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(54) **MENINGOCOCCAL ANTIGENS**

(75) Inventors: **Vincenzo Scarlato**, Siena (IT); **Vega Masignani**, Siena (IT); **Rino Rappuoli**, Siena (IT); **Mariagrazia Pizza**, Siena (IT); **Guido Grandi**, Siena (IT)

Correspondence Address:
MORRISON & FOERSTER LLP
425 MARKET STREET
SAN FRANCISCO, CA 94105-2482 (US)

(73) Assignee: **Chiron Corporation**, Emeryville, CA

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Related U.S. Application Data

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Jan. 14, 1998	(GB)	9800760.2

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(57) **ABSTRACT**

The invention provides proteins from *Neisseria meningitidis* (strains A & B), including amino acid sequences, the corresponding nucleotide sequences, expression data, and serological data. The proteins are useful antigens for vaccines, immunogenic compositions, and/or diagnostics.

FIG. 1A

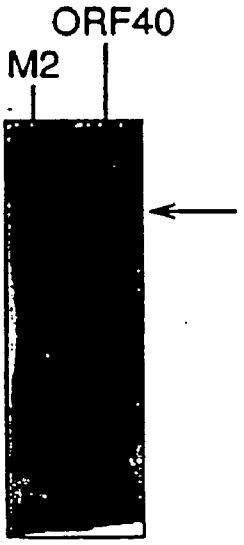


FIG. 1B

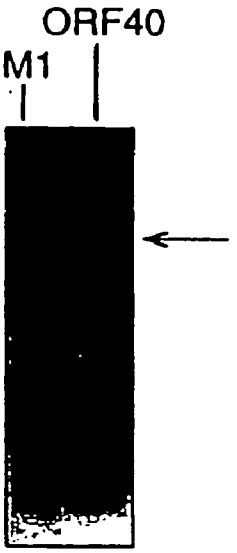
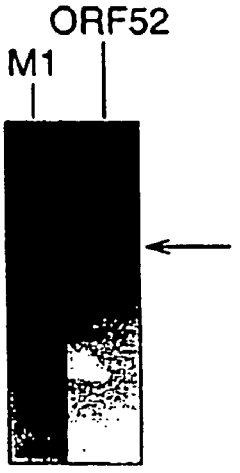


FIG. 4A



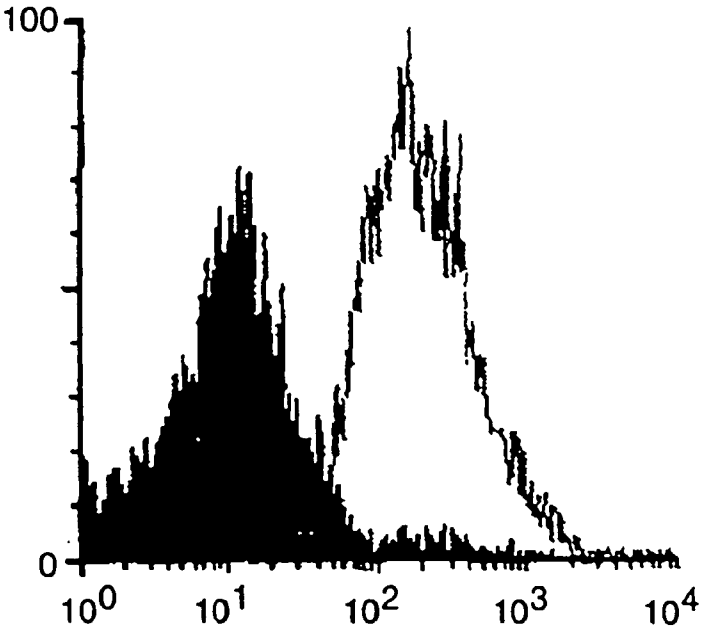


FIG. 1C

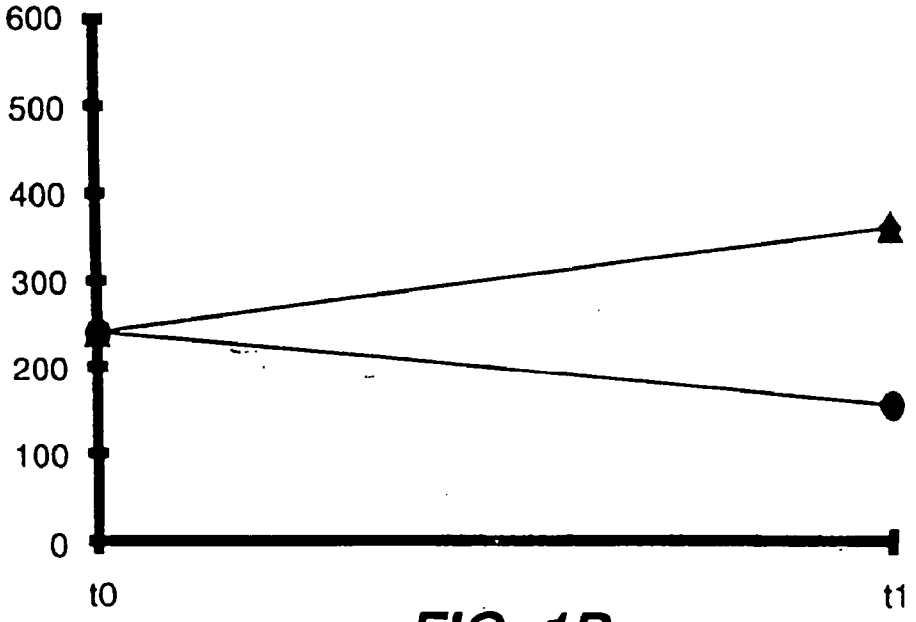


FIG. 1D

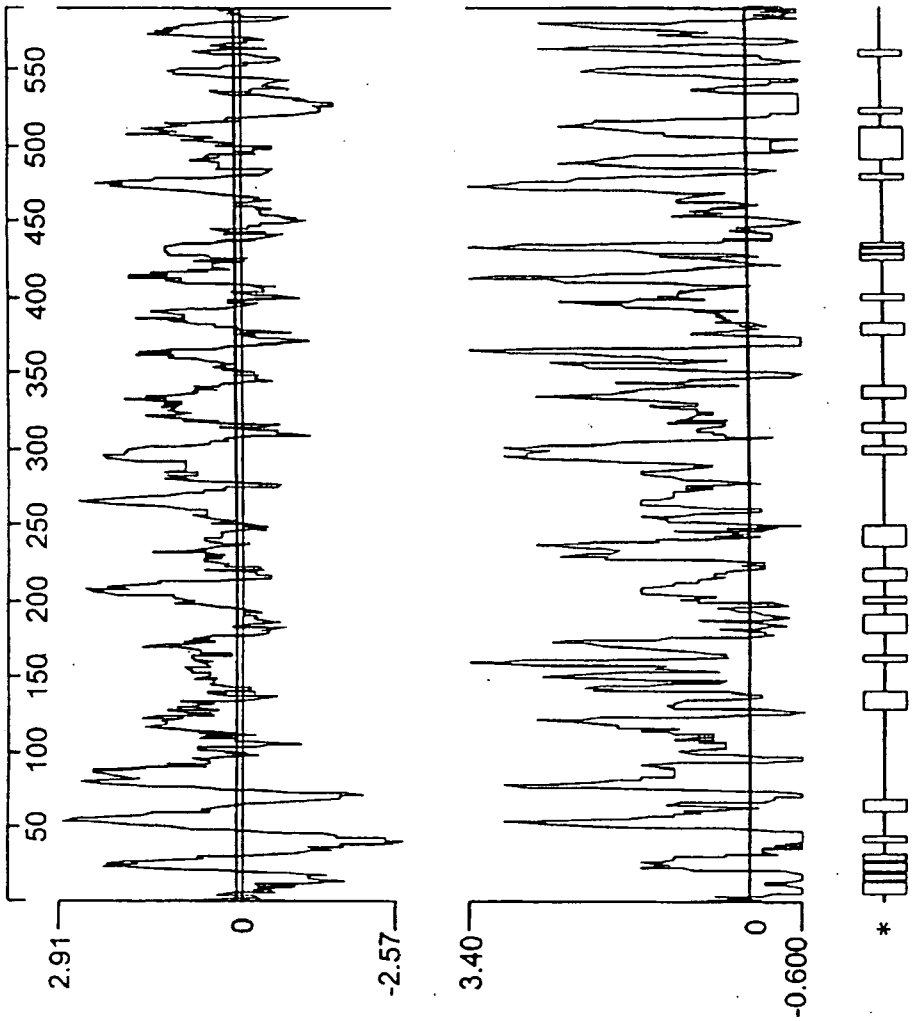


FIG. 1E

FIG. 2A

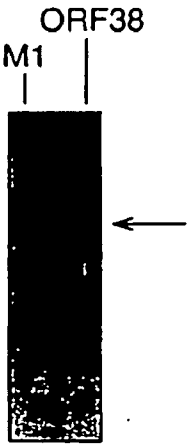


FIG. 2B

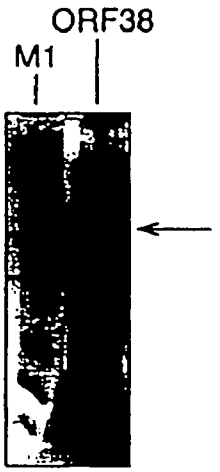


FIG. 2C

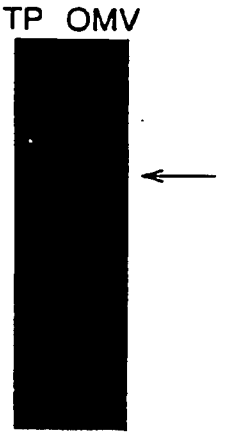
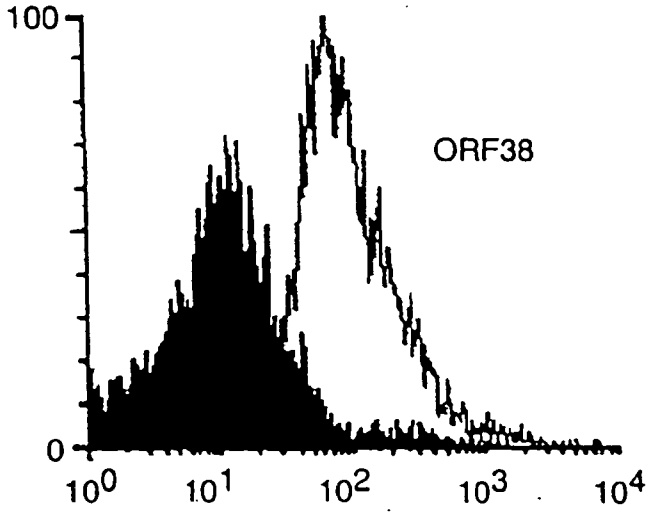
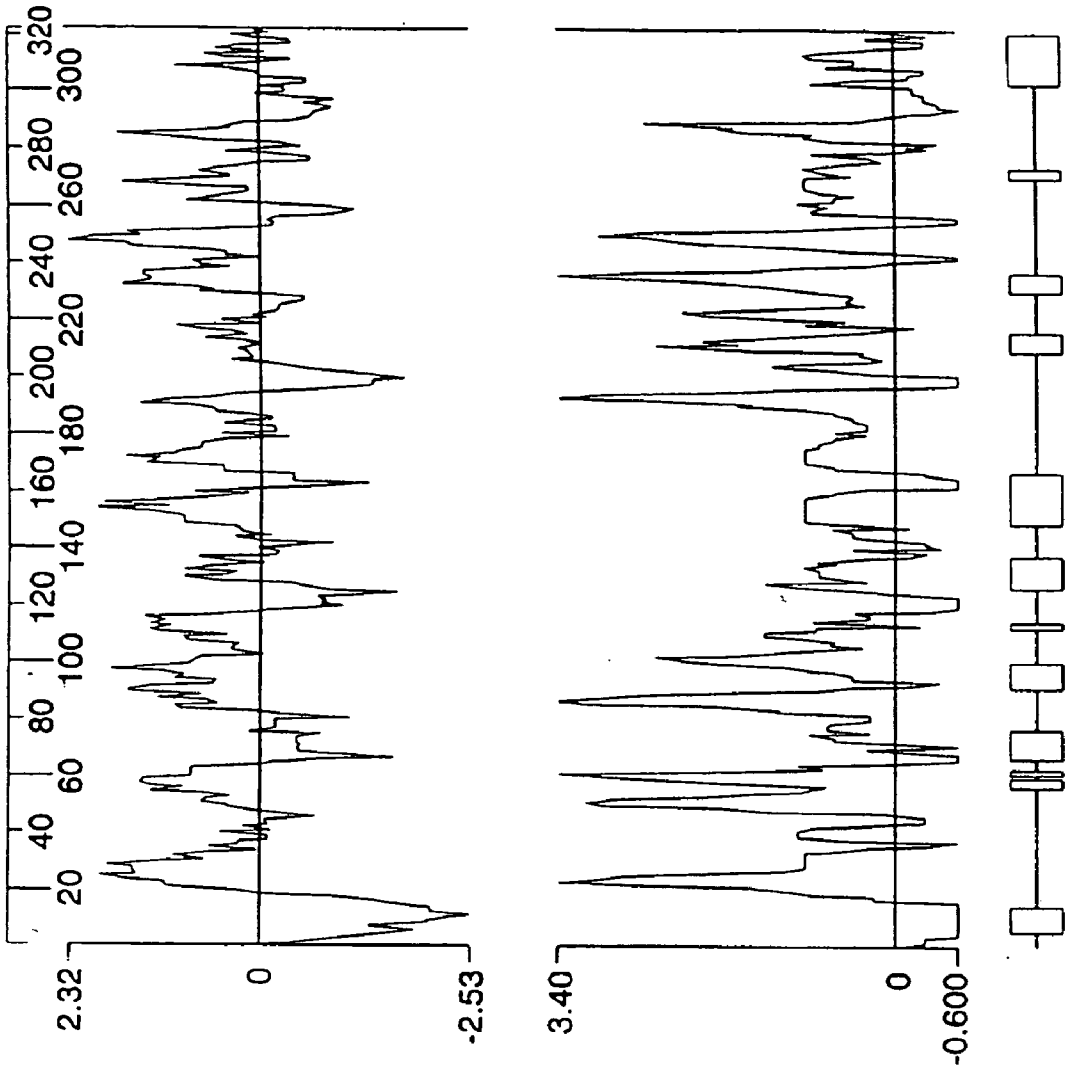


FIG. 2D

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-0.600

FIG. 2E

FIG. 3A

FIG. 3B

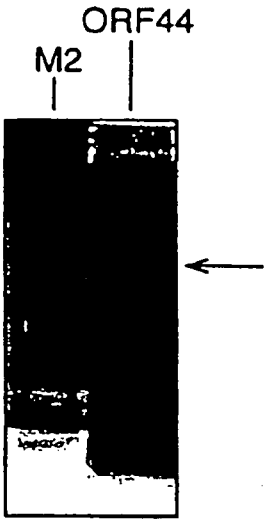
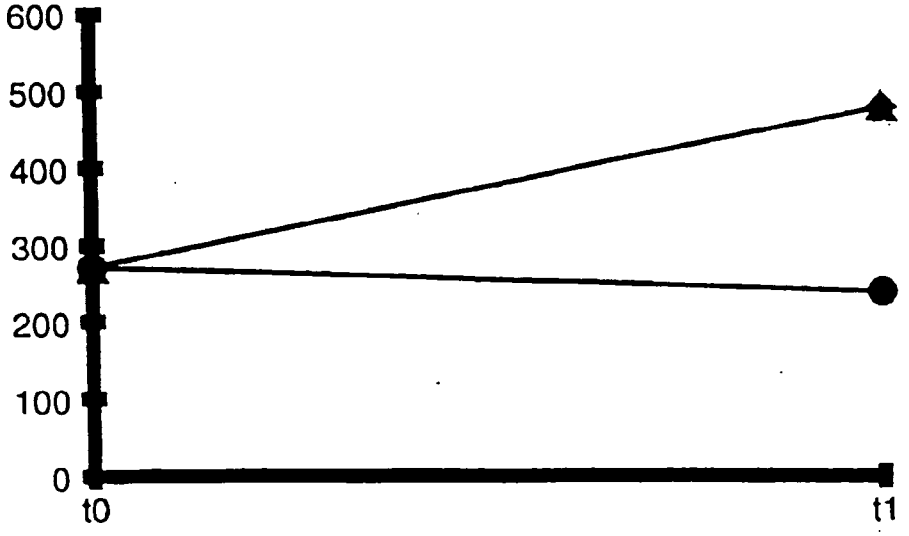
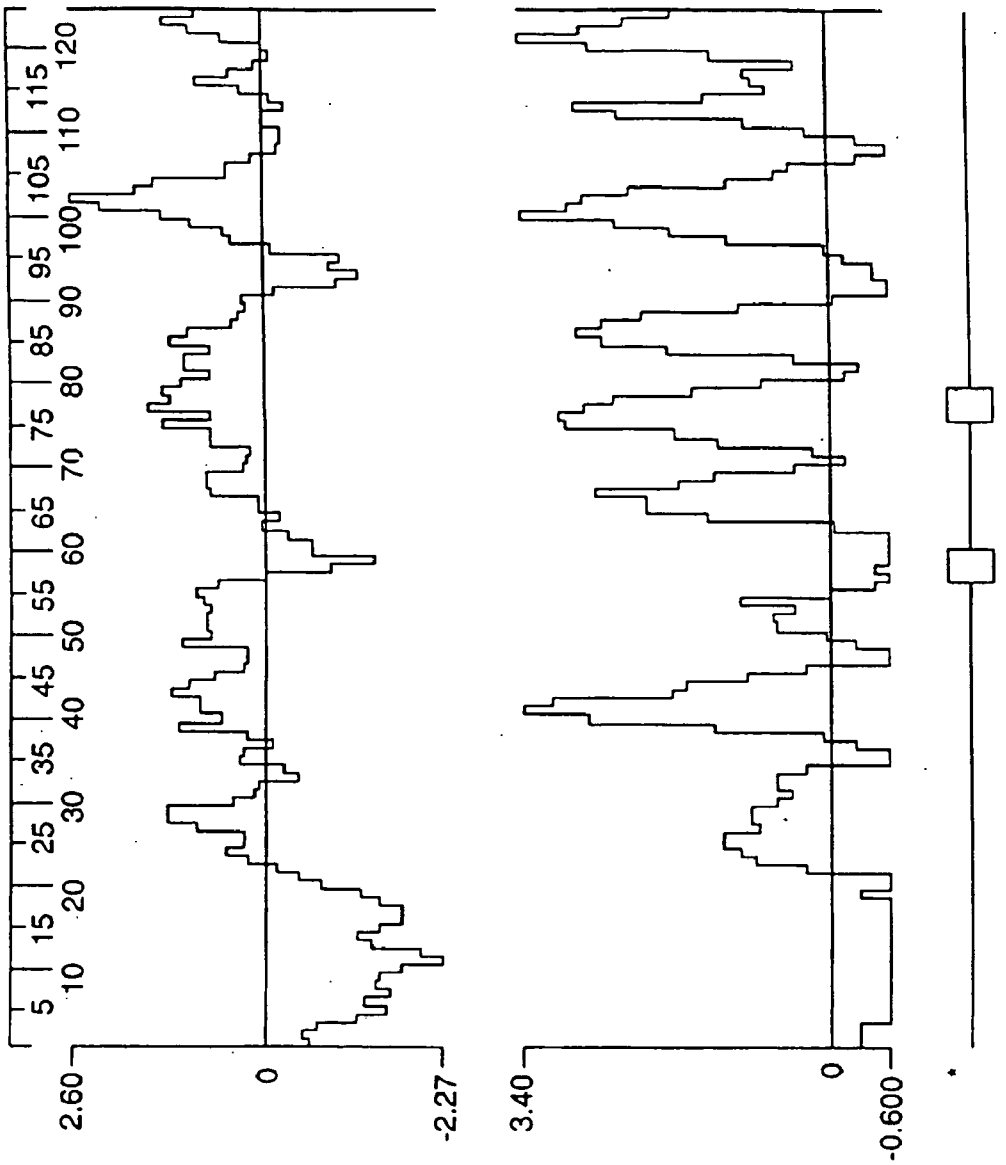


FIG. 3C

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-2.27
3.40
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-0.600

FIG. 3D

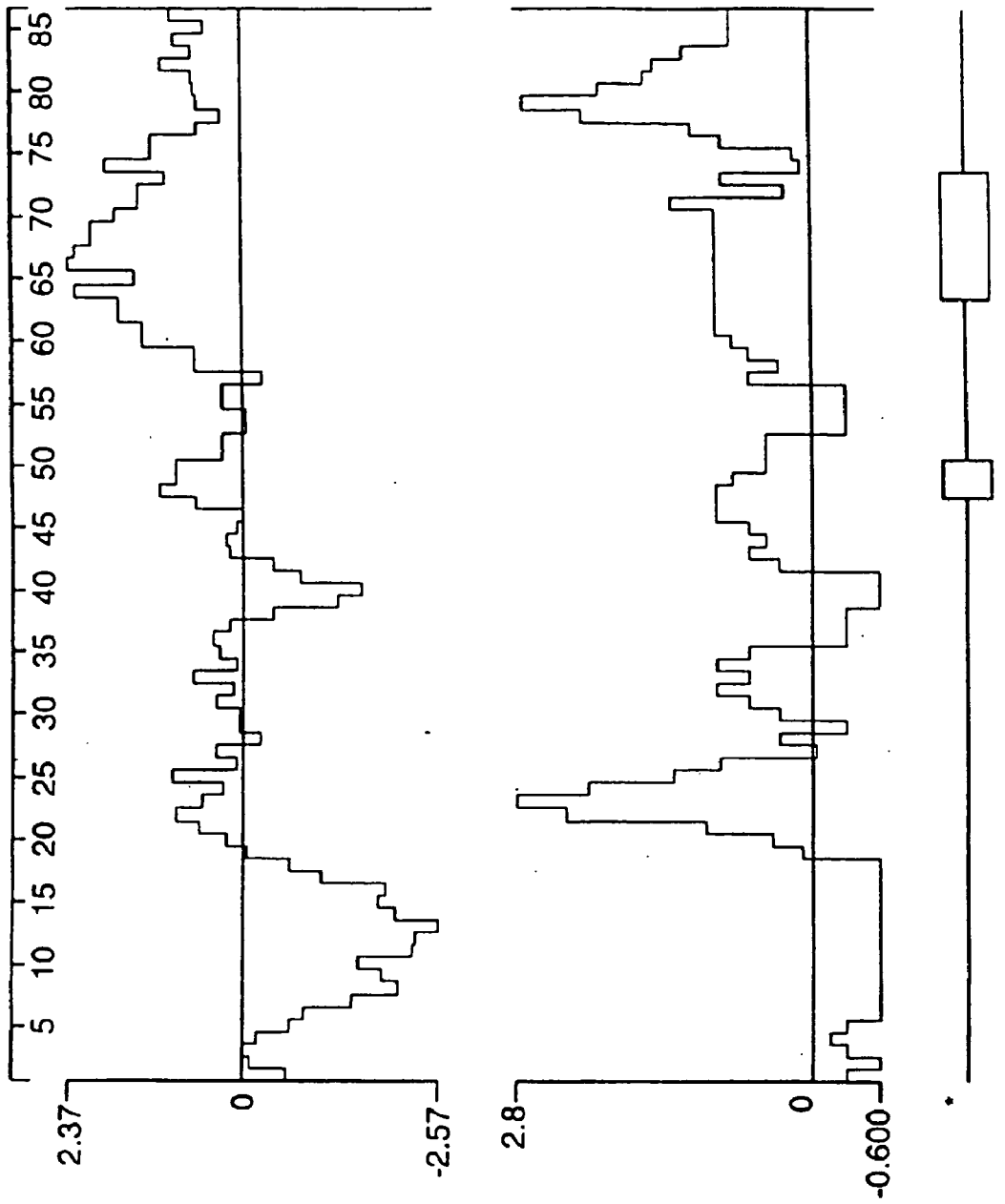


FIG. 4B

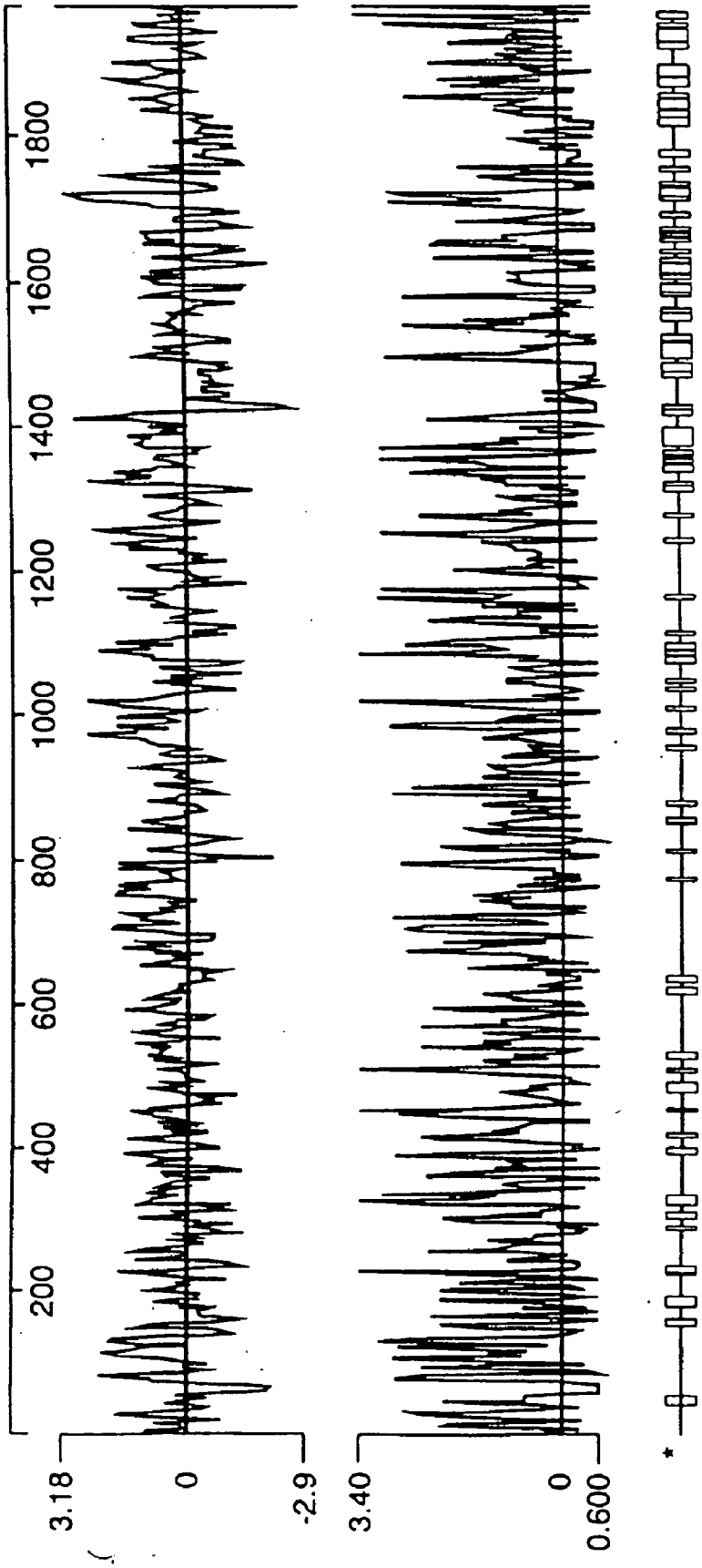
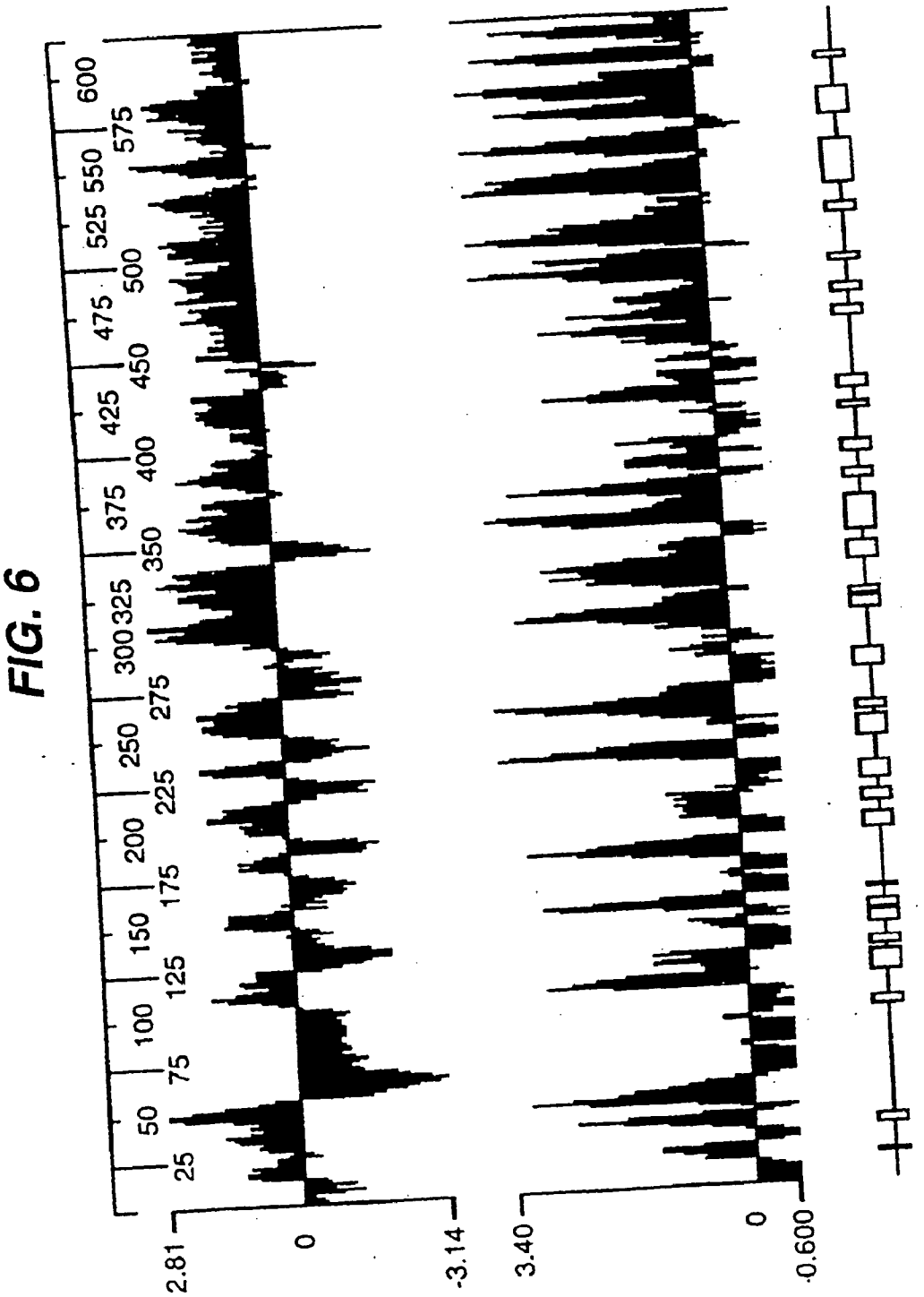


FIG. 5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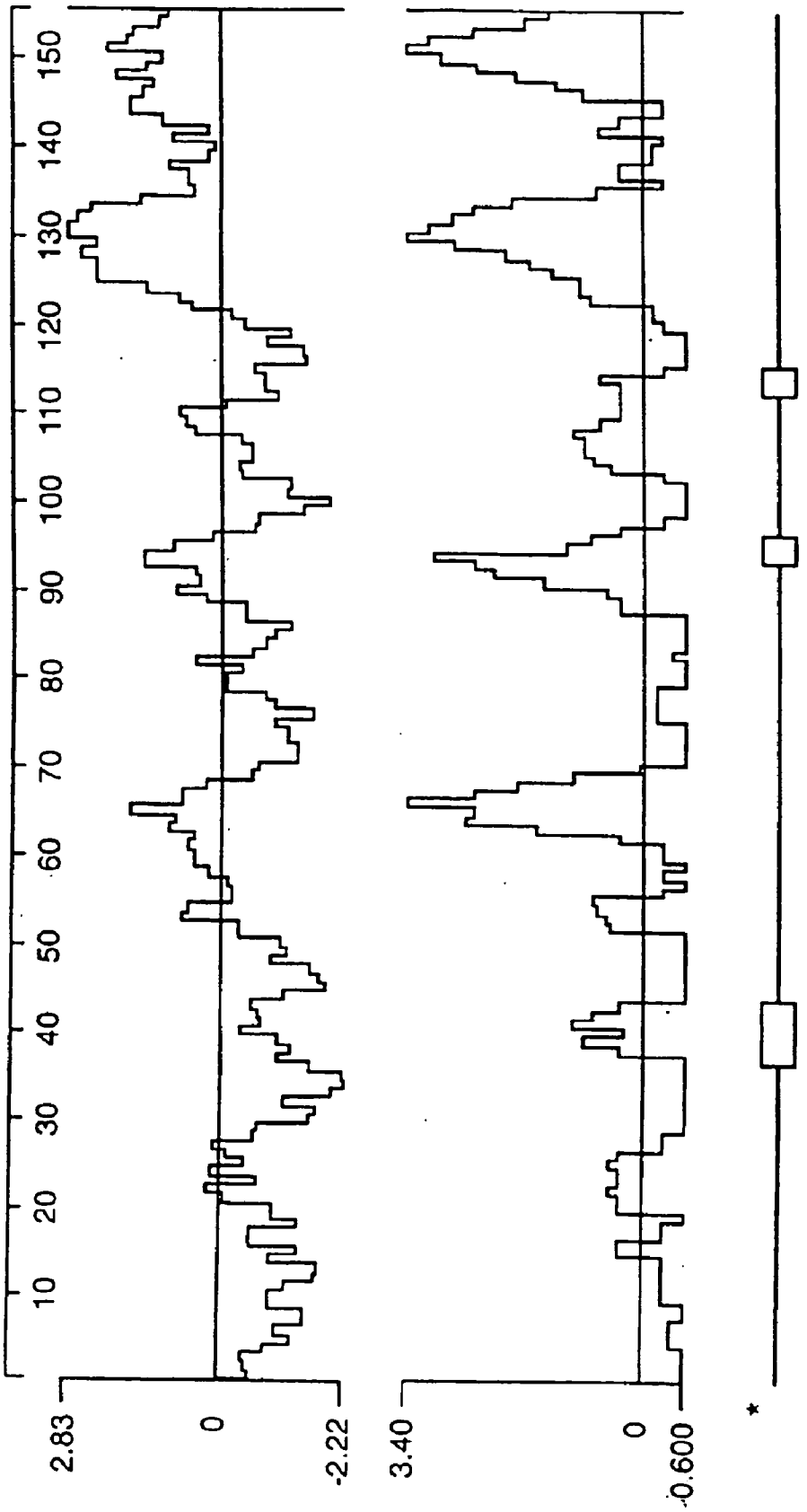
-0.600

FIG. 6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-0.600

FIG. 7

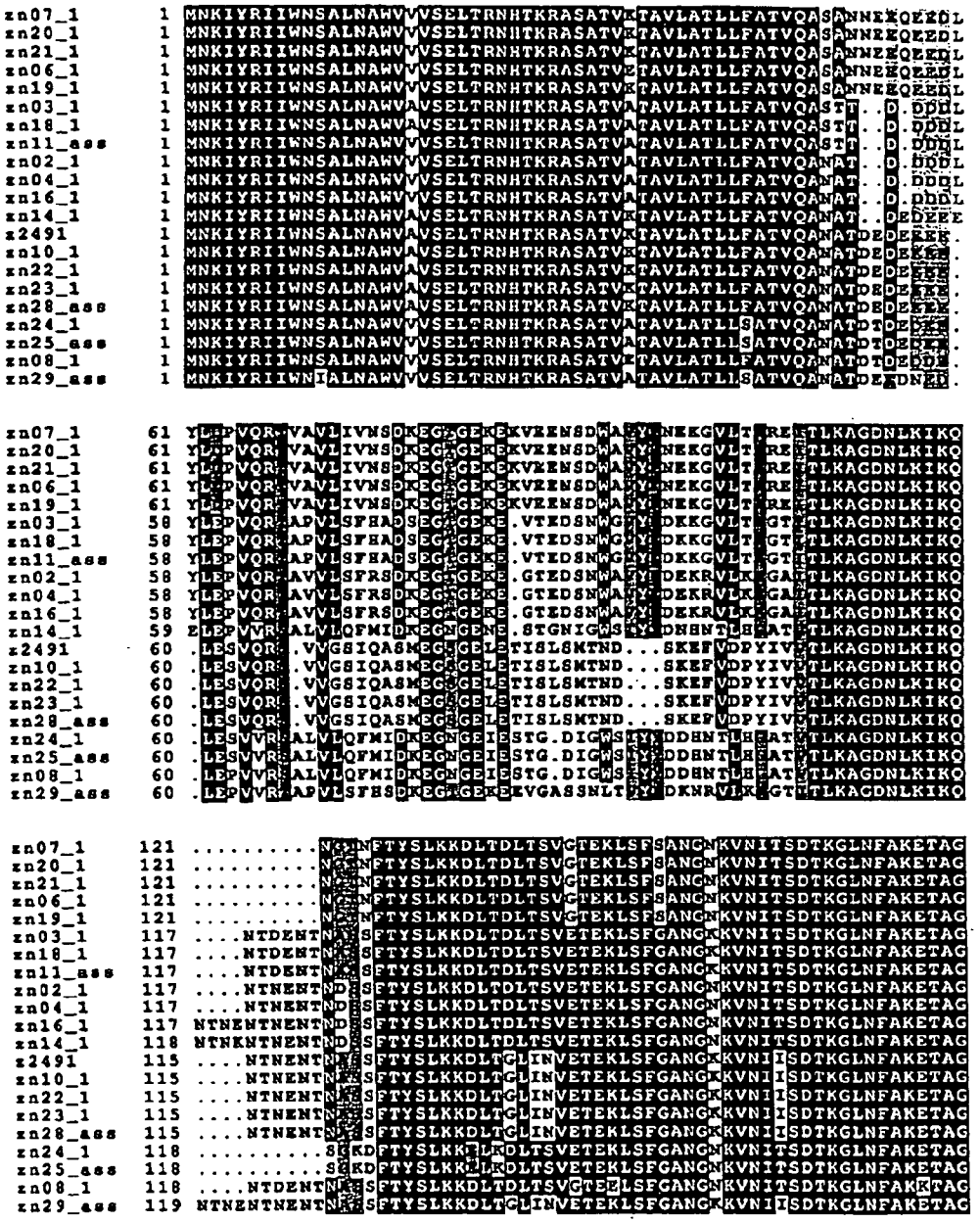

FIG. 8A

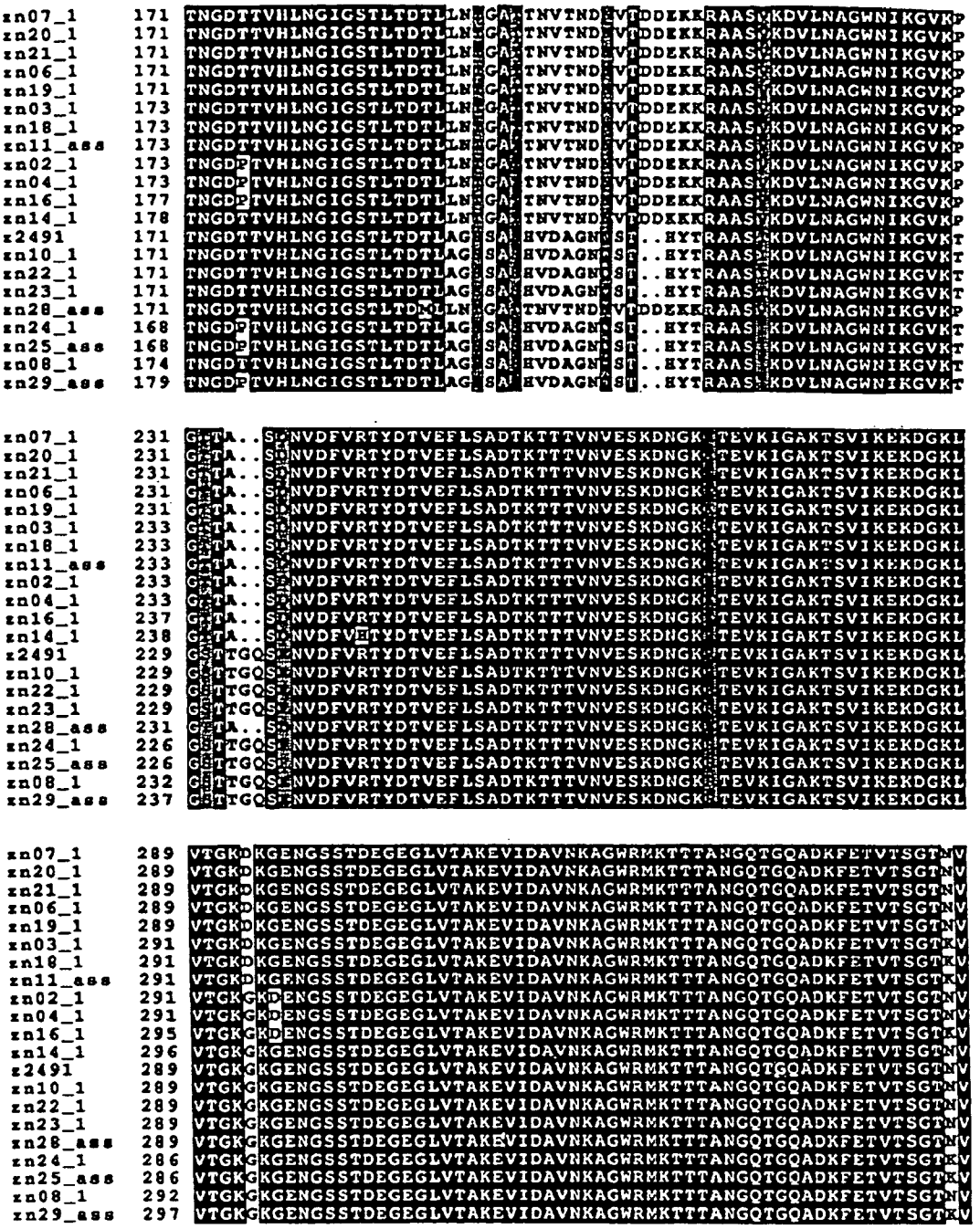
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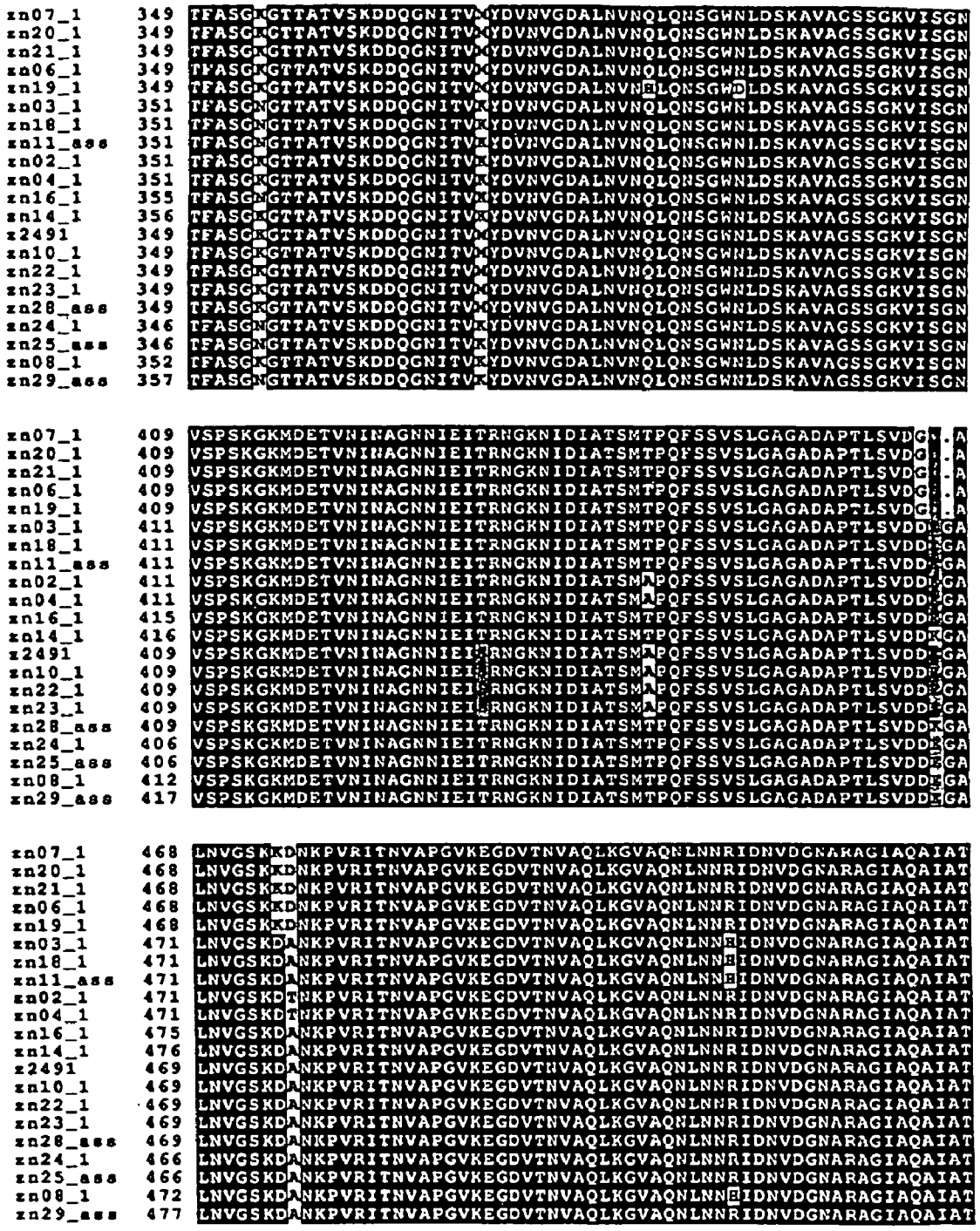
FIG. 8B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zn02_1 411 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDIGA
zn04_1 411 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDIGA
zn16_1 415 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDIGA
zn14_1 416 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGA
z2491 409 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDIGA
zn10_1 409 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDIGA
zn22_1 409 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDIGA
zn23_1 409 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDIGA
zn28_ass 409 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGA
zn24_1 406 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGA
zn25_ass 406 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGA
zn08_1 412 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDIGA
zn29_ass 417 VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGA
zn07_1 468 LNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn20_1 468 LNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn21_1 468 LNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn06_1 468 LNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn19_1 468 LNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn03_1 471 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNEIDNVDGNARAGIAQAIAT
zn18_1 471 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNEIDNVDGNARAGIAQAIAT
zn11_ass 471 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNEIDNVDGNARAGIAQAIAT
zn02_1 471 LNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn04_1 471 LNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn16_1 475 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn14_1 476 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
z2491 469 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn10_1 469 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn22_1 469 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn23_1 469 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn28_ass 469 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn24_1 466 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn25_ass 466 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
zn08_1 472 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNEIDNVDGNARAGIAQAIAT
zn29_ass 477 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT

FIG. 8C

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zn07_1      528 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn20_1      528 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn21_1      528 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn06_1      528 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn19_1      528 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn03_1      531 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn18_1      531 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn11_ass    531 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn02_1      531 AGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn04_1      531 AGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn16_1      535 AGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASV
zn14_1      536 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
z2491       529 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn10_1      529 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn22_1      529 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn23_1      529 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn28_ass    529 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn24_1      526 AGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASV
zn25_ass    526 AGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASV
zn08_1      532 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
zn29_ass    537 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV

zn07_1      588 GYQW*
zn20_1      588 GYQW*
zn21_1      588 GYQW*
zn06_1      588 GYQW*
zn19_1      588 GYQW*
zn03_1      591 GYQW*
zn18_1      591 GYQW*
zn11_ass    591 GYQW*
zn02_1      591 GYQW*
zn04_1      591 GYQW*
zn16_1      595 GYQW*
zn14_1      596 GYQW*
z2491       589 GYQW*
zn10_1      589 GYQW*
zn22_1      589 GYQW*
zn23_1      589 GYQW*
zn28_ass    589 GYQW*
zn24_1      586 GYQW*
zn25_ass    586 GYQW*
zn08_1      592 GYQW*
zn29_ass    597 GYQW*
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FIG. 8D

MENINGOCOCCAL ANTIGENS

[0001] This application is a continuation-in-part of international patent application PCT/IB99/00103, filed Jan. 14, 1999, from which priority is claimed under 35 U.S.C. § 119.

[0002] This invention relates to antigens from the bacterium *Neisseria meningitidis*.

BACKGROUND

[0003] *Neisseria meningitidis* is a non-motile, gram negative diplococcus human pathogen. It colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoeae*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

[0004] *N. meningitidis* causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks (see Lieberman el al. (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat et al (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae, N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat et al (1997) supra).

[0005] Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol. 46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H. influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger W D "New and Improved Vaccines Against Meningococcal Disease" in: *New Generation Vaccines*, supra, pp. 469-488; Lieberman et al (1996) supra; Costantino et al (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

[0006] Meningococcus B remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of α(2-8)-linked N-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the N-acetyl groups with N-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular?*Clin Microbiol Rev* 7(4):559-575).

[0007] Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman J T (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28). Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

[0008] A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (eg. EP-A-0467714, WO96/29412), but this is by no means complete. The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae*.

[0009] The Invention

[0010] The invention provides proteins comprising the *N. meningitidis* amino acid sequences disclosed in the examples.

[0011] It also provides proteins comprising sequences homologous (ie. having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of sequence identity is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These homologous proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between the proteins is preferably determined by the Smith-Waterman homology search algorithm as implemented in the MPSRCH program (Oxford Molecular), using an affine gap search with parameters gap open penalty=12 and gap extension penalty=1.

[0012] The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

[0013] The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis etc.) and in various forms (eg. native, fusions etc.). They are preferably prepared in substantially pure form (ie. substantially free from other *N. meningitidis* or host cell proteins).

[0014] According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

[0015] According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences disclosed in the examples. In addition, the invention provides nucleic acid comprising sequences homologous (ie. having sequence identity) to the *N. meningitidis* nucleotide sequences disclosed in the examples.

[0016] Furthermore, the invention provides nucleic acid which can hybridise to the *N. meningitidis* nucleic acid disclosed in the examples, preferably under "high stringency" conditions (eg. 65° C. in a 0.1×SSC, 0.5% SDS solution).

[0017] Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences and, depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

[0018] According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

[0019] It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

[0020] Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, from genomic or cDNA libraries, from the organism itself etc.) and can take various forms (eg. single stranded, double stranded, vectors, probes etc.).

[0021] In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also peptide nucleic acids (PNA) etc.

[0022] According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (eg. expression vectors) and host cells transformed with such vectors.

[0023] According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents, or as immunogenic compositions.

[0024] The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (eg. as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of: (i) a medicament for treating or preventing infection due to Neisserial bacteria; (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria; and/or (iii) a reagent which can raise antibodies against Neisserial bacteria Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain A, strain B or strain C.

[0025] The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

[0026] According to further aspects, the invention provides various processes.

[0027] A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

[0028] A process for producing protein or nucleic acid of the invention is provided, wherein the protein or nucleic acid is synthesised in part or in whole using chemical means.

[0029] A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

[0030] A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

[0031] Unlike the sequences disclosed in PCT/IB98/01665, the sequences disclosed in the present application are believed not to have any significant homologs in *N. gonorrhoeae*. Accordingly, the sequences of the present invention also find use in the preparation of reagents for distinguishing between *N. meningitidis* and *N. gonorrhoeae*.

[0032] A summary of standard techniques and procedures which may be employed in order to perform the invention (eg. to utilise the disclosed sequences for vaccination or diagnostic purposes) follows. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

[0033] General

[0034] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature eg. Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D. N Glover ed. 1985); *Oligonucleotide Synthesis* (M. J. Gait ed, 1984); *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription and Translation* (B. D. Hames &

S. J. Higgins eds. 1984); *Animal Cell Culture* (R. I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J. H. Miller and M. P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D. M. Weir and C. C. Blackwell eds 1986).

[0035] Standard abbreviations for nucleotides and amino acids are used in this specification.

[0036] All publications, patents, and patent applications cited herein are incorporated in full by reference. In particular, the contents of UK patent applications 9800760.2, 9819015.0 and 9822143.5 are incorporated herein.

[0037] Definitions

[0038] A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

[0039] The term "comprising" means "including" as well as "consisting" eg. a composition "comprising" X may consist exclusively of X or may include something additional to X, such as X+Y.

[0040] A "conserved"*Neisseria* amino acid fragment or protein is one that is present in a particular Neisserial protein in at least x % of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an animo acid is "conserved" in a particular Neisserial protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria*.

[0041] The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a Neisserial sequence is heterologous to a mouse host cell. A further examples would be two epitopes from the same or different proteins which have been assembled in a single protein in an arrangement not found in nature.

[0042] An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

[0043] A "mutant" sequence is defined as DNA, RNA or amino acid sequence differing from but having sequence identity with the native or disclosed sequence. Depending on the particular sequence, the degree of sequence identity between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more, calculated using the Smith-Waterman algorithm as described above). As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs essentially at the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions (eg. see U.S. Pat. No. 5,753,235).

[0044] Expression Systems

[0045] The Neisserial nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, baculoviruses, plants, bacteria, and yeast.

[0046] i. Mammalian Systems

[0047] Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation [Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual,* 2nd ed.]

[0048] Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallotheionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible), depending on the promoter can be induced with glucocorticoid in hormone-responsive cells.

[0049] The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter [Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell,* 2nd ed.]. Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer [Dijkema et al (1985) *EMBO J.* 4:761] and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus [Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777] and from human cytomegalovirus [Boshart et al. (1985) *Cell* 41:521]. Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion [Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237].

[0050] A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by in vitro incubation with cyanogen bromide.

[0051] Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either in vivo or in vitro. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus triparite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

[0052] Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation [Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B. D. Hames and D. M. Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105]. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminater/polyadenylation signals include those derived from SV40 [Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*].

[0053] Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers; introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 [Gluzman (1981) *Cell* 23:175] or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replicaton systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 [Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946] and pHEBO [Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074].

[0054] The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

[0055] Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (eg. Hep G2), and a number of other cell lines.

[0056] ii. Baculovirus Systems

[0057] The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

[0058] After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant-virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, inter alia, Invitrogen, San Diego Calif. ("MaxBac" kit). These techniques are generally

known to those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No.* 1555 (1987) (hereinafter "Summers and Smith").

[0059] Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its owned set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

[0060] Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

[0061] The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.,* 42:177) and a prokaryotic ampicillin-resistance (amp) gene and origin of replication for selection and propagation in *E. coli.*

[0062] Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3) transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

[0063] Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

[0064] DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene,* 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human α-interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacq-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA,* 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA,* 7:99, can also be used to provide for secretion in insects.

[0065] A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by in vitro incubation with cyanogen bromide.

[0066] Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

[0067] After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus—usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5 kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art (See Summers and Smith supra; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91 The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

[0068] The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in

size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. "Current Protocols in Microbiology" Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, supra; Miller et al. (1989).

[0069] Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, inter alia: *Aedes aegypti, Autographa californica, Bombyx mori, Drosophila melanogaster, Spodoptera frugiperda*, and *Trichoplusia ni* (WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

[0070] Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, eg. Summers and Smith supra.

[0071] The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, eg. HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, eg. proteins, lipids and polysaccharides.

[0072] In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

[0073] iii. Plant Systems

[0074] There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. Pat. No. 5,693,506; U.S. Pat. No. 5,659,122; and U.S. Pat. No. 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., Nucleic Acids Research 15:2515-2535 (1987); Wirsel et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R. L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell,* 2:1027-1038 (1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci* 84:1337-1339 (1987)

[0075] Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker, and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Reptr,* 11(2):165-185.

[0076] Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

[0077] The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

[0078] A heterologous coding sequence may be for any protein relating to the present invention. The sequence

encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

[0079] Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

[0080] The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet,* 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature,* 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature,* 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta,* 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA,* 79, 1859-1863, 1982.

[0081] The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

[0082] All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria, Lotus, Medicago, Onobrychis, Trifolium, Trigonella, Vigna, Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Sinapis, Atropa, Capsicum, Datura, Hyoscyamus, Lycopersion, Nicotiana, Solanum, Petunia, Digitalis, Majorana, Cichorium, Helianthus, Lactuca, Bromus, Asparagus, Antirrhinum, Hererocallis, Nemesia, Pelargonium, Panicum, Pennisetum, Ranunculus, Senecio, Salpiglossis, Cucumis, Browaalia, Glycine, Lolium, Zea, Triticum, Sorghum*, and *Datura.*

[0083] Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

[0084] In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

[0085] iv. Bacterial Systems

[0086] Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) [Raibaud et al. (1984) *Annu. Rev. Genet.* 18:173]. Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

[0087] Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples

include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (lac) [Chang et al. (1977) *Nature* 198:1056], and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (trp) [Goeddel et al. (1980) *Nuc. Acids Res.* 8:4057; Yelverton et al. (1981) *Nucl. Acids Res.* 9:731; U.S. Pat. No. 4,738,921; EP-A-0036776 and EP-A-0121775]. The g-laotamase (bla) promoter system [Weissmann (1981) "The cloning of interferon and other mistates." In *Interferon* 3 (ed I. Gresser)], bacteriophage lambda PL [Shimatake et al. (1981) *Nature* 292:128] and T5 [U.S. Pat. No. 4,689,406] promoter systems also provide useful promoter sequences.

[**0088**] In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter [U.S. Pat. No. 4,551, 433]. For example, the tac promoter is a hybrid trp-lac promoter comprised of both trp promoter and lac operon sequences that is regulated by the lac repressor [Amann et al. (1983) *Gene* 25:167; de Boer et al. (1983) *Proc. Natl. Acad. Sci.* 80:21]. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system [Studier et al. (1986) *J. Mol. Biol.* 189:113; Tabor et al. (1985) *Proc Natl. Acad. Sci.* 82:1074]. In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO-A-0 267 851).

[**0089**] In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon [Shine et al. (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' and of *E. coli* 16S rRNA [Steitz et al. (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R. F. Goldberger)]. To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site [Sambrook et al. (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*].

[**0090**] A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by in vitro incubation with cyanogen bromide or by either in vivo on in vitro incubation with a bacterial methionine N-terminal peptidase (EPO-A-0 219 237).

[**0091**] Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene [Nagai et al. (1984) *Nature* 309:810]. Fusion proteins can also be made with sequences from the lacZ [Jia et al. (1987) *Gene* 60:197], trpE (Allen et al. (1987) J. Biotechnol. 5:93; Makoff et al. (1989) *J. Gen. Microbiol.* 135:11], and Chey [EP-A-0 324 647] genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (eg. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated [Miller et al. (1989) *Bio/Technology* 7:698].

[**0092**] Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria [U.S. Pat. No. 4,336,336]. The signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either in vivo or in vitro encoded between the signal peptide fragment and the foreign gene.

[**0093**] DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (ompA) [Masui et al. (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb et al. (1984) *EMBO J.* 3:2437] and the *E. coli* alkaline phosphatase signal sequence (phoA) [Oka et al. (1985) *Proc. Natl. Acad. Sci.* 82:7212]. As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* [Palva et al. (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 244 042].

[**0094**] Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the trip gene in *E. coli* as well as other biosynthetic genes.

[**0095**] Usually, the above described components, comprising a promoter, signal sequence (if desired), coding

sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as bacteria The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

[**0096**] Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EP-A-0 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

[**0097**] Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline [Davies et al. (1978) *Annu. Rev. Microbiol.* 32:469]. Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

[**0098**] Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

[**0099**] Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria For example, expression vectors have been developed for, inter alia, the following bacteria: *Bacillus subtilis* [Palva et al. (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541], *Escherichia coli* [Shimatake et al. (1981) *Nature* 292:128; Amann et al. (1985) *Gene* 40:183; Studier et al. (1986) *J. Mol. Biol.* 189:113; EP-A-0 036 776, EP-A-0 136 829 and EP-A-0 136 907], *Streptococcus cremoris* [Powell et al. (1988) *Appl. Environ. Microbiol.* 54:655]; *Streptococcus lividans* [Powell et al. (1988) *Appl. Environ. Microbiol.* 54:655], *Streptomyces lividans* [U.S. Pat. No. 4,745,056].

[**0100**] Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with $CaCl_2$ or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by electroporation. Transformation procedures usually vary with the bacterial species to be transformed. See eg. [Masson et al. (1989) *FEMS Microbiol. Lett.* 60:273; Palva et al. (1982) *Proc. Natl. Acad. Sci USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541, *Bacillus*], [Miller et al. (1988) *Proc. Natl. Acad. Sci.* 85:856; Wang et al. (1990) *J. Bacteriol.* 172:949, *Campylobacter*], [Cohen et al. (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower et al. (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H. W. Boyer and S. Nicosia); Mandel et al. (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim Biophys. Acta* 949:318; *Escherichia*], [Chassy et al. (1987) *FEMS Microbiol. Lett.* 44:173 *Lactobacillus*]; [Fiedler et al. (1988) *Anal. Biochem* 170:38, *Pseudomonas*]; [Augustin et al. (1990) *FEMS Microbiol. Lett.* 66:203, *Staphylococcus*], [Barany et al. (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry et al. (1981) *Infect Immun.* 32:1295; Powell et al. (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti et al. (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412, *Streptococcus*].

[**0101**] v. Yeast Expression

[**0102**] Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

[**0103**] Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences. Examples include alcohol dehydrogenase (ADH) (EP-A-0 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO-A-0 329 203). The yeast PHO5 gene, encoding acid phosphatase, also provides useful promoter sequences [Myanohara et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:1].

[**0104**] In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Pat. Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the ADH2, GAL4, GAL10, OR PHO5 genes, combined with the tran-

scriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EP-A-0 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, inter alia, [Cohen et al. (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff et al. (1981) *Nature* 283:835; Hollenberg et al. (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg et al. (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K. N. Timmis and A. Puhler); Mercerau-Puigalon et al. (1980) *Gene* 11:163; Panthier et al. (1980) *Curr. Genet.* 2:109;].

[0105] A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by in vitro incubation with cyanogen bromide.

[0106] Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See eg. EP-A-0 196 056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (eg. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (eg. WO88/024066).

[0107] Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either in vivo or in vitro. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

[0108] DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EP-A-0 012 873; JPO. 62,096,086) and the A-factor gene (U.S. Pat. No. 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EP-A-0 060 057).

[0109] A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Pat. Nos. 4,546,083 and 4,870,008; EP-A-0 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (eg. see WO 89/02463.)

[0110] Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

[0111] Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 [Botstein et al. (1979) *Gene* 8:17-24], pCl/1 [Brake et al. (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646], and YRp17 [Stinchcomb et al. (1982) *J. Mol. Biol.* 158:157]. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See eg. Brake et al., supra.

[0112] Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome [Orr-Weaver et al. (1983) *Methods in Enzymol.* 101:228-245]. An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver et al., supra. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced [Rine et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:6750]. The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

[0113] Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as ADE2, HIS4, LEU2,

TRP1, and ALG7, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of CUP1 allows yeast to grow in the presence of copper ions [Butt et al. (1987) *Microbiol, Rev.* 51:351].

[0114] Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

[0115] Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors have been developed for, inter alia, the following yeasts: *Candida albicans* [Kurtz, et al. (1986) *Mol. Cell. Biol.* 6:142], *Candida maltosa* [Kunze, et al. (1985) *J. Basic Microbiol.* 25:141]. *Hansenula polymorpha* [Gleeson, et al. (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp et al. (1986) *Mol. Gen. Genet.* 202:302], *Kluyveromyces fragilis* [Das, et al. (1984) *J. Bacteriol.* 158:1165], *Kluyveromyces lactis* [De Louvencourt et al. (1983) *J. Bacteriol.* 154:737; Van den Berg et al. (1990) *Bio/Technology* 8:135], *Pichia guillerimondii* [Kunze et al. (1985) *J. Basic Microbiol.* 25:141], *Pichia pastoris* [Cregg, et al. (1985) *Mol. Cell. Biol.* 5:3376; U.S. Pat. Nos. 4,837,148 and 4,929,555], *Saccharomyces cerevisiae* [Hinnen et al. (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito et al. (1983) *J. Bacteriol.* 153:163], *Schizosaccharomyces pombe* [Beach and Nurse (1981) *Nature* 300:706], and *Yarrowia lipolytica* [Davidow, et al. (1985) *Curr. Genet.* 10:380471 Gaillardin, et al (1985) *Curr. Genet.* 10:49].

[0116] Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See eg. [Kurtz et al. (1986) *Mol. Cell. Biol.* 6:142; Kunze et al. (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson et al. (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp et al. (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das et al. (1984) *J. Bacteriol.* 158:1165; De Louvencourt et al. (1983) *J. Bacteriol.* 154:1165; Van den Berg et al. (1990) *Bio/Technology* 8:135; *Kluyveromyces*]; [Cregg et al. (1985) *Mol. Cell. Biol.* 5:3376; Kunze et al. (1985) *J. Basic Microbiol.* 25:141; U.S. Pat. Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen et al. (1978) *Proc. Natl. Acad. Sci. USA* 75;1929; Ito et al. (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow et al. (1985) *Curr. Genet.* 10:39; Gaillardin et al. (1985) *Curr. Genet.* 10:49; *Yarrowia*].

[0117] Antibodies

[0118] As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies. Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying Neisserial proteins.

[0119] Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 μg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by in vitro immunization using methods known in the adt, which for the purposes of this invention is considered equivalent to in vivo immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25° C. for one hour, followed by incubating at 4° C. for 2-18 hours. The serum is recovered by centrifugation (eg. 1,000 g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

[0120] Monoclonal antibodies are prepared using the standard method of Kohler & Milstein [*Nature* (1975) 256:495-96], or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (eg. hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either in vitro (eg. in tissue culture bottles or hollow fiber reactors), or in vivo (as ascites in mice).

[0121] If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific

therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I, or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

[0122] Pharmaceutical Compositions

[0123] Pharmaceutical compositions can comprise either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

[0124] The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

[0125] For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

[0126] A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

[0127] Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

[0128] Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

[0129] Delivery Methods

[0130] Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

[0131] Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

[0132] Vaccines

[0133] Vaccines according to the invention may either be prophylactic (ie. to prevent infection) or therapeutic (ie. to treat disease after infection).

[0134] Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid, usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

[0135] Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59™ (WO 90/14837; Chapter 10 in Vaccine design: the subunit and adjuvant approach, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, Mass.), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% plu-

ronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi™ adjuvant system (RAS), (Ribi Immunochem, Hamilton, Mont.) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL+CWS (Detox™); (3) saponin adjuvants, such as Stimulon™ (Cambridge Bioscience, Worcester, Mass.) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (eg. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (eg. gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ are preferred.

[0136] As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)ethylamine (MTP-PE), etc.

[0137] The immunogenic compositions (eg. the immunising antigen/immunogen/polypeptide/protein/nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

[0138] Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

[0139] Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (eg. nonhuman primate, primate, etc.), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctors assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

[0140] The immunogenic compositions are conventionally administered parenterally, eg. by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (eg. WO98/20734). Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

[0141] As an alternative to protein-based vaccines, DNA vaccination may be employed [eg. Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly et al. (1997) *Annu Rev Immunol* 15:617-648; see later herein].

[0142] Gene Delivery Vehicles

[0143] Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in in vivo or ex vivo modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence in vivo can be either constitutive or regulated.

[0144] The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picomavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

[0145] Retroviral vectors are well known in the art and we contemplate that any retroviral gene therapy vector is employable in the invention, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retrovirus eg. MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

[0146] Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

[0147] These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see U.S. Pat. No. 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

[0148] Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines

are made from human parent cells (eg. HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

[0149] Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia, Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC Nol VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Md. or isolated from known sources using commonly available techniques.

[0150] Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, U.S. Pat. No. 5,219,740, U.S. Pat. No. 4,405,712, U.S. Pat. No. 4,861,719, U.S. Pat. No. 4,980,289, U.S. Pat. No. 4,777,127, U.S. Pat. No. 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Rain (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

[0151] Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102, WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (ie. there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in U.S. Pat. No. 5,478,745. Still other vectors are those disclosed in Carter U.S. Pat. No. 4,797,368 and Muzyczka U.S. Pat. No. 5,139,941, Chartejee U.S. Pat. No. 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in U.S. Pat. No. 5,354,678, U.S. Pat. No. 5,173,414, U.S. Pat. No. 5,139,941, and U.S. Pat. No. 5,252,479.

[0152] The gene therapy vectors of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in U.S. Pat. No. 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

[0153] Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in U.S. Pat. Nos. 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Ser. No. 08/405,627, filed Mar. 15, 1995, WO94/21792, WO92/10578, WO95/07994, U.S. Pat. No. 5,091,309 and U.S. Pat. No. 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Md. or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see U.S. Ser. No. 08/679,640).

[0154] DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

[0155] Other viral vectors suitable for use in the present invention include those derived from poliovirus, for

example ATCC VR-58 and those described in Evans, Nature 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem L*401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in U.S. Pat. No. 4,603,112 and U.S. Pat. No. 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in U.S. Pat. No. 5,166,057 and in Enami (1990) *Proc Nail Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Triniti virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

[0156] Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see U.S. Ser. No. 08/366,787, filed Dec. 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see U.S. Ser. No. 08/240,030, filed May 9, 1994, and U.S. Ser. No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in U.S. Pat. No. 5,149,655, ionizing radiation as described in U.S. Pat. No. 5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

[0157] Particle mediated gene transfer may be employed, for example see U.S. Ser. No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu & Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

[0158] Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and U.S. Pat. No. 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

[0159] Liposomes that can act as gene delivery vehicles are described in U.S. Pat. No. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in U.S. S No. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin et al (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. Pat. No. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. Pat. No. 5,206,152 and WO92/11033

[0160] Exemplary liposome and polycationic gene delivery vehicles are those described in U.S. Pat. Nos. 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697, and WO91/14445; in EP-0524968; and in Stryer, Biochemistry, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

[0161] A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

[0162] Delivery Methods

[0163] Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the

subject; (2) delivered ex vivo, to cells derived from the subject; or (3) in vitro for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

[0164] Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

[0165] Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in eg. WO93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells.

[0166] Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

[0167] Polynucleotide and Polypeptide Pharmaceutical Compositions

[0168] In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

[0169] A. Polypeptides

[0170] One example are polypeptides which include, without limitation: asioloorosomucoid (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of *plasmodium falciparum* known as RII.

[0171] B. Hormones, Vitamins, etc.

[0172] Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

[0173] C. Polyalkylenes, Polysaccharides, etc.

[0174] Also, polyalkylene glycol can be included with the desired polynucleotides/polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethlylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

[0175] D. Lipids, and Liposomes

[0176] The desired polynucleotide/polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

[0177] Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

[0178] Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

[0179] Cationic liposomes are readily available. For example, N[1-2,3-dioleyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner supra). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boerhinger). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Nail. Acad. Sci. USA* 75:41944198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

[0180] Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphoshatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

[0181] The liposomes can comprise multilammelar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) Cell 17:77); Deamer & Bangham (1976) *Biochim. Biophys. Acia* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348); Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

[0182] E. Lipoproteins

[0183] In addition, lipoproteins can be included with the polynucleotide/polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, DL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

[0184] Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

[0185] A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

[0186] The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) Annu Rev. Biochem 54:699; Law (1986) Adv. Exp Med. Biol. 151:162; Chen (1986) J Biol Chem 261:12918; Kane (1980) Proc Natl Acad Sci USA 77:2465; and Utermann (1984) Hum Genet 65:232.

[0187] Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

[0188] Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (supra); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J. Clin. Invest* 64:743-750. Lipoproteins can also be produced by in vitro or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acia* 30: 443. Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Techniologies, Inc., Stoughton, Mass., USA. Further description of lipoproteins can be found in Zuckermann et al. PCT/US97/14465.

[0189] F. Polycationic Agents

[0190] Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide/polypeptide to be delivered.

[0191] Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

[0192] The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic aid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

[0193] Organic polycationic agents include: spermine, spermidine, and purtrescine.

[0194] The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

[0195] Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin™, and lipofectAMINE™ are monomers that form polycationic complexes when combined with polynucleotides/polypeptides.

[0196] Immunodiagnostic Assays

[0197] Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

[0198] Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, etc.) required for the conduct of the assay, as well as suitable set of assay instructions.

[0199] Nucleic Acid Hybridisation

[0200] "Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions

that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook et al. [supra] Volume 2, chapter 9, pages 9.47 to 9.57.

[0201] "Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200° C. below the calculated Tm of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook et al. at page 9.50.

[0202] Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 g for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy yeast gene can be detected with an exposure time of only 1 hour starting with 1 μg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/μg. For a single-copy mammalian gene a conservative approach would start with 10 μg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/μg, resulting in an exposure time of 24 hours.

[0203] Several factors can affect the melting temperature (Tm) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$Tm = 81 + 16.6(\log_{10} Ci) + 0.4[\%\ (G+C)] - 0.6(\%\ \text{formamide}) - 600/n - 1.5(\%\ \text{mismatch}).$$

[0204] where Ci is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

[0205] In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (ie. stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

[0206] In general, convenient hybridization temperatures in the presence of 50% formamide are 42° C. for a probe with is 95% to 100% homologous to the target fragment, 37° C. for 90% to 95% homology, and 32° C. for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

[0207] Nucleic Acid Probe Assays

[0208] Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

[0209] The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

[0210] The probe sequence need not be identical to the Neisserial sequence (or its complement)—some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

[0211] The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic

applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

[0212] Probes may be produced by synthetic procedures, such as the triester method of Matteucci et al. [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea et al. [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

[0213] The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated eg. backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase in vivo half-life, alter RNA affinity, increase nuclease resistance etc. [eg. see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [eg. see Corey (1997) *TIBTECH* 15:224-229; Buchardt et al. (1993) *TIBTECH* 11:384-386].

[0214] Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis et al. [*Meth. Enzymol.* (1987) 155: 335-350]; U.S. Pat. Nos. 4,683,195 and 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

[0215] A thermostable polymerase creases copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

[0216] Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook et al [supra]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

BRIEF DESCRIPTION OF THE DRAWINGS

[0217] **FIGS. 1-7** show biochemical data and sequence analysis pertaining to Examples 1, 2, 3, 7, 13, 16 and 19, respectively, with ORFs 40, 38, 44, 52, 114, 41 and 124. M1 and M2 are molecular weight markers. Arrows indicate the position of the main recombinant product or, in Western blots, the position of the main *N. meningitidis* immunoreactive band. TP indicates *N. meningitidis* total protein extract; OMV indicates *N. meningitidis* outer membrane vesicle preparation. In bactericidal assay results: a diamond (♦) shows preimmune data; a triangle (▲) shows GST control data; a circle (●) shows data with recombinant *N. meningitidis* protein. Computer analyses show a hydrophilicity plot (upper), an antigenic index plot (middle), and an AMPHI analysis (lower). The AMPHI program has been used to predict T-cell epitopes [Gao et al. (1989) *J. Immunol.* 143:3007; Roberts et al. (1996) *AIDS Res Hum Retrovir* 12:593; Quakyi et al. (1992) *Scand J Immunol* suppl. 11:9) and is available in the Protean package of DNASTAR, Inc. (1228 South Park Street, Madison, Wis. 53715 USA).

[0218] **FIG. 8** shows an alignment comparison of amino acid sequences for ORF 40 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLES

[0219] The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, along with their putative translation products. Not all of the nucleic acid sequences are complete ie. they encode less than the full-length wild-type protein. It is believed at present that none of the DNA sequences described herein have significant homologs in *N. gonorrhoeae*.

[0220] The examples are generally in the following format:

- [0221] a nucleotide sequence which has been identified in *N. meningitidis* (strain B)
- [0222] the putative translation product of this sequence
- [0223] a computer analysis of the translation product based on database comparisons
- [0224] a corresponding gene and protein sequence identified in *N. meningitidis* (strain A)
- [0225] a description of the characteristics of the proteins which indicates that they might be suitably antigenic
- [0226] results of biochemical analysis (expression, purification, ELISA, FACS etc.)

[0227] The examples typically include details of sequence homology between species and strains. Proteins that are similar in sequence are generally similar in both structure and function, and the homology often indicates a common evolutionary origin. Comparison with sequences of proteins of known function is widely used as a guide for the assignment of putative protein function to a new sequence and has proved particularly useful in whole-genome analyses.

[0228] Sequence comparisons were performed at NCBI (http://www.ncbi.nlm.nih.gov) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul et al. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

[0229] Dots within nucleotide sequences (eg. position 288 in Example 12) represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame.

In the same way, double-underlined nucleotides were removed. Lower case letters (eg. position 589 in Example 12) represent ambiguities which arose during alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

[0230] Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti et al. [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

[0231] Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

[0232] Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (http://www.psort.nib-b.ac.jp). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

[0233] Various tests can be used to assess the in vivo immunogenicity of the proteins identified in the examples. For example, the proteins can be expressed recombinantly and used to screen patient sera by immunoblot A positive reaction between the protein and patient serum indicates that the patient has previously mounted an immune response to the protein in question ie. the protein is an immunogen. This method can also be used to identify immunodominant proteins.

[0234] The recombinant protein can also be conveniently used to prepare antibodies eg. in a mouse. These can be used for direct confirmation that a protein is located on the cell-surface. Labelled antibody (eg. fluorescent labelling for FACS) can be incubated with intact bacteria and the presence of label on the bacterial surface confirms the location of the protein.

[0235] In particular, the following methods (A) to (S) were used to express, purify and biochemically characterise the proteins of the invention:

[0236] A) Chromosomal DNA Preparation

[0237] *N. meningitidis* strain 2996 was grown to exponential phase in 100 ml of GC medium, harvested by centrifugation, and resuspended in 5 ml buffer (20% Sucrose, 50 mM Tris-HCl, 50 mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10 ml lysis solution (50 mM NaCl, 1% Na-Sarkosyl, 50 μg/ml Proteinase K), and the suspension was incubated at 37° C. for 2 hours. Two phenol extractions (equilibrated to pH 8) and one $ChCl_3$/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes ethanol, and was collected by centrifugation. The pellet was washed once with 70% ethanol and redissolved in 4 ml buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The DNA concentration was measured by reading the OD at 260 nm.

[0238] B) Oligonucleotide Design

[0239] Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by deducing the 5'-end amplification primer sequence immediately downstream from the predicted leader sequence.

[0240] The 5' primers included two restriction enzyme recognition sites (BamHI-NdeI, BamHI-NheI, or EcoRI-NheI, depending on the gene's own restriction pattern); the 3' primers included a XhoI restriction site. This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using either BamHI-XhoI or EcoRI-XhoI), and pET21b+ (using either NdeI-XhoI or NheI-XhoI).

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5'end primer tail:
CGCGGATCCCATATG          (BamHI-NdeI)
CGCGGATCCGCTAGC          (BamHI-NheI)
CCGGAATTCTAGCTAGC        (EcoRI-NheI)

3'-end primer tail:
CCCGCTCGAG               (XhoI)
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[0241] As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridised to the sequence to be amplified. The number of hybridizing nucleotides depended on the melting temperature of the whole primer, and was determined for each primer using the formulae:

T_m=4 (*G*+*C*)+2 (*A*+*T*) (tail excluded)

T_m=64.9+0.41 (% *GC*)−600/*N* (whole primer)

[0242] The average melting temperature of the selected oligos were 65-70° C. for the whole oligo and 50-55° C. for the hybridising region alone.

[0243] Table I shows the forward and reverse primers used for each amplification. Oligos were synthesized by a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2 ml NH_4OH, and deprotected by 5 hours incubation at 56° C. The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were then centrifuged and the pellets resuspended in either 100 μl or 1 ml of water. OD_{260} was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration was determined and adjusted to 2-10 pmol/μl.

TABLE I

PCR primers

ORF	Primer	Sequence	Restriction sites
ORF 38	Forward	CGCGGATCCCATATG-TCGCCGCAAAATTCCGA <SEQ ID 112>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTTGCCGCGTTAAAAGC <SEQ ID 113>	XhoI

TABLE I-continued

		PCR primers	
ORF	Primer	Sequence	Restriction sites
ORF 40	Forward	CGCGGATCCCATATG-ACCGTGAAGACCGCC <SEQ ID 114>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGA <SEQ ID 115>	XhoI
ORF 41	Forward	CGCGGATCCCATATG-TATTTGAAACAGCTCCAAG <SEQ ID 116>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTCTGGGTGAATGTTA <SEQ ID 117>	XhoI
ORF 44	Forward	GCGGATCCCATATG-GGCACGGACAACCCC <SEQ ID 118>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ACGTGGGGAACAGTCT <SEQ ID 119>	XhoI
ORF 51	Forward	GCGGATCCCATATG-AAAAATATTCAAGTAGTTGC <SEQ ID 120>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AAGTTTGATTAAACCCG <SEQ ID 121>	XhoI
ORF 52	Forward	CGCGGATCCCATATG-TGCCAACCGCAATCCG <SEQ ID 122>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTTTCCAGCTCCGGCA <SEQ ID 123>	XhoI
ORF 56	Forward	GCGGATCCCATATG-GTTATCGGAATATTACTCG <SEQ ID 124>	BamHI-NdeI
	Reverse	CCCGCTCGAG-GGCTGCAGAAGCTGG <SEQ ID 125>	XhoI
ORF 69	Forward	CGCGGATCCCATATG-CGGACGTGGTTGGTTTT <SEQ ID 126>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATATCTTCCGTTTTTTTCAC <SEQ ID 127>	XhoI
ORF 82	Forward	CGC GGATCCGCTAGC-GTAAATTTATTATTTTTAGAA <SEQ ID 128>	BamHI-NheI
	Reverse	CCCGCTCGAG-TCCAACTCATTGAAGTA <SEQ ID 129>	XhoI
ORF 114	Forward	CGCGGATCCCATATG-AATAAAGGTTTACATCGCAT <SEQ ID 130>	BamHI-NheI
	Reverse	CCCGCTCGAG-AATCGCTGCACCGGCT <SEQ ID 131>	XhoI
ORF 124	Forward	CGCGGATCCCATATG-ACTGCCTTTTCGACA <SEQ ID 132>	BamHI-NheI
	Reverse	CCCGCTCGAG-GCGTGAAGCGTCAGGA <SEQ ID 133>	XhoI

[0244] C) Amplification

[0245] The standard PCR protocol was as follows: 50-200 ng of genomic DNA were used as a template in the presence of 20-40 μM of each oligo, 400-8004M dNTs solution, 1×PCR buffer (including 1.5 mM $MgCl_2$), 2.5 units TaqI DNA polymerase (using Perkin-Elmer AmpliTaQ, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase).

[0246] In some cases, PCR was optimised by the addition of 10 μl DMSO or 50 μl 2M betaine.

[0247] After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95° C.), each sample underwent a double-step amplification: the first 5 cycles were performed using as the hybridization temperature the one of the oligos excluding the restriction enzymes tail, followed by 30 cycles performed according to the hybridization temperature of the whole length oligos. The cycles were followed by a final 10 minute extension step at 72° C.

[0248] The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95° C.	30 seconds 50–55° C.	30–60 seconds 72° C.

-continued

	Denaturation	Hybridisation	Elongation
Last 30 cycles	30 seconds 95° C.	30 seconds 65–70° C.	30–60 seconds 72° C.

[0249] The elongation time varied according to the length of the ORF to be amplified.

[0250] The amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

[0251] The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a suitable volume to be loaded on a 1% agarose gel. The DNA fragment corresponding to the right size band was then eluted and purified from gel, using the Qiagen Gel Extraction Kit, following the instructions of the manufacturer. The final volume of the DNA fragment was 30 μl or 500 of either water or 10 mM Tris, pH 8.5.

[0252] D) Digestion of PCR Fragments

[0253] The purified DNA corresponding to the amplified fragment was split into 2 aliquots and double-digested with:

[0254] NdeI/XhoI or NheI/XhoI for cloning into pET-21b+ and further expression of the protein as a C-terminus His-tag fusion

[0255] BamHI/XhoI or EcoRI/XhoI for cloning into pGEX-KG and further expression of the protein as N-terminus GST fusion.

[0256] EcoRI/PstI, EcoRI/SalI, SalI/PstI for cloning into pGex-His and further expression of the protein as N-terminus His-tag fusion

[0257] Each purified DNA fragment was incubated (37° C. for 3 hours to overnight) with 20 units of each restriction enzyme (New England Biolabs) in a either 30 or 40 μl final volume in the presence of the appropriate buffer. The digestion product was then purified using the QIAquick PCR purification kit, following the manufacturer's instructions, and eluted in a final volume of 30 or 50 μl of either water or 10 mM Tris-HCl, pH 8.5. The final DNA concentration was determined by 1% agarose gel electrophoresis in the presence of titrated molecular weight marker.

[0258] E) Digestion of the Cloning Vectors (pET22B, pGEX-KG, pTRC-His A, and pGex-His)

[0259] 10 μg plasmid was double-digested with 50 units of each restriction enzyme in 200 μl reaction volume in the presence of appropriate buffer by overnight incubation at 37° C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick-Gel Extraction Kit and the DNA was eluted in 50 μl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260} of the sample, and adjusted to 50 μg/μl. 1 μl of plasmid was used for each cloning procedure.

[0260] The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream to the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia).

[0261] F) Cloning

[0262] The fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 μl, a molar ratio of 3:1 fragment/vector was ligated using 0.5 μl of NEB T4 DNA ligase (400 units/μl), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

[0263] In order to introduce the recombinant plasmid in a suitable strain, 100 μl *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37° C. for 3 minutes, then, after adding 800 μl LB broth, again at 37° C. for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 μl of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

[0264] The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37° C. in either 2 ml (pGEX or pTC clones) or 5 ml (pET clones) LB broth+100 μg/ml ampicillin. The cells were then pelletted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 μl. 5 μl of each individual miniprep (approximately 1 g) were digested with either NdeI/XhoI or BamHI/XhoI and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1 Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

[0265] G) Expression

[0266] Each ORF cloned into the expression vector was transformed into the strain suitable for expression of the recombinant protein product. 1 μl of each construct was used to transform 30 μl of *E. coli* BL21 (pGEX vector), *E. coli* TOP 10 (pTRC vector) or *E. coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E. coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2 ml LB+Amp (100 μg/ml), incubated at 37° C. overnight, then diluted 1:30 in 20 ml of LB+Amp (100 μg/ml) in 100 ml flasks, making sure that the OD_{600} ranged between 0.1 and 0.15. The flasks were incubated at 30° C. into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1 mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30° C., the final concentration of the sample was checked by OD. In order to check expression, 1 ml of each sample was removed, centrifuged in a microfuge, the pellet resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000 g and the pellet resuspended in PBS for further use.

[0267] H) GST-Fusion Proteins Large-Scale Purification.

[0268] A single colony was grown overnight at 37° C. on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37° C.) to OD_{550} 0.8-1. Protein expression was induced with 0.2 mM IPTG followed by three hours incubation. The culture was centrifuged at 800 rpm at 4° C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40 W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was collected and mixed with 150 μl Glutatione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4° C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1 ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2 ml cold PBS until the flow-through reached OD_{280} of 0.02-0.06. The GST-fusion protein was eluted by addition of 70011 cold Glutathione elution buffer (10 mM reduced glutathione, 50 mM Tris-HCl) and fractions collected until the OD_{280} was 0.1. 21 μl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M2) (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26 kDa, this value must be added to the MW of each GST-fusion protein.

[0269] I) His-Fusion Solubility Analysis

[0270] To analyse the solubility of the His-fusion expression products, pellets of 3 ml cultures were resuspended in buffer M1 [500 μl PBS pH 7.2]. 25 μl lysozyme (10 mg/ml) was added and the bacteria were incubated for 15 min at 4° C. The pellets were sonicated for 30 sec at 40 W using a Branson sonifier B-15, frozen and thawed twice and then separated again into pellet and supernatant by a centrifugation step. The supernatant was collected and the pellet was resuspended in buffer M2 [8M urea, 0.5M NaCl, 20 mM imidazole and 0.1M NaH_2 PO_4] and incubated for 3 to 4 hours at 4° C. After centrifugation, the supernatant was collected and the pellet was resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20 mM imidazole and 0.1M NaH_2PO_4] overnight at 4° C. The supernatants from all steps were analysed by SDS-PAGE.

[0271] J) His-Fusion Large-Scale Purification.

[0272] A single colony was grown overnight at 37° C. on a LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600 ml fresh medium and allowed to grow at the optimal temperature (20-37° C.) to OD_{550} 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4° C., the supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml of either (i) cold buffer A (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8) for soluble proteins or (ii) buffer B (urea 8M, 10 mM Tris-HCl, 100 mM phosphate buffer, pH 8.8) for insoluble proteins.

[0273] The cells were disrupted by sonication on ice for 30 sec at 40 W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again.

[0274] For insoluble proteins, the supernatant was stored at −20° C., while the pellets were resuspended in 2 ml buffer C (6M guanidine hydrochloride, 100 mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes.

[0275] Supernatants were collected and mixed with 150 μl Ni^{2+}-resin (Pharmacia) (previously washed with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4° C. The resin was washed twice with 10 ml buffer A or B for 10 minutes, resuspended in 1 ml buffer A or B and loaded on a disposable column. The resin was washed at either (i) 4° C. with 2 ml cold buffer A or (ii) room temperature with 2 ml buffer B, until the flow-through reached OD_{280} of 0.02-0.06.

[0276] The resin was washed with either (i) 2 ml cold 20 mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) or (ii) buffer D (urea 8M, 10 mM Tris-HCl, 100 mM phosphate buffer, pH 6.3) until the flow-through reached the $O.D_{280}$ of 0.02-0.06. The His-fusion protein was eluted by addition of 700 μl of either (i) cold elution buffer A (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) or (ii) elution buffer B (urea 8M, 10 mM Tris-HCl, 100 mM phosphate buffer, pH 4.5) and fractions collected until the $O.D_{280}$ was 0.1. 21 μl of each fraction were loaded on a 12% SDS gel.

[0277] K) His-Fusion Proteins Renaturation

[0278] 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μg/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50 mM phosphate buffer, 5 mM reduced glutathione, 0.5 mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4° C. for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50 mM phosphate buffer, 5 mM reduced glutathione, 0.5 mM oxidised glutathione, pH 8.8) for 12-14 hours at 4° C. Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

[0279] L) His-Fusion Large-Scale Purification

[0280] 500 ml of bacterial cultures were induced and the fusion proteins were obtained soluble in buffer M1, M2 or M3 using the procedure described above. The crude extract of the bacteria was loaded onto a Ni-NTA superflow column (Qiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer of the fusion proteins. Unbound material was eluted by washing the column with the same buffer. The specific protein was eluted with the corresponding buffer containing 500 mM imidazole and dialysed against the corresponding buffer without imidazole. After each run the columns were sanitized by washing with at least two column volumes of 0.5 M sodium hydroxide and reequilibrated before the next use.

[0281] M) Mice Immunisations

[0282] 20 μg of each purified protein were used to immunise mice intraperitoneally. In the case of ORF 44, CD1 mice

were immunised with $Al(OH)_3$ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For ORF 40, CD1 mice were immunised using Freund's adjuvant, rather than $Al(OH)_3$, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for ORF 38, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49.

[0283] N) ELISA Assay (Sera Analysis)

[0284] The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37° C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7 ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD_{620}. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 2 hours at room temperature and then overnight at 4° C. with stirring. 100 μl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4° C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 μl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37° C. Wells were washed three times with PBT. 200 μl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN_3 in PBS) were added to each well and the plates incubated for 90 minutes at 37° C. Wells were washed three times with PBT. 100 μl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37° C. Wells were washed three times with PBT buffer. 100 μl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 μl of H_2O) were added to each well and the plates were left at room temperature for 20 minutes. 100 μl H_2SO_4 was added to each well and OD_{490} was followed. The ELISA was considered positive when OD_{490} was 2.5 times the respective pre-immune sera.

[0285] O) FACScan Bacteria Binding Assay Procedure.

[0286] The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37° C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8 ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD_{620}. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000 rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA, 0.4% NaN_3) and centrifuged for 5 minutes at 4000 rpm. Cells were resuspended in blocking buffer to reach OD_{620} of 0.07. 100 μl bacterial cells were added to each well of a Costar 96 well plate. 100 μl of diluted (1:200) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4° C. Cells were centrifuged for 5 minutes at 4000 rpm, the supernatant aspirated and cells washed by addition of 200 μl/well of blocking buffer in each well. 100 μl of R-Phicoerytin conjugated $F(ab)_2$ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4° C. Cells were spun down by centrifugation at 4000 rpm for 5 minutes and washed by addition of 200 μl/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μl/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan setting were: FL1 on, FL2 and FL3 off; FSC-H threshold: 92; FSC PMT Voltage: E 02; SSC PMT: 474; Amp. Gains 7.1; FL-2 PMT: 539; compensation values: 0.

[0287] P) OMV Preparations

[0288] Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20 mM Tris-HCl. Heat inactivation was performed at 56° C. for 30 minutes and the bacteria disrupted by sonication for 10 minutes on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000 g for 10 minutes and the total cell envelope fraction recovered by centrifugation at 50000 g at 4° C. for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000 g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000 g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10 mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

[0289] Q) Whole Extracts Preparation

[0290] Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1 ml of 20 mM Tris-HCl. Heat inactivation was performed at 56° C. for 30 minutes.

[0291] R) Western Blotting

[0292] Purified proteins (500 ng/lane), outer membrane vesicles (5 μg) and total cell extracts (25 μg) derived from MenB strain 2996 were loaded on 15% SDS-PAGE and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150 mA at 4° C., in transferring buffer (0.3% Tris base, 1.44% glycine, 20% methanol). The membrane was saturated by overnight incubation at 4° C. in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37° C. with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

[0293] S) Bactericidal Assay

[0294] MC58 strain was grown overnight at 37° C. on chocolate agar plates. 5-7 colonies were collected and used

to inoculate 7 ml Mueller-Hinton broth. The suspension was incubated at 37° C. on a nutator and let to grow until OD_{620} was 0.5-0.8. The culture was aliquoted into sterile 1.5 ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD_{620} of 0.5, diluted 1:20000 in Gey's buffer and stored at 25° C.

[0295] 50 μl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25 μl of diluted mice sera (1:100 in Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4° C. 25 μl of the previously described bacterial suspension were added to each well. 25 μl of either heat-inactivated (56° C. waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22 μl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37° C. with rotation and then 22 μl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1 hour were counted.

[0296] Table II gives a summary of the cloning, expression and purification results.

TABLE II

	Cloning, expression and purification			
ORF	PCR/cloning	His-fusion expression	GST-fusion expression	Purification
orf 38	+	+	+	His-fusion
orf 40	+	+	+	His-fusion
orf 41	+	n.d.	n.d.	
orf 44	+	+	+	His-fusion
orf 51	+	n.d.	n.d.	
orf 52	+	n.d.	+	GST-fusion
orf 56	+	n.d.	n.d.	
orf 69	+	n.d.	n.d.	
orf 82	+	n.d.	n.d.	
orf 114	+	n.d.	+	GST-fusion
orf 124	+	n.d.	n.d.	

Example 1

[0297] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1>:

```
   1 ACACTGTTGT TTGCAACGGT TCAGGCAAGT GCTAACCAAT GAAGAGCAAG
  51 AAGAAGATTT ATATTTAGAC CCCGTACAAC GCACTGTTGC CGTGTTGATA
 101 GTCAATTCCG ATAAAGAAGG CACGGGAGAA AAAGAAAAAG TAGAAGAAAA
 151 TTCAGATTGG GCAGTATATT TCAACGAGAA AGGAGTACTA ACAGCCAGAG
 201 AAATCACCyT CAAAGCCGGC GACAACCTGA AAATCAAACA AAACGGCACA
 251 AACTTCACCT ACTCGCTGAA AAALGACCTC ACAGATCTGA CCAGTGTTGG
 301 AACTGAAAAA TTATCGTTTA GCGCAAACGG CAATAAAGTC AACATCACAA
 351 GCGACACCAA AGGCTTGAAT TTTGCGAAAG AAACGGCTGG sACGAACGgC
 401 GACACCACGG TTCATCTGAA CGGTATTGGT TCGACTTTGA CCGATACGCT
 451 GCTGAATACC GGAGCGACCA CAAACGTAAC CAACGACAAC GTTACCGATG
 501 ACGAGAAAAA ACGTGCGGCA AGCGTTAAAG ACGTATTAAA CGCTGGCTGG
 551 AACATTAAAG GCGTTAAACC CGGTACAACA GCTTCCGATA ACGTTGATTT
 601 CGTCCGCACT TACGACACAG TCGAGTTCTT GAGCGCAGAT ACGAAAACAA
 651 CGACTGTTAA TGTGGAAAGC AAAGACAACG GCAAGAAAAC CGAAGTTAAA
 701 ATCGGTGCGA AGACTTCTGT TATTAAAGAA AAAGAC...
```

[0298] This corresponds to the amino acid sequence <SEQ ID 2; ORF40>:

```
   1..TLLFATVQAS ANQEEQEEDL YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN
  51   SDWAVYFNEK GVLTAREITX KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG
 101   TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
 151   LNTGATTNVT NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF
 201   VRTYDTVEFL SADTKTITVN VESKDNGKKT EVKIGAXTSV IKEKD...
```

[0299] Further work revealed the complete DNA sequence <SEQ ID 3>:

```
   1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT
  51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTACAACG
 201 CACTGTTGCC GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA
 251 AAGAAAAAGT AGAAGAAAAT TCAGATTGGG CAGTATATTT CAACGAGAAA
 301 GGAGTACTAA CAGCCAGAGA AATCACCCTC AAAGCCGGCG ACAACCTGAA
 351 AATCAAACAA AACGGCACAA ACTTCACCTA CTCGCTGAAA AAAGACCTCA
 401 CAGATCTGAC CAGTGTTGGA ACTGAAAAAT TATCGTTTAG CGCAAACGGC
 451 AATAAAGTCA ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA
 501 AACGGCTGGG ACGAACGGCG ACACCACGGT TCATCTGAAC GGTATTGGTT
 551 CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
 601 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA
 651 CGTATTAAAC GCTGGCTGGA ACATTAAAGG CGTTAAACCC GGTACAACAG
 701 CTTCCGATAA CGTTGATTTC GTCCGCACTT ACGACACAGT CGAGTTCTTG
 751 AGCGCAGATA CGAAAACAAC GACTGTTAAT GTGGAAAGCA AAGACAACGG
 801 CAAGAAAACC GAAGTTAAAA TCGGTGCGAA GACTTCTGTT ATTAAAGAAA
 851 AAGACGGTAA GTTGGTTACT GGTAAAGACA AAGGCGAGAA TGGTTCTTCT
 901 ACAGACGAAG GCGAAGGCTT AGTGACTGCA AAAGAAGTGA TTGATGCAGT
 951 AAACAAGGCT GGTTGGAGAA TGAAAACAAC AACCGCTAAT GGTCAAACAG
1001 GTCAAGCTGA CAAGTTTGAA ACCGTTACAT CAGGCACAAA TGTAACCTTT
1051 GCTAGTGGTA AAGGTACAAC TGCGACTGTA AGTAAAGATG ATCAAGGCAA
1101 CATCACTGTT ATGTATGATG TAAATGTCGG CGATGCCCTA AACGTCAATC
1151 AGCTGCAAAA CAGCGGTTGG AATTTGGATT CCAAAGCGGT TGCAGGTTCT
1201 TCGGGCAAAG TCATCAGCGG CAATGTTTCG CCGAGCAAGG GAAAGATGGA
1251 TGAAACCGTC AACATTAATG CCGGCAACAA CATCGAGATT ACCCGCAACG
1301 GTAAAAATAT CGACATCGCC ACTTCGATGA CCCCGCAGTT TTCCAGCGTT
1351 TCGCTCGGCG CGGGGGCGGA TGCGCCCACT TTGAGCGTGG ATGGGGACGC
1401 ATTGAATGTC GGCAGCAAGA AGGACAACAA ACCCGTCCGC ATTACCAATG
1451 TCGCCCCGGG CGTTAAAGAG GGGGATGTTA CAAACGTCGC ACAACTTAAA
1501 GGCGTGGCGC AAAACTTGAA CAACCGCATC GACAATGTGG ACGGCAACGC
1551 GCGTGCGGGC ATCGCCCAAG CGATTGCAAC CGCAGGTCTG GTTCAGGCGT
1601 ATTTGCCCGG CAAGAGTATG ATGGCGATCG GCGGCGGCAC TTATCGCGGC
1651 GAAGCCGGTT ACGCCATCGG CTACTCCAGT ATTTCCGACG GCGGAAATTG
```

-continued

```
1701 GATTATCAAA GGCACGGCTT CCGGCAATTC GCGCGGCCAT TTCGGTGCTT

1751 CCGCATCTGT CGGTTATCAG TGGTAA
```

[0300] This corresponds to the amino acid sequence <SEQ ID 4; ORF40-1>:

```
   1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS

  51 ANNEEQEEDL YLDFVQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK

 101 GVLTAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSMIG

 151 NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT

 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF VRTYDTVEFL

 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGKLVT GKDKGENGSS

 301 TDEGEGLVTA KEVIDAYNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF

 351 ASGKGTTATV SKDDQGNITV NYDVNVGDAL NVNQLQNSGW NLDSKAVAGS

 401 SGKVISGNVS PSKGKMDETV NINAGNNIEI TRNGKNIDIA TSHTPQFSSV

 451 SLGAGADAPT LSVDGDALNV GSKKDNKPVR ITNVAPGVKE GOVTNVAQLK

 501 GVAQNLNNRI DNVDGNARAG ZAQAIATAGL VQAYLPGKSM MAIGGGTYRG

 551 EAGYAIGYSS ISDGGNWIIK GTASGNSRGH FGASASVGYQ W*
```

[0301] Further work identified the corresponding gene in strain A of *N. meningitidis* <SEQ ID 5>:

```
   1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGNGT

  51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG

 101 TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT TCAGGCGAAT

 151 GCTACCGATG AAGATGAAGA AGAAGAGTTA GAATCCGTAC AACGCTCTGT

 201 CGTAGGGAGC ATTCAAGCCA GTATGGAAGG CAGCGGCGAA TTGGAAACGA

 251 TATCATTATC AATGACTAAC GACAGCAAGG AATTTGTAGA CCCATACATA

 301 GTAGTTACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AAAACACCAA

 351 TGAAAACACC AATGCCAGTA GCTTCACCTA CTCGCTGAAA AAAGACCTCA

 401 CAGGCCTGAT CAATGTTGAN ACTGAAAAAT TATCGTTTGG CGCAAACGGC

 451 AAGAAAGTCA ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA

 501 AACGGCTGGG ACGAACGGCG ACACCACGGT TCATCTGAAC GGTATCGGTT

 551 CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG

 601 GGTAACCNAA GTACACATTA CACTCGTGCA GCAAGTATTA AGGATGTGTT

 651 GAATGCGGGT TGGAATATTA AGGGTGTTAA ANNNGGCTCA ACAACTGGTC

 701 AATCAGAAAA TGTCGATTTC GTCCGCACTT ACGACACAGT CGAGTTCTTG

 751 AGCGCAGATA CGNAAACAAC GACNGTTAAT GTGGAAAGCA AAGACAACGG

 801 CAAGAGAACC GAAGTTAAAA TCGGTGCGAA GACTTCTGTT ATTAAAGAAA

 851 AAGACGGTAA GTTGGTTACT GGTAAAGGCA AAGGCGAGAA TGGTTCTTCT
```

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```
 901 ACAGACGAAG GCGAAGGCTT AGTGACTGCA AAAGAAGTGA TTGATGCAGT

 951 AAACAAGGCT GGTTGGAGAA TGAAAACAAC AACCGCTAAT GGTCAAACAG

1001 GTCAAGCTGA CAAGTTTGAA ACCGTTACAT CAGGCACAAA TGTAACCTTT

1051 GCTAGTGGTA AAGGTACAAC TGCGACTGTA AGTAAAGATG ATCAAGGCAA

1101 CATCACTGTT ATGTATGATG TAAATGTCGG CGATGCCCTA AACGTCAATC

1151 AGCTGCAAAA CAGCGGTTGG AATTTGGATT CCAAAGCGGT TGCAGGTTCT

1201 TCGGGCAAAG TCATCAGCGG CAATGTTTCG CCGAGCAAGG GAAAGATGGA

1251 TGAAACCGTC AACATTAATG CCGGCAACAA CATCGACATT AGCCGCAACG

1301 GTAAAAATAT CGACATCGCC ACTTCGATGG CGCCGCAGTT TTCCAGCGTT

1351 TCGCTCGGCG CGGGGGCAGA TGCGCCCACT TTAAGCGTGG ATGACGAGGG

1401 CGCGTTGAAT GTCGGCAGCA AGGATGCCAA CAAACCCGTC CGCATTACCA

1451 ATGTCGCCCC GGGCGTTAAA GANGGGGATG TTACAAACGT CNCACAACTT

1501 AAAGGCGTGG CGCAAAACTT GAACAACCGC ATCGACAATG TGGACGGCAA

1551 CGCGCGTGCN GGCATCGCCC AAGCGATTGC AACCGCAGGT CTGGTTCAGG

1601 CGTATCTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG CACTTATCGC

1651 GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG ACGGCGGAAA

1701 TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC CATTTCGGTG

1751 CTTCCGCATC TGTCGGTTAT CAGTGGTAA
```

[0302] This encodes a protein having amino acid sequence <SEQ ID 6; ORF40a>:

```
   1 MNKIYRIIWN SALNPXVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN

  51 ATDEDEKEEL ESVQRSVVGS IQASMEGSGE LETISLSHTN DSKEFVDPYI

 101 VVTLKAGDNL KIKONTHENT NASSFTYSLK KDLTGLINVX TEKLSFGANG

 151 KKVNIISDTK GLNFAXETAG TNGDTTVHLN GIGSTLTDTL AGSSASHVDA

 201 GNXSTHYTRA ASIKDVLNAG WNIKGVKXGS TTGQSENVDF VRTYDTVEFL

 251 SADTXTTTVN VESKDNGKRT EVXIGAXTSV IKEKDGKLVT GKGKGENGSS

 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF

 351 ASGKGTTATV SXDDQGNITV MYDVNVGDAL NVNQLONSGW NLDSKAVAGS

 401 SGKVISGNVS PSKGKMDETV NINAGNNIEI SRNGKNIDIA TSMAPQFSSV

 451 SLGAGADAPT LSVDDEGALN VGSKDANKPV RITNVAPGVK XGDVTNVXQL

 501 KGVAQNLNNR IDNYOGNARA GIAQAIATAG LVQAYLPGKS NNAIGGGTYR

 551 GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY QW
```

[0303] The originally-identified partial strain B sequence (ORF40) shows 65.7% identity over a 254 aa overlap with ORF40a:

```
                                          10        20        30
orf40.pep                               TLLFATVQASANQEEQEEDLYLDPVQRTVA
                                        |||||||||:|::|::||:|  : |||:|
orf40a    SALNAXVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL--ESVQRSV-
```

-continued

```
                 20        30        40        50        60

                 40        50        60        70        80
orf40.pep VLIVNSDKEGTGEKEKVEEN-SDWAVYFNEKGVLTAREITXKAGDNLKIKQN------GT
          |  :::: ||:|| | :  : :: :  | :  ::    :| ||||||||||       ::
orf40a    VGSIQASMEGSGELETISLSMTNDSKEFVDPYIV----VTLKAGDNLKIKQNTNENTNAS
           70        80        90       100       110       120

              90       100       110       120       130       140
orf40.pep NFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIG
          :||||||||||  | :| ||||||:|||:|||| |||||||||||||||||||||||||
orf40a    SFTYSLKKDLTGLINVXTEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIG
              130       140       150       160       170       180

              150       160       170       180       190       200
orf40.pep STLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA--SDNVDFV
          ||||||| :::|: :|   | :  :  ||||:|||||||||||||| |:|:  |:|||||
orf40a    STLTDTLAGSSAS-HVDAGNXST-HYTRAASIKDVLNAGWNIKGVKXGSTTGQSENVDFV
              190       200       210       220       230       240

                210       220       230       240
orf40.pep RTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD
          |||||||||||||  |||||||||||||:||||||||||||||
orf40a    RTYDTVEFLSADTXTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSST
                250       260       270       280       290       300
```

[0304] The complete strain B sequence (ORF44-1) and ORF40a show 83.7% identity in 601 aa overlap:

```
                        10        20        30        40        50        60
orf40-1.pep   MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
              |||||||||||||||  |:|||||||||||||||||||||||||||||||:|::|::||:|
orf40a        MNKIYRIIWNSALNAXVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                        10        20        30        40        50        60

                        70        80        90       100       110       119
orf40-1.pep   YLDPVQRTVAVLIVNSDKEGTGEKEKVEEN-SDWAVYFNEKGVLTAREITLKAGDNLKIK
                : |||:| |  :::: ||:|| | :  : :: :  | :  ::    :||||||||||
orf40a        --ESVQRSV-VGSIQASMEGSGELETISLSMTNDSKEFVDPYIV----VTLKAGDNLKIK
                          70        80        90       100       110

            120             130       140       150       160       170
orf40-1.pep   QN------GTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNG
              ||      :::|||||||||| | :| ||||||:|||:|||| ||||||||||||||||
orf40a        QNTNENTNASSFTYSLKKDLTGLINVXTEKLSFGANGKKVNIISDTKGLNFAKETAGTNG
                  120       130       140       150       160       170

                  180       190       200       210       220       230
orf40-1.pep   DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
              |||||||||||||||| :::|: :|    | :  :  ||||:|||||||||||||| |:|
orf40a        DTTVHLNGIGSTLTDTLAGSSAS-HVDAGNXST-HYTRAASIKDVLNAGWNIKGVKXGST
                  180       190       200       210       220       230

                    240       250       260       270       280       290
orf40-1.pep   A--SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTG
              :  |:|||||||||||||||| |||||||||||||:|||||||||||||||||||||||
orf40a        TGQSENVDFVRTYDTVEFLSADTXTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG
                    240       250       260       270       280       290

                    300       310       320       330       340       350
orf40-1.pep   KDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFA
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf40a        KGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFA
                    300       310       320       330       340       350

                    360       370       360       390       400       410
orf40-1.pep   SGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf40a        SGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP
                    360       370       360       390       400       410

                    420       430       440       450       460       470
orf40-1.pep   SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNV
```

-continued

```
                    ||||||||||||||||||:||||||||||||:||||||||||||||||||| : ||||
orf40a              SKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNV
                          420        430        440        450        460        470

                          480        490        500        510        520        530
orf40-1.pep         GSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL
                    |||  ||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
orf40a              GSKDANKPVRITNVAPGVKXGDVTNVXQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL
                        480        490        500        510        520        530

                          540        550        560        570        580        590
orf40-1.pep         VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf40a              VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ
                          540        550        560        570        580        590

orf40-1.pep         WX
                    ||
orf40a              WX
```

[0305] Computer analysis of these amino acid sequences gave the following results:

[0306] Homology with Hsf Protein Encoded by the Type b Surface Fibrils Locus of *H. influenzae* (Accession Number U41852)

[0307] ORF40 and Hsf protein show 54% aa identity in 251 aa overlap:

```
Orf40     1 TLLFATVQASANQEEQEEDLYLDPVQRTVAVLVINSDXXXXXXXXXXXXNSDWAVYFNEK 60
            TLLFATVQA+A  E++E    LDPV RT  VL  +SD           NS+W +YF+ K
Hsf      41 TLLFATVQANATDEDEE----LDPVVRTAPVLSFHSDKEGTGEKEVTE-NSNWGIYFDNK 95

Orf40    61 GVLTAREITXKAGDNLKIKQN------GTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVN 114
            GVL A  IT KAGDNLKIKQN       ++FTYSLKKDLTDLTSV TEKLSF ANG+KV+
Hsf      96 GVLKAGAITLKAGDNLKIKQNTDESTNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVD 155

Orf40   115 ITSDTKGLNFAKETAGTNGDTTVhLNGIGSTLTDTLLNTGAXXXXXXXXXXXXXEKKRAAS 174
            ITSD  GL  AK      G+  VHLNG+ STL D + NTG             EK RAA+
Hsf     156 ITSDANGLKLAK-----TGNGNVHLNGLDSTLPDAVTNTGVLSSSSFTPNDV-EKTRAAT 209

Orf40   175 VKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKI 234
            VKDVLNAGWNIKG K      ++VD V  Y+ VEF++ D  T  V ++K+NGK TEVK
Hsf     210 VKDVLNAGWNIKGAKTAGGNVESVDLVSAYNNVEFITGDKNTLDVVLTAKENGKTTEVKF 269

Orf40   235 GAKTSVIKEKD 245
              KTSVIKEKD
Hsf     270 TPKTSVIKEKD 280
```

[0308] ORF40a also shows homology to Hsf:

```
gi|1666683 (U41852) hsf gene product [Haemophilus influenzae] Length = 2353
Score = 153 (67.7 bits), Expect = 1.5-116, Sum P(11) = 1.5e-116
Identities = 33/36 (91%), Positives = 34/36 (94%)
Query:   16 VAVSELTRNHTKRASATVKTAVLATLLFATVQANAT 51
            V VSELTR HTKRASATV+TAVLATLLFATVQNAT
Sbjct:   17 VVVSELTRTHTKRASATVETAVLATLLFATVQANAT 52

Score = 161 (71.2 bits), Expect = 1.5e-116, Sum P(11) 1.5e-116
Identities = 32/38 (84%), Positives = 36/38 (94%)
Query:  101 VTLKAGDNLKIKQNTNENTNASSFTYSLKKDLTGLINV 138
            +TLAGDNLKIKQNT+E+TNASSFTYSLKKDLT L +V
Sbjct:  103 ITLKAGDNLKIKQNTDESTNASSFFYSLKKDLTDLTSV 140

Score = 110 (48.7 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
Identities = 21/29 (72%), Positives = 25/29 (86%)
Query:  138 VTEKLSFGANGKKVNIISDTKGLNFAKET 166
            V++KLS G NG KVNI SDTKGLNFAK++
```

-continued

```
Sbjct: 1439 VSDKLSLGTNGNKVNITSDTXGLNFAKDS 1467

Score = 85 (37.6 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
Identities = 18/32 (56%), Positives = 20/32 (62%)
Query:  169 TNGDTTVHLNGIGSTLTDTLAGSSASHVDAGN 200
            T  D  +HLNGI STLTDTL  S A+    GN
Sbjct: 1469 TGDDANIHLNGIASTLTDTLLNSGATTNLGGN 1500

Score = 92 (40.7 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
Identities = 16/19 (84%), Positives = 19/19 (100%)
Query:  206 RAASIKOVLNAGWNIKGVK 224
            RAAS+KDVLNAGWN++GVK
Sbjct: 1509 RAASVKDVLNAGWNVRGVK 1527

Score = 90 (39.8 bits), Expect = 1.5e-116, Sum P(11) = 1.5e-116
Identities = 17/28 (60%), Positives 20/28 (71%)
Query:  226 STTGQSENVDFVRTYDTVEFLSADTTTT 253
            S   Q EN+DFV TYDTV+F+S D  TT
Sbjct: 1530 SANNQVENIDFVATYDTVDFVSGDKDTT 1557
```

[0309] Based on homology with Hsf, it was predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

[0310] ORF40-1 (61 kDa) was cloned in pET and pGex vectors and expressed in *E. coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. **FIG. 1A** shows the results of affinity purification of the His-fusion protein, and **FIG. 1B** shows the results of expression of the GST-fusion in *E. coli*. Purified His-fusion protein was used to immunise mice, whose sera were used for FACS analysis (**FIG. 1C**), a bactericidal assay (**FIG. 1D**), and ELISA (positive result). These experiments confirm that ORF40-1 is a surface-exposed protein, and that it is a useful immunogen.

[0311] **FIG. 1E** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF40-1.

Example 2

[0312] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 7>

```
   1 ATGTFACGTt TGACTGCtTT AGCCGTATGC ACCGCCCTCG CTTTGGGCGC

  51 GTGTT[]GCCG CAAAATTCCG ACTCTGCCCC ACAAGCCAAA GaACAG-
     GCGG

 101 TTTCCGCCGC ACAAACCGAA GgCGCGTCCG TTACCGTCAA AACCGCGCGC

 151 GGCGACGTTC AAATACCGCA AAACCCCGAA CGCATCGCCG TTTACGATTT

 201 GGGTATGCTC GACACCTTGA GCAAACTGGG CGTGAAAACC GGTTTGTCCG

 251 TCGATAAAAA CCGCCTGCCG TATTTAGAGG AATATTTCAA AACGACAAAA

 301 CCTGCcGGCA CTTTGTTCGA GCCGGATTAC GAAACGCTCA ACGCTTACAA

 351 ACCGCAGCTC ATCATCATCG GCAGCCGCGC CgCCAAGGCG TTTGACAAAT

 401 TGAAcGAAAT CGCGCCGACC ATCGrmwTGA CCGCCGATAC CGCCAACCTC

 451 AAAGAAAGTG CCAArGAGGC ATCGACGCTG GCGCAAATCT TC..
```

[0313] This corresponds to the amino acid sequence <SEQ ID 8; ORF38>:

```
   1 MLRLTALAVC TALALGACSP QNSDSAPOAK EQAVSAAQTE GASVTVKTAR

  51 GDVQIPQNPE RIAVYDLGHL DTLSKLGVKT GLSVDKNRLP YLEEYFKTTK

 101 PAGTLFEPDY ETLNAYKPQL IIIGSRAAKA FDKLNEIAPT IXXTADTANL

 151 KESAKEASTL AQIF..
```

[0314] Further work revealed the complete nucleotide sequence <SEQ ID 9>:

```
   1 ATGTTACGTT TGACTGCTTT AGCCGTATGC ACCGCCCTCG CTTTGGGCGC
  51 GTGTTCGCCG CAAAATTCCG ACTCTGCCCC ACAAGCCAAA GAACAGGCGG
 101 TTTCCGCCGC ACAAACCGAA GGCGCGTCCG TTACCGTCAA AACCGCGCGC
 151 GGCGACGTTC AAATACCGCA AAACCCCGAA CGCATCGCCG TTTACGATTT
 201 GGGTATGCTC GACACCTTGA GCAAACTGGG CGTGAAAACC GGTTTGTCCG
 251 TCGATAAAAA CCGCCTGCCG TATTTAGAGG AATATTTCAA AACGACAAAA
 301 CCTGCCGGCA CTTTGTTCGA GCCGGATTAC GAAACGCTCA ACGCTTACAA
 351 ACCGCAGCTC ATCATCATCG GCAGCCGCGC CGCCAAGGCG TTTGACAAAT
 401 TGAACGAAAT CGCGCCGACC ATCGAAATGA CCGCCGATAC CGCCAACCTC
 451 AAAGAAAGTG CCAAAGAGCG CATCGACGCG CTGGCGCAAA TCTTCGGCAA
 501 ACAGGCGGAA GCCGACAAGC TGAAGGCGGA AATCGACGCG TCTTTTGAAG
 551 CCGCGAAAAC TGCCGCACAA GGTAAGGGCA AAGGTTTGGT GATTTTGGTC
 601 AACGGCGGCA AGATGTCGGC TTTCGGCCCG TCTTCACGCT TGGGCGGCTG
 651 GCTGCACAAA GACATCGGCG TTCCCGCTGT CGATGAATCA ATTAAAGAAG
 701 GCAGCCACGG TCAGCCTATC AGCTTTGAAT ACCTGAAAGA GAAAAATCCC
 751 GACTGGCTGT TTGTCCTTGA CCGAAGCGCG GCCATCGGCG AAGAGGGTCA
 801 GGCGGCGAAA GACGTGTTGG ATAATCCGCT GGTTGCCGAA ACAACCGCTT
 851 GGAAAAAAGG ACAGGTCGTG TACCTCGTTC CTGAAACTTA TTTGGCAGCC
 901 GGTGGCGCGC AAGAGCTGCT GAATGCAAGC AAACAGGTTG CCGACGCTTT
 951 TAACGCGGCA AAATAA
```

[0315] This corresponds to the amino acid sequence <SEQ ID 10; ORF38-1>:

```
   1 MLRLTALAVC TALALGACSP QNSDSAPQAK EQAVSAAQTE GASVTVKTAR
  51 GDVQIPQNPE RIAVYDLQIL DTLSXLGVKT GLSVDKNRLP YLEEYFKTTK
 101 PAGTLFEPDY ETLNAYKPQL IIIGSRAAKA FDKLNEIAPT IENTADTANL
 151 KESAKERIDA LAQIFGKQAE ADKLKAEIDA SFEAAKTAAQ GKGKGLVILV
 201 NGGKMSAFGP SSRLGGWLKK DIGVPAVDES IKEGSHGQPI SFEYLKEKNP
 251 DWLFVLDRSA AIGEEGQAAK DVLDNPLVAE TTAWKKGQVV YLVPETYLAA
 301 GGAQELLNAS KQVADAFNAA K*
```

[0316] Computer analysis of this amino acid sequence reveals a putative prokaryotic membrane lipoprotein lipid attachment site (underlined).

[0317] Further work identified the corresponding gene in strain A of *N. meningitidis* <SEQ ID 11>:

```
   1 ATGTTACGTT TGACTGCTTT AGCCGTATGC ACCGCCCTCG CTTTGGGCGC
  51 GTGTTCGCCG CAAAATTCCG ACTCTGCCCC ACAAGCCAAA GAACAGGCGG
```

-continued

```
101 TTTCCGCCGC ACAATCCGAA GGCGTGTCCG TTACCGTCAA AACGGCGCGC

151 GGCGATGTTC AAATACCGCA AAACCCCGAA CGTATCGCCG TTTACGATTT

201 GGGTATGCTC GACACCTTGA GCAAACTGGG CGTGAAAACC GGTTTGTCCG

251 TCGATAAAAA CCGCCTGCCG TATTTAGAGG AATATTTCAA AACGACAAAA

301 CCTGCCGGAA CTTTGTTCGA GCCGGATTAC GAAACGCTCA ACGCTTACAA

351 ACCGCAGCTC ATCATCATCG GCAGCCGCGC AGCCAAAGCG TTTGACAAAT

401 TGAACGAAAT CGCGCCGACC ATCGAAATGA CCGCCGATAC CGCCAACCTC

451 AAAGAAAGTG CCAAAGAGCG TATCGACGCG CTGGCGCAAA TCTTCGGCAA

501 AAAGGCGGAA GCCGACAAGC TGAAGGCGGA AATCGACGCG TCTTTTGAAG

551 CCGCGAAAAC TGCCGCGCAA GGCAAAGGCA AGGGTTTGGT GATTTTGGTC

601 AAcGGCGGCA AGATGTCCGC CTTCGGCCCG TCTTCACGAC TGGGCGGCTG

651 GCTGCACAAA GACATCGGCG TTCCCGCTGT TGACGAAGCC ATCAAAGAAG

701 GCAGCCACGG TCAGCCTATC AGCTTTGAAT ACCTGAAAGA GAAAAATCCC

751 GACTGGCTGT TTGTCCTTGA CCGCAGCGCG GCCATCGGCG AAAAGGGTCA

601 GGCGGCGAAA GACGTGTTGA ACAATCCGCT GGTTGCCGAA ACAACCGCTT

851 GGAAAAATGG ACAAGTCGTT TACCTTGTTC CTGAAACTTA TTTGGCAGCC

901 GGTGGCGCGC AAGAGCTACT GAATGCAAGC AAACAGGTTG CCGACGCTTT

951 TAACGCGGCA AAATAA
```

[**0318**] This encodes a protein having amino acid sequence <SEQ ID 12; ORF38a>:

```
  1 MLRLTALAVC TALALGACSP QNSDSAPOAK EQAVSAAQSE GVSVTVKTAR

 51 GDVQIPQNPE RIAVYDLGHL DTLSKLGVKT GLSVDKNRLP YLEEYFKTTK

101 PAGTLFEPDY ETLNAYKPQL IIIGSRAAKA FDKLNEIAPT IENTADTANL

151 KESAKERIDA LAOIFGKKAE ADKLKAEIDA SFEAAKTAAQ GKGKGLVILV

201 NGGKMSAFGP SSRLGGWLHK DIGVPAVDEA IKEGSHGQPI SFEYLKEKNP

251 DWLFVLDRSA AIGEEGQAAK DVLNNPLVAE TTAWKKGQVV YLVPETYLAA

301 GGAQELLNAS KQVAOAFWAA K*
```

[**0319**] The originally-identified partial strain B sequence (ORF38) shows 95.2% identity over a 165 aa overlap with ORF38a:

```
                10        20        30        40        50        60
orf38.pep MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQTEGASVTVKTARGDVQIPQNPE
          ||||||||||||||||||||||||||||||||||||||:||:||||||||||||||||||
orf38a    MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQSEGVSVTVKTARGDVQIPQNPE
                10        20        30        40        50        60

                70        80        90       100       110       120
orf38.pep RIAVYDLGMLDTLSKLGVKTGLSVDKNRLPYLEEYFKTTKPAGTLFEPDYETLNAYKPQL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf38a    RIAVYDLGMLDTLSKLGVKTGLSVDKNRLPYLEEYFKTTKPAGTLFEPDYETLNAYKPQL
                70        80        90       100       110       120
```

-continued

```
                130       140       150       160
orf38.pep IIIGSRAAKAFDKLNEIAPTIXXTADTANLKESAKE-ASTLAQIF
          ||||||||||||||||||||  ||||||||||||  ::|||||
orf39a    IIIGSRAAKAFDKLNEIAPTIEMTADTANLKESAKERIDALAQIFGKKAEADKLKAEIDA
                130       140       150       160

orf38a    SFEAAKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGVPAVDEAIKEGSHGQPI
                190       200       210       220       230       240
```

[0320] The complete strain B sequence (ORF38-1) and ORF38a show 98.4% identity in 321 aa overlap:

```
orf38a.pep  MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQSEGVSVTVKTARGDVQIPQNPE
            ||||||||||||||||||||||||||||||||||||||:||:||||||||||||||||||
orf38-1     MLRLTALAVCTALALGACSPQNSDSAPQAKEQAVSAAQTEGASVTVKTARGDVQIPQNPE

orf38a.pep  RIAVYDLGMLDTLSKLGVKTGLSVDKNRLPYLEEYFKTTKPAGTLFEPDYETLNAYKPQL
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf38-1     RIAVYDLGMLDTLSKLGVKTGLSVDKNRLPYLEEYFKTTKPAGTLFEPDYETLNAYKPQL

orf38a.pep  IIIGSRAAKAFDKLNEIAPTIEMTADTANLKESAKERIDALAQIFGKKAEADKLKAEIDA
            ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
orf38-1     IIIGSRAAKAFDKLNEIAPTIEMTADTANLKESAKERIDALAQIFGKQAEADKLKAEIDA

orf38a.pep  SFEAAKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGVPAVDEAIKEGSHGQPI
            ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
orf38-1     SFEAAKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGVPAVDESIKEGSHGQPI

orf38a.pep  SFEYLKEKNPDWLFVLDRSAAIGEEGQAAKDVLNNPLVAETTAWKKGQVVYLVPETYLAA
            ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
orf38-1     SFEYLKEKNPDWLFVLDRSAAIGEEGQAAKDVLDNPLVAETTAWKKGQVVYLVPETYLAA

orf38a.pep  GGAQELLNASKQVADAFNAAK
            |||||||||||||||||||||
orf38-1     GGAQELLNASKQVADAFNAAK
```

[0321] Computer analysis of these sequences revealed the following:

[0322] Homology with a Lipoprotein (lipo) of *C. jejuni* (Accession Number X82427)

[0323] ORF38 and lipo show 38% aa identity in 96 aa overlap:

```
Orf38:  40 EGASVTVKTARGDVQIPQNPERIAVYDLGMLDTLSKLGVKTGLS-VKDNRLPYLEEYFKT 98
           EG S  VK  + G+ + P+NP  ++ + DLG+LDT   L +   ++ V    LP   + FK
Lipo:   51 EGDSFLVKDSLGENKTPKNPSKVVILDLGILDTFDALKLNDKVAGVPAKNLPKYLQQFKN 110

Orf38:  99 TKPAGTLFEPDYETLNAYKPQLIIIGSRAAKAFDKL 134
               G + + D+E +NA KP LIII  R +K +DKL
Lipo:  111 KPSVGGVQQVDFEAINALKPDLIIISGRQSKFYDKL 146
```

[0324] Based on this analysis, it was predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

[0325] ORF38-1 (32 kDa) was cloned in pET and pGex vectors and expressed in *E. coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. **FIG. 2A** shows the results of affinity purification of the His-fusion protein, and **FIG. 2B** shows the results of expression of the GST-fusion in *E. coli*. Purified His-fusion protein was used to immunise mice, whose sera were used for Western blot analysis (**FIG. 2C**) and FACS analysis (**FIG. 2D**). These experiments confirm that ORF38-1 is a surface-exposed protein, and that it is a useful immunogen.

[0326] **FIG. 2E** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF38-1.

Example 3

[0327] The following *N. meningitidis* DNA sequence was identified <SEQ ID 13>:

```
1  ATGAAACTTC TGACCACCGC AATCCTGTCT TCCGCAATCG CGCTCAGCAG

51 TATGGCTGCC GCCGCTGGCA CGGACAACCC CACTGTTGCA AAAAAAACCG
```

-continued

```
101 TCAGCTACGT CTGCCAGCAA GGTAAAAAAG TCAAAGTAAC CTACGGCTTC

151 AACAAACAGG GTCTGACCAC ATACGCTTCC GCCGTCATCA ACGGCAAACG

201 CGTGCAAATG CCTGTCAATT TGGACAAATC CGACAATGTG GAAACATTCT

251 ACGGCAAAGA AGGCGGTTAT GTTTTGGGTA CCGGCGTGAT GGATGGCAAA

301 TCCTACCGCA AACAGCCCAT TATGATTACC GCACCTGACA ACCAAATCGT

351 CTTCAAAGAC TGTTCCCCAC GTTAA
```

[0328] This corresponds to the amino acid sequence <SEQ ID 14; ORF44>:

```
  1 MKLLTTAILS SAIALSSMAA AAGTDWPTVA KKTVSYVCQQ GKKVKVTYGF

 51 NKQGLTTYAS AVINGKRVQH PVNLDKSDNV ETFYGKEGGY VLGTGVMDGK

101 SYRKQPIHIT APDNQIVFKD CSPR*
```

[0329] Computer analysis of this amino acid sequence predicted the leader peptide shown underlined.

[0330] Further work identified the corresponding gene in strain A of *N. meningitidis* <SEQ ID 15>:

```
  1 ATGAAACTTC TGACCACCGC AATCCTGTCT TCCGCAATCG CGCTCAGCAG

 51 TATGGCTGCT GCTGCCGGCA CGAACAACCC CACCGTTGCC AAAAAAACCG

101 TCAGCTACGT CTGCCAGCAA GGTAAAAAAG TCAAAGTAAC CTACGGCTTT

151 AACAAACAGG GCCTGACCAC ATACGCTTCC GCCGTCATCA ACGGCAAACG

201 TGTGCAAATG CCTGTCAATT TGGACAAATC CGACAATGTG GAAACATTCT

251 ACGGCAAAGA AGGCGGTTAT GTTTTGGGTA CCGGCGTGAT GGATGGCAAA

301 TCCTATCGCA AACAGCCTAT TATGATTACC GCACCTGACA ACCAAATCGT

351 CTTCAAAGAC TGTTCCCCAC GTTAA
```

[0331] This encodes a protein having amino acid sequence <SEQ ID 16; ORF44a>:

```
  1 MKLLTTAILS SAIALSSMAA AAGTNNPTVA KKTVSYVCQQ GKKVKVTYGF

 51 NKQGLTTYAS AVINGKRVQM PVNLDKSDNV ETFYGKEGGY VLGTGVMDGK

101 SYRKQPIMIT APDNQIVFKD CSPR*
```

[0332] The strain B sequence (ORF44) shows 99.2% identity over a 124 aa overlap with ORF44a:

```
                 10        20        30        40        50        60
orf44.pep MKLLTTAILSSAIALSSMAAAAGTDNPTVAKKTVSYVCQQGKKVKVTYGFNKQGLTTYAS
          ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
orf44a    MKLLTTAILSSAIALSSMAAAAGTNNPTVAKKTVSYVCQQGKKVKVTYGFNKQGLTTYAS
                 10        20        30        40        50        60
```

-continued

```
        70        80        90       100       110       120
orf44.pep AVINGKRVQMPVNLDKSDNVETFYGKEGGYVLGTGVMDGKSYRKQPIMITAPDNQIVFKD
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf44a    AVINGKRVQMPVNLDKSDNVETFYGKEGGYVLGTGVMDGKSYRKQPIMITAPDNQIVFKD
                  70        80        90       100       110       120

orf44.pep CSPRX
          |||||
orf44a    CSPRX
```

[0333] Computer analysis gave the following results:

[0334] Homology with the LecA Adhesin of *Eikenella corrodens* (Accession Number D78153)

[0335] ORF44 and LecA protein show 45% aa identity in 91 aa overlap:

```
Orf44   33 TVSYVCQQGKKVKVTYGFNKQGLTTYASAVINGKRVQMPVNLDKSDNVETFYGKEGGYVL 92
           +V+YVCQQG+++ V Y FN  G+ T A   +N + +++P NL  SDNV+T +    GY L
LecA   135 SVAYVCQQGRRLNVNYRFNSAGVPTSAELRVNNRNLRLPYNLSASDNVDTVF-SANGYRL 193

Orf44   93 GTGVHDGKSYRKQPIHITAPDNQIVFKDCSP 123
             T  MD  +YR Q I+++AP+ Q+++KDCSP
LecA   194 TTNAMDSANYRSQDIIVSAPNGQNLYKDCSP 224
```

[0336] Based on homology with the adhesin, it was predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

[0337] ORF44-1 (11.2 kDa) was cloned in pET and pGex vectors and expressed in *E. coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. **FIG. 3A** shows the results of affinity purification of the His-fusion protein, and **FIG. 3B** shows the results of expression of the GST-fusion in E-coli. Purified His-fusion protein was used to immunise mice, whose sera were used for ELISA, which gave positive results, and for a bactericidal assay (**FIG. 3C**). These experiments confirm that ORF44-1 is a surface-exposed protein, and that it is a useful immunogen.

[0338] **FIG. 3D** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF44-1.

Example 4

[0339] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>

```
   1 GGCACCGAAT TCAAAACCAC CCTTTCCGGA GCCGACATAC AGGCAGGGGT
  51 GGGTGAAAAA GCCCGAGCCG ATGCGAAAAT TATCCTAAAA GGCATCGTTA
 101 ACCGCATCCA AACCGAAGAA AAGCTGGAAT CCAACTCGAC CGTATGGCAA
 151 AAGCAGGCCG GAAGCGGCAG CACGGTTGAA ACGCTGAAGC TACCGAGCTT
 201 TGAAGGGCCG GCACTGCCTA AGCTGACCGC TCCCGGCGGC TATATCGCCG
 251 ACATCCCCAA AGGCAACCTC AAAACCGAAA TCGAAAAGCT GGCCAAACAG
 301 CCCGAATATG CCTATCTGAA ACAGCTTCAG ACGGTCAAGG ACGTGAACTG
 351 GAACCAAGTA CAGCTCGCTT ACGACAAATG GGACTATAAA CAGGAAGGCC
 401 TAACCGGAGC CGGAGCCGCA ATTANCGCAC TGGCCGTTAC CGTGGTCACC
 451 TCAGGCGCAG GAACCGGAGC CGTATTGGGA TTAANACGNG TGGCCGCCGC
 501 CGCAACCGAT GCAGCATTT...
```

[0340] This corresponds to the amino acid sequence <SEQ ID 18; ORF49>:

```
   1 GTEFKTTLSG ADIQAGVGEK ARADPKIILK GIVNRIQTEE KLESNSTVWQ

  51 KQAGSGSTVE TLKLPSFEGP ALPKLTAPGG YIADIPKGNL KTEIEKLAKQ
```

-continued

```
101 PEYAYLKQLQ TVKDVNWNQV QLAYDKWDYK QEGLTCAGAA IXALAVTVVT

151 SGAGTGAVLG LXRVAAAATD AAF..
```

[0341] Further work revealed the complete nucleotide sequence <SEQ ID 19>:

```
   1 ATGCAACTGC TGGCAGCCGA AGGCATTCAC CAACACCAAT TGAATGTTCA

  51 GAAAAGTACC CGTTTCATCG GCATCAAAGT GGGTAAAAGC AATTACAGCA

 101 AAAACGAGCT GAACGAAACC AAACTGCCCG TACGCGTTAT CGCCCAAACA

 151 GCCAAAACCC GTTCCGGCTG GGATACCGTA CTCGAAGGCA CCGAATTCAA

 201 AACCACCCTT TCCGGAGCCG ACATACAGGC AGGGGTGGGT GAAAAAGCCC

 251 GAGCCGATGC GAAAATTATC CTAAAAGGCA TCGTTAACCG CATCCAAACC

 301 GAAGAAAAGC TGGAATCCAA CTCGACCGTA TGGCAAAAGC AGGCCGGAAG

 351 CGGCAGCACG GTTGAAACGC TGAAGCTACC GAGCTTTGAA GGGCCGGCAC

 401 TGCCTAAGCT GACCGCTCCC GGCGGCTATA TCGCCGACAT CCCCAAAGGC

 451 AACCTCAAAA CCGAAATCGA AAAGCTGGCC AAACAGCCCG AATATGCCTA

 501 TCTGAAACAG CTTCAGACGG TCAAGGACGT GAACTGGAAC CAAGTACAGC

 551 TCGCTTACGA CAAATGGGAC TATAAACAGG AAGGCCTAAC CGGAGCCGGA

 601 GCCGCAATTA TCGCACTGGC CGTTACCGTG GTCACCTCAG GCGCAGGAAC

 651 CGGAGCCGTA TTGGGATTAA ACGGTGCGGC CGCCGCCGCA ACCGATGCAG

 701 CATTTGCCTC TTTGGCCAGC CAGGCTTCCG TATCGTFCAT CAACAACAAA

 751 CGCAATATCG GTAACACCCT GAAAGAGCTG GGCAGAAGCA GCACGGTGAA

 801 AAATCTGATG GTTGCCGTCG CTACCGCAGG CGTAGCCGAC AAAATCGGTG

 851 CTTCGGCACT GAACAATGTC AGCGATAAGC AGTGGATCAA CAACCTGACC

 901 GTCAACCTGG CCAATGCGGG CAGTGCCGCA CTGATTAATA CCGCTGTCAA

 951 CGGCGGCAGC CTGAAAGACA ATCTGGAAGC GAATATCCTT GCGGCTTTGG

1001 TGAATACTGC GCATGGAGAG GCAGCAAGTA AAATCAAACA GTTGGATCAG

1051 CACTACATTG CCCATAAGAT TGCCCATGCC ATAGCGGGCT GTGCGGCAGC

1101 GGCGGCGAAT AAGGGCAAGT GTCAAGATGG TGCGATCGGT GCGGCGGTCG

1151 GTGAAATCCT TGGCGAAACC CTACTGGACG GCAGAGACCC TGGCAGCCTG

1201 AATGTGAAGG ACAGGGCAAA AATCATTGCT AAGGCGAAGC TGGCAGCAGG

1251 GGCGGTTGCG GCGTTGAGTA AGGGGGATGT GAGTACGGCG GCGAATGCGG

1301 CTGCTGTGGC GGTAGAGAAT AATTCTTTAA ATOATATACA GGATCGTTTG

1351 TTGAGTGGAA ATTATGCTTT ATGTATGAGT GCAGGAGGAG CAGAAAGCTT

1401 TTGTGAGTCT TATCGACCAC TGGGCTTGCC ACACTTTGTA AGTGTTTCAG

1451 GAGAAATGAA ATTACCTAAT AAATTCGGGA ATCGTATGGT TAATGGAAAA

1531 TTAATTATTA ACACTAGAAA TGGCAATGTA TATTTCTCTG TAGGTAAAAT

1551 ATGGAGTACT GTAAAATCAA CAAAATCAAA TATAAGTGGG GTATCTGTCG

1601 GTTGGGTTTT AAATGTTTCC CCTAATGATT ATTTAAAAGA AGCATTTATG
```

-continued

```
1651 AATGATTTCA GAAATAGTAA TCAAAATAAA GCCTATGCAG AAATGATTTC

1701 CCAGACTTTG GTAGGTGAGA GTGTTGGTGG TAGTCTTTGT CTGACAAGAG

1751 CCTGCTTTTC GGTAAGTTCA ACAATATCTA AATCTAAATC TCCTTTTAAA

1801 GATTCAAAAA TTATTGGGGA AATCGGTTTG GGAAGTGGTG TTGCTGCAGG

1851 AGTAGAAAAA ACAATATACA TAGGTAACAT AAAAGATATT GATAAATTTA

1901 TTAGTGCAAA CATAAAAAAA TAG
```

[0342] This corresponds to the amino acid sequence <SEQ ID 20; ORF49-1>:

```
   1 MQLLAAEGIH QHQLNVQKST RFIGIKVGKS NYSKNELNET KLPVRVIAQT

  51 AKTRSGWDTV LEGTEFKTTL SGADIQAGVG EKARADAKII LKGIVNRIQT

 101 EEKLESNSTV WQKQAGSGST VETLKLPSFE GPALPKLTAP GGYIADIPKG

 151 NLKTEIEKLA KQPEYAYLKQ LQTVKDVNWN QVQLAYDKWD YKQEGLTGAG

 201 AAIIALAVTV VTSGAGTGAV LGLNGAAAAA TDAAFASLAS QASVSFINNK

 251 GNIGNTLKEL GRSSTVKNLM VAVATAGVAD KIGASALNNV SDKQWINNLT

 301 VNLANAGSAA LINTAVNGGS LKDNLEANIL AALVNTAHGE AASKIKQLDQ

 351 HYIAHKIAHA IAGCAAAAAN KGKCQDGAIG AAVGEILGET LLDGRDPGSL

 401 NVKDRAKIIA KAKLAAGAVA ALSKGDVSTA ANAAAVAVEN NSLNDIQDRL

 451 LSGNYALCNS AGGAESFCES YRPLGLPHFV SVSGENKLPN KFGNRNVNGK

 501 LIINTRNGNV YFSVGKIWST VKSTKSNISG VSVGWVLNVS PNDYLKEASM

 551 NDFRNSNQNK AYAEMISQTL VGESVGGSLC LTRACFSVSS TISKSKSPFK

 601 DSKIIGEIGL GSGVAAGVEK TIYIGNIKDI DKFISANIKK *
```

[0343] Computer analysis predicts a transmembrane domain and also indicates that ORF49 has no significant amino acid homology with known proteins. A corresponding ORF from *N. meningitidis* strain A was, however, identified:

[0344] ORF49 shows 86.1% identity over a 173 aa overlap with an ORF (ORF49a) from strain A of *N. meningitidis*:

```
                                                  10        20        30
orf49.pep                                       GTEFKTTLSGADIQAGVGEKARADAKIILK
                                                ||||||||:|||||||| ||||:|||||||
orf49a    SKNELNETKLPVRVVAQXAATRSGWDTVLEGTEFKTTLAGADIQAGVXEKARVDAKIILK
               40        50        60        70        80        90

                  40        50        60        70        80        90
orf49.pep GIVNRIQTEEKLESNSTVWQKQAGSGSTVETLKLPSFEGPALPKLTAPGGYIADIPKGNL
          |||||||:|||||:|||||||||| |||:|||||||||:|: |||:|||||||:|||||||
orf49a    GIVNRIQSEEKLETNSTVWQKQAGRGSTIETLKLPSFESPTPPKLSAPGGYIVDIPKGNL
               100       110       120       130       140       150

                 100       110       120       130       140       150
orf49.pep KTEIEKLAKQPEYAYLKQLQTVKDVNWNQVQLAYDKWDYKQEGLTGAGAAIXALAVTVVT
          |||||||:|||||||||||||::|::||||||||||:||||||||| ||||| ||||||||
orf49a    KTEIEKLSKQPEYAYLKQLQVAKNINWNQVQLAYDRWDYKQEGLTEAGAAIIALAVTVVT
               160       170       180       190       200       210

                 160       170
```

-continued

```
orf49.pep SGAGTGAVLGLXRVAAAATDAAF
          |||||||||||  : ||||||||
orf49a    SGAGTGAVLGLNGAXAAATDAAFASLASQASVSFINNKGDVGKTLKELGRSSTVKNLVVA
               220       230       240       250       260       270
```

[**0345**] ORF49-1 and ORF49a show 83.2% identity in 457 aa overlap:

```
orf49a.pep  XQLLAEEGIHKHELDVQKSRRFIGIKVGXSNYSKNELNETKLPVRVVAQXAATRSGWDTV
             |||| ||||:|:|:|||| |||||||| ||||||||||||||||:||:| ||||||||
orf49-1     MQLLAAEGIHQHQLNVQKSTRFIGIKVGKSNYSKNELNETKLPVRVIAQTAKTRSGWDTV

orf49a.pep  LEGTEFKTTLAGADIQAGVXEKARVDAKIILKGIVNRIQSEEKLETNSTVWQKQAGRGST
            ||||||||||:|||||||| ||||:|||||||||||||:|||||:|||||||||| |||
orf49-1     LEGTEFKTTLSGADIQAGVGEKARADAXIILKGIVNRIQTEEKLESNSTVWQKQAGSGST

orf49a.pep  IETLKLPSFESPTPPKLSAPGGYIVDIPKGNLKTEIEKLSKQPEYAYLKQLQVAKNINWN
            :|||||||||:|: |||:||||||:|||||||||||||:||||||||||::|::|||
orf49-1     VETLKLPSFEGPALPKLTAPGGYIADIPKGNLKTEIEKLAKQPEYAYLKQLQTVKDVNWN

orf49a.pep  QVQLAYDRWDYKQEGLTEAGAAIIALAVTVVTSGAGTGAVLGLNGAXAAATDAAFASLAS
            |||||||:||||||||| |||||||||||||||||||||||||||| ||||||||||||
orf49-1     QVQLAYDKWDYKQEGLTGAGAAIIALAVTVVTSGAGTGAVLGLNGAAAAATDAAFASLAS

orf49a.pep  QASVSFINNKGDVGKTLKELGRSSTVKNLVVAAATAGVADKIGASALXNVSDKQWINNLT
            ||||||||||::|:|||||||||||||:||:||||||||||||| ||||||||||||
orf49-1     QASVSFINNKGNIGNTLKELGRSSTVKNLMVAVATAGVADKIGASALNNVSDKQWINNLT

orf49a.pep  VNLANAGSAALINTAVNGGSLKDXLEANILAALVNTAHGEAASKIKQLDQHYIVHKIAHA
            |||||||||||||||||||||| |||||||||||||||||||||||||||||:||||||
orf49-1     VNLANAGSAALINTAVNGGSLKDNLEANILAALVNTAHGEAASKIKQLDQHYIAHKIAHA

orf49a.pep  IAGCAAAAANKGKCQDGAIGAAVGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVS
            |||||||||||||||||||||||||||||:||:| :|::| :|::|:| :|:|: :||:||:|:
orf49-1     IAGCAAAAANKGKCQDGAIGAAVGEILGETLLDGRDPGSLNVKDRAKIIAKAKLAAGAVA

orf49a.pep  GVVGGDVNAAANAAEVAVKNNQLSDXEGREFDNEMTACAKQNXPQLCRKNTVKKYQNVAD
            ::  |||::||||| |||:||:|:| : | :::::: |
orf49-1     ALSKGDVSTAANAAAVAVENNSLNDIQDRLLSGNYALCMSAGGAESFCESYRPLGLPHFV

orf49a.pep  KRLAASIAICTDISRSTECRTIRKQHLIDSRSLHSSWEAGLIGKDDEWYKLFSKSYTQAD

orf49-1     SVSGEMKLPNKFGNRMVNGKLIINTRNGNVYFSVGKIWSTVKSTKSNISGVSVGWVLNVS
```

[**0346**] The complete length ORF49a nucleotide sequence <SEQ ID 21> is:

```
   1 NTGCAACTGC TGGCAGAAGA AGGCATCCAC AAGCACGAGT TGGATGTCCA

  51 AAAAAGCCGC CGCTTTATCG GCATCAAGGT AGGTNAGAGC AATTACAGTA

 101 AAAACGAACT GAACGAAACC AAATTGCCTG TCCGCGTCGT CGCCCAAANT

 151 GCAGCCACCC GTTCAGGCTG GGATACCGTG CTCGAAGGTA CCGAATTCAA

 201 AACCACGCTG GCCGGTGCCG ACATTCAGGC AGGTGTANGC GAAAAAGCCC

 251 GTGTCGATGC GAAAATTATC CTCAAAGGCA TTGTGAACCG TATCCAGTCG

 301 GAAGAAAAAT TAGAAACCAA CTCAACCGTA TGGCAGAAAC AGGCCGGACG

 351 CGGCAGCACT ATCGAAACGC TAAAACTGCC CAGCTTCGAA AGCCCTACTC

 401 CGCCCAAATT GTCCGCACCC GGCGGNTATA TCGTCGACAT TCCGAAAGGC

 451 AATCTGAAAA CCGAAATCGA AAAGCTGTCC AAACAGCCCG AGTATGCCTA
```

-continued

501 TCTGAAACAG CTCCAAGTAG CGAAAAACAT CAACTGGAAT CAGGTGCAGC

551 TTGCTTACGA CAGATGGGAC TACAAACAGG AGGGCTTAAC CGAAGCAGGT

601 GCGGCGATTA TCGCACTGGC CGTTACCGTG GTCACCTCAG GCGCAGGAAC

651 CGGAGCCGTA TTGGGATTAA ACGGTGCGNC CGCCGCCGCA ACCGATGCAG

701 CATTCGCCTC TTTGGCCAGC CAGGCTTCCG TATCGTTCAT CAACAACAAA

751 GGCGATGTCG GCAAAACCCT GAAAGAGCTG GGCAGAAGCA GCACGGTGAA

801 AAATCTGGTG GTTGCCGCCG CTACCGCAGG CGTAGCCGAC AAAATCGGCG

851 CTTCGGCACT GANCAATGTC AGCGATAAGC AGTGGATCAA CAACCTGACC

901 GTCAACCTAG CCAATGCGGG CAGTGCCGCA CTGATTAATA CCGCTGTCAA

951 CGGCGGCAGC CTGAAAGACA NTCTGGAAGC GAATATCCTT GCGGCTTTGG

1001 TCAATACCGC GCATGGAGAA GCAGCCAGTA AAATCAAACA GTTGGATCAG

1051 CACTACATAG TCCACAAGAT TGCCCATGCC ATAGCGGGCT GTGCGGCAGC

1101 GGCGGCGAAT AAGGGCAAGT GTCAGGATGG TGCGATAGGT GCGGCTGTGG

1151 GCGAGATAGT CGGGGAGGCT TTGACAAACG GCAAAAATCC TGACACTTTG

1201 ACAGCTAAAG AACGCGAACA GATTTTGGCA TACAGCAAAC TGGTTGCCGG

1251 TACGGTAAGC GGTGTGGTCG GCGGCGATGT AAATGCGGCG GCGAATGCGG

1301 CTGAGGTAGC GGTGAAAAAT AATCAGCTTA GCGACTAAGA GGGTAGAGAA

1351 TTTGATAACG AAATGACTGC ATGCGCCAAA CAGAATANTC CTCAACTGTG

1401 CAGAAAAAAT ACTGTAAAAA AGTATCAAAA TGTTGCTGAT AAAAGACTTG

1451 CTGCTTCGAT TGCAATATGT ACGGATATAT CCCGTAGTAC TGAATGTAGA

1501 ACAATCAGAA AACAACATTT GATCGATAGT AGAAGCCTTC ATTCATCTTG

1551 GGAAGCAGGT CTAATTGGTA AAGATGATGA ATGGTATAAA TTATTCAGCA

1601 AATCTTACAC CCAAGCAGAT TTGGCTTTAC AGTCTTATCA TTTGAATACT

1651 GCTGCTAAAT CTTGGCTTCA ATCGGGCAAT ACAAAGCCTT TATCCGAATG

1701 GATGTCCGAC CAAGGTTATA CACTTATTTC AGGAGTTAAT CCTAGATTCA

1751 TTCCAATACC AAGAGGGITF GTAAAACAAA ATACACCTAT TACTAATGTC

1801 AAATACCCGG AAGGCATCAG TTTCGATACA AACCTANAAA GACATCTGGC

1851 AAATGCTGAT GGTTTTAGTC AAGAACAGGG CATTAAAGGA GCCCATAACC

1901 GCACCAATNT TATGGCAGAA CTAAATTCAC GAGGAGGANG NGTAAAATCT

1951 GAAACCCANA CTGATATTGA AGGCATTACC CGAATTAAAT ATGAGATTCC

2001 TACACTAGAC AGGACAGGTA AACCTGATGG TGGATTTAAG GAAATTTCAA

2051 GTATAAAAAC TGTTTATAAT CCTAAAAANT TTTNNGATGA TAAAATACTT

2101 CAAATGGCTC AANATGCTGN TTCACAAGGA TATTCAAAAG CCTCTAAAAT

2151 TGCTCAAAAT GAAAGAACTA AATCAATATC GGAAAGAAAA AATGTCATTC

2201 AATTCTCAGA AACCTTTGAC GGAATCAAAT TTAGANNNTA TNTNGATGTA

2251 AATACAGGAA GAATTACAAA CATTCACCCA GAATAATTTA A

[0347] This encodes a protein having amino acid sequence <SEQ ID 22>:

```
  1 XQLLAEEGIH KHELDVQKSR RFIGIKVGXS NYSKNELNET KLPVRVVAQX
 51 AATRSGWDTV LEGTEFKTTL AGADIQAGVX EKARVOAKII LKGIVNRIQS
101 EEKLETNSTV WQKQAGRGST IETLKLPSFE SPTPPKLSAP GGYIVDIPKG
151 NLKTEIEKLS KQPEYAYLKQ LQVAKNINWN QVQLAYDRWD YKQEGLTEAG
201 AAIIALAVTV VTSGAGTGAV LGLNGAXAAA TORAFASLAS QASVSFINNK
251 GDVGKTLKEL GRSSTVKNLV VAAATAGVAD KIGASALXNV SDKQNINNLT
301 VNLANAGSAA LINTAVNGGS LKDXLEANIL AALVNTAHGE AASKIKQLDQ
351 HYIVHKIAHA IAGCAAAAAN KGKCQDGAIG AAVGEIVGEA LTNGKNPDTL
401 TAKEREQILA YSKLVAGTVS GVVGGDVNAA ANAAEVAVKN NQLSDXEGRE
451 FDWEHTACAK QNXPQLCRXN TVKKYQNVAD KRLAASIAIC TDISRSTECR
501 TIRKQHLIDS RSLHSSWEAG LIGKDDEWYK LFSKSYTQAD LALOSYHLNT
551 AAKSWLQSGN TKPLSEWNSD QGYTLISGVN PRFIPIPRGF VKQNTPITNV
601 KYPEGISFDT NLXRHLATAD GFSQEQGIKG AHNRTNXMAE LNSRGGXVKS
651 ETXTDIEGIT RIKYEIPTLD RTGKPDGGFK EISSIKTVYN FKXFKDDKIL
701 QMAQXAXSQG YSKASKIAQN ERTKSISERK NVIQFSETFD GIKFRXYXDV
751 NTGRITNIHP E
```

[0348] Based on the presence of a putative transmembrane domain, it is predicted that these proteins from *N. meningitidis*, and their epitopes, could be useful antigens for vaccines or diagnostics.

Example 5

[0349] The following partial DNA sequence was identified in *N. meningitidis* SEQ ID 23>

```
  1..CGGATCGTTG TAGGTTTGCG GATTTCTTGC GCCGTAGTCA CCGTAGTCCC
 51  AAGTATAACC CAAGGCTTTG TCTTCGCCTT TCATTCCGAT AAGGGATATG
101  ACGCTTTGGT CGGTATAGCC GTCTTGGGAA CCTTTGTCCA CCCAACGCAT
151  ATCTGCCTGC GGATTCTCAT TGCCGCTTCT TGGCTGCTGA TTTTTCTGCC
201  TTCGCGTTTT TCAACTTCGC GCTTGAGGGC TTCGGCATAT TTGTCGGCCA
251  ACGCCATTTC TTTCGGATGC AGCTGCCTAT TGTTCCAATC TACATTCGCA
301  CCCACCACAG CACCACCACT ACCACCAGTT GCATAG
```

[0350] This corresponds to the amino acid sequence <SEQ ID 24; ORF50>:

```
  1..RIVVGLRISC AVVTVVPSIT QGFVFAFHSD KGYDALVGIA VLGTFVHPTH

 51ICLRILIAAS WLLIFLPSRF STSRLRASAY LSANAISFGC SCLLFQSTFA

101PTTAPPLPPV A*
```

[0351] Computer analysis predicts two transmembrane domains and also indicates that ORF50 has no significant amino acid homology with known proteins.

[0352] Based on the presence of a putative transmembrane domain, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 6

[0353] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 25>

```
   1..AAGTTTGACT TTACCTGGTT TATTCCGGCG GTAATCAAAT ACCGCCGGTT
  51  GTTTTTTGAA GTATTGGTGG TGTCGGTGGT GTTGCAGCTG TTTGCGCTGA
 101  TTACGCCTCT GTTTTTCCAA GTGGTGATGG ACAAGGTGCT GGTACATCGG
 151  GGATTCTCTA CTTTGGATGT GGTGTCGGTG GCTTTGTTGG TGGTGTCGCT
 201  GTTTGAGATT GTGTTGGGCG GTTTGCGGAC GTATCTGTTT GCACATACGA
 251  CTTCACGTAT TGATGTGGAA TTGGGCGCGC GTTTGTTCCG GCATCTGCTT
 301  TCCCTGCCTT TATCCTATTT CGAGCACAGA CGAGTGGGTG ATACGGTGGC
 351  TCGGGTGCGG GAATTGGAGC AGATTCGCAA TTTCTTGACC GGTCAGGCGC
 401  TGACTTCGGT GTTGGATTTG GCGTTTTCGT TTATCTTTCT GGCGGTGATG
 451  TGGTATTACA GCTCCACTCT GACTTGGGTG GTATTGGCTT CGTTG.....
                                  //
1451  ..........  ..........  ..........  ..........  ..........
1501  ..........  ..........  ..........  ..........  ..ATTTGCGC
1551  CAACCGGACG GTGCTGATTA TCGCCCACCG TCTGTCCACT GTTAAAACGG
1601  CACACCGGAT CATTGCCATG GATAAAGGCA GGATTGTGGA AGCGGGAACA
1651  CAGCAGGAAT TGCTGGCGAA CG..AACGGA TATTACCGCT ATCTGTATGA
1701  TTTACAGAAC GGGTAG
```

[0354] This corresponds to the amino acid sequence <SEQ ID 26; ORF39>:

```
1   ..KFDFTWFIPA VIKYRRLFFE VLVVSVVLQL FALITPLFFQ VVMDKVLVHR
51    GFSTLDVVSV ALLVVSLFEI VLGGLRTYLF AHTTSRIDVE LGARLFRHLL
101   SLPLSYFEHP RVGDTVARVR ELEQIRNFLT GQALTSVLDL AFSFIFLAVM
151   WYYSSTLTWV VLASL..... ..........  ..........  ..........
                              //
501   ..........  ....ICANRT VLIIAHRLST VKTAHRIIAH DKGRIVEAGT
551   QQELLANXNG YYRYLYDLQN G*
```

[0355] Further work revealed the complete nucleotide sequence <SEQ ID 27>:

```
   1 ATGTCTATCG TATCCGCACC GCTCCCCGCC CTTTCCGCCC TCATCATCCT
  51 CGCCCATTAC CACGGCATTG CCGCCAATCC TGCCGATATA CAGCATGAAT
 101 TTTGTACTTC CGCACAGAGC GATTTAAATG AAACGCAATG GCTGTTAGCC
```

-continued

151 GCCAAATCTT TGGGATTGAA GGCAAAGGTA GTCCGCCAGC CTATTAAACG

201 TTTGGCTATG GCGACTTTAC CCGCATTGGT ATGGTGTGAT GACGGCAACC

251 ATTTCATTTT GGCCAAAACA GACGGTGAGG GTGAGCATGC CCAATTTTFG

301 ATACAGGATT TGGTTACGAA TAAGTCTGCG GTATTGTCTT TTGCCGAATT

351 TTCTAACAGA TATTCGGGCA AACTGATATT GGTTGCTTCC CGCGCTTCGG

401 TATTGGGCAG TTTGGCAAAG TTTGACTTTA CCTGGTTTAT TCCGGCGGTA

451 ATCAAATACC GCCGGTTGTT TTTTGAAGTA TTGGTGGTGT CGGTGGTGTT

501 GCAGCTGTTT GCGCTGATTA CGCCTCTGTT TTTCCAAGTG GTGATGGACA

551 AGGTGCTGGT ACATCGGGGA TTCTCTACTT TGGATGTGGT GTCGGTGGCT

601 TTGTTGGTGG TGTCGCTGTT TGAGATTGTG TTGGGCGGTT TGCGGACGTA

651 TCTGTTTGCA CATACGACTT CACGTATTGA TGTGGAATTG GGCGCGCGTT

701 TGTTCCGGCA TCTGCTTTCC CTGCCTTTAT CCTATTTCGA GCACAGACGA

751 GTGGGTGATA CGGTGGCTCG GGTGCGGGAA TTGGAGCAGA TTCGCAATTT

801 CTTGACCGGT CAGGCGCTGA CTTCGGTGTT GGATTTGGCG TTTTCGTTTA

951 TCTTTCTGGC GGTGATGTGG TATTACAGCT CCACTCTGAC TTGGGTGGTA

901 TTGGCTTCGT TGCCTGCCTA TGCGTTTTGG TCGGCATTTA TCAGTCCGAT

951 ACTGCGGACG CGTCTGAACG ATAAGTTCGC GCGCAATGCA GACAACCAGT

1001 CGTTTTTAGT AGAAAGCATC ACTGCGGTGG GTACGGTAAA GGCGATGGCG

1051 GTGGAGCCGC AGATGACGCA GCGTTGGGAC AATCAGTTGG CGGCTTATGT

1101 GGCTTCGGGA TTTCGGGTAA CGAAGTTGGC GGTGGTCGGC CAGCAGGGGG

1151 TGCAGCTGAT TCAGAAGCTG GTGACGGTGG CGACGTTGTG GATTGGCGCA

1201 CGGCTGGTAA TTGAGAGCAA GCTGACGGTG GGGCAGCTGA TTGCGTTTAA

1251 TATGCTCTCG GGACACGTGG CGGCGCCTGT TATCCGTTTG GCGCAGTTGT

1301 GGCAGGATTT CCAGCAGGTG GGGATTTCGG TGGCGCGTTT GGGGGATATT

1351 CTGAATGCGC CGACCGAGAA TGCGTCTTCG CATTTGGCTT TGCCCGATAT

1401 CCGGGGGGAG ATTACGTTCG AACATGTCGA TTTCCGCTAT AAGGCGGACG

1451 GCAGGCTGAT TTTGCAGGAT TTGAACCTGC GGATTCCGGC GGGGGAAGTG

1501 CTGGGGATTG TGGGACGTTC GGGGTCGGGC AAATCCACAC TCACCAAATT

1551 GGTGCAGCGT CTGTATGTAC CGGAGCAGGG ACGGGTGTTG GTGGACGGCA

1601 ACGATTTGGC TTTGGCCGCT CCTGCCTGGC TGCGGCGGCA GGTCGGCGTG

1651 GTCTTGCAGG AGAATGTGCT GCTCAACCGC AGCATACGCG ACAATATCGC

1701 GCTGACGGAT ACGGGTATGC CGCTGGAACG CATTATCGAA GCAGCCAAAC

1751 TGGCGGGCGC ACACGAGTTT ATTATGGAGC TGCCGGAAGG CTACGGCACC

1801 GTGGTGGGCG AACAAGGGGC CGGCTTGTCG GGCGGACAGC GGCAGCGTAT

1951 TGCGATTGCC CGCGCGTTAA TCACCAATCC GCGCATTCTG ATTTTTGATG

1901 AAGCCACCAG CGCGCTGGAT TATGAAAGTG AACGAGCGAT TATGCAGAAC

1951 ATGCAGGCCA TTTGCGCCAA CCGGACGGTG CTGATTATCG CCCACCGTCT

2001 GTCCACTGTT AAAACGGCAC ACCGGATCAT TGCCATGGAT AAAGGCAGGA

-continued

```
2051 TTGTGGAAGC GGGAACACAG CAGGAATTGC TGGCGAAGCC GAACGGATAT

2101 TACCGCTATC TGTATGATTT ACAGAACGGG TAG
```

[0356] This corresponds to the amino acid sequence <SEQ ID 28; ORF39-1>:

```
   1 MSIVSAPLPA LSALIILAMY HGIAANPADI QHEFCTSAQS DLNETQWLLA

  51 AKSLGLKAKV VRQPIKRLAM ATLPALVWCD DGNHFILAKT DGEGEHAQFL

 101 IQDLVTNKSA VLSFAEFSNR YSGKLILVAS RASVLGSLAK FDFTWFIPAV

 151 IKYRRLFFEV LVVSVVLQLF ALITPLFFQV VMDKVLVHRG FSTLDVVSVA

 201 LLVVSLFEIV LGGLRTYLFA HTTSRIDVEL GARLFRHLLS LPLSYFEHPA

 251 VGDTVARVRE LEQIRNFLTG QALTSVLDLA FSFIFLAVMW YYSSTLTWVV

 301 LASLPAYAFW SAFISPILRT RLNDKFAPNA DNQSFLVESI TAVGTVKAMA

 351 VEPQHTQRWD NQLAAYVASG FRVTKLAVVG QQGVQLIQKL VTVATLWIGA

 401 RLVIESRLTV GQLIAFNMLS GQVAAPVIRL AQLWQDFQQV GISVARLGDI

 451 VVAPTENASS HLALPDIRGE ITFEHVDFRY KADGRLILQD LNLRIRAGEV

 501 LGIVGRSGSG KSTLTKLVQR LYVPEQGRVL VDGNDLALAA PAWLRRQVGV

 551 VLQENVLLNR SIRDNIALTD TGNPLERIIE AAKLAGAHEF IMELPEGYGT

 601 VVGEQGAGLS GGQRQRIAIA RALITNPRIL IFDEATSALD YESERAINQN

 651 MQAICANRTV LIIAHRLSTV KTAHRIIAND KGRIVEAGTQ QELLAKPNGY

 701 YRYLYDLQNG *
```

[0357] Computer analysis of this amino acid sequence gave the following results:

[0358] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[0359] ORF39 shows 100% identity over a 165 aa overlap with an ORF (ORF39a) from strain A of *N. meningitidis*:

```
                                              10        20        30
orf39.pep                                   KFDFTWFIPAVIKYRRLFFEVLVVSVVLQL
                                            ||||||||||||||||||||||||||||||
orf39a      AVLSFAEFSNRYSGKLILVASRASVLGSLAKFDFTWFIPAVIKYRRLFFEVLVVSVVLQL
          110       120       130       140       150       160

                    40        50        60        70        80        90
orf39.pep   FALITPLFFQVVMDKVLVHRGFSTLDVVSVALLVVSLFEIVLGGLRTYLFAHTTSRIDVE
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      FALITPLFFQVVMDKVLVHRGFSTLDVVSVALLVVSLFEIVLGGLRTYLFAHTTSRIDVE
          170       180       190       200       210       220

                  100       110       120       130       140       150
orf39.pep   LGARLFRHLLSLPLSYFEHRRVGDTVARVRELEQIRNFLTGQALTSVLDLAFSFIFLAVM
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      LGARLFRHLLSLPLSYFEHRRVGDTVARVRELEQIRNFLTGQALTSVLDLAFSFIFLAVM
          230       240       250       260       270       280
```

-continued

```
                  160       170       180       190       200       210
orf39.pep   WYYSSTLTWVVLASLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXICANRTVLIIAHRLSTV
            ||||||||||||||||
orf39a      WYYSSTLTWVVLASLPAYAFWSAFISPILRTRLNDKFARNADNQSFLVESITAVGTVKAM
          290       300       310       320       330       340
```

[0360] ORF39-1 and ORF39a show 99.4% identity in 710 aa overlap:

```
orf39-1.pep MSIVSAPLPALSALIILAHYHGIAANPADIQHEFCTSAQSDLNETQWLLAAKSLGLKAKV
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      MSIVSAPLPALSALIILAHYHGIAANPADIQHEFCTSAQSDLNETQWLLAAKSLGLKAKV

orf39-1.pep VRQPIKRLAMATLPALVWCDDGNHFILAKTDGEGEHAQFLIQDLVTNKSAVLSFAEFSNR
            |||||||||||||||||||||||||||||| ||||:|||||:|||||||||||||||
orf39a      VRQPIKRLAMATLPALVWCDDGNHFILAKTDGGGEHAQYLIQDLTTNKSAVLSFAEFSNR

orf39-1.pep YSGKLILVASRASVLGSLAKFDFTWFIPAVIKYRRLFFEVLVVSVVLQLFALITPLFFQV
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      YSGKLILVASRASVLGSLAKFDFTWFIPAVIKYRRLFFEVLVVSVVLQLFALITPLFFQV

orf39-1.pep VMDKVLVHRGFSTLDVVSVALLVVSLFEIVLGGLRTYLFAHTTSRIDVELGARLFRHLLS
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      VMDKVLVHRGFSTLDVVSVALLVVSLFEIVLGGLRTYLFAHTTSRIDVELGARLFRHLLS

orf39-1.pep LPLSYFEHRRVGDTVARVRELEQIRNFLTGQALTSVLDLAFSFIFLAVMWYYSSTLTWVV
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      LPLSYFEHRRVGDTVARVRELEQIRNFLTGQALTSVLDLAFSFIFLAVMWYYSSTLTWVV

orf39-1.pep LASLPAYAFWSAFISPILRTRLNDKFARNADNQSFLVESITAVGTVKAMAVEPQMTQRWD
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      LASLPAYAFWSAFISPILRTRLNDKFARNADNQSFLVESITAVGTVKAMAVEPQMTQRWD

orf39-1.pep NQLAAQVASGFRVTKLAVVGQQGVQLIQKLVTVATLWIGARLVIESKLTVGQLIAFNMLS
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      NQLAAQVASGFRVTKLAVVGQQGVQLIQKLVTVATLWIGARLVIESKLTVGQLIAFNMLS

orf39-1.pep GQVAAPVIRLAQLWQDFQQVGISVARLGDILNAPTENASSHLALPDIRGEITFEHVDFRY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      GQVAAPVIRLAQLWQDFQQVGISVARLGDILNAPTENASSHLALPDIRGEITFEHVDFRY

orf39-1.pep KADGRLILQDLNLRIRAGEVLGIVGRSGSGKSTLTKLVQRLYVPEQGRVLVDGNDLALAA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      KADGRLILQDLNLRIRAGEVLGIVGRSGSGKSTLTKLVQRLYVPEQGRVLVDGNDLALAA

orf39-1.pep PAWLRRQVGVVLQENVLLNRSIRDNIALTDTGMPLERIIEAAKLAGAHEFIHELPEGYGT
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      PAWLRRQVGVVLQENVLLNRSIRDNIALTDTGMPLERIIEAAKLAGAHEFIHELPEGYGT

orf39-1.pep VVGEQGAGLSGGQRQRIAIARALITNPRILIFDEATSALDYESERAIMQNMQAICANRTV
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      VVGEQGAGLSGGQRQRIAIARALITNPRILIFDEATSALDYESERAIMQNMQAICANRTV

orf39-1.pep LIIAHRLSTVKTAHRIIAMDKGRIVEAGTQQELLAKPNGYYRYLYDLQNGX
            ||||||||||||||||||||||||||||||||||||||||||||||||||
orf39a      LIIAHRLSTVKTAHRIIAMDKGRIVEAGTQQELLAKPNGYYRYLYDLQNGX
```

[0361] The complete length ORF39a nucleotide sequence <SEQ ID 29> is:

```
   1 ATGTCTATCG TATCCGCACC GCTCCCCGCC CTTTCCGCCC TCATCATCCT

  51 CGCCCATYAC CACGGCATTG CCGCCAATCC TGCCGATATA CAGCATGAAT

 101 TTTGTACTTC CGCACAGAGC GATTTAAATG AAACGCAATG GCTGTTAGCC

 151 GCCAAATCTT TGGGATTGAA GGCAAAGGTA GTCCGCCAGC CTATTAAACG

 201 TTTGGCTATG GCGACTTTAC CCGCATTGGT ATGGTGTGAT GACGGCAACC
```

-continued

```
 251 ATTTTATTTT GGCTAAAACA GACGGTGGGG GTGAGCATGC CCAATATCTA
 301 ATACAGGATT TAACTACGAA TAAGTCTGCG GTATTGTCTT TTGCCGAATT
 351 TTCTAACAGA TATTCGGGCA AACTGATATT GGTTGCTTCC CGCGCTTCGG
 401 TATTGGGCAG TTTGGCAAAG TTTGACTTTA CCTGGTTTAT TCCGGCGGTA
 451 ATCAAATACC GCCGGTTGTT TTTTGAAGTA TTGGTGGTGT CGGTGGTGTT
 501 GCAGCTGTTT GCGCTGATTA CGCCTCTGTT TTTCCAAGTG GTGATGGACA
 551 AGGTGCTGGT ACATCGGGGA TTCTCTATTT TGGATGTGGT GTCGGTGGCT
 601 TTGTTGGTGG TGTCGCTGTT TGAGATTGTG TTGGGCGGTT TGCGGACGTA
 651 TCTGTTTGCA CATACGACTT CACGTATTGA TGTGGAATTG GGCGCGCGTT
 701 TGTTCCGGCA TCTGCTTTCC CTGCCTTTAT CCTATTTCGA GCACAGACGA
 751 GTGGGTGATA CGGTGGCTCG GGTGCGGGAA TTGGAGCAGA TTCGCAATTT
 801 CTTGACCGGT CAGGCGCTGA CTTCGGTGTT GGATTTGGCG TTTTCGTTTA
 951 TCTTTCTGGC GGTGATGTGG TATTACAGCT CCACTCTGAC TTGGGTGGTA
 901 TTGGCTTCGT TGCCTGCCTA TGCGTTTTGG TCGGCATTTA TCAGTCCGAT
 951 ACTGCGGACG CGTCTGAACG ATAAGTTCGC GCGCAATGCA GACAACCAGT
1001 CGTTTTTAGT AGAAAGCATC ACTGCGGTGG GTACGGTAAA GGCGATGGCG
1051 GTGGAGCCGC AGATGACGCA GCGTTGGGAC AATCAGTTGG CGGCTTATGT
1101 GGCTTCGGGA TTTCGGGTAA CGAAGTTGGC GGTGGTCGGC CAGCAGGGGG
1151 TGCAGCTGAT TCAGAAGCTG GTGACGGTGG CGACGTTGTG GATTGGCGCA
1201 CGGCTGGTAA TTGAGAGCAA GCTGACGGTG GGGCAGCTGA TTGCGTTTAA
1251 TATGCTCTCG GGACAGGTGG CGGCGCCTGT TATCCGTTTG GCGCAGTTGT
1301 GGCAGGATTT CCAGCAGGTG GGGATTTCGG TGGCGCGTTT CGGGGATATT
1351 CTGAATGCGC CGACCGAGAA TGCGTCTTCG CATTTGGCTT TGCCCGATAT
1401 CCGGGGGGAG ATTACGTTCG AACATGTCGA TTTCCGCTAT AAGGCGGACG
1451 GCAGGCTGAT TTTGCAGGAT TTGAACCTGC GGATTCGGGC GGGGGAAGTG
1501 CTGGGGATTG TGGGACGTTC GGGGTCGGGC AAATCCACAC TCACCAAATT
1551 GGTGCAGCGT CTGTATGTAC CGGCGCAGGG ACGGGTGTTG GTGGACGGCA
1601 ACGATTTGGC TTTGGCCGCT CCTGCTTGGC TGCGGCGGCA GGTCGGCGTG
1651 GTCTTGCAGG AGAATGTGCT GCTCAACCGC AGCATACGCG ACAATATCGC
1701 GCTGACGGAT ACGGGTATGC CGCTGGAACG CATTATCGAA GCAGCCAAAC
1751 TGGCGGGCGC ACACGAGTTT ATTATGGAGC TGCCGGAAGG CTACGGCACC
1801 GTGGTGGGCG AACAAGGGGC CGGCTTGTCG GGCGGACAGC GGCAGCGTAT
1851 TGCGATTGCC CGCGCGTTAA TCACCAATCC GCGCATTCTG ATTTTTGATG
1901 AAGCCACCAG CGCGCTGGAT TATGAAAGTG AACGAGCGAT TATGCAGAAC
1951 ATGCAGGCCA TTTGCGCCAA CCGGACGGTG CTGATTATCG CCCACCGTCT
2001 GTCCACTGTT AAAACGGCAC ACCGGATCAT TGCCATGGAT AAAGGCAGGA
2051 TTGTGGAAGC GGGAACACAG CAGGAATTGC TGGCGAAGCC GAACGGATAT
2101 TACCGCTATC TGTATGATTT ACAGAACGGG TAG
```

[0362] This encodes a protein having amino acid sequence <SEQ ID 30>:

```
   1 MSIVSAPLPA LSALIILAHY HGIAANPADI QHEFCTSAQS DLNETQWLLA

  51 AKSLGLKAKV VRQPIKRLAN ATLPALVWCD DGNHFILAKT DGGGEHAQYL

 101 IQDLTTNKSA VLSFAEFSNR YSGKLILVAS RASVIASLAX FDFTWFIPAV

 151 IKYRRLFFEV LVVSVVLQLF ALITPLFFQV VNDKVLVHRG FSTLDVVSVA

 201 LLVVSLFEIV LGGLRTYLFA HTTSRIDVEL GARLFRHLLS LPLSYFEHRR

 251 VGDTVARVRE LEQIRNFLTG QALTSVLDLA FSFIFLAVMW YYSSTLTWVV

 301 LASLPAYAFW SAFISPILRT RLNDKFARNA ONQSFLVESI TAVGTVKAMA

 351 VEPQNTQRWD NQLAAYVASG FRVTKLAVVG QQGVQLIQKL VTVATLWIGA

 401 RLVIESKLTV GQLIAFNHLS GQVAAPVIRL AQLWQOFQQV GISVARLGDI

 451 LNAPTENASS HLALPDIRGE ITFEHVDFRY KADGRLILQD LNLRIRAGEV

 501 LGIVGRSGSG KSTLTKLVQR LYVPAQGRVL VDGNDLALAA PAWLREQVGV

 551 VLQENVLLNR SIRDNIALTD TGMPLERIIE AAKLAGAHEF IHPLPEGYGT

 601 VVGEQGAGLS GGQRQRIAIA RALITNPRIL IFDEATSALD YESERAIMQN

 651 NQAICANRTV LIIAHRLSTV KTAMRIIAMD KGRIVEAGTQ QELLAKPNGY

 701 YRYLYOLQNG *
```

[0363] ORF39a is homologous to a cytolysin from *A. pleuropneumoniae*:

```
sp|P26760|RT1B_ACTPL RTX-I TOXIN DETERMINANT B (TOXIN RTX-I SECRETION ATP-
BINDING PROTEIN) (APX-IB) (HLY-IB) (CYTOLYSIN IB) (CLY-IB)
>gi|97137|pir||D43599 cytolysin IB - Actinobacillus pleuropneumoniae
(serotype 9) >gi|36944 (X61112) ClyI-B protein [Actinobacillus
pleuropneumoniae] Length = 707 Score = 931 bits (2379), Expect =0.0
Identities = 472/690 (68%), Positives = 540/690 (77%),
Gaps = 3/690 (0%)
Query:  20 YHGIAANPADIQHEFCTSAQSDLNETQWXXXXXXXXXXXXVVRQPIKRLAMATLPALVWC 79
           YH IA NP +++H+F    +  L+ T W             V++ I RLA   LPALVW
Sbjct:  20 YHNIAVNPEELKHKFDLEGKG-LDLTAWLLAAKSLELKAKQVKKAIDRLAFIALPALVWR 78

Query:  80 DDGNHFILAKTDGGGEHAQYLIQDLTTNKSAVLSFAEFSNRYSGKLILVASRASVLGSLA 139
           +DG HFIL K D   E  +YLI DL T+   +L  AEF + Y GKLILVASRAS++G LA
Sbjct:  79 EDGKHFILTKIDN--EAKKYLIFDLETHNPRILEQAEFESLYQGKLILVASRASIVGKLA 136

Query: 140 KFDFTWFIPAVIKYRRXXXXXXXXXXXXXXXXXITPLFFQVVMDKVLVHRGFXXXXXXXX 199
           KFDFTWFIPAVIKYR+                 ITPLFFQVVMDKVLVHRGF
Sbjct: 137 KFDFTWFIPAVIKYRKIFIETLIVSIFLQIFALITPLFFQVVMDKVLVHRGFSTLNVITV 196

Query: 200 XXXXXXXFEIVLGGLRTYLFAHTTSRIDVELGARLFRHLLSLPLSYFEHRRVGDTVARVR 259
                 FEIVL GLRTY+FAH+TSRIDVELGARLFRHLL+LP+SYFE+RRVGDTVARVR
Sbjct: 197 ALAIVVLFEIVLNGLRTYIFAHSTSRIDVELGARLFRHLLALPISYFENRRVGDTVARVR 256

Query: 260 ELEQIRNFLTGQALTSVLDLAFSFIFLAVMWYYSSTLTWVVLASLPAYAFWSAFISPILR 319
           EL+QIRNFLTGQALTSVLDL FSFIF AVMWYYS  LT V+L SLP Y  WS FISPILR
Sbjct: 257 ELDQIRNFLTGQALTSVLDIMFSFIFFAVMWYYSPKLTLVILGSLPFYNGWSIFISPILR 316

Query: 320 TRLNDKFARNADNQSFLVESITAVGTVKAMAVEPQNTQRWDNQLAAYVASGFRVTKLAVV 379
            RL++KFAR ADNQSFLVES+TA+ T+KA+AV PQMT  WD QLA+YV++GFRVT LA +
Sbjct: 317 RRLDEKFARGADNQSFLVESVTAINTIKALAVTPQMTNTWDKQLASYVSAGFRVTTLATI 376

Query: 380 GQQGVQLIQKLVTVATLWIGARLVIESKLTVGQLIAFNNLSGQVAAPVIRLAQLWQDFQQ 439
           GQQGVQ IQK+V V TLW+GA LVI   L++GQLIAFNNLSGQV APVIRLAQLWQDFQQ
Sbjct: 377 GQQGVQFIQKVVNVITLWLGAMLVISGDLSIGQLIAFNNLSGQVIAPVIRLAQLWQDFQQ 436

Query: 440 VGISVAPLGDILNAPTENASSHLALPDIRGEITFEHVDFRYKADGRLILQDLNLRIRAGE 499
           VGISV RLGD+LN+PTE+    LALP+I+G+ITF ++ FRYX D  +IL D+NL I+ GE
```

-continued

```
Sbjct: 437 VGISVTRLGDVLNSPTESYQGKLALPEIKGDITFRNIRFRYXPDAPVILNDVNLSIQQGE 496

Query: 500 VLGIVGRSGSGKSTLTKLVQRLYVPAOGRVLVDGNDLALAAPAWLRRQVGVVLQENVLLN 559
           V+GIVGRSGSGKSTLTKL+QR Y+P  G+VL+DG+DLALA P WLRRQVGVVLQ+NVLLN
Sbjct: 497 VIGIVGRSGSGKSTLTKLIQRFYIPENGQVLIDGHDLALADPNWLRRQVGVVLQDNVLLN 556

Query: 560 RSIRDNIALTDTGMPLERIIEAAKLAGAIIEFINELPEGYGTVVGEQGNLSGGQRQRIAI 619
           RSIRDNIAL D GMP+E+I+ AAKLAGAHEFI EL EGY T+VGEQGAGLSGGQRQRIAI
Sbjct: 557 RSIRDNIALADPGMPMEKIVHAAKLAGAHEFISELREGYNTIVGEOGAGLSGGQRQRIAI 616

Query: 620 ARALITNPRILIFDEATSALDYESERAIMQNMQAICANRTVLIIAHRLSTVKTAHRIIAM 679
           ARAL+ NP+ILIFDEATSALDYESE IM+NM  IC  RTV+IIAHRLSTVK A RII M
Sbjct: 617 ARALVNNPKILIFDEATSALDYESEHIIMRNMHQICKGRTVIIIAHRLSTVKNADRIIVM 676

Query: 680 DKGRIVEAGTQQELLAKPNGYYRYLYDLQN 709
           +KG+IVE G  +ELLA PNG Y YL+ LQ+
Sbjct: 677 EKGQIVEQGKHKELLADPNGLYHYLHQLQS 706
```

[0364] Homology with the HlyB Leucotoxin Secretion ATP-Binding Protein of *Haemophilus actinomycetemcomitans* (Accession Number X53955)

[0365] ORF39 and HlyB protein show 71% and 69% amino acid identity in 167 and 55 overlap at the N- and C-terminal regions, respectively:

```
Orf39    1 KFDFTWFIPAVIKYRRXXXXXXXXXXXXXXXXXXITPLFFQVVMDKVLVHRGFXXXXXXXX 60
           KFDFTWFIPAVIKYR+                    ITPLFFQVVMDKVLVHRGF
HlyB   137 KFDFTWFIPAVIKYRKIFIETLIVSIFLQIFALITPLFFQVVMDKVLVHRGFSTLNVITV 196

Orf39   61 XXXXXXXFEIVLGGLRTYLFAHTTSRIDVELGARLFRHLLSLPLSYFEHRRVGDTVARVR 120
                 FEI+LGGLRTY+FAH+TSRIDVELGARLFMLL+LP+SYFE RRVGDTVARVR
HlyB   197 ALAIVVLFEIILGGLRTYVFAHSTSRIDVELGARLFRHLLALPISYFEARRVGDTVARVR 256

Orf39  121 ELEQIRNFLTGQALTSVLDLAFSFIFLAVMWYYSSTLTWVVLASLIC 167
           EL+QIRNFLTGQALTS+LDL FSFIF AVMWYYS  LT VVL SL C
HlyB   257 ELDQIRNFLTGQALTSILDLLFSFIFFAVMWYYSPKLTLVVLGSLPC 303
                                        //

Orf39  166 ICANRTVLIIAHRLSTVKTAHRIIAMDKGRIVEAGTQQELLANXNGYYRYLYDLQ 220
    IC
NRTV-
LII-
AHRL-
STVK A
RII
MDKG
I+E
G  QELL
+  G Y
YL+ LQ
HlyB   651 ICQNRTVLIIAHRLSTVKNADRIIVMDKGEIIEQGKHQELLKDEKGLYSYLHQLQ 705
```

[0366] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 7

[0367] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 31>

```
  1 ATGAAATACT TGATCCGCAC CGCCTTACTC GCAGTCGCAG CCGCCGGCAT

 51 CTACGCCTGC CAACCGCAAT CCGAAGCCGC AGTGCAAGTC AAGGCTGAAA
```

-continued

```
101 ACAGCCTGAC CGCTATGCGC TTAGCCGTCG CCGACAAACA GGCAGAGATT

151 GACGGGTTGA ACGCCCAAAk sGACGCCGAA ATCAGA...
```

[0368] This corresponds to the amino acid sequence SEQ ID 32; ORF52>:

```
  1 MKYLIRTALL AVAAAGIYAC QPQSEAAVQV KAZNSLTANR LAVADKQAEI

 51 DGLNAQXDAE IR..
```

[0369] Further work revealed the complete nucleotide sequence <SEQ ID 33>:

```
  1 ATGAAATACT TGATCCGCAC CGCCTTACTC GCAGTCGCAG CCGCCGGCAT

 51 CTACGCCTGC CAACCGCAAT CCGAAGCCGC AGTGCAAGTC AAGGCTGAAA

101 ACAGCCTGAC CGCTATGCGC TTAGCCGTCG CCGACAAACA GGCAGAGATT

151 GACGGGTTGA ACGCCCAAAT CGACGCCGAA ATCAGACAAC GCGAAGCCGA

201 AGAATTGAAA GACTACCGAT GGATACACGG CGACGCGGAA GTGCCGGAGC

251 TGGAAAAATG A
```

[0370] This corresponds to the amino acid sequence <SEQ ID 34; ORF52-1>:

```
  1 MKYLIRTALL AVAAAGIYAC QPQSEAAVQV KAENSLTAMR LAVADKQAEI

 51 DGLNAQIDAE IRQREAEELK DThWIHGDAE VPELEK
```

[0371] Computer analysis of this amino acid sequence predicts a prokaryotic membrane lipoprotein lipid attachment site (underlined).

[0372] ORF52-1 (7 kDa) was cloned in the pGex vectors and expressed in *E. coli*, as described above. The products of protein expression and purification were analyzed by SDS-PAGE. **FIG. 4A** shows the results of affinity purification of the GST-fusion. **FIG. 4B** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF52-1.

[0373] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 8

[0374] The following DNA sequence was identified in *N. meningitidis* <SEQ ID 35>

```
  1 ATGGTTATCG GAATATTACT CGCATCAAGC AAGCATGCTC TTGTCATTAC

 51 TCTATTGTTA AATCCCGTCT TCCATGCATC CAGTTGCGTA TCGCGTTSGG

101 CAATACGGAA TAAAATCTGC TGTTCTGCTT TGGCTAAATT TGCCAAATTG

151 TTTATTGTTT CTTTAGGAGC AGCTTGCTTA GCCGCCTTCG CTTTCGACAA

201 CGCCCCCACA GGCGCTTCCC AAGCGTTGCC TTCCGTTACC GCACCCGTGG

251 CGATTCCCGC GCCCGCTTCG GCAGCCTGA
```

[0375] This corresponds to the amino acid sequence <SEQ ID 36; ORF56>:

```
  1 MVIGILLASS KHALVITLLL NPVFHASSCV SRXAIRNKIC CSALAKFAKL

 51 FIVSLGAACL AAFAFDNAPT GASQALPTVT APVAIPAPAS AA*
```

[0376] Further work revealed the complete nucleotide sequence <SEQ ID 37>:

```
   1 ATGGCTTGTA CAGGTTTGAT GGTTTTTCCG TTAATGGTYA TCGGAATATT

  51 ACTTGCATCA AGCAAGCCTG CTCCTTTCCT TACTCTATTG TTAAATCCCG

 101 TCTTCCATGC ATCCAGTTGC GTATCGCGTT GGGCAATACG GAATAAAATC

 151 TGCTGTTCTG CTTTGGCTAA ATTTGCCAAA TTGTTTATTG TTTCTTTAGG

 201 AGCAGCTTGC TTAGCCGCCT TCGCTTTCGA CAACGCCCCC ACAGGCGCTT

 251 CCCAAGCGTT GCCTACCGTT ACCGCACCCG TGGCGATTCC CGCGCCCGCT

 301 TCGGCAGCCT GA
```

[0377] This corresponds to the amino acid sequence <SEQ ID 38; ORF56-1>:

```
   1 MACTGLMVFP LNVZGILLAS SKPAPFLTLL LNPVFHASSC VSRWAIRNKI

  51 CCSALAKFAK LFIVSLGAAC LAAFAFDNAP TGASQALPTV TAPVAIPAPA

 101 SAA*
```

[0378] Computer analysis of this amino acid sequence predicts a leader peptide (underlined) and suggests that ORF56 might be a membrane or periplasmic protein.

[0379] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 9

[0380] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>

```
   1 ATGTTCAGTA TTTTAAATGT GTTTCTTCAT TGTATTCTGG CTTGTGTAGT

  51 CTCTGGTGAG ACGCCTACTA TATTTGGTAT CCTTGCTCTT TTTTACTTAT

 101 TGTATCTTTC TTATCTTGCT GTTTTTAAGA TTTTCTTTTC TTTTTTCTTA

 151 GACAGAGTTT CACTCCGGTC TCCCAGGCTG GAGTGCAAAT GGCATGACCC

 201 TTTGGCTCAC TGGCTCACGG CCACTTCTGC TATTCTGCCG CCTCAGCCTC

 251 CAGGG...
```

[0381] This corresponds to the amino acid sequence <SEQ ID 40; ORF63>:

```
  1 MFSILNVFLR CILACVVSGE TPTIFGILAL FYLLYLSYLA VFKIFFSFFL

 51 DRVSLRSPRL ECKWNDPLAH WLTATSAILP PQPPG...
```

[0382] Computer analysis of this amino acid sequence predicts a transmembrane region.

[0383] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 10

[0384] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>

```
  1..GTGCGGACGT GGTTGGTTTT TTGGTTGCAG CGTTTGAAAT ACCCGTTGTT

 51   GCTTTGGATT GCGGATATGT TGCTGTACCG GTTGTTGGGC GGCGCGGAAA

101   TCGAATGCGG CCGTTGCCCT GTGCCGCCGA TGACGGATTG GCAGCATTTT

151   TTGCCGGCGA TGGGAACGGT GTCGGCTTGG GTGGCGGTGA TTTGGGCATA

201   CCTGATGATT GAAAGTGAAA AAAACGGAAG ATATTGA
```

[0385] This corresponds to the amino acid sequence <SEQ ID 42; ORF69>:

```
  1 ..VRTWLVFWLQ RLKYPLLLWI ADNLLYRLLG GAE1ECGRCP VPPMTDWQHF

 51   LPANGTVSAW VAVIWAYLMI ESEKNGRY*
```

[0386] Computer analysis of this amino acid sequence predicts a transmembrane region.

[0387] A corresponding ORF from strain A of *N. meningitidis* was also identified:

[0388] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[0389] ORF69 shows 96.2% identity over a 78 aa overlap with an ORF (ORF69a) from strain A of *N. meningitidis*:

```
                  10        20        30        40        50        60
orf69.pep VRTWLVFWLQRLKYPLLLWIADMLLYRLLGGAEIECGRCPVPPMTDWQHFLPAMGTVSAW
          |||||||||||||||||| ||||||||||||||||||||||||||||||:||||:||
orf69a    VRTWLVFWLQRLKYPLLLCIADMLLYRLLGGAEIECGRCPVPPMTDWQHFLPTMGTVAAW
                  10        20        30        40        50        60

                  70        79
orf69.pep VAVIWAYLMIESEKNGRYX
          |||||||||||||||||||
orf69a    VAVIWAYLMIESEKNGRYX
                  70        79
```

[0390] The ORF69a nucleotide sequence <SEQ ID 43> is:

```
   1 GTGCGGACGT GGTTGGTTTT TTGGTTGCAG CGTTTGAAAT ACCCGTTGTT

  51 GCTTTGTATT GCGGATATGC TGCTGTACCG GTTGTTGGGC GGCGCGGAAA

 101 TCGAATGCGG CCGTTGCCCT GTACCGCCGA TGACGGATTG GCAGCATTTT

 151 TTGCCGACGA TGGGAACGGT GGCGGCTTGG GTGGCGGTGA TTTGGGCATA

 201 CCTGATGATT GAAAGTGAAA AAAACGGAAG ATATTGA
```

[0391] This encodes a protein having amino acid sequence <SEQ ID 44>:

```
  1 VRTWLVFWLQ RLKYPLLLCI ADMLLYRLLG GAEIECGRCP VPPNTDWQHF
 51 LPTMGTVAAW VAVIWAYLMI ESEKNGRY*
```

[0392] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 11

[0393] The following DNA sequence was identified in *N. meningitidis* <SEQ ID 45>

```
   1 ATGTTTCAAA ATTTTGATTT GGGCGTGTTC CTGCTTGCCG TCCTCCCCGT
  51 GCTGCCCTCC ATTACCGTCT CGCACGTGGC GCGCGGCTAT ACGGCGCGCT
 101 ACTGGGGAGA CAACACTGCC GAACAATACG GCAGGCTGAC ACTGAACCCC
 151 CTGCCCCATA TCGATTTGGT CGGCACAATC ATCgTACCGC TGCTTACTTT
 201 GATGTTCACG CCCTTCCTGT TCGGCTGGGC GCGTCCGATT CCTATCGATT
 251 CGCGCAACTT CCGCAACCCG cGCCTTGCCT GGCGTTGCGT TGCCGCGTCC
 301 GGCCCGCTGT CGAATCTAGC GATGGCTGTw CTGTGGGGCG TGGTTTTGGT
 351 GCTGACTCCG TATGTCGGCG GGGCGTATCA GATGCCGTTG GCTCAAATGG
 401 CAAACTACGG TATTCTGATC AATGCGATTC TGTTCGCGCT CAACATCATC
 451 CCCATCCTGC CTTGGGACGG CGGCATTTTC ATCGACACCT TCCTGTCGGC
 501 GAAATATTCG CAAGCGTTCC GCAAAATCGA ACCTTATGGG ACGTGGATTA
 551 TCCTACTGCT GATGCTGACC SGGGTTTTGG GTGCGTTTAT wGCACCGATT
 601 sTGCGGmTGc GTGATTGCrT TTGTGCAGAT GTwCGTCTGA CTGGCTTTCA
 651 GACGGCATAA
```

[0394] This corresponds to the amino acid sequence <SEQ ID 46; ORF77>:

```
   1 MFQNFDLGVF LLAVLPVLPS ITVSNVARGY TARYWGDNTA EQYGRLTLNP
  51 LPHIDLVGTI IVPLLTLMFT PFLFGWPRPI PIDSRNFRNP RLAWRCVAAS
 101 GPLSNLAMAV LWGVVLVLTP YVGGAYQMPL AQMANYGILI NAILFPLNII
 151 PILPWDGGIF IDTFLSAKYS QAFRKIEPYG TWIILLLMLT XVLGAFIAPI
 201 XRXRDCXCAD VRLTGFQTA*
```

[0395] Further work revealed the complete nucleotide sequence <SEQ ID 47>:

```
   1 ATGTTTCAAA ATTTTGATTT GGGCGTGTTT CTGCTTGCCG TCCTGCCCGT
  51 GCTGCTCTCC ATTACCGTCA GGGAGGTGGC GCGCGGCTAT ACGGCGCGCT
 101 ACTGGGGAGA CAACACTGCC GAACAATACG GCAGGCTGAC ACTGAACCCC
```

-continued

```
151 CTGCCCCATA TCGATTTGGT CGGCACAATC ATCGTACCGC TGCTTACTTT

201 GATGTTCACG CCCTTCCTGT TCGGCTGGGC GCGTCCGATT CCTATCGATT

251 CGCGCAACTT CCGCAACCCG CGCCTTGCCT GGCGTTGCGT TGCCGCGTCC

301 GGCCCGCTGT CGAATCTAGC GATGGCTGTT CTGTGGGGCG TGGTTTTGGT

351 GCTGACTCCG TATGTCGGCG GGGCGTATCA GATGCCGTTG GCTCAAATGG

401 CAAACTACGG TATTCTGATC AATGCGATTC TGTTCGCGCT CAACATCATC

451 CCCATCCTGC CTTGGGACGG CGGCATTTTC ATCGACACCT TCCTGTCGGC

501 GAAATATTCG CAAGCGTTCC GCAAAATCGA ACCTTATGGG ACGTGGATTA

551 TCCTACTGCT GATGCTGACC GGGGTTTTGG GTGCGTTTAT TGCACCGATT

601 GTGCGGCTGG TGATTGCGTT TGTGCAGATG TTCGTCTGA
```

[0396] This corresponds to the amino acid sequence <SEQ ID 48; ORF77-1>:

```
  1 MFQNFDLGVF LLAVLPVLLS ITVREVARGY TARYWGDNTA EQYGRLTLNP

 51 LPHIDLVGTI IVPLLTLMFT PFLFGWARPI PIDSRNFRNP RLAWRCVAAS

101 GPLSNLAMAV LWGVVLVLTP YVGGAYQMPL AQMANYGILI NAILFALNII

151 PILPWDGGIF IDTFLSAXYS QAYRRIEPYG TWIILLLNLT GVLGAFIAPI

201 VRLVIAFVQH FV*
```

[0397] Computer analysis of this amino acid sequence reveals a putative leader sequence and several transmembrane domains.

[0398] A corresponding ORF from strain A of *N. meningitidis* was also identified:

[0399] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[0400] ORF77 shows 96.5% identity over a 173 aa overlap with an ORF (ORF77a) from strain A of *N. meningitidis:*

```
                 10        20        30        40        50        60
ort77.pep MFQNFDLGVFLLAVLPVLPSITVSHVARGYTARYWGDNTAEQYGRLTLNPLPHIDLVGTI
                                    ||||||||||||||||||||||||||||||||||
orf77a                              RGYTARYWGDNTAEQYGRLTLNPLPHIDLVGTI
                                           10        20        30

                 70        80        90       100       110       120
orf77.pep IVPLLTLMFTPFLFGWARPIPIDSRNFRNPRLAWRCVAASGPLSNLAMAVLWGVVLVLTP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf77a    IVPLLTLMFTPFLFGWARPIPIDSRNFRNPRLAWRCVAASGPLSNLAMAVLWGVVLVLTP
               40        50        60        70        80        90

                130       140       150       160       170       180
orf77.pep YVGGAYQMPLAQMANYGILINAILFALNIIPILPWDGGIFIDTFLSAKYSQAFRKIEPYG
          ||||||||||||||| ||||||| |||||||||||||||||||| ||||||||||||
orf77a    YVGGAYQMPLAQMANYXILINAILXALNIIPILPWDGGIFIDTFLSAKXSQAFRKIEPYG
              100       110       120       130       140       150
```

-continued

```
                190       200       210       220
orf77.pep TWIILLLMLTGVLGAFIAPIVRLVIAFVQMFVX
          |||| |||||||||| |||||:||||||||||||
orf77a    TWIIXLLMLTGVLGAXIAPIVQLVIAFVQMFVX
              160       170       180
```

[0401] ORF77-1 and ORF77a show 96.8% identity in 185 aa overlap:

```
                    10        20        30        40        50        60
orf77-1.pep MFQNFDLGVFLLAVLPVLLSITVREVARGYTARYWGDNTAEQYGRLTLNPLPHIDLVGTI
                                        ||||||||||||||||||||||||||||||||||
orf77a                                  RGYTARYWGDNTAEQYGRLTLNPLPHIDLVGTI
                                                10        20        30

                    70        80        90       100       110       120
orf77-1.pep IVPLLTLMFTPFLFGWARPIPIDSRNFRNPRLAWRCVAASGPLSNLAMAVLWGVVLVLTP
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf77a      IVPLLTLMFTPFLFGWARPIPIDSRNFRNPRLAWRCVAASGPLSNLAMAVLWGVVLVLTP
                 40        50        60        70        80        90

                   130       140       150       160       170       180
orf77-1.pep YVGGAYQMPLAQMANYGILINAILFALNIIPILPWDGGIFIDTFLSAKYSQAFRKIEPYG
            |||||||||||||||| ||||||| ||||||||||||||||||||| ||||||||||||
orf77a      YVGGAYQMPLAQMANYXILINAILXALNIIPILPWDGGIFIDTFLSAKXSQAFRKIEPYG
                100       110       120       130       140       150

                   190       200       210
orf77-1.pep TWIILLLMLTGVLGAFIAPIVRLVIAFVQMFVX
            |||| |||||||||| |||||:||||||||||||
orf77a      TWIIXLLMLTGVLGAXIAPIVQLVIAFVQMFVX
                160       170       180
```

[0402] A partial ORF77a nucleotide sequence <SEQ ID 49> was identified:

```
  1  ..CGCGGCTATA CAGCGCGCTA CTGGGGTGAC AACACTGCCG AACAATACGG

 51  CAGGCTGACA CTGAACCCCC TGCCCCATAT CGATTTGGTC GGCACAATCA

101  TCGTACCGCT GCTTACTTTG ATGTTTACGC CCTTCCTGTT CGGCTGGGCG

151  CGTCCGATTC CTATCGATTC GCGCAACTTC CGCAACCCGC GCCTTGCCTG

201  GCGTTGCGTT GCCGCGTCCG GCCCGCTGTC GAATCTGGCG ATGGCTGTTC

251  TGTGGGGCGT GGTTTTGGTG CTGACTCCGT ATGTCGGTGG GGCGTATCAG

301  ATGCCGTTGG CNCAAATGGC AAACTACNNN ATTCTGATCA ATGCGATTCT

351  GTNCGCGCTC AACATCATCC CCATCCTGCC TTGGGACGGC GGCATTTTCA

401  TCGACACCTT CCTGTCGGCN AAATANTCGC AAGCGTTCCG CAAAATCGAA

451  CCTTATGGGA CGTGGATTAT CCNGCTGCTT ATGCTGACCG GGGTTTTGGG

501  TGCGTNTATT GCACCGATTG TGCAGCTGGT GATTGCGTTT GTGCAGATGT

551  TCGTCTGA
```

[0403] This encodes a protein having amino acid sequence <SEQ ID 50>:

```
  1  ..RGYTARYWGD NTAEQYGRLT LNPLPHIDLV GTIIVPLLTL MFTPFLFGWA

 51   RPIPIDSRNF RNPRLAWRCV AASGFLSNLA MAVLWGVVLV LTPYVGGAYQ
```

-continued

```
101  MPLAQNANYX ILINAILXAL NIIPILPWDG GIFIDTFLSA KXSQAFRKIE

151  PYGTWIIXLL MLTGVLGAXI APIVQLVIAF VQNFV*
```

[0404] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 12

[0405] The following partial DNA sequence was identified in *N. meningitidis* SEQ ID 51>

```
   1 ATGAACCTGA TTTCACGTTA CATCATCCGT CAAATGGCGG TTATGGCGGT

  51 TTACGCGCTC CTTGCCTTCC TCGCTTTGTA CAGCTTTTTT GAAATCCTGT

 101 ACGAAACCGG CAACCTCGGC AAAGGCAGTT ACGGCATATG GGAAATGCTG

 151 GGCTACACCG CCCTCAAAAT GCCCGCCCGC GCCTACGAAC TGATTCCCCT

 201 CGCCGTCCTT ATCGGCGGAC TGGTCTCCCT CAGCCAGCTT GCCGCCGGCA

 251 GCGAACTGAC CGTCATCAAA GCCAGCGGCA TGAGCACCAA AAAGCTGCTG

 301 TTGATTCTGT CGCAGTTCGG TTTTATTTTT GCTATTGCCA CCGTCGCGCT

 351 CGGCGAATGG GTTGCGCCCA CACTGAGCCA AAAAGCCGAA AACATCAAAG

 401 CCGCCGCCAT CAACGGCAAA ATCAACACCG GCAATACCGG CCTTTGGCTG

 451 AAAGAAAAAA ACAGCGTGAT CAATGTGCGC GAAATGTTGC CCGACCAT..
```

[0406] This corresponds to the amino acid sequence SEQ ID 52; ORF112>:

```
   1 HNLISRYIIR QMAVMAVYAL LAFLALYSFF EILYETGNLG KGSYGIWEML

  51 GYTALIQPAR AYELIPLAVL IGGLVSLSQL AAGSELTVIK ASGNSTKKLL

 101 LILSQFGFIF AIATVPLGEW VAPTLSQKAE NIKAAAINGK ISTGNTGLWL

 151 KEKNSVINVR EHLPDH...
```

[0407] Further work revealed further partial nucleotide sequence <SEQ ID 53>:

```
   1 ATGAACCTGA TTTCACGTTA CATCATCCGT CAAATGGCGG TTATGGCGGT

  51 TTACGCGCTC CTTGCCTTCC TCGCTTTGTA CAGCTTTTTT GAAATCCTGT

 101 ACGAAACCGG CAACCTCGGC AAAGGCAGTT ACGGCATATG GGAAATGCTG

 151 GGCTACACCG CCCTCAAAAT GCCCGCCCGC GCCTACGAAC TGATTCCCCT

 201 CGCCGTCCTT ATCGGCGGAC TGGTCTCCCT CAGCCAGCTT GCCGCCGGCA

 251 GCGAACTGAC CGTCATCAAA GCCAGCGGCA TGAGCACCAA AAAGCTGCTG

 301 TTGATTCTGT CGCAGTTCGG TTTTATTTTT GCTATTGCCA CCGTCGCGCT

 351 CGGCGAATGG GTTGCGCCCA CACTGAGCCA AAAAGCCGAA AACATCAAAG

 401 CCGCCGCCAT CAACGGCAAA ATCAGCACCG GCAATACCGG CCTTGCTCTG
```

-continued

```
451 AAAGAAAAAA ACAGCTTAAT CAATGTGCGC GAAATGTTGC CCGACCATAC

501 GCTTTTGGGC ATCAAAATTT GGGCGCGCAA CGATAAAAAC GAATTGGCAG

551 AGGCAGTGGA AGCCGATTCC GCCGTTTTGA ACAGCGACGG CAGTTGGCAG

601 TTGAAAAACA TCCGCCGCAG CACGCTTGGC GAAGACAAAG TCGAGGTCTC

651 TATTGCGGCT GAAGAAAACT GGCCGATTTC CGTCAAACGC AACCTGATGG

701 ACGTATTGCT CGTCAAACCC GACCAAATGT CCGTCGGCGA ACTGACCACC

751 TACATCCGCC ACCTCCAAAA CAACAGCCAA AACACCCGAA TCTACGCCAT

601 CGCATGGTGG CGCAAATTGG TTTACCCCGC CGCAGCCTGG GTGATGGCGC

851 TCGTCGCCTT TGCCTTTACC CCGCAAACCA CCCGCCACGG CAATATGGGC

901 TTAAAACTCT TCGGCGGCAT CTGTSTCGGA TTGCTGTTCC ACCTTGCCGG

951 ACGGCTCTTT GGGTTTACCA GCCAACTCGG...
```

[**0408**] This corresponds to the amino acid sequence <SEQ ID 54; ORF112-1>:

```
  1 MNLISRYIIR QMAVMAVYAL LAFLALYSFF EILYETGNLG KGSYGIWEHL

 51 GYTALKMPAR AYELIPLAVL IGGLVSLSQL AAGSELTVIK ASGMSTKKLL

101 LILSQFGFIF AIATVALGEW VAPTLSQKAE NIKAAAINGK ISTGNTGLWL

151 KEKNSXINVR EHLPDHTLLG IKIWARNDKN ELAEAVEADS AVLNSDGSWQ

201 LKNIRRSTLG EDKVEVSIAA EENWPISVKR NLTDVLLVKP DQMSVGELTT

251 YIRHLONNSQ NTRIYAIAWW RKLVYPAAAW VMALVAFAFT PQTTRHGNMG

301 LKLFGGICXG LLFHLAGRLF GFTSQL...
```

[**0409**] Computer analysis of this amino acid sequence predicts two transmembrane domains.

[**0410**] A corresponding ORF from strain A of *N. meningitidis* was also identified:

[**0411**] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[**0412**] ORF112 shows 96.4% identity over a 166 aa overlap with an ORF (ORF112a) from strain A of *N. meningitidis*:

```
                10        20        30        40        50        60
orf112.pep  MNLISRYIIRQMAVMAVYALLAFLALYSFFEILYETGNLGKGSYGIWEMLGYTALKMPAR
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||
orf112a     MNLISRYIIRQMAVMAVYALLAFLALYSFFEILYETGNLGKGSYGIWEMXGYTALKMXAR
                10        20        30        40        50        60

                70        80        90       100       110       120
orf112.pep  AYELIPLAVLIGGLVSLSQLAAGSELTVIKASGMSTKKLLLILSQFGFIFAIATVALGEW
            ||||:|||||||||||| |||||||||:||||||||||||||||||||||||||||||||
orf112a     AYELMPLAVLIGGLVSXSQLAAGSELTVIKASGMSXKKLLLILSQFGFIFAIATVALGEW
                70        80        90       100       110       120
```

-continued

```
                  130       140       150       160
orf112.pep  VAPTLSQKAENIKAAAINGKISTGNTGLWLKEKNSVINVREMLPDH
            ||||||||||||||||||||||||||||||||||:||||||||||
orf112a     VAPTLSQKAENIKAAAINGKISTGNTGLWLKEKNSIINVREMLPDHTLLGIKIWARNDKN
                  130       140       150       160

orf112a     ELAEAVEADSAVLNSDGSWQLKNIRRSTLGEDKVEVSIAAEEXWPISVKRNLMDVLLVKP
                  190       200       210       220       230       240
```

[0413] A partial ORF112a nucleotide sequence <SEQ ID 55> was identified:

```
   1 ATGAACCTGA TTTCACGTTA CATCATCCGT CAAATGGCGG TTATGGCGGT
  51 TTACGCGCTC CTTGCCTTCC TCGCTTTGTA CAGCTTTTTT GAAATCCTGT
 101 ACGAAACCGG CAACCTCGGC AAAGGCAGTT ACGGCATATG GGAAATGNTG
 151 GGNTACACCG CCCTCAAAAT GNCCGCCCGC GCCTACGAAC TGATGCCCCT
 201 CGCCGTCCTT ATCGGCGGAC TGGTCTCTNT CAGCCAGCTT GCCGCCGGCA
 251 GCGAACTGAN CGTCATCAAA GCCAGCGGCA TGAGCACCAA AAAGCTGCTG
 301 TTGATTCTGT CGCAGTTCGG TTTTATTTTT GCTATTGCCA CCGTCGCGCT
 351 CGGCGAATGG GTTGCGCCCA CACTGAGCCA AAAAGCCGAA AACATCAAAG
 401 CCGCGGCCAT CAACGGCAAA ATCAGTACCG GCAATACCGG CCTTTGGCTG
 451 AAAGAAAAAA ACAGCATTAT CAATGTGCGC GAAATGTTGC CCGACCATAC
 501 CCTGCTGGGC ATTAAAATCT GGGCCCGCAA CGATAAAAAC GAACTGGCAG
 551 AGGCAGTGGA AGCCGATTCC GCCGTTTTGA ACAGCGACGG CAGTTGGCAG
 601 TTGAAAAACA TCCGCCGCAG CACGCTTGGC GAAGACAAAG TCGAGGTCTC
 651 TATTGCGGCT GAAGAAAANT GGCCGATTTC CGTCAAACGC AACCTGATGG
 701 ACGTATTGCT CGTCAAACCC GACCAAATGT CCGTCGGCGA ACTGACCACC
 751 TACATCCGCC ACCTCCAAAN NNACAGCCAA AACACCCGAA TCTACGCCAT
 801 CGCATGGTGG CGCAAATTGG TTTACCCCGC CGCAGCCTGG GTGATGGCGC
 851 TCGTCGCCTT TGCCTTTACC CCGCAAACCA CCCGCCACGG CAATATGGGC
 901 TTAAAANTCT TCGGCGGCAT CTGTCTCGGP TTGCTGTTCC ACCTTGCCGG
 951 NCGGCTCTTC NGGTTTACCA GCCAACTCTA CGGCATCCCG CCCTTCCTCG
1001 NCGGCGCACT ACCTACCATA GCCTTCGCCT TGCTCGCCGT TTGGCTGATA
1051 CGCAAACAGG AAAAACGCTA A
```

[0414] This encodes a protein having amino acid sequence <SEQ ID 56>:

```
   1 MNLISRYIIR QMAVMAVYAL LAFLALYSFF EILYETGNLG KGSYGIWEMK
  51 GYTALKMXAR AYELMPLAVL IGGLVSXSQL AAGSELXVIX ASGNSTKKLL
 101 LILSQFGFIF AIATVALGEV VAPTLSQKAE NIKAAAINGK ISTGNTGLWL
 151 KEKNSIINVR EMLPDHTLLG IKIWAIWDKN ELAEAVFADS AVLNSDGSWQ
 201 LKNIRRSTLG EDKVEVSIAA EEXWPISVKR NLMDVLLVKP DQMSVGELTT
 251 YIRHLQXXSQ NTRIYAIAWW RKLVYPAAAW VMALVAFAFT PQTTRHGNMG
```

-continued

```
301 LKXFGGICLG LLFHLAGRLF XFTSQLYGIP PFLXGALPTI AFALLAVWLI

351 RKQEKR*
```

[0415] ORF112a and ORF112-1 show 96.3% identity in 326 aa overlap:

```
orf112a.pep MNLISRYIIRQMAVMAVYALLAFLALYSFFEILYETGNLGKGSYGIWEMXGYTALKMXAR
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||
orf112-1    MNLISRYIIRQMAVMAVYALLAFLALYSFFEILYETGNLGKGSYGIWEMLGYTALKMXAR

orf112a.pep AYEIIPLAVLIGGLVSXSQLAAGSELXVIKASGHSTKKLLLILSQFGFIFAIATVALGEW
            ||||:|||||||||||  |||||||||:||||||||||||||||||||||||||||||||
orf112-1    AYEIIPLAVLIGGLVSLSQLAAGSELTVIKASGHSTKKLLLILSQFGFIFAIATVALGEW

orf112a.pep VAPTLSQKAENIKAAAAINGKISTGNTGLWLKEKNSIINVREMLPDHTLLGIKIWARNDKN
            |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
orf112-1    VAPTLSQKAENIKAAAAINGKISTGNTGLWLKEKNSXINVREMLPDHTLLGIKIWARNDKN

orf112a.pep ELAEAVEADSAVLNSDGSWQLKNIRRSTLGEDKVEVSIAAEEXWPISVKRNLMDVLLVKP
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
orf112-1    ELAEAVEADSAVLNSDGSWQLKNIRRSTLGEDKVEVSIAAEENWPISVKRNLMDVLLVKP

orf112a.pep DQMSVGELTTYIRHLQXXSQNTRIYAIAWWRKLVYPAAAWVMALVAFAFTPQTTRHGNMG
            ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
orf112-1    DQMSVGELTTYIRHLQXXSQNTRIYAIAWWRKLVYPAAAWVMALVAFAFTPQTTRHGNMG

orf112a.pep LKXFGGICLGLLFHLAGRLFXFTSQLYGIPPFLXGALPTIAFALLAVWLIRKQEXRX
            || ||||| |||||||||||| |||||
orf112-1    LKLFGGICXGLLFHLAGRLFGFTSQL
```

[0416] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 13

[0417] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>

```
  1..GCAGTAGCCG AAACTGCCAA CAGCCAGGGC AAAGGTAAAC AGGCAGGCAG

 51  TTCGGTTTCT GTTTCACTGA AAACTTCAGG CGACCTTTGC GGCAAACTCA

101  AAACCACCCT TAAAACTTTG GTCTGCTCTT TGGTTTCCCT GAGTATGGTA

151  TTGCCTGCCC ATGCCCAAAT TACCACCGAC AAATCACCAC CTAAAAACCA

201  GCAGGTCGTT ATCCTTAAAA CCAACACTGG TGCCCCCTTG GTGAATATCC

251  AAACTCCGAA TGGACGCGGA TTGAGCCACA ACCGCTA.TA CGCATTTGAT

301  GTTGACAACA AAGGGGCAGT GTTAAACAAC GACCGTAACA ATAATCCGTT

351  TGTGGTCAAA GGCAGTGCGC AATTGATTTT GAACGAGGTA CGCGGTACGG

401  CTAGCAAACT CAACGGCATC GTTACCGTAG GCGGTCAAAA GGCCGACGTG

451  ATTATTGCCA ACCCCAACGG CATTACCGTT AATGGCGGCG GCTTTAAAAA

501  TGTCGGTCGG GGCATCTTAA CTACCGGTGC GCCCCAAATC GGCAAAGACG

551  GTGCACTGAC AGGATTTGAT GTGCGTCAAG GCACATTGGA CCGTAGTAGC

601  AGCAGGTTGG AATGATAAAG GCGGAGCmrm yTACACCGGG GTACTTGCTC

651  GTGCAGTTGC TTTGCAGGGG AAATTwmmGG GTAAA.AACT GGCGGTTTCT
```

-continued

```
701  ACCGGTCCTC AGAAAGTAGA TTACGCCAGC GGCGAAATCA GTGCAGGTAC

751  GGCAGCGGGT ACGAAACCGA cTATTGCCCT TGATACTGCC GCACTGGGCG

901  GTATGTACGC CGACAGCATC ACACTGATTG CCAATGAAAA AGGCGTAGGC

951  GTCTAA
```

[0418] This corresponds to the amino acid sequence <SEQ ID 58; ORF114>:

```
  1..AVAETANSQG KGKQAGSSVS VSLKTSGDLC GKLKTTLKTL VCSLVSLSHV

 51  LPAHAQITTD KSAPKNQQVV ILKTNTGAPL VNIQTPNGRG LSHNRXYAFD

101  VDNKGAVLNN DRNNNPFVVK GSAQLILNEV RGTASKLNGI VTVGGQKADV

151  IIANPNGITV NGGGFXNVGR GILTTGAPQI GKDGALTGFD VVKAHVTVXA

201  AGWNDKGGAX YTGVLAPAVA LQGKXXGLXL AVSTGPQKVD YASGEISAGT

251  AAGTKPTIAL DTAALGGNYA DSITLIANEX GVGV*
```

[0419] Further work revealed the complete nucleotide sequence SEQ ID 59>:

```
   1 ATGAATAAAG GTTTACATCG CATTATCTTT AGTAAAAAGC ACAGCACCAT

  51 GGTTGCAGTA GCCGAAACTG CCAACAGCCA GGGCAAAGGT AAACAGGCAG

 101 GCAGTTCGGT TTCTGTTTCA CTGAAAACTT CAGGCGACCT TTGCGGCAAA

 151 CTCAAAACCA CCCTTAAAAC TTTGGTCTGC TTTTTGGTTT CCCTGAGTAT

 201 GGTATTGCCT GCCCATGCCC AAATTACCAC CGACAAATCA GCACCTAAAA

 251 ACCAGCAGGT CGTTATCCTT AAAACCAACA CTGGTGCCCC CTTGGTGAAT

 301 ATCCAAACTC CGAATGGACG CGGATTGAGC CACAACCGCT ATACGCAGTT

 351 TGATGTTGAC AACAAAGGGG CAGTGTTAAA CAACGACCGT AACAATAATC

 401 CGTTTGTGGT CAAAGGCAGT GCGCAATTGA TTTTGAACGA GGTACGCGGT

 451 ACGGCTAGCA AACTCAACGG CATCGTTACC GTAGGCGGTC AAAAGGCCGA

 501 CGTGATTATT GCCAACCCCA ACGGCATTAC CGTTAATGGC GGCGGCTTTA

 551 AAAATGTCGG TCGGGGCATC TTAACTACCG GTGCGCCCCA AATCGGCAAA

 601 GACGGTGCAC TGACAGGATT TGATGTGCGT CAAGGCACAT TGACCGTAGG

 651 AGCAGCAGGT TGGAATGATA AAGGCGGAGC CGACTACACC GGGGTACTTG

 701 CTCGTGCAGT TGCTTTGCAG GGGAAATTAC AGGGTAAAAA CCTGGCGGTT

 751 TCThCCGGTC CTCAGAAAGT AGATTACGCC AGCGGCGAAA TCAGTGCAGG

 801 TACGGCAGCG GGTACGAAAC CGACTATTGC CCTTGATACT GCCGCACTGG

 951 GCGGTATGTA CGCCGACACC ATCACACTGA TTGCCAATGA AAAAGGCGTA

 901 GGCGTCAAAA ATGCCGGCAC ACTCGAAGCG GCCAAGCAAT TGATTGTGAC

 951 TTCGTCAGGC CGCATTGAAA ACAGCGGCCG CATCGCCACC ACTGCCGACG

1001 GCACCGAAGC TTCACCGACT TATCTCTCCA TCGAAACCAC CGAAAAAGGA

1051 GCGGCAGGCA CATTTATCTC CAATGGTGGT CGGATCGAGA GCAAAGGCTT
```

-continued

1101 ATTGGTTATT GAGACGGGAG AAGATATCAG CTTGCGTAAC GGAGCCGTGG

1151 TGCAGAATAA CGGCAGTCTC CCAGCTACCA CGGTATTAAA TGCTGGTCAT

1201 AATTTGGTGA TTGAGAGCAA AACTAATGTG AACAATGCCA AAGGCCCGGC

1251 TACTCTGTCG GCCGACGGCC GTACCGTCAT CAAGGAGGCC AGTATTCAGA

1301 CTGGCACTAC CGTATACAGT TCCAGCAAAG GCAACGCCGA ATTAGGCAAT

1351 AACACACGCA TTACCGGGGC AGATGTTACC GTATTATCCA ACGGCACCAT

1401 CAGCAGTTCC GCCGTAATAG ATGCCAAAGA CACCGCACAC ATCGAAGCAG

1451 GCAAACCGCT TTCTTTGGAA GCTTCAACAG TTACCTCCGA TATCCGCTTA

1501 AACGGAGGCA GTATCAAGGG CGGCAAGCAG CTTGCTTTAC TGGCAGACGA

1551 TAACATTACT GCCAAAACTA CCAATCTGAA TACTCCCGGC AATCTGTATG

1601 TTCATACAGG TAAAGATCTG AATTIGAATG TTGATAAAGA TTTGTCIGCC

1651 GCCAGCATCC ATTTGAAATC GGATAACGCT GCCCATATTA CCGGCACCAG

1701 TAAAACCCTC ACTGCCTCAA AAGACATGGG TGTGGAGGCA GGCTCGCTGA

1751 ATGTTACCAA TACCAATCTG CGTACCAACT CGGGTAATCT GCACATTCAG

1801 GCAGCCAAAG GCAATATTCA GCTTCGCAAT ACCAAGCTGA ACGCAGCCAA

1851 GGCTCTCGAA ACCACCGCAT TGCAGGGCAA TATCGTTTCA GACGGCCTTC

1901 ATGCTGTTTC TGCAGACGGT CATGTATCCT TATCGGCCAA CGGTAATGCC

1951 GACTTTACCG GTCACAATAC CCTGACAGCC AAGGCCGATG TCAATGCAGG

2001 ATCGGTTGGT AAAGGCCGTC TGAAAGCAGA CAATACCAAT ATCACTTCAT

2051 CTTCAGGAGA TATTACGTTG GTTGCCGGCA ACGGTATTCA GCTTGGTGAC

2101 GGAAAACAAC GCAATTCAAT CAACGGAAAA CACATCAGCA TCAAAAACAA

2151 CGGTGGTAAT GCCGACTTAA AAAACCTTAA CGTCCATGCC AAAAGCGGGG

2201 CATTGAACAT TCATTCCGAC CGGGCATTGA GCATAGAAAA TACCAAGCTG

2251 GAGTCTACCC ATAATACGCA TCTTAATGCA CAACACGAAG GGGTAACGCT

2301 CAACCAAGTA GATGCCTACG CACACCGTCA TCTAAGCATT ACCGGCAGCC

2351 AGATTTGGCA AAACGACAAA CTGCCTTCTG CCAACAAGCT GGTGGCTAAC

2401 GGTGTATTGG CACTCAATGC GCGCTATTCC CAAATTGCCG ACAACACCAC

2451 GCTGAGAGCG GGTGCAATCA ACCTTATTGC CGGTACCGCC CTAGTCAAGC

2501 GCGGCAACAT CAATTGGAGT ACCGTTGCGA CCAAAACTTT GGAAGATAAT

2551 GCCGAATTAA AACCATTGGC CGGACGGCTG AATATTGAAG CAGGTAGCGG

2601 CACATTAACC ATCGAACCTG CCAACCGCAT CAGTGCGCAT ACCGACCTGA

2651 GCATCAAAAC AGGCGGAAAA TTGCTGTTGT CTGCAAAAGG AGGAAATGCA

2701 GGTGCGCCTA GTGCTCAAGT TTCCTCATTG GAAGCAAAAG GCAATATCCG

2751 TCTGGTTACA GGAGAAACAG ATTTAAGAGG TTCTAAAATT ACAGCCGGTA

2801 AAAACTTGGT TGTCGCCACC ACCAAAGGCA AGTTGAATAT CGAAGCCGTA

2951 AACAACTCAT TCAGCAATTA TTTTCCTACA CAAAAAGCGG CTGAACTCAA

2901 CCAAAAATCC AAAGAATTGG AACAGCAGAT TGCGCAGTTG AAAAAAAGCT

2951 CGCCTAAAAG CAAGCTGATT CCAACCCTGC AAGAAGAACG CGACCGTCTC

3001 GCTTTCTATA TTCAAGCCAT CAACAAGGAA GTTAAAGGTA AAAAACCCAA

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3051 AGGCAAAGAA TACCTGCAAG CCAAGCTTTC TGCACAAAAT ATTGACTTGA

3101 TTTCCGCACA AGGCATCGAA ATCAGCGGTT CCGATATTAC CGCTTCCAAA

3151 AAACTGAACC TTCACGCCGC AGGCGTATTG CCAAAGGCAG CAGATTCAGA

3201 GGCGGCTGCT ATTCTGATTG ACGGCATAAC CGACCAATAT GAAATTGGCA

3251 AGCCCACCTA CAAGAGTCAC TACGACAAAG CTGCTCTGAA CAAGCCTTCA

3301 CGTTTGACCG GACGTACAGG GGTAAGTATT CATGCAGCTG CGGCACTCGA

3351 TGATGCACGT ATTATTATCG GTGCATCCGA AATCAAAGCT CCCTCAGGCA

3401 GCATAGACAT CAAAGCCCAT AGTGATATTG TACTGGAGGC TGGACAAAAC

3451 GATGCCTATA CCTTCTTAAA AACCAAAGGT AAAAGCGGCA AAATCATCAG

3501 AAAAACCAAG TTTACCAGCA CCCGCGACCA CCTGATTATG CCAGCCCCCG

3551 TCGAGCTGAC CGCCAACGGC ATAACGCTTC AGGCAGGCGG CAACATCGAA

3601 GCTAATACCA CCCGCTTCAA TGCCCCTGCA GGTAAAGTTA CCCTGGTTGC

3651 GGGTGAAGAG CTGCAACTGC TGGCAGAASA AGGCATCCAC AAGCACGAGT

3701 TGGATGTCCA AAAAAGCCGC CGCTTTATCG GCATCAAGGT AGGCAAGAGC

3751 AATTACAGTA AAAACGAACT GAACGAAACC AAATTGCCTG TCCGCGTCGT

3801 CGCCCAAACT GCAGCCACCC GTTCAGGCTG GGATACAGTG CTCGAAGGTA

3051 CCGAATTCAA AACCACGCTG GCCGGTGCGG ACATTCAGGC AGGTGTAGGC

3901 GAAAAAGCCC GTGCCGATGC GAAAATTATC CTCAAAGGCA TTGTGAACCG

3951 TATCCAGTCG GAAGAAAAAT TAGAAACCAA CTCAACCGTA TGGCAGAAAC

4001 AGGCCGGACG CGGCAGCACT ATCGAAACGC TGAAACTGCC CAGCTTCGAA

4051 AGCCCTACTC CGCCCAAACT GACCGCCCCC GGTGGCTATA TCGTCGACAT

4101 TCCGAAAGGC AATTTGAAAA CCGAAATCGA AAAGCTGGCC AAACAGCCCG

4151 AGTATGCCTA TCTGAAACAG CTCCAAGTAG CGAAAAACGT CAACTGGAAC

4201 CAGGTGCAAC TGGCTTACGA TAAATGGGAC TATAAGCAGG AAGGCTTAAC

4251 CAGAGCCGGT GCAGCGATTG TTACCATAAT CGTAACCGCA CTGACTTATG

4301 GATACGGCGC AACCGCAGCG GGCGGTGTAG CCGCTTCAGG AAGTAGTACA

4351 GCCGCAGCTG CCGGAACAGC CGCCACAACG ACAGCAGCAG CTACTACCGT

4401 TTCTACAGCG ACTGCCATGC AAACCGCTGC TTTAGCCTCC TTGTATAGCC

4451 AAGCAGCTGT ATCCATCATC AATAATAAAG GTGATGTCGG CAAAGCGTTG

4501 AAAGATCTCG GCACCAGTGA TACGGTCAAG CAGATTGTCA CTTCTGCCCT

4551 GACGGCGGGT GCATTAAATC AGATGGGCGC AGATATIGCC CAATTGAACA

4601 GCAAGGTAAG AACCGAACTG TTCAGCAGTA CGGGCAATCA AACTATTGCC

4651 AACCTTGGAG GCAGATTGGC TACCAATCTC AGTAATGCAG GTATCTCAGC

4701 TGGTATCAAT ACCGCCGTCA ACGGCGGCAG CCTGAAAGAC AACTTAGGCA

4751 ATGCCGCATT AGGAGCATTG GTTAATAGCT TCCAAGGAGA AGCCGCCAGC

4801 AAAATCAAAA CAACCTTCAG CGACGATTAT GTTGCCAAAC AGTTCGCCCA

4851 CGCTTTGGCT GGGTGTGTTA GCGGATTGGT ACAAGGAAAA TGTAAAGACG

4901 GGGCAATTGG CGCAGCAGTT GGGGAAATCG TAGCCGACTC CATGCTTGGC

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```
4951 GGCAGAAACC CTGCTACACT CAGCGATGCG GAAAAGCATA AGGTTATCAG

5001 TTACTCGAAG ATTATTGCCG GCAGCGTGGC GGCACTCAAC GGCGGCGATG

5051 TGAATACTGC GGCGAATGCG GCTGAGGTGG CGGTAGTGAA TAATGCTTTG

5101 AATTTTGACA GTACCCCTAC CAATGCGAAA AAGCATCAAC CGCAGAAGCC

5151 CGACAAAACC GCACTGGAAA AAATTATCCA AGGTATTATG CCTGCACATG

5201 CAGCAGGTGC GATGACTAAT CCGCAGGATA AGGATGCTGC CATTTGGATA

5251 AGCAATATCC GTAATGGCAT CACAGGCCCG ATTGTGATTA CCAGCTATGG

5301 GGTTTATGCT GCAGGTTGGA CAGCTCCGCT GATCGGTACA GCGGGTAAAT

5351 TAGCTATCAG CACCTGCATG GCTAATCCTT CTGGTTGTAC TGTCATGGTC

5401 ACTCAGGCTG CCGAAGCGGG CGCGGGAATC GCCACGGGTG CGGTAACGGT

5451 AGGCAACGCT TGGGAAGCGC CTGTGGGGGC GTTGTCGAAA GCGAAGGCGG

5501 CCAAGCAGGC TATACCAACC CAGACAGTTA AAGAACTTGA TGGCTTACTA

5551 CAAGAATCAA AAAATATAGG TGGTGTAAAT ACACGAATAA ATATAGCGAA

5601 TAGTACTACT CGATATACAC CAATGAGACA AACGGGACAA CCGCTATCTG

5651 CTGGCTTTGA GCATGTFCTT GAGGGGGACT TCCATAGGCC TATTGCGAAT

5701 AACCGTTCAG TTTTTACCAT CTCCCCAAAT GAATTGAAGG TTATACTTCA

5751 AAGTAATAAA GTAGTTTCTT CTCCCGTATC GATGACTCCT GATGGCCAAT

5801 ATATGCGGAC TGTCGATGTA GGAAAAGTTA TTGGTACTAC TTCTATTAAA

5651 GAAGGTGGAC AACCCACAAC TACAATTAAA GTATTTACAG ATAAGTCAGG

5901 AAATTTGATT ACTACATACC CAGTAAAAGG AAACTAA
```

[**0420**] This corresponds to the amino acid sequence <SEQ ID 60; ORF114-1>:

```
  1 HNKGLHRIIF SXKHSTMVAV AETANSQGKG KQAGSSVSVS LKTSGDLCGK

 51 LKTTLKTLVC SLVSLSHVLP AHAQITTDKS APKNQQVVIL KFNTGAPLVN

101 IQTPNGRGLS HNRYTQFDVD NKGAVLNNDR NNNPFVVKGS AQLILNEVRG

151 TASKLNGIVT VGGQKADVII ANPNGITVNG GGFKNVGRGI LTTGAPQIGK

201 DGALTGFDVR QGTLTVGAAG WNDKGGADYT GVLAAAVALQ GKLQGKLLAV

251 STGFQKVDYA SGEISAGTAA GTKPTIALDT AALGGHYADS ITLIANEKGV

301 GVKNAGTLKA AXQLIVTSSG RIENSGRIAT TADGTFASPT YLSIETTEKG

351 AAGTFISNGG RIESKGLLVI ETGEDISLRN GAVVQINGSR PATTVLNAGH

401 HLVIESKTNV NNAKGFATLS ADGRTVIKEA SIQTGTTVYS SSKGTAELGN

451 NTRZTGADVT VLSNGTISSS AVIDAKOTAN IEAGKPLSLT ASTVTSDIRL

501 NGGSIKGGKQ LALLADDNIT AXTTNLNTPG NLYVHTGKDL NIMVDKDLSA

551 ASIHLKSDNA AHITGTSKTL TASKDMGVEA GSLNVTNTNL RTNSGNLHIQ

601 AAKGNIQLRN TKLNAAKALE TTALQGNIVS OGLHAVSADG HVSLLANGNA

651 DFTGHNTLTA KADVNAGSVG KGRLKADNTN ITSSSGDITL VAGNGIQLGD

701 GKQRNSINGK HISIKNNGGN ADLIQLNVHA KSGALNIHSD RALSIENTKL
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```
 751 ESTRNTHLNA QHERVTLNQV DAYAHRHLSI TGSQIWQNOK LPSANKLVTN

 801 GVLALNARYS QIADNTTLRA GAINLTAGTA LVKRGNINWS TVSTKTLEDN

 851 AELKPLAGRL NIEAGSGTLT IEPANRISAH TDLSIKTGGK LLLSAKGGNA

 901 GAFSAQVSSL EAKGNIRLVT GETDLRGSKI TAGKNLVVAT TKGKLNIEAV

 951 NNSFSNYFPT QKAAELNQKS KELEQQIAQL KKSSPKSKLI PTLQEERDRL

1001 AFYIQAINKE VKGKKPKGKE YLQAKLSAQN IDLISAQGIE ISGSDITASK

1051 KLNLHAAGVL PKAADSEAAA ILIDGITDQY EIGKPTYKSH YOKAALNKPS

1101 RLTGRTGVSI HAAAALDDAR IIIGASEIKA FSGSIDIKAH SDIVLEAGQN

1151 DAYTFLKTKG KSGKIIRXTK FTSTRDHLIM PAPVELTANG ITLQAGGNIE

1201 ANTTRFNAPA GKVTLVAGEE LQLLAEEGIH KHELDVQKSR RFIGIKVGKS

1251 NYSKNELNET KLPVRVVAQT AATRSGWDTV LEGTEFKTTL AGADIQAGVG

1301 EKAPADAKII LKGIVNRIQS EEKLETNSTV WQKQAGRGST IETLKLPSFE

1351 SPTPPKLTAP GGYIVDIPKG NLKTEIEKLA KQPEPEYLKQ LQVAKNVNWN

1401 QVQLAYDKWD YKQEGLTRAG AAIVTIIVTA LTYGYGATAA GGVAASGSST

1451 AAAAGTAATT TAAATTVSTA TANQTAALAS LYSQAAVSII NNKGDVGKAL

1501 KDLGTSDTVK QIVISALTAG ALNQMGADIA QLNSKVRTEL FSSTGVQTIA

1551 NLGGRLATNL SNAGISAGIN TAVNGGSLKD NLGNAALGAL VNSFQGEAAS

1601 KIKTTFSDDY VAKQFAHALA GCVSGLVQGK CKDGAIGAAV GEIVADSNLG

1651 GRNPATLSDA EKHKVISYSK IIAGSVAALN GGDVNTAANA AEVAVVNNAL

1701 NFDSTPTNAK KNQPQKPDKT ALEKIIQGIM PAHAAGAMTN PQDKDAAIWI

1751 SNIRNGITGP IVITSYGVYA AGWTAPLIGT AGKLAISTCM ANPSGCTVNV

1801 TQAAEAGAGI ATGAVTVGNA WEAPVGALSK AKAAKQAIPT QTVKELDGLL

1851 QESKNIGAVN TRINIANSTT RYTPNRQTGQ PVSAGFENVL EGHFHRPIAN

1901 NRSVFTXSPN ELKVILQSNK VVSSPVSMTP DGQYNRTVDV GKVIGTTSIK

1951 EGGQPTTTIK VFTDKSGNLI TTYPVKGN*
```

[0421] Computer analysis of this amino acid sequence predicts a transmembrane region and also gives the following results:

[0422] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[0423] ORF114 shows 91.9% identity over a 284 aa overlap with an ORF (ORF114a) from strain A of *N. meningitidis*:

```
                                    10        20        30        40
orf114.pep                    AVAETANSQGKGKQAGSSVSVSLKTSGDLCGKLKTTLKTLVC
                              ||||||||||||||||||||||||||||||||||||||||||
orf114a     MNKGLHRIIFSKKHSTMVAVAETANSQGKGKQAGSSVSVSLKTSGDLCGKLKTTLKTLVC
                   10        20        30        40        50        60

                  50        60        70        80        90       100
orf114.pep  SLVSLSMVLPAHAQITTDKSAPKNQQVVILKTNTGAPLVNIQTPNGRGLSHNRXYAFDVD
            |||||||      |||||||||||| ||||||||||||||||||||||||||   ||||
orf114a     SLVSLSMXXXXXXQITTDKSAPKNXQVVILKTNTGAPLVNIQTPNGRGLSHNRYTQFDVD
                   70        80        90        100       110       120
```

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                110       120       130       140       150       160
orf114.pep  NKGAVLNNDRNNNPFVVKGSAQLILNEVRGTALKLNGIVTVGGQKADVIIANPNGITVNG
            ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
orf114a     NKGAVLNNDRNNNPFLVKGSAQLILNEVRGTASKLNGIVTVGGQKADVIIANPNGITVNG
                130       140       150       160       170       180

                170       180       190       200       210       220
orf114.pep  GGFKNVGRGILTTGAPQIGKDGALTGFDVVKAHWTVXAAGWNDKGGAXYTGVLARAVALQ
||||||||||| ||||||||||||||| ::  || |||||||||| ||||||||||
orf114a     GGFKNVGRGILTIGAPQIGKDGALTGFDVRQGTLTVAAAGWNDKGGADYTGVLARAVALQ
                190       200       210       220       230       240

                230       240       250       260       270       290
orf114.pep  GKXXGKXLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGMYADSITLIANEKGV
            ||  || ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
orf114a     GKLQGKNLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGMYADSITLIAXEKGV
                250       260       270       280       290       300

orf114.pep  GVX
            ||
orf114a     GVKNAGTLEAAKQLIVTSSGRIENSGRIATTADGTEASPTYLXIETTEKGAXGTFISNGG
                310       320       330       340       350       360
```

[**0424**] The complete length ORF114a nucleotide sequence <SEQ ID 61> is:

```
   1 ATGAATAAAG GTTTACATCG CATTATCTTT AGTAAAAAGC ACAGCACCAT

  51 GGTTGCAGTA GCCGAAACTG CCAACAGCCA GGGCAAAGGT AAACAGGCAG

 101 GCAGTTCGGT TTCTGTTTCA CTGAAAACTT CAGGCGACCT TTGCGGCAAA

 151 CTCAAAACCA CCCTTAAAAC CTTGGTCTGC TCTTTGGTTT CCCTGAGTAT

 201 GGNATTNCNN NNCNNTNCCC AAATTACCAC CGACAAATCA GCACCTAAAA

 251 ACCANCAGGT CGTTATCCTT AAAACCAACA CTGGTGCCCC CTTGGTGAAT

 301 ATCCAAACTC CGAATGGACG CGGATTGAGC CACAACCGCT ATACGCAGTT

 351 TGATGTTGAC AACAAAGGGG CAGTGTTAAA CAACGACCGT AACAATAATC

 401 CGTTTCTGGT CAAAGGCAGT GCGCAATTGA TTTTGAACGA GGTACGCGGT

 451 ACGGCTAGCA AACTCAACGG CATCGTTACC GTAGGCGGTC AAAAGGCCGA

 501 CGTGATTATT GCCAACCCCA ACGGCATTAC TGTTAATGGC GGCGGCTTTA

 551 AAAATGTCGG TCGGGGCATC TTAACTATCG GTGCGCCCCA AATCGGCAAA

 601 GACGGTGCAC TGACAGGATT TGATGTGCGT CAAGGCACAT TGACCGTAGG

 651 AGCAGCAGGT TGGAATGATA AAGGCGGAGC CGACTACACC GGGGTACTTG

 701 CTCGTGCAGT TGCTTTGCAG GGGAAATTAC AAGGTAAAAA CCTGGCGGTT

 751 TCTACCGGTC CTCAGAAAGT AGATTACGCC AGCGGCGAAA TCAGTGCAGG

 801 TACGGCAGCG GGTACGAAAC CGACTATTGC CCTTGATACT GCCGCACTGG

 951 GCGGTATGTA CGCCGAGAAA ATCACACTGA TTGCCAATGA AAAAGGCGTA

 901 GGcGTCAAAA ATGCCGGCAC ACTCGAAGCG GCCAAGCAAT TGATTGTGAC

 951 TTCGTCAGGC CGCATTGAAA ACAGCGGCCG CATCGCCACC ACTGCCGACG

1001 GCACCGAAGC TTCACCGACT TATCTNNCNA TCGAAACCAC CGAAAAAGGA

1051 GCNNCAGGCA CATTTATCTC CAATGGTGGT CGGATCGAGA GCAAAGGCTT

1101 ATTGGTTATT GAGACGGGAG AAGATATCAT CTTGCGTAAC GGAGCCGTGG
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1151 TGCAGAATAA CGGCAGTCGC CCAGCTACCA CGGTATTAAA TGCTGGTCAT

1201 AATTTGGTGA TTGAGAGTAA AACTAATGTG AACAATGCCA AAGGCTCGNC

1251 TAATCTGTCG GCCGGCGGTC GTACTACGAT CAATGATGCT ACTATTCAAG

1301 CGGGCAGTTC CGTGTACAGC TCCACCAAAG GCGATACTGA NTTGGGTGAA

1351 AATACCCGTA TTATTGCTGA AAACGTAACC GTATTATCTA ACGGTAGTAT

1401 TGGCAGTGCT GCTGTAATTG AGGCTAAAGA CACTGCACAC ATTGAATCGG

1451 GCAAACCGCT TTCTTTAGAA ACCTCGACCG TTGCCTCCAA CATCCGTTTG

1501 AACAACGGTA ACATTAAAGG CGGAAAGCAG CTTGCTTTAC TGGCAGACGA

1551 TAACATTACT GCCAAAACTA CCAATCTGAA TACTCCCGGC AATCTGTATG

1601 TTCATACAGG TAAAGATCTG AATTTGAATG TTGATAAAGA TTTGTCTGCC

1651 GCCAGCATCC ATTTGAAATC GGATAACGCT GCCCATATTA CCGGCACCAG

1701 TAAAACCCTC ACTGCCTCAA AAGACATGGG TGTGGAGGCA GGCTTGCTGA

1751 ATGTTACCAA TACCAATCTG CGTACCAACT CGGGTAATCT GCACATTCAG

1801 GCAGCCAAAG GCAATATTCA GCTTCGCAAT ACCAAGCTGA ACGCAGCCAA

1851 GGCTCTCGAA ACCACCGCAT TGCAGGGCAA TATCGTTTCA GACGGCCTTC

1901 ATGCTGTTTC TGCAGACGGT CATGTATCCT TATTGGCCAA CGGTAATGCC

1951 GACTTTACCG GTCACAATAC CCTGACAGCC AAGGCCGATG TCNATGCAGG

2001 ATCGGTTGGT AAAGGCCGTC TGAAAGCAGA CAATACCAAT ATCACTTCAT

2051 CTTCAGGAGA TATTACGTTG GTTGCCGNNN NCGGTATTCA GCTTGGTGAC

2101 GGAAAACAAC GCAATTCAAT CAACGGAAAA CACATCAGCA TCAAAAACAA

2151 CGGTGGTAAT GCCGACTTAA AAAACCTTAA CGTCCATGCC AAAAGCGGGG

2201 CATTGAACAT TCATTCCGAC CGGGCATTGA GCATAGAAAA TACNAAGCTG

2251 GAGTCTACCC ATAATACGCA TCTTAATGCA CAACACGAGC GGGTAACGCT

2301 CAACCAAGTA GATGCCTACG CACACCGTCA TCTAAGCATT ANCGGCAGCC

2351 AGATTTGGCA AAACGACAAA CTGCCTTCTG CCAACAAGCT GGTGGCTAAC

2401 GGTGTATTGG CAATCAATGC GCGCTATTCC CAAATTGCCG ACAACACCAC

2451 GCTGAGAGCG GGTGCAATCA ACCTTACTGC CGGTACCGCC CTAGTCAAGC

2501 GCGGCAACAT CAATTGGATT ACCGTTTCGA CCAAGACTTT GGAAGATAAT

2551 GCCGAATTAA AACCATTGGC CGGACGGCTG AATATTGAAG CAGGTAGCGG

2601 CACATTAACC ATCGAACCTG CCAACCGCAT CAGTGCGCAT ACCGACCTGA

2651 GCATCAAAAC AGGCGGAAAA TTGCTGTTGT CTGCAAAAGG AGGAAATGCA

2701 GGTGCGCNTA GTGCTCAAGT TTCCTCATTG GAAGCAAAAG GCAATATCCG

2751 TCTGGTTACA GGAGNAACAG ATTTAAGAGG TTCTAAAATT ACAGCCGGTA

2901 AAAACTTGGT TGTCGCCACC ACCAAAGGCA AGTTGAATAT CGAAGCCGTA

2951 AACAACTCAT TCAGCAATTA TTTTCNTACA CAAAAAGNGN NNGNNCTCAA

2901 CCAAAAATCC AAAGAATTGG AACAACAGAT TGCGCAGTIG AAAAAAAGCT

2951 CGCNTAAAAG CAAGCTGATT CCAACCCTGC AAGAAGAACG CGACCGTCTC

3001 GCTTTCTATA TTCAAGCCAT CAACAAGGAA GTTAAAGGTA AAAAACCCAA

3051 AGGCAAAGAA TACCTGCAAG CCAAGCTTTC TGCACAAAAT ATTGACTTGA

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3101 TTTCCGCACA AGGCATCGAA ATCAGCGGTT CCGATATTAC CGCTTCCAAA
3151 AAACTGAACC TTCACGCCGC AGGCGTATTG CCAAAGGCAG CAGATTCAGA
3201 GGCGGCTGCT ATTCTGATTG ACGGCATAAC CGACCAATAT GAAATTGGCA
3251 AGCCCACCTA CAAGAGTCAC TACGACAAAG CTGCTCTGAA CAAGCCTTCA
3301 CGTTTGACCG GACGTACGGG GGTAAGTATT CATGCAGCTG CGGCACTCGA
3351 TGATGCACGT ATTATTATCG GTGCATCCGA AATCAAAGCT CCCTCAGGCA
3401 GCATAGACAT CAAAGCCCAT AGTGATATTG TACTGGAGGC TGGACAAAAC
3451 GATGCCTATA CCTTCTTAAA AACCAAAGGT AAAAGCGGCA NAATNATCAG
3501 AAAAACNAAG TTTACCAGCA CCNGCGANCA CCTGATTATG CCAGCCCCNG
3551 TCGAGCTGAC CGCCAACGGT ATCACGCTTC ACGCAGGCGG CAACATCGAA
3601 GCTAATACCA CCCGCTTCAA TGCCCCTGCA GGTAAAGTIA CCCTGGTTGC
3651 GGGTGAANAG NTGCAACTGC TGGCAGAAGA AGGCATCCAC AAGCACGAGT
3701 TGGATGTCCA AAAAAGCCGC CGCTTTATCG GCATCAAGGT AGGTNAGAGC
3751 AATTACAGTA AAAACGAACT GAACGAAACC AAATTGCCTG TCCGCGTCGT
3801 CGCCCAAAAT GCAGCCACCC GTTCAGGCTG GGAThCCGTG CTCGAAGGTA
3851 CCGAATTCAA ATCCACGCTG GCCGGTGCCG ACATTCAGGC AGGTGTANGC
3901 GAAAAAGCCC GTGTCGATGC GAAAATCATC CTCAAAGGCA TTGTGAACCG
3951 TATCCAGTCG GAAGAAAAAT TAGAAACCAA CTCAACCGTA TGGCAGAAAC
4001 AGGCCGGACG CGGCAGCACT ATCGAAACGC TAAAACTGCC CAGCTTCGAA
4051 AGCCCTACTC CGCCCAAATT GTCCGCACCC GGCGGNTATA TCGTCGACAT
4101 TCCGAAAGGC AATCTGAAAA CCGAAATCGA AAAGCTGTCC AAACAGCCCG
4151 AGTATGCCtA TCTGAAACAG CTCCAAGTAG CGAAAAACAT CAACTGGAAT
4201 CAGGTGCAGC TTGCTTACGA CAGATGGGAC TACAAACAGG AGGGCTTAAC
4251 CGAAGCAGGT GCGGCGATTA TCGCACTGGC CGTTACCGTG GTCACCTCAG
4301 GCGCAGGAAC CGGAGCCGTA TTGGGATTAA ACGGTGCGNC CGCCGCCGCA
4351 ACCGATGCAG CATTCGCCTC TTTGGCCAGC CAGGCTTCCG TATCGTTCAT
4401 CAACAACAAA GGCGATGTCG GCAAAACCCT GAAAGAGCTG GGCAGAAGCA
4451 GCACGGTGAA AAATCTGGTG GTTGCCGCCG CTACCGCAGG CGTAGCCGAC
4501 AAAATCGGCG CTTCGGCACT GANCAATGTC AGCGATAAGC AGTGGATCAA
4551 CAACCTGACC GTCAACCTAG CCAATGNCGG GCAGTGCCGC ACTGAttaa
```

[**0425**] This encodes a protein having amino acid sequence <SEQ ID 62>:

```
   1 MNKGLHRIIF SKKHSTMVAV AETANSQGKG KQAGSSVSVS LKTSGDLCGK
  51 LKTTLKTLVC SLVSLSMXXX XXXQITTDKS APIDXQVVIL KTNTGAPLVN
 101 IQTPNGRGLS HNRYTQFDVD NKGAVLNNDR NNNPFLVKGS AQLILNEVRG
 151 TASKLNGIVT VGGQKADVII ANPNGITVNG GGFKNVGRGI LTIGAPQIGK
 201 DGALTGFDVR QGTLTVGAAG WNDKGGADYT GVLARAVALQ GKLQGKNLAV
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 251 STGPQKVDYA SGEISAGTAA GTKPTIALDT AALGGMYADS ITLTAXEKGV

 301 GVKNAGTLEA AKQLIVTSSG RIENSGRIAT TADGTEASPT YLXIETTEKG

 351 AXGTFISNGG RIESKGLLVI ETGEDIXLPA GAVVQNNGSR PATTVLNAGH

 401 NLVIESKTNV NNAXGSXNLS AGGRTTINDA TIQAGSSVYS STKGDTXLGE

 451 NTRIIAENVT VLSNGSIGSA AVIEAKDTAN IESGKPLSLE TSTVASNIRL

 501 NNGNIKGGKQ LALLADDNIT AKTTNLNTPG NLYVHTGKDL NLNVDKDLSA

 551 ASIHLKSDNA AHITGTSKTL TASKDNGVEA GLLNVTNTNL RTNSGNLHIQ

 601 AAKGNZQLRH TKLNAAKALE TTALQGNIVS DGLHAVSADG HVSLLANGNA

 651 DFTGHNTLTA KADVXAGSVG KGRLKADNTN ITSSSGDITL VAXXGIQLGD

 701 GKQRNSINGK HISIKNNGGN ADLKNLNVHA KSGALNIHSO RALSIENTKL

 751 ESTHNTHLNA QHERVTLNQV DAYAHRHLSI XGSQIWQNDK LPSANKLVAN

 801 GVLAXNARYS QIADNTTLRA CAINLTAGTA LVKRGNINWS TVSTKTLEDN

 851 AELKPLAGRL NIEAGSGTLT IEFANRISAH TDLSIKTGGK LLLSAXGGNA

 901 GAXSAQVSSL EAKGNIRLVT GXTDLRGSKI TAGKNLVVAT TKGKLNIEAV

 951 NNSFSNYFXT QKXXXLNQKS KELEOQIAQL KKSSXKSKLI PTLQEERDRL

1001 AFYIQAINKE VKGKKPKGKE YLQAXLSAQN IDLISAQGIE ISGSDITASK

1051 KLNLHAAGVL PKAADSEAAA ILIDGITOQY EIGKPTYKSH YDKAALNKPS

1101 RLTGRTGVSI HAAAALDDAR IIIGASEIKA PSGSIDIKAR SDIVLEAGQN

1151 DAYTFLXTKG KSGXXIRKTK FTSTXXHLIM PAPVELTANG ITLQAGGNIE

1201 ANTTRFHAPA GKVTLVAGEK XQLLAEEGIK KHELDVQKSR RFIGIKVGXS

1251 NYSINELNET KLPVRVVAQX AATRSGWDTV LEGTEFKTTL AGADIQAGVX

1301 EKARVQAXII LKGIVNRIQS EEKLETNSTV WQKQAGRGST IETLKLPSFE

1351 SPTPPKLSAP GGYIVDIPKG NLKTEIEKLS KQPEYAYLKQ LQVAKNINWN

1401 QVQLAYQRWD YKQEGLTEAG AAIIALAVTV VTSGAGTGAV LGLNGAXAAA

1451 TDAAFASLAS QASVSFINNK GDVGKTLKEL GRSSTVKNLV VAAATAGVAD

1501 KIGASALXNV SDKQWINNLT VNLANXGQCR TD*
```

[0426] ORF114-1 and ORF114a show 89.8% identity in 1564 aa overlap

```
orf114a.pep MNKGLHRIIFSKKHSTMVAVAETANSQGKGKQAGSSVSVSLKTSGDLCGKLKTTLKTLVC
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    MNKGLHRIIFSKKHSTMVAVAETANSQGKGKQAGSSVSVSLKTSGDLCGKLKTTLKTLVC

orf114a.pep SLVSLSMXXXXXXQITTDKSAPKNXQVVILKTNTGAPLVNIQTPNGRGLSHNRYTQFDVD
            |||||||       |||||||||||| ||||||||||||||||||||||||||||||||||
orf114-1    SLVSLSMXXXXXXQITTDKSAPKNQQVVILKTNTGAPLVNIQTPNGRGLSHNRYTQFDVD

orf114a.pep NKGAVLNNDRNNNPFLVKGSAQLILNEVRGTASKLNGIVTVGGQKADVIIANPNGITVNG
            ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    NKGAVLNNDRNNNPFVVKGSAQLILNEVRGTASKLNGIVTVGGQKADVIIANPNGITVNG

orf114a.pep GGFKNVGRGILTIGAPQIGKDGALTGFDVRQGTLTVGAAGWNDKGGADYTGVLARAVALQ
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    GGFKNVGRGILTTGAPQIGKDGALTGFDVRQGTLTVGAAGWNDKGGADYTGVLARAVALQ

orf114a.pep GKLQGKNLAVSTGFQKVDYASGEISAGTAAGTKPTIALDTAALGGMYADSITLIAXEKGV
```

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
orf114-1    GKLOGKNLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGMYADSITLIANEKGV

orf114a.pep GVKNAGTLEAAXQLIVTSSGRIENSGRIATTADGTLASPTYLXIETTEKGAXGTFISNGG
            |||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
orf114-1    GVKNAGTLEAAXQLIVTSSGRIENSGRIATTADGTLASPTYLSIETTEKGAAGTFISNGG

orf114a.pep RIESKGLLVIETGEDIXLRNGAVVQNNGSRPATTVLNAGHNLVIESKTNVNNAKGSXNLS
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||  :||
orf114-1    RIESKGLLVIETGEDISLRNGAVVQNNGSRPATTVLNAGHNLVIESKTNVNNAKGPANLS

orf114a.pep AGGRTTINDATIQAGSSVYSSTKGDTXLGENTRIIAENVTVLSNGSIGSAAVIEAKDTAH
            | |||:|::|:||:|::||||:||:: ||:|||| : :|||||||:|:|||:||||||
orf114-1    ADGRTVIKEASIQTGTTVYSSSKGNAELGNNTRITGADVTVLSNGTISSSAVIDAKDTAH

orf114a.pep IESGKPLSLETSTVASNIRLNNGNIKGGKQLALLADDNITAKTTNLNTPGNLYVHTGKDL
            ||:|||||||:|||:|:||||:|:||||||||||||||||||||||||||||||||||||
orf114-1    IEAGKPLSLEASTVTSDIRLNGGSIKGGKQLALLADDNITAKTTNLNTPGNLYVHTGKDL

orf114a.pep NLNVDKDLSAASIHLKSDNAAHITGTSKTLTASKDMGVEAGLLNVTNTNLRTNSGNLHIQ
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
orf114-1    NLNVDKDLSAASIHLKSDNAAHITGTSKTLTASKDMGVEAGSLNVTNTNLRTNSGNLHIQ

orf114a.pep AAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSADGHVSLLANGNADFTGHNTLTA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    AAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSADGHVSLLANGNADFTGHNTLTA

orf114a.pep KADVXAGSVGKGRLKADNTNITSSSGDITLVAXXGIQLGDGKQRNSINGKHISIKNNGGN
            |||| |||||||||||||||||||||||||||  ||||||||||||||||||||||||||
orf114-1    KADVNAGSVGKGRLKADNTNITSSSGDITLVAGNGIQLGDGKQRNSINGKHISIKNNGGN

orf114a.pep ADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTHLNAQHERVTLNQVDAYAHRHLSI
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    ADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTHLNAQHERVTLNQVDAYAHRHLSI

orf114a.pep XGSQIWQNDKLPSANKLVANGVLAXNARYSQIADNTTLRAGAINLTAGTALVKRGNINWS
            :||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
orf114-1    TGSQIWQNDKLPSANKLVANGVLALNARYSQIADNTTLRAGAINLTAGTALVKRGNINWS

orf114a.pep TVSTKTLEDNAELKPLAGRLNIEAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    TVSTKTLEDNAELKPLAGRLNIEAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNA

orf114a.pep GAXSAQVSSLEAKGNIRLVTGXTDLRGSKITAGKNLVVATTKGKLNIEAVNNSFSNYFXT
            || |||||||||||||||||| |||||||||||||||||||||||||||||||||||| |
orf114-1    GAPSAQVSSLEAKGNIRLVTGETDLRGSKITAGKNLVVATTKGKLNIEAVNNSFSNYFPT

orf114a.pep QKXXXLNQKSKELEQQIAQLKKSSXKSKLIPTLQEERDRLAFYIQAINKEVKGKKPKGKE
            ||   ||||||||||||||||||| |||||||||||||||||||||||||||||||||||
orf114-1    QKAAELNQKSKELEQQIAQLKKSSPKSKLIPTLQEERDRLAFYIQAINKEVKGKKPKGKE

orf114a.pep YLQAKLSAQNIDLISAQGIEISGSDITASKKLNLHAAGVLPKAADSEAAAILIDGITDQY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    YLQAKLSAQNIDLISAQGIEISGSDITASKKLNLHAAGVLPKAADSEAAAILIDGITDQY

orf114a.pep EIGKPTYKSHYDKAALNKPSRLTGRTGVSIHAAAALDDARIIIGASEIKAPSGSIDIKAH
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf114-1    EIGKPTYKSHYDKAALNKPSRLTGRTGVSIHAAAALDDARIIIGASEIKAPSGSIDIKAH

orf114a.pep SDIVLEAGQNDAYTFLXTKGKSGXXIRKTKFTSTXXHLIMPAPVELTANGITLQAGGNIE
            |||||||||||||||| ||||||  |||||||||  ||||||||||||||||||||||||
orf114-1    SDIVLEAGQNDAYTFLKTKGKSGKIIRKTKFTSTRDHLIMPAPVELTANGITLQAGGNIE

orf114a.pep ANTTRFNAPAGKVTLVAGEXXQLLAEEGIHKHELDVQKSRRFIGIKVGXSNYSKNELNET
            |||||||||||||||||||  ||||||||||||||||||||||||||| |||||||||||
orf114-1    ANTTRFNAPAGKVTLVAGEELQLLAEEGIHKHELDVQKSRRFIGIKVGKSNYSKNELNET

orf114a.pep KLPVRVVAQXAATRSGWDTVLEGTEFKTTLAGADIQAGVXEKARVDAKIILKGIVNRIQS
            |||||||||:||||||||||||||||||||||||||||| ||||:|||||||||||||||
orf114-1    KLPVRVVAQTAATRSGWDTVLEGTEFKTTLAGADIQAGVGEKARADAKIILKGIVNRIQS

orf114a.pep EEKLETNSTVWQKQAGRGSTIETLKLPSFESPTPPKLSAPGGYIVDIPKGNLKTEIEKLS
            ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||:
orf114-1    EEKLETNSTVWQKQAGRGSTIETLKLPSFESPTPPKLSTPGGYIVDIPKGNLKTEIEKLA

orf114a.pep KQPEYAYLKQLQVAKNINWNQVQLAYDRWDYKQEGLTEAGAAIIALAVTVVTSGAGTGAV
            ||||||||||||||||:||||||||||:|||||||||:|||||::: ||::| | |: |:
```

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```
orf114-1    KQPEYAYLKQLQVAKNVNWNQVQLAYDKWDYKQEGLTRAGAAIVTIIVTALTYGYGATAA

orf114a.pep LGLNGA--------------XAATD----------AAFASLASQASVSFINNKGDVGKTL 1477
             |: ::              :||||          ||:||| |||:||:||||||||:|
orf114-1    GGVAASGSSTAAAAGTAATTTAAATTVSTATAMQTAALASLYSQAAVSIINNKGDVGKAL 1500

orf114a.pep KELGRSSTVKNLVVAAATAGVADKIGA----------SALXNVSDKQWINNL----TVNL 1523
            |:|| |:|||::|::| |||: :::||          : | : : :| | ||    ::||
orf114-1    KDLGTSDTVKQIVTSALTAGALNQMGADIAQLNSKVRTELFSSTGNQTIANLGGRLATNL 1560

orf114a.pep ANXGQCRTDX
            :| |
orf114-1    SNAGISAGINTAVN...
```

[0427] Homology with pspA Putative Secreted Protein of *N. meningitidis* (Accession Number AF030941)

[0428] ORF114 and pspA protein show 36% aa identity in 302 aa overlap:

```
Orf114:    1AVAETANSQGKGKQAGSSVSVSL----KTSGDXXXXXXXXXXXXXXXXXXXXXPAHAQ 56
             AVAE  +  GK  Q   + SV +      S                          PA A
pspA:     19AVAENVHRDGKSMQDSEAASVRVTGAASVSSARAAFGFRMAAFSVMLALGVAAFSPAPAS 78

Orf114:   57-ITTDKSAPKNQQVVILKTNTGAPLVNIQTPNGRGLSHNRXYAFDVDNKGAVLNNDRNN- 114
             I  DKSAPKNQQ VIL+T  G P VNIQTP+ +G+S NR   FDVD KG +LNN R+N
pspA:     79GIIADKSAPKNQQAVILQTANGLPQVNIQTPSSQGVSVNRFKQFDVDEKGVILNNSRSNT 138

Orf114:  115----------NPFVVKGSAQLILNEV-RGTASKLNGIVTVGGQKADVIIANPNGITVNGG 163
                       NP + +G A++I+N++     S LNG + VGG++A+V++ANP+GI VNGG
pspA:    139QTQLGGWIQGNPHLARGEARVIVNQIDSSNPSLLNGYIEVGGKRAEVVVANPSGIRVNGG 198

Orf114:  164GFKNVGRGILTTGAPQIGKDGALTGFDVVKAHWTVXAAGWNDKGGAXYTGVLARAVALQG 223
             G  N     LT+G P +  +G LTGFDV      +   G  D   A YT +L+RA  +
papA:    199GLINAASVTLTSGVPVL-NNGNLTGFDVSSGKVVIGGKGL-DTSDADYTRILSRAAEINA 256

Orf114:  224KXXGKXLAVSTGPQKVDYASGEISAGTAAGTK----PTIALDTAALGGMYADSITLIANE 279
               GK + V +G  K+D+        +A  +     PT+A+DTA LGGMYAD ITLI+ +
pspA:    257GVWGKDVKVVSGKNKLDFDGSLAKTASAPSSSDSVTPTVAIDTATLGGMYAQKITLISTD 316

Orf114:  280KG 291
             G
papA:    317NG 318
```

[0429] ORF114a is also homologous to pspA:

```
gil2623258 (AF030941) putative secreted protein
(Neisseria meningitidis) Length = 2273
Score +32 261 bits (659), Expect +32 3e-69
Identities = 203/663 (30%), Positives 314/663 (46%), Gaps 76/663 (11%)

Query:     1 MNKGLHRIIFSKKHSTMVAVAETANSQGKGKQAGSSVSVSLK-----TSGDXXXXXXXXX 55
             MNK  +++IF+KK S M+AVAE  +  GK  Q   + SV +      +S
Sbjct:     1 MNKRCYKVIFNKKRSCMMAVAENVHRDGKSMQDSEAASVRVTGAASVSSARAAFGFRMAA 60

Query:    56 XXXXXXXXXXXXXXXXXQITTKDSAPKNXQVVILKTNTGAPLVNIQTPNGRGLSHNRYT 115
                                I  DKSAPKN Q VIL+T  G P VNIQTP+ +G+S NR+
Sbjct:    61 FSVMLALGVAAFSPAPASGIIADKSAPKNQQAVILQTANGLPQVNIQTPSSQGVSVNRFK 120

Query:   116 QFDVDNKGAVLNNDRNN-----------NPFLVKGSAQLILNEV-RGTASKLNGIVTVGG 163
             QFDVD KG +LNN R+N-----------NP L +G A++I+N++     S LNG + VGG
Sbjct:   121 QFDVDEKGVILNNSRSNTQTQLGGWIQGNPHLARGEARVIVNQIDSSNPSLLNGYIEVGG 180

Query:   164 QKADVIIANPNGITVNGGGFKNVGRGILTIGAPQIGKDGALTGFDVRQGTLTVGAAGWND 223
             ++A+V++ANP+GI VNGGG  N     LT G P +  +G LTGFDV  G + +G  G  D
Sbjct:   181 KRAEVVVANPSGIRVNGGGLINAASVTLTSGVPVL-NNGNLTGFDVSSGKVVIGGKGL-D 238
```

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```
Query:  224 KGGADYTGVLARAVALQGKLQGKNLAVSTGPQKVDYASGEISAGTAAGTK----PTIALD 279
            ADYT +L+RA  +   + GK++ V +G  K+D+        +A  +     PT+A+D
Sbjct:  239 TSDADYTRILSRAAEINAGVWGKDVKVVSGKNKLDFDGSLAKTASAPSSSDSVTPTVAID 298

Query:  280 TAALGGMYADSITLIAXEKGVGVKNAGTLEAAK-QLIVTSSGRIENSGRIATTADGTEAS 338
            TA LGGMYAD ITLI+ + G  ++N G + AA   + +++ G++ NSG I
Sbjct:  299 TATLGGMYADKITLISTDNGAVIRNKGRIFAATGGVTLSADGKLSNSGSI-------DAA 351

Query:  339 PTYLXIETTEKGAXGTFISNGGRIESKGLLVIETGEDIXLRNGAVVQNNGSRPATTVLNA 398
              +  +T +        +  G I S    V++  + I  + G +    GS     + +
Sbjct:  352 EITISAQTVD--------NRQGFIRSGKGSVLKVSDGINNQAGLI----GSAGLLDIRDT 399

Query:  399 GHNLVIESKTNVNNAKGS----XNLSAGGRTTINDATIQAGSSVYSSTKGDTXLGENTRI 454
            G     +S  ++NN  G+     ++S   ++  ND  + A   V S +  D   G+
Sbjct:  400 G-----KSSLHINNTDGTIIAGKDVSLQAKSLDNDGILTAARDV-SVSLHDDFAGKRDIE 453

Query:  455 IAENVTVLSNGSIGSAAVIEAKDTAHIESGKPLSLETSTVASNIRLNNGNIKGGKQLALL 514
              +T  + G + +  +I+A DT  + + +  +  +  + S  R       G     L+
Sbjct:  454 AGRTLTFSTQGRLKNTRIIQAGDTVSLTAAQIDNTVSGKIQSGNRTGLNGKNGITNRGLI 513

Query:  515 ADDNIT-----AKTTNLNTPGNLYVHTGKDLNLNVDKDLSAASIHLKSDNAAHITGTSKT 569
             + IT     AK+ N  T G +Y   G  + +  D  L+           AA
Sbjct:  514 NSNGITLLQTEAKSDNAGT-GRIY---GSRVAVEADTLLNREETVNGETKAA-------V 562

Query:  570 LTASKDMGVEAGXXXXXXXXXXXXSGNLHIQAA---KGNIQLRNTKL-NAAKALETTALQ 625
            + A + + + A              SG+LHI +A      +Q  NT L N + A+E++
Sbjct:  563 IAARERLDIGAREIENREAALLSSSGDLHIGSALNGSRQVQGANTSLHNRSAAIESS--- 619

Query:  626 GNI 628
            GNI
Sbjct:  620 GNI 622

Score +32 37.5 bits (65), Expect = 0.53
Identities = 87/432 (20%), Positives +32 159/432 (36%), Gaps = 62/432 (14%)

Query:  239 LQGKLQGKNLAVSTGPQKVDYASGEISAGTAAGTKPTIALDTAALGGMYADSITLIAXEK 298
            LQG LQGKN+  + G    +  +G I A  A   K        A   + + S T     +
Sbjct: 1023 LQGDLQGKNIFAAAGSDITN--TGSIGAENALLLK--------ASNNIESRSETRSNQNE 1072

Query:  299 GVGVKNAGTLEAAKQLIVTSSGRI--ENSGRIATTADGTEASPTYLXIETTEKGAXG-TF 355
              V+N G + A   L    +G +  +    I  TA            E T +   G T
Sbjct: 1073 QGSVRNIGRV-AGIYLTGRQNGSVLLDAGNNIVLTAS----------ELTNQSEDGQTV 1120

Query:  356 ISNGGRIESKGLLVIETGEDIXLRNGAVVQNNGSRPATTVLNAGHNLVIESK-------T 408
            ++ GG I S    +      I   +  V++   +   +T+   G NL + +K
Sbjct: 1121 LNAGGDIRSDTTGISRNQNTIFDSDNYVIRKEQNEVGSTIRTRG-NLSLNAKGDIRIPAA 1179

Query:  409 NVNNAKGSXNLSAGGRTTINDATIQAGSS--------VYSSTKGDTXLGENTRIIAENVT 460
             V + +G   L+AG      D  ++AG +          Y+   G     + TR +
Sbjct: 1180 EVGSEQGRLKLAAG-----RDIKVEAGKAHTETEDALKYTGRSGGGIKQKMTRHLKNQNG 1234

Query:  461 VLSNGSIGSAAVIEAKDTAHIESGKPLSLETSTVASWIRLNNGNIKGGKQLALLADDNIT 520
              +G++    +I          +G  +  +  T+ S    NN  +K  +  +  A+ N
Sbjct: 1235 QAVSGTLDGKEIILVSGRDITVTGSNIIADNHTILS--AKNNIVLKAAETRSRSAEMNKK 1292

Query:  521 AKTTNLNTPG-NLYVHTGKDLNLNVDKDLSAASIHLKSDN-------AAHITGTSKTLTA 572
             K+  + + G      + KD   N  + +S     + S N          H T T  T+++
Sbjct: 1293 EKSGLMGSGGIGFTAGSKKDTQTNRSETVSHTESVVGSLNGNTLISAGKHYTQTGSTISS 1352

Query:  573 SK-DMGVEAGXXXXXXXXXXXXSGNLHIQAAKG-----NIQLRNTKLNAAKALETTALQG 626
             + D+G+ +G               +  +   KG     ++ + NT + A  A++     G
Sbjct: 1353 PQGDVGISSGKISIDAAQNRYSQESKQVYEQKGVTVAISVPVVNTVMGAVDAVKAVQTVG 1412

Query:  627 NIVSDGLHAVSA 638
              +  ++A++A
Sbjct: 1413 KSKNSRVNAMAA 1424
```

[0430] Amino acids 1-1423 of ORF114-1 were cloned in the pGex vector and expressed in *E. coli*, as described above. GST-fusion expression was visible using SDS-PAGE, and **FIG. 5** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF114-1.

[0431] Based on these results, including the homology with the putative secreted protein of *N. meningitidis* and on the presence of a transmembrane domain, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 14

[0432] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>

```
   1 CGCTTCATTC ATGATGAAGC AGTCGGCAGC AACATCGGCG GCGGCAAAAT
  51 GATTGTTGCA GCCGGGCAGG ATATCAATGT ACGCGGCAnA AGCCTTATTT
 101 CTGATAAGGG CATTGTTTTA AAAGCAGGAC ACGACATCGA TATTTCTACT
 151 GCCCATAATC GCTATACCGG CAATGAATAC CACGAGAGCA wAAAwTCAGG
 201 CGTCATGGGT ACTGGCGGAT TGGGCTTTAC TATCGGTAAC CGGAAAACTA
 251 CCGATGACAC TGATCGTACC AATATTGTsC ATACAGGCAG CATTATAGGC
 301 AGCCTGAaTG GAGACACCGT TACAGTTGCA GGAAACCGCT ACCGACAAAC
 351 CGGCAGTACC GTCTCCAGCC CCGACGGGCG CAATACCGTC ACAGCCAAAw
 401 GCATAGATGT AGAGTTCGCA AACAACCGGT ATGCCACTGA CTACGcCCAT
 451 ACCCAGGGAA CAAAAAGGCC TTACCGTCGC CCTCAATGTC CCGGTTGTCC
 501 AAGCTGCACA AAACTTCATA CAAGCAGCCC AAAATGTGGG CAAAAGTAAA
 551 AATAAACGCG TTAATGCCAT GGCTGCAGCC AATGCTGCAT GGCAGAGTTA
 601 TCAAGCAACC CAACAAATGC AACAATTTGC TCCAAGCAGC AGTGCGGGAC
 651 AAGGTCAAAA CTACAATCAA AGCCCCAGTA TCAGTGTGTC CATTAC.TAC
 701 GGCGAACAGA AAAGTCGTAA CGAGCAAAAA AGACATTACA CCGAAgCGGC
 751 AgCAAGTCAA ATTATCGGCA AAGGGCAAAC CACACTTGCG GCAACAGGAA
 801 GTGGGGAGCA GTCCAATATC AATATTACAG GTTCCGATGT CATCGGCCAT
 951 GCAGGTACTC C.CTCATTGC AAGCAACCAT ATCAGACTCC AATCTGCCAA
 901 ACAGGACGGC AGCGAGCAAA GCAAAAACAA AAGCAGTGGT TGGAATGCAG
 951 GCGTACGTnn CAAAATAGGC AAcGGCATCA GGTTTGGAAT TACCGCCGGA
1001 GGAAATATCG GTAAAGGTAA AGAGCAAGGG GGAAGTACTA CCCACCGCCA
1051 CACCCATGTC GGCAGCACAA CCGGCAAAAC TACCATCCGA AGCGGCGGGG
1101 GATACCACCC TCAAAGGTGT GCAGCTCATC GGCAAAGGCA TACAGGCAGA
1151 TACGCGCAAC CTGCATATAG AAAGTGTTCA AGATACTGAA ACCTATCAGA
1201 GCAAACAGCA AAACGGCAAT GTCCAAGTTt ACTGTCGGTT ACGGATTCAG
1251 TGCAAGCGGC AGTTACCGCC AAAGCAAAGT CAAAGCAGAC CATGCCTCCG
1301 TAACCGGGCA AAgCGGTATT TATGCCGGAG AAGACGGCTA TCAAATyAAA
1351 GTyAGAGACA ACACAGACCT yAAGGGCGGT ATCATCACGT CTAGCCAAAG
1401 CGCAGAAGAT AAGGGCAAAA ACCTTTTTCA GACGGCCACC CTTACTGCCA
1451 GCGACATTCA AAACCACAGC CGCTACGAAG GCAGAAGCTT CGGCATAGGC
1501 GGCAGTTTCG ACCTGAACGG CGGCTGGGAC GGCACGGTTA CCGACAAACA
1551 AGGCAGGCCT ACCGACAGGA TAAGCCCGGC AGCCGGCTAC GGCAGCGACG
1601 GAGACAGCAA AAACAGCACC ACCCGCAGCG GCGTCAACAC CCACAACATA
1651 CACATCACCG ACGAAGCGGG ACAACTTGCC CGAACAGGCA GGACTGCAAA
```

-continued

```
1701 AGAAACCGAA GCGCGTATCT ACACCGGCAT CGACACCGAA ACTGCGGATC

1751 AACACTCAGG CCATCTGAAA AACAGCTTCG AC...
```

[0433] This corresponds to the amino acid sequence <SEQ ID 64; ORF116>:

```
  1..RFIHDEAVGS NIGGGKNIVA AGQDINVRGX SLISDKGIVL KAGADIDIST

 51  AHNRYTGNEY HESXXSGVMG TGGLGFTIGN RKTTDDTDRT NIVHTGSIIG

101  SLNGDTVTVA GNRYRQTGST VSSPEGRNTV TAKXIDVEFA NNRYATDYAH

151  TQEQKGLTVA LNVPVVQAAQ NFIQAAQNVG KSKNKRVNAM AAANAAWQSY

201  QATQQMQQFA PSSSAGQGQN YNQSPSISVS IXYGEQKSRN EQKRNYTEAA

251  ASQIIGKGQT TLAATGSGEQ SNINITGSDV IGHAGTXLIA DNHIRLQSAX

301  QDGSEQSKNK SSGWNAGVRX KIGNGIRFGI TAGGNIGKGK EQGGSTTHRH

351  THVGSTTGKT TIRSGGDTTL KGVQLIGXGI QADTRNLHIE SVQDTETYQS

401  KQQNGNVQVT VGYGFSASGS YRQSKVKADH ASVTGQSGIY AGEDGYQIKV

451  RDNTDLKGGI ITSSQSAEDK GKNLFQTATL TASDIQNHSR YEGRSFGIGG

501  SFDLNGGWDG TVTDKQGRPT DRISPAAGYG SDGDSKNSTT RSGVNTHNIH

551  ITDEAGQLAR TGRTAKETEA RIYTGIDTET ADQHSGHLKN SFD...
```

[0434] Computer analysis of this amino acid sequence gave the following results:

[0435] Homology with pspA Putative Secreted Protein of *N. meningitidis* (Accession Number AF030941)

[0436] ORF116 and pspA protein show 38% aa identity in 502 aa overlap:

```
Orf116:  6    EAVGSNIGGGKMIVAAGQDINVRGXSLISDKGIVLKAGHDIDISTAHNRYTGNEYHESXX 65
              +AV   + G ++I+ +G+DI V G ++I+D   +L A ++I +  A  R    E ++
PspA:    1235 QAVSGTLDGKEIILVSGRDITVTGSNIIADNHTILSAKNNIVLKAAETRSRSAEMNKKEK 1294

Orf116:  66   XXXXXXXXXXXXXXNRKXXXXXXRTNIVHTGSIIGSLNGDTVTVAGNRYRQTGSTVSSPE 125
                           ++K          + HT S++GSLNG+T+  AG   Y QTGST+SSP+
PspA:    1295 SGLMGSGGIGFTAGSKKDTQTNRSETVSHTESVVGSLNGNTLISAGKHYTQTGSTISSPQ 1354

Orf116:  126  GRNTVTAKXIDVEFANNRYATDYAHTQEQKGLTVALNVPXXXX---XXXXXXXXXXGKS 182
              G   +++  I ++ A NRY+ +     EQKG+TVA++VP               GKS
PspA:    1355 GDVGISSGKISIDAAQNRYSQESKQVYEQKGVTVAISVPVVNTVMGAVDAVKAVQTVGKS 1414

Orf116:  183  KNKRVXXXXXXXXXWQSYQATQQMQQFA--PSSSAGQGQNYNQSPSISVSIXYGEQKSRN 240
              KN RV          +   +   +   A  P  +AGQG        ISVS+ YGEQK+ +
PspA:    1415 KNSRVNAMAAANALNKGVDSGVALYNAARNPKKAAGQG--------ISVSVTYGEQKNTS 1466

Orf116:  241  EQKRHYTEAAASQIIGKGQTTLAATGSGEQSNINITGSDVIGHAGTXLIADNHIRLQSAK 300
              E +   T+    +I G G+ +L A+G+G+ S I ITGSDV G  GT L A+N +++++A+
PspA:    1467 ESRIKGTQVQEGKITGGGKVSLTASGAGKDSRITITGSDVYGGKGTRLKAENAVQIEAAR 1526

Orf116:  301  QDGSEQSKNKSSGWNAGVRXKIGNGIRFGITAXXXXXXXXXXXXXSTTHRHTHVGSTTGKT 360
              Q   E+S+NKS+G+NAGV   I  GI FG TA             T +R++H+GS   +T
PspA:    1527 QTHQERSENKSAGFNAGVAIAINKGISFGFTAGANYGKGYGNGDETAYRNSHIGSKDSQT 1586

Orf116:  361  TIRSGGDTTLKGVQLIGKGIQADTRNLHIESVQDTETYQSKQQNGNVQVTVGYGFSASGS 420
               I SGGDT +KG QL GKG+     +LHIES+QDT  ++ KQ+N + QVTVGYGFS  GS
PspA:    1587 AIESGGDTVIKGGQLKGKGVGVTAESLHIESLQDTAVFKGKQENVSAQVTVGYGFSVGGS 1646
```

-continued

```
Orf116:  421  YRQSKVKADHASVTGQSGIYAGEDGYQIKVRDNTDLKGGIITSSQSAEDKGKNLFQTATL 480
              Y +SK  +D+ASV  QSGI+AG DGY+I+V   T L G  + S     DK KNL +T+ +
PspA:    1647 YNRSKSSSDYASVNEQSGIFAGGDGYRIRVNGKTGLVGAAVVSD---ADKSKNLLKTSEI 1703

Orf116:  481  TASDIQNHSRYEGRSFGIGGSF 502
                DIQNH+     + G+ G F
PspA:    1704 WHKDIQNHASAAASALGLSGGF 1725
```

[0437] Based on homology with pspA, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 15

[0438] The following partial DNA sequence was identified in *N. meningitidis* SEQ ID 65>

```
  1..ACGACCGGCA GCCTCGGCGG CATACTGGCC GGCGGCGGCA CTTCCCTTGC

 51  CGCACCGTAT TTGGACAAAG CGGCGGAAAA CCTCGGTCCG GCGGGCAAAG

101  CGGCGGTCAA CGCACTGGGC GGTGCGGCCA TCGGCTATGC AACTGGTGGT

151  AGTGGTGGTG CTGTGGTGGG TGCGAATGTA GATTGGAACA ATAGGCAGCT

201  GCATCCGAAA GAAATGGCGT TGGCCGACAA ATATGCCGAA GCCCTCAAGC

251  GCGAAGTTGA AAAACGCGAA GGCAGAAAAA TCAGCAGCCA AGAAGCGGCA

301  ATGAGAATCC GCAGGCAGAT ATGCGTTGGG TGGACAAAGG TTCCCAAGAC

351  GGCTATACCG ACCAAAGCGT CATATCCCTT ATCGGAATGA
```

[0439] This corresponds to the amino acid sequence <SEQ ID 66; ORF118>:

```
  1..TTGSLGGILA GGGTSLAAPY LDKAAENLGP AGKAAVNALG GAAIGYATGG

 51  SGGAVVGANV DWNNRQLHPK EMALADKYAE ALKREVEKRE GRKISSQEAA

101  MRIRRQICVG WTKVPKTAIP TKASYPLSE*
```

[0440] Computer analysis of this amino acid sequence reveals two putative transmembrane domains.

[0441] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 16

[0442] The following partial DNA sequence was identified in *N. meningitidis* SEQ ID 67>

```
  1..CAATGCCGTC TGAAAAGCTC ACAATYTTAC AGACGGCATT TGTTATGCAA

 51  GTACATATAC AGATTCCCTA TATACTGCCC AGrkGCGTGC GTgGCTGAAG

101  ACACCCCCTA CGCTTGCTAT TTGrAACAGC TCCAAGTCAC CAAAGACGTC

151  AACTGGAACC AGGTACWACT GGCGTACGAC AAATGGGACT ATAAACAGGA

201  AGGCTTAACC GGAGCCGGAG CAGCGATTAT TGCGCTGGCT GTTACCGTGG
```

-continued

```
251  TTACTGCGGG CGCGGGAgCC GGAGCCGCAC TGGGcTTAAA CGGCGCGGCc

301  GCAGCGGCAA CCGATGCCGC ATTCGCCTCG CTGGCCAGCC AGGcTTCCGT

351  ATCGCTCATC AaCAACAAAG GCAATATCGG TAaCACCCTG AAAGAGCTGG

401  GCAGAAGCAG CACGGTGAAA AATCTGATGG TTGCCGTCGc tACCGCAgGC

451  GTagCcgaCA AAATCGGTGC TTCGGCACTG AACAATGTCA GCGATAAGCA

501  GTGGATCAAC AACCTGACCG TCAACCTGGC CAATGCGGGC AGTGCCGCAC

551  TGATTAATAC CGCTGTCAAC GGCGGCAGCc tgAAAGACAA TCTGGAAGCG

601  AATATCCTTG CGGCTTTGGT GAATACTGCG CATGGAGAAG CAGCCAGTAA

651  AATCAAACAG TTGGATCAGC ACTACATTAC CCACAAGATT GCCCaTGCCA

701  TAGCGGGCTG TGCGGcTGCG GCGGCGAATA AGGGCAAGTG TCAGGATGGT

751  GCGATAgGTG CGGCTGTGGG CGAGATAGTC GGGGAgGCTT TGACAAACGG

801  CAAAAATCCT GACACTTTGA CAGCTAAAgA ACGCGaACAG ATTTTGGCAT

851  ACAGCAAACT GGTTGCCGGT ACGGTAAGCG GTGTGGTCGG CGGCGATGTA

901  AATGCGGCGG CGAATGCGGC TGAGGTAGCG GTGAAAAATA ATCAGCTTAG

951  CGACAAAtGA
```

[0443] This corresponds to the amino acid sequence <SEQ ID 68; ORF41>:

```
  1..QCRLKSSQFY RRHLLCKYIY RFPIYCPXAC VAEDTPYACY LXQLQVTKDV

 51  HWNQVXLAYD KWDYKQEGLT GAGAAIIALA VTVVTAGAGA GAALGLNGAA

101  AAATDAAFAS LASQASVSLI NNKGNIGNTL KELGRSSTVK NU4VAVATAG

151  VADKIGASAL NNVSDKQWIN NLTVNLANAG SAALINTAVN GGSLKDNLEA

201  NILAALVNTA HGEAASKIKQ LDQHYITHKI AHAIAGCAAA AANKGKCQDG

251  AIGAAVGEIV GEALTNGKNP DTLTAKEREQ ILAYSKLVAG TVSGVVGGDV

301  NAAANAAEVA VKNNQLSDK*
```

[0444] Further work revealed the complete nucleotide sequence <SEQ ID 69>:

```
   1 ATGCAAGTAA ATATTCAGAT TCCCTATATA CTGCCCAGAT GCGTGCGTGC

  51 TGAAGACACC CCCTACGCTT GCTATTTGAA ACAGCTCCAA GTCACCAAAG

 101 ACGTCAACTG GAACCAGGTA CAACTGGCGT ACGACAAATG GGACTATAAA

 151 CAGGAAGGCT TAACCGGAGC CGGAGCAGCG ATTATTGCGC TGGCTGTTAC

 201 CGTGGTTACT GCGGGCGCGG GAGCCGGAGC CGCACTGGGC TTAAACGGCG

 251 CGGCCGCAGC GGCAACCGAT GCCGCATTCG CCTCGCTGGC CAGCCAGGCT

 301 TCCGTATCGC TCATCAACAA CAAAGGCAAT ATCGGTAACA CCCTGAAAGA

 351 GCTGGGCAGA AGCAGCACGG TGAAAAATCT GATGGTTGCC GTCGCTACCG

 401 CAGGCGTAGC CGACAAAATC GGTGCTTCGG CACTGAACAA TGTCAGCGAT

 451 AAGCAGTGGA TCAACAACCT GACCGTCAAC CTGGCCAATG CGGGCAGTGC
```

-continued

```
 501 CGCACTGATT AATACCGCTG TCAACGGCGG CAGCCTGAAA GACAATCTGG
 551 AAGCGAATAT CCTTGCGGCT TTGGTGAATA CTGCGCATGG AGAAGCAGCC
 601 AGTAAAATCA AACAGTTGGA TCAGCACTAC ATTACCCACA AGATTGCCCA
 651 TGCCATAGCG GGCTGTGCGG CTGCGGCGGC GAATAAGGGC AAGTGTCAGG
 701 ATGGTGCGAT AGGTGCGGCT GTGGGCGAGA TAGTCGGGGA GGCTTTGACA
 751 AACGGCAAAA ATCCTGACAC TTTGACAGCT AAAGAACGCG AACAGATTTT
 801 GGCATACAGC AAACTGGTTG CCGGTACGGT AAGCGGTGTG GTCGGCGGCG
 851 ATGTAAATGC GGCGGCGAAT GCGGCTGAGG TAGCGGTGAA AAATAATCAG
 901 CTTAGCGACA AAGAGGGTAG AGAATTTGAT AACGAAATGA CTGCATGCGC
 951 CAAACAGAAT AATCCTCAAC TGTGCAGAAA AAATACTGTA AAAAAGTATC
1001 AAAATGTTGC TGATAAAAGA CTTGCTGCTT CGATTGCAAT ATGTACGGAT
1051 ATATCCCGTA GTACTGAATG TAGAACAATC AGAAAACAAC ATTTGATCGA
1101 TAGTAGAAGC CTTCATTCAT CTTGGGAAGC AGGTCTAATT GGTAAAGATG
1151 ATGAATGGTA TAAATTATTC AGCAAATCTT ACACCCAAGC AGATTTGGCT
1201 TTACAGTCTT ATCATTTGAA TACTGCTGCT AAATCTTGGC TTCAATCGGG
1251 CAATACAAAG CCTTTATCCG AATGGATGTC CGACCAAGGT TATACACTTA
1301 TTTCAGGAGT TAATCCTAGA TTCATTCCAA TACCAAGAGG GTTTGTAAAA
1351 CAAAATACAC CTATTACTAA TGTCAAATAC CCGGAAGGCA TCAGTTTCGA
1401 TACAAACCTA AAAAGACATC TGGCAAATGC TGATGGTTTT AGTCAAAAAC
1451 AGGGCATTAA AGGAGCCCAT AACCGCACCA ATTTTATGGC AGAACTAAAT
1501 TCACGAGGAG GACGCGTAAA ATCTGAAACC CAAACIGATA TTGAAGGCAT
1551 TACCCGAATT AAATATGAGA TTCCTACACT AGACAGGACA GGTAAACCTG
1601 ATGGTGGATT TAAGGAAATT TCAAGTATAA AAACTGTTTA TAATCCTAAA
1651 AAATTTTCTG ATGATAAAAT ACTTCAAATG GCTCAAAATG CTGCTTCACA
1701 AGGATATTCA AAAGCCTCTA AAATTGCTCA AAATGAAAGA ACTAAATCAA
1751 TATCGGAAAG AAAAAATGTC ATTCAATTCT CAGAAACCTT TGACGGAATC
1801 AAATTTAGAT CATATTTTGA TGTAAATACA GGAAGAATTA CAAACATTCA
1851 CCCAGAATAA
```

[**0445**] This corresponds to the amino acid sequence <SEQ ID 70; ORF41-1>:

```
   1 MQVNIQIPYI LPRCVRAEDT PYACYLKQLQ VTKDVNWNQV QLAYOKWDYK
  51 QEGLTGAGAA IIALAVTVVT AGAGAGAALG LNGAAAAATD AAFASLASQA
 101 SVSLINNKGN IGNTLKELGR SSTVKNLHVA VATAGVADKI GASALNNVSD
 151 KQWINNLTVN LANAGSAALI NTAVNGGSLX DNLEANILAA LVNTAHGEAA
 201 SKIKQLDQHY ITHKIAHAIA GCAAAAANKG KCQDGAIGAA VGEIVGEALT
 251 NGKNPDTLTA KEREQILAYS KLVAGTVSGV VGGDVNAAAN AAEVAVKNNQ
 301 LSDKLGREFD NEMTACAKQN NPQLCRKNTV KKYQNVADKR LAASIAICTD
```

-continued

```
351 ISRSTECRTI RKQHLIDSRS LHSSWEAGLX GKDDEWYKLF SKSYTQADLA

401 LQSYHLNTAA KSWLOSGNTK PLSEWNSDQG YTLISGVNPR FIPIPRGFVK

451 QHTFITNVKY PEGISFDTNL KRMLANADGF SQKQGIKGAH NRTNFNAELN

501 SRGGRVKSET QTDIEGITRI KYEIPTLDRT GKPDGGFKEI SSIKTVYNPK

551 KFSDDKILQH AQNAASQGYS KASKIAQNER TKSISERKNV IQFSETFDGI

601 KFRSYFDVNT GRITNIHPE*
```

[0446] Computer analysis of this amino acid sequence predicts a transmembrane domain, and homology with an ORF from *N. meningitidis* (strain A) was also found.

[0447] ORF41 shows 92.8% identity over a 279 aa overlap with an ORF (ORF41a) from strain A of *N. meningitidis:*

```
          10        20        30        40        50        60        69
orf41.pep   YRRHLLCKYIYRFPIYCPXACVAEDTPYACYLXQLQVTKDVNWNQVXLAYDKWDYKQEGL
                                          11 1111:1::11111 1111:11111111
orf41a                                    YLKQLQVAXNINWNQVQLAYDRWDYKQEGL
                                                    10        20        30

          70        80        90       100       110       120       129
orf41.pep   TGAGAAIIALAVTVVTAGAGAGAALGLNGAAAAATDAAFASLASQASVSLINNKGNIGNT
            | ||||||||||||||:|||:||:|||||| |||||||||||||||||:|||||::|:|
orf41a      TEAGAAIIALAVTVVTSGAGTGAVLGLNGAXAAATDAAFASLASQASVSFINNKGDVGKT
                     40        50        60        70        80        90

          130       140       150       160       170       180       189
orf41.pep   LKELGRSSTVKNLMVAVATAGVADKIGASALNNVSDKQWINNLTVNLANAGSAALINTAV
            |||||||||||||:||:||||||||||||||| |||||||||||||||||||||||||||
orf41a      LKELGRSSTVKNLVVAAATAGVADKIGASALXNVSDKQWINNLTVNLANAGSAALINTAV
                    100       110       120       130       140       150

          190       200       210       220       230       240       249
orf41.pep   NGGSLKDNLEANILAALVNTAHGEAASKIKQLDQHYITHKIAHAIAGCAAAAANKGKCQD
            ||||||| |||||||||||||||||||||||||||:|||||||||||||||||||||||
orf41a      NGGSLKDXLEANILAALVNTAHGEAASKIKQLDQHYIVHKIAHAIAGCAAAAANKGKCQD
                    160       170       180       190       200       210

          250       260       270       280       290       300       309
orf41.pep   GAIGAAVGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAAEV
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf41a      GAIGAAVGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAAEV
                    220       230       240       250       260       270

          310       320
orf41.pep   AVKNNQLSDKX
            |||||||||
orf41a      AVKNNQLSDXEGREFDNENTACAKQNXPQLCRXWIVKKYQNVADKRLAASIAICTDISRS
                    280       290       300       310       320       330
```

[0448] A partial ORF41a nucleotide sequence <SEQ ID 71> is:

```
  1 TATCTGAAAC AGCTCCAAGT AGCGAAAAAC ATCAACTGGA ATCAGGTGCA

 51 GCTTGCTTAC GACAGATGGG ACTACAAACA GGAGGGCTTA ACCGAAGCAG

101 GTGCGGCGAT TATCGCACTG GCCGTTACCG TGGTCACCTC AGGCGCAGGA

151 ACCGGAGCCG TATTGGGATT AAACGGTGCG NCCGCCGCCG CAACCGATGC

201 AGCATTCGCC TCTTTGGCCA GCCAGGCTTC CGTATCGTTC ATCAACAACA

251 AAGGCGATGT CGGCAAAACC CTGAAAGAGC TGGGCAGAAG CAGCACGGTG
```

-continued

```
 301 AAAAATCTGG TGGTTGCCGC CGCTACCGCA GGCGTAGCCG ACAAAATCGG
 351 CGCTTCGGCA CTGANCAATG TCAGCGATAA GCAGTGGATC AACAACCTGA
 401 CCGTCAACCT AGCCAATGCG GGCAGTGCCG CACTGATTAA TACCGCTGTC
 451 AACGGCGGCA GCCTGAAAGA CANTCTGGAA GCGAATATCC TTGCGGCTTT
 501 GGTCAATACC GCGCATGGAG AAGCAGCCAG TAAAATCAAA CAGTTGGATC
 551 AGCACTACAT AGTCCACAAG ATTGCCCATG CCATAGCGGG CTGTGCGGCA
 601 GCGGCGGCGA ATAAGGGCAA GTGTCAGGAT GGTGCGATAG GTGCGGCTGT
 651 GGGCGAGATA GTCGGGGAGG CTTTGACAAA CGGCAAAAAT CCTGACACTT
 701 TGACAGCTAA AGAACGCGAA CAGATTTTGG CATACAGCAA ACTGGTTGCC
 751 GGTACGGTAA GCGGTGTGGT CGGCGGCGAT GTAAATGCGG CGGCGAATGC
 801 GGCTGAGGTA GCGGTGAAAA ATAATCAGCT TAGCGACNAA GAGGGTAGAG
 851 AATTTGATAA CGAAATGACT GCATGCGCCA AACAGAATAN TCCTCAACTG
 901 TGCAGAAAAA ATACTGTAAA AAAGTATCAA AATGTTGCTG ATAAAAGACT
 951 TGCTGCTTCG ATTGCAATAT GTACGGATAT ATCCCGTAGT ACTGAATGTA
1001 GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT TCATTCATCT
1051 TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTCAG
1101 CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTTGAATA
1151 CTGCTGCTAA ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA
1201 TGGATGTCCG ACCAAGGTTA TACACTTATT TCAGGAGTTA ATCCTAGATT
1251 CATTCCAATA CCAAGAGGGT TTGTAAAACA AAATACACCT ATTACTAATG
1301 TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTANA AAGACATCTG
1351 GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCCATAA
1401 CCGCACCAAT NTTATGGCAG AACTAAATTC ACGAGGAGGA NGNGTAAAAT
1451 CTGAAACCCA NACTGATATT GAAGGCATTA CCCGAATTAA ATATGATATT
1501 CCTACACTAG ACAGGACAGG TAAACCTGAT GGTGGATTTA AGGAAATTTC
1551 AAGTATAAAA ACTGTTTATA ATCCTAAAAA NTTTTNNGAT GATAAAATAC
1601 TTCAAATGGC TCAANATGCT GNTTCACAAG GATATTCAAA AGCCTCTAAA
1651 ATTGCTCAAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT
1701 TCAATTCTCA GAAACCTTTG ACGGAATCAA ATTTAGANNN TATNTNGATG
1751 TAAATACAGG AAGAATTACA AACATTCACC CAGAATAA
```

[0449] This encodes a protein having the partial amino acid sequence <SEQ ID 72>:

```
  1 YLKQLQVAKN INWNQVQLAY DRWDYKQEGL TEAGAAIIAL AVTVVTSGAG
 51 TGAVLGLNGA XAAATDAAFA SLASQASVSF INNKGDVGKT LKELGRSSTV
101 KNLVVAAATA GVADKIGASA LXNVSDKQWI NNLTVNLANA GSAALINTAV
151 NGGSLKDXLE ANILAALVNT AHGEAASKIK QLDQHYIVRK IAHAIAGCAA
201 AAANKGKCQD GAIGAAVGEI VGEALTNGKN PDTLTAKERE QILAYSKLVA
```

-continued

```
251 GTVSGVVGGD VNAAANAAEV AVKNNQLSDX EGREFONENT ACAKQNXPQL

301 CRKNTVKKYQ NVADKRLAAS IAICTDISRS TECRTIRKQH LIDSRSLHSS

351 WEAGLIGKDD EWYKLFSKSY TQADLALQSY BLNTAAKSWL QSGNTKPLSE

401 VNSDQGYTLI SGVNPRFIFI PRGFVKQNTP ITNVKYPEGI SFDTNLXRHL

451 ANADGFSQEQ GIKGAHNRTN XMAELNSRGG XVKSETXTDI EGITRIKYEI

501 PTLDRTGKPD GGFKEISSIK TVYNPKXFXD DKILQMAQXA XSQGYSKASK

551 IAQNERTKSI SERKNVIQFS ETFDGIKFRX YXDVNTGRIT NIHPE*
```

[**0450**] ORF41a and ORF41-1 show 94.8% identity in 595 aa overlap:

```
                                        10        20        30
orf41a.pep                          YLKQLQVAKNINWNQVQLAYDRWDYKQEGLTEAGAA
                                    |||||||:|::||||||||||:|||||||||| ||||
orf41-1     MQVNIQIPYILPRCVRAEDTPYACYLKQLQVTKDVNWNQVQLAYDKWDYKQEGLTGAGAA
                   10        20        30        40        50        60

              40        50        60        70        80        90
orf41a.pep  IIALAVTVVTSGAGTGAVLGLNGAXAAATDAAFASLASQASVSFINNKGDVGKTLKELGR
            ||||||||||:|||:||:|||||| ||||||||||||||||||:|||||::|:|||||||
orf41-1     IIALAVTVVTAGAGAGAALGLNGAAAAATDAAFASLASQASVSLINNKGNIGNTLKELGR
                  70        80        90       100       110       120

             100       110       120       130       140       150
orf41a.pep  SSTVKNLVVAAATAGVADKIGASALXNVSDKQWINNLTVNLANAGSAALINTAVNGGSLK
            |||||||:||:|||||||||||||| ||||||||||||||||||||||||||||||||||
orf41-1     SSTVKNLMVAVATAGVADKIGASALNNVSDKQWINNLTVNLANAGSAALINTAVNGGSLK
                  130       140       150       160       170       180

             160       170       180       190       200       210
orf41a.pep  DXLEANILAALVNTAHGEAASKIKQLDQHYIVHKIAHAIAGCAAAAANKGKCQDGAIGAA
            | ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
orf41-1     DNLEANILAALVNTAHGEAASKIKQLDQHYITHKIAHAIAGCAAAAANKGKCQDGAIGAA
                  190       200       210       220       230       240

             220       230       240       250       260       270
orf41a.pep  VGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAAEVAVKNNQ
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf41-1     VGEIVGEALTNGKNPDTLTAKEREQILAYSKLVAGTVSGVVGGDVNAAANAAEVAVKNNQ
                  250       260       270       280       290       300

             280       290       300       310       320       330
orf41a.pep  LSDXEGREFDNEMTACAKQNXPQLCRKNTVKKYQNVADKRLAASIAICTDISRSTECRTI
            ||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
orf41-1     LSDKEGREFDNEMTACAKQNNPQLCRKNTVKKYQNVADKRLAASIAICTDISRSTECRTI
                  310       320       330       340       350       360

             340       350       360       370       380       390
orf41a.pep  RKQHLIDSRSLHSSWEAGLIGKODEWYKLFSKSYTQADLALQSYHLNTAMCSWLQSGNTK
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf41-1     RKQHLIDSRSLHSSWEAGLIGKDDEWYKLFSKSYTQADLALQSYHLNTAAXSWLOSGNTK
                  370       380       390       400       410       420

             400       410       420       430       440       450
orf41a.pep  PLSEWMSDQGYTLISGVNPRFIPIPRGFVKQNTPITNVKYPEGISFDTNLXRHLANADGF
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
orf41-1     PLSEWMSDQGYTLISGVNPRFIPIPRGFVKQNTPITNVKYPEGISFDTNLKRHLANADGF
                  430       440       450       460       470       480

             460       470       480       490       500       510
orf41a.pep  SQEQGIKGAHNRTNXMAELNSRGGXVKSETXTDIEGITRIKYEIPTLDRTGKPDGGFKEI
            ||:|||||||||| ||||||||| ||||| ||||||||||||||||||||||||||||||
orf41-1     SQKQGIKGAHNRTNFMAELNSRGGRVKSETQTDIEGITRIKYEIPTLDRTGKPDGGFKEI
                  490       500       510       520       530       540

             520       530       540       550       560       570
```

-continued

```
orf41a.pep  SSIKTVYNPKXFXDDKILQMAQXAXSQGYSKASKIAQNERTKSISERKNVIQFSETFDGI
            |||||||||| | ||||||||| | ||||||||||||||||||||||||||||||||||
orf41-1     SSIKTVYNPKKFSDDKILQMAQNAASQGYSKASKIAQNERTKSISERKNVIQFSETFDGI
                   550       560       570       580       590       600

             580       590
orf41a.pep  KFRXYXDVNTGRITNIHPEX
            ||| | ||||||||||||||
orf41-1     KFRSYFDVNTGRITNIHPEX
                   610       620
```

[0451] Amino acids 25-619 of ORF41-1 were amplified as described above. **FIG. 6** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF41-1.

[0452] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 17

[0453] The following DNA sequence was identified in *N. meningitidis* <SEQ ID 73>

```
   1 ATGGCAATCA TTACATTGTA TTATTCTGTC AATGGTATTT TAAATGTATG
  51 TGCAAAAGCA AAAAATATTC AAGTAGTTGC CAATAATAAG AATATGGTTC
 101 TTTTTGGGTT TTTGGSmrGC ATCATCGGCG GTTCAACCAA TGCCATGTCT
 151 CCCATATTGT TAATATTTTT GCTTAGCGAA ACAGAAAATA AAAATcgTAT
 201 CGTAAAATCA AGCAATCTAT GCTATCTTTT GGCGAAAATT GTTCAAATAT
 251 ATATGCTAAG AGACCAGTAT TGGTTATTAA ATAAGAGTGA ATACGdTTTA
 301 ATATTTTTAC TGTCCGTATT GTCTGTTATT GGATTGTATG TTGGAATTCG
 351 GTTAAGGACT AAGATTAGCC CAaATTTTTT TAAAATGTTA ATTTTTATTG
 401 tTTTATTGGT ATTGGCtCTG AAAATCGGGC AttCGGGTTT AAtCAAACTT
 451 TAA
```

[0454] This corresponds to the amino acid sequence <SEQ ID 74; ORF51>:

```
   1 HAIITLYYSV NGILNVCAKA KNIQVVANNK NMVLFGFLXX IICGSTNANS
  51 PILLIFLLSE TENKNRIVKS SNLCYLLAKI VQIYMLRDQY WLLNKSEYXL
 101 IFLLSVLSVI GLYVGIRLRT KISPNFFKML IFIVLLVLAL KIGHSGLIKL
 151 *
```

[0455] Further work revealed the complete nucleotide sequence <SEQ ID 75>:

```
   1 ATGCAAGAAA TAATGCAATC TATCGTTTTT GTTGCTGCCG CAATACTGCA
  51 CGGAATTACA GGCATGGGAT TTCCGATGCT CGGTACAACC GCATTGGCTT
 101 TTATCATGCC ATTGTCTAAG GTTGTTGCCT TGGTGGCATT ACCAAGCCTG
 151 TTAATGAGCT TGTTGGTTCT ATGCAGCAAT AACAAAAAGG GTTTTTGGCA
```

-continued

```
201 AGAGATTGTT TATTATTTAA AAACCTATAA ATTGCTTGCT ATCGGCAGCG

251 TCGTTGGCAG CATTTTGGGG GTGAAGTTGC TTTTGATACT TCCAGTGTCT

301 TGGCTGCTTT TACTGATGGC AATCATTACA TTGTATTATT CTGTCAATGG

351 TATTTTAAAT GTATGTGCAA AAGCAAAAAA TATTCAAGTA GTTGCCAATA

401 ATAAGAATAT GGTTCTTTTT GGGTTTTTGG CAGGCATCAT CGGCGGTTCA

451 ACCAATGCCA TGTCTCCCAT ATTGTTAATA TTTTTGCTTA GCGAAACAGA

501 AAATAAAAAT CGTATCGTAA AATCAAGCAA TCTATGCTAT CTTTTGGCGA

551 AAATTGTTCA AATATATATG CTAAGAGACC AGTATTGGTT ATTAAATAAG

601 AGTGAATACG GTTTAATATT TTTACTGTCC GTATTGTCTG TTATTGGATT

651 GTATGTTGGA ATTCGGTTAA GGACTAAGAT TAGCCCAAAT TTTTTTAAAA

701 TGTTAATTTT TATTGTTTTA TTGGTATTGG CTCTGAAAAT CGGGCATTCG

751 GGTTTAATCA AACTTTAA
```

[0456] This corresponds to the amino acid sequence <SEQ ID 76; ORF51-1>:

```
  1 MQEIMQSIVF VAAAILHGIT GMGFPMLGTT ALAFIMPLSK VVALVALPSL

 51 LMSLLVLCSN NKKGFWQEIV YYLKTYKLLA IGSVVGSILG VKLLLILPVS

101 WLLLLMAIIT LYYSVNGILN VCAKAKNIQV VANNKNNVLF GFLAGIIGGS

151 TNAMSPILLI FLLSETENKN RIVKSSNLCY LLAKIVQIYN LRDQYWLLNK

201 SEYGLIFLLS VLSVIGLYVG IRLRTKISPN FFKMLIFIVL LVLALKIGHS

251 GLIKL*
```

[0457] Computer analysis of this amino acid sequence reveals three putative transmembrane domains. A corresponding ORF from strain A of *N. meningitidis* was also identified:

[0458] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[0459] ORF51 shows 96.7% identity over a 150 aa overlap with an ORF (ORF51a) from strain A of *N. meningitidis*:

```
                                                 10        20        30
orf51.pep                                       MAIITLYYSVNGILNVCAKAKNIQVVANNK
                                                ||||||||||||||||||||||||||||||
orf51a    YKLLAIGSVVGSILGVKLLLILPVSWLLLLMAIITLYYSVNGILNVCAKAKNIQVVANNK
             80        90        100       110       120       130

                   40        50        60        70        80        90
orf51.pep NMVLFGFLXXIIGGSTNAMSPILLIFLLSETENKNRIVKSSNLCYLLAKIVQIYMLRDQY
          |||||||| ||||||||||||||||||||||||||:||||||||||||||||||||||
orf51a    NMVLFGFLAGIIGGSTNAMSPILLIFLLSETENKNRIAKSSNLCYLLAKIVQIYMLRDQY
            140       150       160       170       180       190

                  100       110       120       130       140       150
orf51.pep WLLNKSEYXLIFLLSVLSVIGLYVGIRLRTKISPNFFKMLIFIVLLVLALKIGHSGLIKL
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||:||||||
orf51a    WLLNKSEYGLIFLLSVLSVIGLYVGIRLRTKISPNFFKMLIFIVLLVLALKIGYSGLIKL
            200       210       220       230       240       250
```

[0460] ORF51-1 and ORF51a show 99.2% identity in 255 aa overlap:

```
orf51a.pep  MQEIMQSIVFVAAAILHGITGMGFPMLGTTALAFIMPLSKVVALVALPSLLMSLLVLCSN
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf51-1     MQEIMQSIVFVAAAILHGITGMGFPMLGTTALAFIMPLSKVVALVALPSLLMSLLVLCSN

orf51a.pep  NKKGFWQEIVYYLKTYKLLAIGSVVGSILGVKLLLILPVSWLLLLMAIITLYYSVNGILN
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf51-1     NKKGFWQEIVYYLKTYKLLAIGSVVGSILGVKLLLILPVSWLLLLMAIITLYYSVNGILN

orf51a.pep  VCAKAKNIQVVANNKNMVLFGFLAGIIGGSTNAMSPILLIFLLSETENKNRIAKSSNLCY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
orf51-1     VCAKAKNIQVVANNKNMVLFGFLAGIIGGSTNAMSPILLIFLLSETENKNRIVKSSNLCY

orf51a.pep  LLAKIVQIYMLRDQYWLLNKSEYGLIFLLSVLSVIGLYVGIRLRTKISPNFFKMLIFIVL
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf51-1     LLAKIVQIYMLRDQYWLLNKSEYGLIFLLSVLSVIGLYVGIRLRTKISPNFFKMLIFIVL

orf51a.pep  LVLALKIGYSGLIKLX
            ||||||||:|||||||
orf51-1     LVLALKIGHSGLIKLX
```

[0461] The complete length ORF51a nucleotide sequence SEQ D 77> is:

```
   1 ATGCAAGAAA TAATGCAATC TATCGTTTTT GTTGCTGCCG CAATACTGCA

  51 CGGAATTACA GGCATGGGAT TTCCGATGCT CGGTACAACC GCATTGGCTT

 101 TTATCATGCC ATTGTCTAAG GTTGTTGCCT TGGTGGCATT ACCAAGCCTG

 151 TTAATGAGCT TGTTGGTTCT ATGCAGCAAT AACAAAAAGG GTTTTTGGCA

 201 AGAGATTGTT TATTATTTAA AAACCTATAA ATTGCTTGCT ATCGGCAGCG

 251 TCGTTGGCAG CATTTTGGGG GTGAAGTTGC TTTTGATACT TCCAGTGTCT

 301 TGGCTGCTTT TACTGATGGC AATCATTACA TTGTATTATT CTGTCAATGG

 351 TATTTTAAAT GTATGTGCAA AAGCAAAAAA TATTCAAGTA GTTGCCAATA

 401 ATAAGAATAT GGTTCTTTTT GGGTTTTTGG CAGGCATCAT CGGCGGTTCA

 451 ACCAATGCCA TGTCTCCCAT ATTGTTAATA TTTTTGCTTA GCGAAACAGA

 501 GAATAAAAAT CGTATCGCAA AATCAAGCAA TCTATGCTAT CTTTTGGCAA

 551 AAATTGTTCA AATATATATG CTAAGAGACC AGTATTGGTT ATThAATAAG

 601 AGTGAATACG GTTTAATATT TTTACTGTCC GTATTGTCTG TTATTGGATT

 651 GTATGTTGGA ATTCGGTTAA GGACTAAGAT TAGCCCAAAT TTTTTTAAAA

 701 TGTTAATTTT TATTGTTTTA TTGGTATTGG CTCTGAAAAT CGGGTATTCA

 751 GGTTTAATCA AACTTTAA
```

[0462] This encodes a protein having amino acid sequence <SEQ ID 78>:

```
   1 MQEIMQSIVF VAAAILHGIT GMGFPNLGTT ALAFIMPLSK VVALVALPSL

  51 LMSLLVLCSN NKKGFWQEIV YYLKTYKLLA IGSVVGSILG VKLLLILPVS

 101 WLLLLMAIIT LYYSVNGILN VCAKAKNIQV VANNKNMVLF GFLAGIIGGS

 151 TNAMSFILLI FLLSETENKN RIAXSSNLCY LLAKIVQIYM LRDQYWLLNK
```

-continued

201 SEYGLIFLLS VLSVIGLYVG IRLRTKISPN FFKMLIFIVL LVLALKIGYS

251 GLIKL*

[0463] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 18

[0464] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>

```
  1 ATGAGACATA TGAAAATACA AAATTATTTA CTAGTATTTA TAGTTTTACA
 51 TATAGCCTTG ATAGTAATTA ATATAGTGTT TGGTTATTTT GTTTTTCTAT
101 TTGATTTTTT TGCGTTTTTG TTTTTTGCAA ACGTCTTTCT TGCTGTAAAT
151 TTATTATTTT TAGAAAAAAA CATAAAAAAC AAATTATTGT TTTTATTGCC
201 GATTTCTATT ATTATATGGA TGGTAATTCA TATTAGTATG ATAAATATAA
251 AATTTTATAA ATTTGAGCAT CAAATAAAGG AACAAAATAT ATCCTCGATT
301 ACTGGGGTGA TAAAACCACA TGATAGTTAT AATTATGTTT ATGACTCAAA
351 TGGATATGCT AAATTAAAAG ATAATCATAG ATATGGTAGG GTAATTAGAG
401 AAACACCTTA TATTGATGTA GTTGCATCTG ATGTTAAAAA TAAATCCATA
451 AGATTAAGCT TGGTTTGTGG TATTCATTCA TATGCTCCAT GTGCCAATTT
501 TATAAAATTT GTCAGG..
```

[0465] This corresponds to the amino acid sequence <SEQ ID 80; ORF82>:

```
  1 MRHMKIQNYL LVFIVLHIAL IVINIVFGYF VFLFDFFAFL FFANVFLAVN
 51 LLFLEKNIKN KLLFLLPISI IIWMVIHISM INIKFYKFEH QIKEQNISSI
101 TGVIKPNDSY NYVYDSNGYA KLKDWHRYGR VIRETPYIDV VASDVKNKSI
151 RLSLVCGIHS YAPCANFIKF VR..
```

[0466] Further work revealed the complete nucleotide sequence SEQ ID 81>:

```
  1 ATGAGACATA TGAAAAATAA AAATTATTTA CTAGTATTTA TAGTTTTACA
 51 TATAGCCTTG ATAGTAATTA ATATAGTGTT TGGTTATTTT GTTTTTCTAT
101 TTGATTTTTT TGCGTTTTTG TTTTTTGCAA ACGTCTTTCT TGCTGTAAAT
151 TTATTATTTT TAAAAAAAAA CATAAAAAAC AAATTATTGT TTTTATTGCC
201 GATTTCTATT ATTATATGGA TGGTAATTCA TATTAGTATG ATAAATATAA
251 AATTTTATAA ATTTGAGCAT CAAATAAAGG AACAAAATAT ATCCTCGATT
301 ACTGGGGTGA TAAAACCACA TGATAGTTAT AATTATGTTT ATGACTCAAA
351 TGGATATGCT AAATTAAAAG ATAATCATAG ATATGGTAAG GTAATTAGAG
```

-continued

```
401 AAACACCTTA TATTGATGTA GTTGCATCTG ATGTTAAAAA TAAATCCATA

451 AGATTAAGCT TGGTTTGTGG TATFCATTCA TATGCFCCAT GTGCCAATTT

501 TATAAAATTT GCAAAAAAAC CTGTTAAAAT TTATTTTTAT AATCAACCTC

551 AAGGAGATTT TATAGATAAT GTAATATTTG AAATTAATGA TGGAAACAAA

601 AGTTTGTACT TGTTAGATAA GTATAAAACA TTTTTTCTTA TTGAAAACAG

651 TGTTTGTATC GTATTAATTA TTTTATATTT AAAATTTAAT TTGCTTTTAT

701 ATAGGACTTA CTTCAATGAG TTGGAATAG
```

[0467] This corresponds to the amino acid sequence <SEQ ID 82; ORF82-1>:

```
  1 MRHMKNKNYL LVFIVLHIAL IVINIVFGYF VFLFDFFAFL FFANVFLAVN

 51 LLFLEKNIKH KLLFLLPISI IIWMVIHISH INIKFYKFEH QIKEQNISSI

101 TGVIKPHDSY NYVYDSNGYA KLKDNHRYGR VIRETPYIDV VASDVKNKSI

151 RLSLVCGIHS YAPCANFIKF AKKPVKIYFY NQPQGDFIDN VIFEINDGNK

201 SLYLLDKYKT FFLIENSVCI VLIILYLKFN LLLYRTYFNE LE*
```

[0468] Computer analysis of this amino acid sequence reveals a predicted leader peptide.

[0469] A corresponding ORF from strain A of *N. meningitidis* was also identified:

[0470] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[0471] ORF82 shows 97.1% identity over a 172 aa overlap with an ORF (ORF82a) from strain A of *N. meningitidis*:

```
                 10         20         30         40         50         60
orf82 pep   MRHMKIQNYLLVFIVLHIALIVINIVFGYFVFLFDFFAFLFFANVFLAVNLLFLEKNIKN
            ||||| :||||||||||:||||||||||||||||||||||||||||||||||||||||||
orf82a      MRHMKIKNYLLVFIVLHITLIVINIVFGYFVFLFDFFAFLFFANVFLAVNLLFLEKNIKN
                 10         20         30         40         50         60

                 70         80         90        100        110        120
orf82 pep   KLLFLLPISIIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf82a      KLLFLLPISIIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKFHDSYNYVYDSNGYA
                 70         80         90        100        110        120

       130        140        150        160        170
orf82 pep   KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFVR
            ||||||||||||||||||||||||||||||||||||||||||||||||||||::
orf82a      KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY
                   130        140        150        160        170

orf82a.pep  MRHMKNKNYLLVFIVLHITLIVINIVFGYFVFLFDFFAFLFFANVFLAVNLLFLEKNIKN
            ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
orf82-1     MRHMKNKNYLLVFIVLHIALIVINIVFGYFVFLFDFFAFLFFANVFLAVNLLFLEKNIKN

orf82a.pep  KLLFLLPISIIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf82-1     KLLFLLPISIIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA

orf82a.pep  KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf82-1     KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY
```

-continued

```
orf82a.pep  NQPQGDFIDNVIFEINKGKKSLYLLDKYKTFFLIENSVCIVLIILYLKFNLLLYRTYFNE
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf82-1     NQPQGDFIDNVIFEINKGKKSLYLLDKYKTFFLIENSVCIVLIILYLKFNLLLYRTYFNE

orf82a.pep  LEX
            |||
orf82-1     LEX
```

[**0472**] ORF82a and ORF82-1 show 99.2% identity in 242 aa overlap:

```
orf82a.pep  MRHMKNKNYLLVFIVLHITLIVININVFGYGVFLFDFFAFLFFANVFLAVNLLFLEKNIKN
            ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
orf82-1     MRHMKNKNYLLVFIVLHIALIVININVFGYGVFLFDFFAFLFFANVFLAVNLLFLEKNIKN

orf82a.pep  KLLFLLPISIIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf82-1     KLLFLLPISIIIWMVIHISMINIKFYKFEHQIKEQNISSITGVIKPHDSYNYVYDSNGYA

orf82a.pep  KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
orf82-1     KLKDNHRYGRVIRETPYIDVVASDVKNKSIRLSLVCGIHSYAPCANFIKFAKKPVKIYFY

orf82a.pep  NQPQGDFIDNVIFEINDGKKSLYLLDKYKTFFLIENSVCIVLIILYLKFNLLLYRTYFNE
            ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
orf82-1     NQPQGDFIDNVIFEINDGNKSLYLLDKYKTFFLIENSVCIVLIILYLKFNLLLYRTYFNE

orf82a.pep  LEX
            |||
orf82-1     LEX
```

[**0473**] The complete length ORF82a nucleotide sequence <SEQ D 83> is:

```
   1 ATGAGACATA TGAAAAATAA AAATTATTTA CTAGTATTTA TAGTTTTACA

  51 TATAACCTTG ATAGTAATTA ATATAGTGTT TGGTTATTTT GTTTTTCTAT

 101 TTGATTTTTT TGCGTTTTTG TTTTTTGCAA ACGTCTTTCT TGCTGTAAAT

 151 TTATTATTTT TAGAAAAAAA CATAAAAAAC AAATTATTGT TTTTATTGCC

 201 GATTTCTATT ATTATATGGA TGGTAATTCA TATTAGTATG ATAAATATAA

 251 AATTTTATAA ATTTGAGCAT CAAATAAAGG AACAAAATAT ATCCTCGATT

 301 ACTGGGGTGA TAAAACCACA TGATAGTTAT AATTATGTTT ATGACTCAAA

 351 TGGATATGCT AAATTAAAAG ATAATCATAG ATATGGTAGG GTAATTACAG

 401 AAACACCTTA TATTGATGTA GTIGCATCTG ATGTTAAAAA TAAATCCATA

 451 AGATIAAGCT TGGTTTGTGG TATTCATTCA TATGCTCCAT GTGCCAATTT

 501 TATAAAATTT GCAAAAAAAC CTGTTAAAAT TTATTTTTAT AATCAACCTC

 551 AAGGAGATTT TATAGATAAT GTAATATTTG AAATTAATGA TGGAAAAAAA

 601 AGTTTGTACT TGTTAGATAA GTATAAAACA TTTTTTCTTA TTGAAAACAG

 651 TGTTTGTATC GTATTAATTA TTTTATATTT AAAATTTAAT TTGCTTTTAT

 701 ATAGGACTTA CTTCAATGAG TTGGAATAG
```

[0474] This encodes a protein having amino acid sequence <SEQ ID 84>:

```
  1 MRHMKNKNYL LVFIVLHITL IVINIVFGYF VFLFDFFAFL FFANVFLAVN
 51 LLFLEKNIKN KLLFLLPISI IIWMVIHISM INIKFYKFEH QIKEQNISSI
101 TGVIKPHDSY NYVYDSNGYA KLKDNHRYGR VIRETPYIDV VASDVIQKSI
151 RLSLVCGIHS YAPCANFIKF AXKPVKIYFY NQPQGDFXDN VIFEINDGKK
201 SLYLLDKYKT FFLIENSVCI VLIILYLKFN LLLYRTYFNE LE*
```

[0475] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 19

[0476] The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>

```
  1..ACCCCCAACA GCGTGACCGT CTTGCCGTCT TTCGGCGGAT TCGGGCGTAC
 51  CGGCGCGACC ATCAATGCAG CAGGCGGGGT CGGCATGACT GCCTTTTCGA
101  CAACCTTAAT TTCCGTAGCC GAGGGCGCGG TTGTAGAGCT GCAGGCCGTG
151  AGAGCCAAAG CCGTCAATGC AACCGCCGCT TGCATTTTTA CGGTCTTGAG
201  TAAGGACATT TTCGATTTCC TTTTTATTTT CCGTTTTCAG ACGGCTGACT
251  TCCGCCTGTA TTTTCGCCAA AGCCATGCCG ACAGCGTGCG CCTTGACTTC
301  ATATTTAAAA GCTTCCGCGC GTGCCAGTTC CAGTTCGCGC GCATAGTTTT
351  GAGCCGACAA CAGCAGGGCT TGCGCCTTGT CGCGCTCCAT CTTGTCGATG
401  ACCGCCTGCA GCTTCGCAAA TGCCGACTFG TAGCCTTGAT GGTGCGACAC
451  AGCCAAGCCC GTGCCGACAA GCGCGATAAT GGCAATCGGT TGCCAGTAAT
501  TCGCCAGCAG TTTCACGAGA TTCATTCTCG ACCTCCTGAC GCTTCACGCT
551  GA
```

[0477] This corresponds to the amino acid sequence <SEQ ID 86; ORF124>:

```
  1..TPNSVTVLPS FGGFGRTGAT INAAGGVGMT AFSTTLISVA EGAVVELQAV
 51  RAKAVNATAA CIFTVLSKDI FDFLFIFRFQ TADFRLYFRQ SHADSVRLDF
101  IFKSFRACQF QFARIVLSRQ QQGLRLVALH LVDORLQLRX CRLVALMVRH
151  SQARADKRDN GNRLPVIRQQ FHEIHSRPPD ASR*
```

[0478] Computer analysis of this amino acid sequence predicts a transmembrane domain.

[0479] Further work revealed the complete nucleotide sequence SEQ ID 87>:

```
  1 ATGACTGCCT TTCGACAAC CTTAATTTCC GTAGCCGAGG GCGCGGTTGT
```

-continued

```
 51 AGAGCTGCAG GCCGTGAGAG CCAAAGCCGT CAATGCAACC GCCGCTTGCA

101 TTTTTACGGT CTTGAGTAAG GACATTTTCG ATTTCCTTTT TATTTTCCGT

151 TTTCAGACGG CTGACTTCCG CCTGTTTTTT CGCCAAAGCC ATGCCGACAG

201 CGTGCGCCTT GACTTCATAT TTTTTAGCTT CCGcGCGTGC CAGTTCCAGT

251 TCGCGCGCAT AGTTTTGAGC CGACAACAGC AGGGCTTGCG CCTTGTCGCG

301 CTCCATCTTG TCGATGACCG CCTGCTGCTT CGCAAATGCC GACTTGTAGC

351 CTTGATGGTG CGACACAGCC AAGCCCGTGC CGACAAGCGC GATAATGGCA

401 ATCGGTTGCC AGTTATTCGC CAGCAGTTTC ACGAGATTCA TTCTCGACCT

451 CCTGACGCTT CACGCTGA
```

[**0480**] This corresponds to the amino acid sequence SEQ ID 88; ORF124-1>:

```
  1 MTAFSTTLIS VAEGAVVELQ AVRAKAVNAT AACIFTVLSK DIFDFLFIFR

 51 FQTADFRLFF RQSHADSVRL DFIFFSFRAC QFQFARIVLS RQQQGLRLVA

101 LHLVDDRLLL RKCRLVAIMV RHSQARADKR DNGNRLPVIR QQFHEIHSRP

151 PDASR*
```

[**0481**] A corresponding ORF from strain A of *N. meningitidis* was also identified:

[**0482**] Homology with a Predicted ORF from *N. meningitidis* (Strain A)

[**0483**] ORF124 shows 87.5% identity over a 152 aa overlap with an ORF (ORF124a) from strain A of *N. meningitidis*:

```
                  10        20        30        40        50        60
orf124.pep  TPNSVTVLPSFGGFGRTGATINAAGGVGMTAFSTTLISVAEGAVVELQAVRAKAVNATAA
                                      ||||||||||||||||:|||||| ||||||:|||
orf124a                               MTAFSTTLISVAEGALVELQAVMAKAVNTTAA
                                             10        20        30

                  70        80        90       100       110       120
orf124.pep  CIFTVLSKDIFDFLFIFRFQTADFRLYFRQSHADSVRLDFIFKSFRACQFQFARIVLSRQ
            ||||||||||||||||||||||||||:|||||||:|||||||  |||:  |||| :|||||
orf124a     CIFTVLSKDIFDFLFIFRFQTADFRLFFRQSHADGVRLDFIFFSFRTRLFQFAGVVLSRQ
                  40        50        60        70        80        90

                 130       140       150       160       170       180
orf124.pep  QQGLRLVALHLVDDRLQLRKCRLVALMVRHSQARADKRDNGNRLPVIRQQFHEIHSRPPD
            ||||||||||:::||| ||| ||||||||| |:|||||:||||||||||||||||||||
orf124a     QQGLRLVALHFLNDRLLLRKSRLVALMVRHRQTRADKRDDGNRLPVIRQQFHEIHSRPPD
                 100       110       120       130       140       150

orf124.pep  ASRX
            :
orf124a     VX
```

[**0484**] ORF124a and ORF124-1 show 89.5% identity in 152 aa overlap:

```
orf124-1.pep MTAFSTTLISVAEGAVVELQAVRAKAVNATAACIFTVLSKDIFDFLFIFRFQTADFRLFF
             ||||||||||||||:|||||| |||||:||||||||||||||||||||||||||||||
```

-continued

```
orf124a       MTAFSTTLISVAEGALVELQAVMAKAVNTTAACIFTVLSKDIFDFLFIFRFQTADFRLFF

orf124-1.pep  RQSHADSVRLDFIFFSFRACQFQFARIVLSRQQQGLRLVALHLVDDRLLLRKCRLVALMV
              ||||||:||||||||||||:  |||| :|||||||||||||:::||||||| |||||||
orf124a       RQSHADGVRLDFIFFSFRTRLFQFAGVVLSRQQQGLRLVALHFLNDRLLLRKSRLVALMV

orf124-1.pep  RHSQARADKRDNGNRLPVIRQQFHEIHSRPPDASRX
              || |:||||||:|||||||||||||||||||:
orf124a       RHRQTRADKRDDGNRLPVIRQQFHEIHSRPPDVX
```

[0485] The complete length ORF124a nucleotide sequence <SEQ ID 89> is:

```
   1 ATGACCGCCT TTTCGACAAC CTTAATTTCC GTAGCCGAGG GCGCGCTTGT

  51 AGAGCTGCAA GCCGTGATGG CCAAAGCCGT CAATACAACC GCCGCCTGCA

 101 TTTTTACGGT CTTGAGTAAG GACATTTTCG ATTTCCTTTT TATTTTCCGT

 151 TTTCAGACGG CTGACTTCCG CCTGTTTTTT CGCCAAAGCC ATGCCGACGG

 201 CGTGCGCCTT GACTTCATAT TTTTTAGCTT CCGCACGCGC CTGTTCCAGT

 251 TCGCGGGCGT AGTTTTGAGC CGACAACAGC AGGGCTTGCG CCTTGTCGCG

 301 CTTCATTTTC TCAATGACCG CCTGCTGCTT CGCAAAAGCC GACTTGTAGC

 351 CTTGATGGTG CGACACCGCC AAACCCGTGC CGACAAGCGC GATGATGGCA

 401 ATCGGTTGCC AGTTATTCGC CAGCAGTTTC ACGAGATTCA TTCTCGACCT

 451 CCTGACGTTT GA
```

[0486] This encodes a protein having amino acid sequence <SEQ ID 90>:

```
   1 MTAFSTTLIS VAEGALVELQ AVNAXAVNTT AACIFTVLSK DIFDFLFIFR

  51 FQTADFRLFF RQSHADGVRL DFIFFSFRTR LFQFAGVVLS RQQQGLRLVA

 101 LHFLNDELLL RKSRLVALHV RHRQTRADKR DDGNRLPVIR QQFHEIHSRP

 151 PDV*
```

[0487] ORF124-1 was amplified as described above. **FIG. 7** shows plots of hydrophilicity, antigenic index, and AMPHI regions for ORF124-1.

[0488] Based on this analysis, it is predicted that this protein from *N. meningitidis*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 20

[0489] Table III lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 40 among different strains.

TABLE III

List of Neisseria Strains Used for Gene Variability Study of ORF 40

Identification number	Strains	Source/reference
	Group B	
zn02__1	BZ198	R. Moxon/Seiler et al., 1996
zn03__1	NG3/88	R. Moxon/Seiler et al., 1996

TABLE III-continued

List of Neisseria Strains Used for Gene Variability Study of ORF 40

Identification number	Strains	Source/reference
zn04__1	297-0	R. Moxon/Seiler et al., 1996
zn06__1	BZ147	R. Moxon/Seiler et al., 1996
zn07__1	BZ169	R. Moxon/Seiler et al., 1996
zn08__1	528	R. Moxon/Seiler et al., 1996
zn10__1	BZ133	R. Moxon/Seiler et al., 1996
zn11__1ass	NGE31	R. Moxon/Seiler et al., 1996
zn14__1	NGH38	R. Moxon/Seiler et al., 1996
zn16__1	NGH15	R. Moxon/Seiler et al., 1996
zn18__1	BZ232	R. Moxon/Seiler et al., 1996
zn19__1	BZ83	R. Moxon/Seiler et al., 1996
zn20__1	44/76	R. Moxon/Seiler et al., 1996
zn21__1	MC58	R. Moxon

TABLE III-continued

List of Neisseria Strains Used for Gene Variability Study of ORF 40

Identification number	Strains	Source/reference
	Group A	
zn22__1	205900	R. Moxon
zn23__1	F6124	R. Moxon
z2491__1	Z2491	R. Moxon/Maiden et al., 1998
	Group C	
zn24__1	90/18311	R. Moxon
zn25__1ass	93/4286	R. Moxon

TABLE III-continued

List of Neisseria Strains Used for Gene Variability Study of ORF 40

Identification number	Strains	Source/reference
	Others	
zn28__1ass	860800 (group Y)	R. Moxon/Maiden et al., 1998
zn29__1ass	E32 (group Z)	R. Moxon/Maiden et al., 1998

References:

Seiler A. et al., Mol. Microbiol., 1996, 19(4): 841–856.
Maiden et al., Proc. Natl. Acad. Sci. USA, 1998, 95: 3140–3145.

[0490] The amino acid sequences for each listed strain are as follows:

>Z2491 <SEQ ID 91>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKISGNVSPSKADEMDETV
NINAGNNIEISRNGKNIDIATSNAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
RINVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVWDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN02_1 <SEQ ID 92>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
PVQRTAVLSFRSDKEGTGEKEGTEDSHGGAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE
NTNDSSFTYSLKKDLTDLTSVETEKLSFGAAGNKVNITSDTKGLNFAKETAGTAGDPTVH
LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
DFVRTYDTVEFLSADTKTTTNVSKDNGKKTEVICIGAIVTSVIKEKDGKLVTGKGKDENG
SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
TVSKODQGNITVRYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGRMDE
TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
KSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN03_1 <SEQ ID 93>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
PVQRTAPVLSFHADSEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTDE
NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH
LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
DFVRTYDTVEFLSADTRTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
KSMMAIGGDTYRGEAGYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYQW*

>ZN04_1 <SEQ ID 94>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
PVQRTAPVLSFHADSEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTDE
NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH
LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
DFVRTYDTVEFLSADTRTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
KSMMAIGGDTYRGEAGYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYQW*

>ZN06_1 <SEQ ID 95>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKISGNVSPSKADEMDETV

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NINAGNNIEISRNGKNIDIATSNAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
RINVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVWDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN07_1 <SEQ ID 96>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKISGNVSPSKADEMDETV
NINAGNNIEISRNGKNIDIATSNAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
RINVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVWDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN08_1 <SEQ ID 97>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVETAVLATLLFATVQANATDTDEDDEL
EPVVRSALVLQFMIDKEGNGEIESTGDIGWSIYYDDHNTLHGATVTLKAGDNLKIKQNTD
ENTNASSFTYSLKKDLTDLTSVGTEELSFGANGNKVNITSDTKGLNFAKKTAGTNGDTTV
HLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSEN
VDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGEN
GSSTEDGEGELVTAKEVIDAVNKAGWRMKTTANGQTGQADKFETVTSGTNVTFASGKGTT
ATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKISGNAVSPSKGKMD
ETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPLTLSVDDEALNVGSKDAN
KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLP
GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN10_1 <SEQ ID 98>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
NINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGYTRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN11_1 ASS <SEQ ID 99>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
PVQRTAPVLSFHADSEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTDE
NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH
LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
DFVRTYDTVEFLSADTRTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
KSMMAIGGDTYRGEAGYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYQW*

>ZN14_1 <SEQ ID 100>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVETAVLATLLFATVQANATDTDEDDEL
EPVVRSALVLQFMIDKEGNGEIESTGDIGWSIYYDDHNTLHGATVTLKAGDNLKIKQNTD
ENTNASSFTYSLKKDLTDLTSVGTEELSFGANGNKVNITSDTKGLNFAKKTAGTNGDTTV
HLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSEN
VDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGEN
GSSTEDGEGELVTAKEVIDAVNKAGWRMKTTANGQTGQADKFETVTSGTNVTFASGKGTT
ATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKISGNAVSPSKGKMD
ETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPLTLSVDDEALNVGSKDAN
KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLP
GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN16_1 <SEQ ID 101>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE
NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN
GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW*

>ZN18_1 <SEQ ID 102>

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MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
PVQRTAPVLSFHADSEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTDE
NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH
LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
DFVRTYDTVEFLSADTRTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
KSMMAIGGDTYRGEAGYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYQW*

>ZN19_1 <SEQ ID 103>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN20_1 <SEQ ID 104>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN21_1 <SEQ ID 105>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN22_1 <SEQ ID 106>
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ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGYTRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN23_1 <SEQ ID 107>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
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GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGYTRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN24_1 <SEQ ID 108>
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLSATVQANATDTDEDEEL
ESVVRSALVLQFMIDKEGNGEIESTGDIGWSIYYDDHNTLHGATVTLKAGDNLKIKQSGK
DFTYSLKKELKDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIG
STLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDFVRT
YDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSSTDE

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GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATVSKD
DQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN
AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRIT
NVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQAYLPGKSMMA
IGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW*

>ZN25_ASS <SEQ ID 109>
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ESVVRSALVLQFMIDKEGNGEIESTGDIGWSIYYDDHNTLHGATVTLKAGDNLKIKQSGK
DFTYSLKKELKDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIG
STLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDFVRT
YDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSSTDE
GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATVSKD
DQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN
AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRIT
NVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQAYLPGKSMMA
IGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW*

>ZN28_ASS <SEQ ID 110>
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
MMAIGGGYTRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW*

>ZN29_ASS <SEQ ID 111>
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NENTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN
GDPTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTT
GQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGK
GKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFAS
GNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS
KGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVVEAGALNVG
SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
*

[0491] **FIG. 8** shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 40, further confirming its utility as an antigen for both vaccines and diagnostics.

[0492] It will be appreciated that the invention has been described by means of example only, and that modifications may be made whilst remaining within the spirit and scope of the invention.

Appendix 1

[0493]

Scarlato, Continuation of U.S. App. Ser. No. 10/695,499, filed herewith	Ruelle, U.S. Pat. No. 6,780,419
18. (New) An isolated polypeptide comprising a member selected from the group consisting of (a) the amino acid sequence of SEQ ID NO: 4; and (b) an immunogenic fragment of at least 15 contiguous amino acids of SEQ ID NO: 4, wherein the immunogenic fragment, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell meditated immune response that recognizes the isolated polypeptide SEQ ID NO: 4.	1. An isolated polypeptide comprising a member selected from the group consisting of (a) the amino acid sequence of SEQ ID NO: 2; (b) an immunogenic fragment of at least 15 contiguous amino acids of SEQ ID NO: 2; wherein the immunogenic fragment, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell meditated immune response that recognizes the isolated polypeptide SEQ ID NO: 2.
19. (New) The isolated polypeptide of claim 18, wherein the polypeptide is according to (a).	2. The isolated polypeptide of claim 1, wherein the polypeptide is according to (a).
20. (New) The isolated polypeptide of claim 18, wherein the polypeptide is according to (b).	3. The isolated polypeptide of claim 1, wherein the polypeptide is according to (b).

-continued

Scarlato, Continuation of U.S. App. Ser. No. 10/695,499, filed herewith	Ruelle, U.S. Pat. No. 6,780,419
21. (New) The isolated polypeptide of claim 18, wherein the immunogenic fragment of (b) comprises at least 20 contiguous amino acids of SEQ ID NO: 4; wherein the immunogenic fragment, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell meditated immune response that recognizes the isolated polypeptide SEQ ID NO: 4.	4. The isolated polypeptide of claim 1, wherein the immunogenic fragment of (b) comprises at least 20 contiguous amino acids of SEQ ID NO: 2; wherein the immunogenic fragment, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell meditated immune response that recognizes the isolated polypeptide SEQ ID NO: 2.
22. (New) The isolated polypeptide of claim 18, wherein the isolated polypeptide consists of SEQ ID NO: 4.	5. The isolated polypeptide of claim 1, wherein the isolated polypeptide consists of SEQ ID NO: 2.
23. (New) A fusion protein comprising the isolated polypeptide of claim 18.	6. A fusion protein comprising the isolated polypeptide of claim 1.
24. (New) An immunogenic composition comprising the polypeptide of claim 18, and a pharmaceutically acceptable carrier.	7. An immunogenic composition comprising the polypeptide of claim 1, and a pharmaceutically acceptable carrier.
25. (New) The isolated polypeptide of claim 18, wherein the isolated polypeptide is a recombinant polypeptide.	9. The isolated polypeptide of claim 1, wherein the isolated polypeptide is a recombinant polypeptide.
26. (New) The isolated polypeptide of claim 19, wherein the isolated polypeptide is a recombinant polypeptide.	10. The isolated polypeptide of claim 2, wherein the isolated polypeptide is a recombinant polypeptide.
27. (New) The isolated polypeptide of claim 20, wherein the isolated polypeptide is a recombinant polypeptide.	11. The isolated polypeptide of claim 3, wherein the isolated polypeptide is a recombinant polypeptide.
28. (New) An immunogenic composition comprising the isolated polypeptide of claim 19.	12. An immunogenic composition comprising the isolated polypeptide of claim 2.
29. (New) An immunogenic composition comprising the isolated polypeptide of claim 20.	13. An immunogenic composition comprising the isolated polypeptide of claim 3.
30. (New) A fusion protein comprising the isolated polypeptide of claim 19.	14. A fusion protein comprising the isolated polypeptide of claim 2.
31. (New) A fusion protein comprising the isolated polypeptide of claim 20.	15. A fusion protein comprising the isolated polypeptide of claim 3.

Appendix 2

[0494]

Added Claim #	Written Description Support in the Current Application (Continuation of Application No. 10/695,499)	Written Description Support in Application No. PCT/IB99/00103
Claims 18–31	Throughout the application and at least at the following citations: Page 3, lines 2–24; Page 31, line 7 to page 34, line 17; Page 52, lines 10–18; Page 65, line 3 to page 70, line 3.	Throughout the application and at least at the following citations: Page 2, line 29 to page 3, line 20; Page 30, line 6 to page 33, line 11; Page 50, lines 12–20; Page 61, line 11 to page 66, line 6.
Claims 23, 30, and 31	Throughout the application and at least at the following citations: Page 3, lines 24–27; Page 9, line 26 to page 10, line 4; Page 21, lines 1–22.	Throughout the application and at least at the following citations: Page 3, lines 21–24; Page 9, lines 11–18; Page 20, line 6 to page 21, line 4.
Claims 25–27	Throughout the application and at least at the following citations: Page 3, lines 24–27;	Throughout the application and at least at the following citations: Page 3, lines 17–20;

-continued

Added Claim #	Written Description Support in the Current Application (Continuation of Application No. 10/695,499)	Written Description Support in Application No. PCT/IB99/00103
	Page 8, line 15 to page 28, line 23.	Page 8, line 1 to page 27, line 25.

Appendix 3

Disclosure of Constructive Reductions to Practice within the Scope of the Interfering Subject Matter in Application No. GB 9800760.2, filed Jan. 14, 1998

[0495]

Number of Amino Acids in Fragment	Location in ORF40 of Application No. GB 9800760.2	Location in SEQ 2 of '419 Patent
25	Residues 85–109	Residues 127–151
16	Residues 111–126	Residues 153–168
98	Residues 131–228	Residues 173–270
16	Residues 230–245	Residues 272–287

SEQUENCE LISTING

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cacgggagaa aaagaaaaag tagaagaaaa ttcagattgg gcagtatatt tcaacgagaa 180

aggagtacta acagccagag aaatcaccyt caaagccggc gacaacctga aaatcaaaca 240

aaacggcaca aacttcacct actcgctgaa aaaagacctc acagatctga ccagtgttgg 300

aactgaaaaa ttatcgttta gcgcaaacgg caataaagtc aacatcacaa gcgacaccaa 360

aggcttgaat tttgcgaaag aaacggctgg sacgaacggc gacaccacgg ttcatctgaa 420

cggtattggt tcgactttga ccgatacgct gctgaatacc ggagcgacca caaacgtaac 480

caacgacaac gttaccgatg acgagaaaaa acgtgcggca agcgttaaag acgtattaaa 540

cgctggctgg aacattaaag gcgttaaacc cggtacaaca gcttccgata acgttgattt 600

cgtccgcact tacgacacag tcgagttctt gagcgcagat acgaaaacaa cgactgttaa 660

tgtggaaagc aaagacaacg gcaagaaaac cgaagttaaa atcggtgcga agacttctgt 720

tattaaagaa aaagac 736

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<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (70)
<223> OTHER INFORMATION: unknown

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Glu Glu Asp Leu Tyr Leu Asp Pro Val Gln Arg Thr Val Ala Val Leu
20 25 30

Ile Val Asn Ser Asp Lys Glu Gly Thr Gly Glu Lys Glu Lys Val Glu
35 40 45

Glu Asn Ser Asp Trp Ala Val Tyr Phe Asn Glu Lys Gly Val Leu Thr
50 55 60

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

Asn Gly Thr Asn Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu
85 90 95

Thr Ser Val Gly Thr Glu Lys Leu Ser Phe Ser Ala Asn Gly Asn Lys
100 105 110

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

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

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Thr Leu Thr Asp Thr Leu Leu Asn Thr Gly Ala Thr Thr Asn Val Thr
145                 150                 155                 160

Asn Asp Asn Val Thr Asp Asp Glu Lys Lys Arg Ala Ala Ser Val Lys
                165                 170                 175

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

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

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

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

Ile Lys Glu Lys Asp
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<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 3

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acactgttgt ttgcaacggt tcaggcaagt gctaacaatg aagagcaaga agaagattta    180

tatttagacc ccgtacaacg cactgttgcc gtgttgatag tcaattccga taaagaaggc    240

acgggagaaa aagaaaaagt agaagaaaat tcagattggg cagtatattt caacgagaaa    300

ggagtactaa cagccagaga aatcaccctc aaagccggcg acaacctgaa aatcaaacaa    360

aacggcacaa acttcaccta ctcgctgaaa aaagacctca cagatctgac cagtgttgga    420

actgaaaaat tatcgtttag cgcaaacggc aataaagtca acatcacaag cgacaccaaa    480

ggcttgaatt ttgcgaaaga aacggctggg acgaacggcg acaccacggt tcatctgaac    540

ggtattggtt cgactttgac cgatacgctg ctgaataccg gagcgaccac aaacgtaacc    600

aacgacaacg ttaccgatga cgagaaaaaa cgtgcggcaa gcgttaaaga cgtattaaac    660

gctggctgga acattaaagg cgttaaaccc ggtacaacag cttccgataa cgttgatttc    720

gtccgcactt acgacacagt cgagttcttg agcgcagata cgaaaacaac gactgttaat    780

gtggaaagca aagacaacgg caagaaaacc gaagttaaaa tcggtgcgaa gacttctgtt    840

attaaagaaa aagacggtaa gttggttact ggtaaagaca aaggcgagaa tggttcttct    900

acagacgaag gcgaaggctt agtgactgca aaagaagtga ttgatgcagt aaacaaggct    960

ggttggagaa tgaaaacaac aaccgctaat ggtcaaacag gtcaagctga caagtttgaa   1020

accgttacat caggcacaaa tgtaaccttt gctagtggta aaggtacaac tgcgactgta   1080

agtaaagatg atcaaggcaa catcactgtt atgtatgatg taaatgtcgg cgatgcccta   1140

aacgtcaatc agctgcaaaa cagcggttgg aatttggatt ccaaagcggt tgcaggttct   1200

tcgggcaaag tcatcagcgg caatgtttcg ccgagcaagg gaaagatgga tgaaaccgtc   1260

aacattaatg ccggcaacaa catcgagatt acccgcaacg gtaaaaatat cgacatcgcc   1320

acttcgatga ccccgcagtt ttccagcgtt tcgctcggcg cgggggcgga tgcgcccact   1380
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ttgagcgtgg atggggacgc attgaatgtc ggcagcaaga aggacaacaa acccgtccgc   1440

attaccaatg tcgccccggg cgttaaagag ggggatgtta caaacgtcgc acaacttaaa   1500

ggcgtggcgc aaaacttgaa caaccgcatc gacaatgtgg acggcaacgc gcgtgcgggc   1560

atcgcccaag cgattgcaac cgcaggtctg gttcaggcgt atttgcccgg caagagtatg   1620

atggcgatcg gcggcggcac ttatcgcggc gaagccggtt acgccatcgg ctactccagt   1680

atttccgacg gcggaaattg gattatcaaa ggcacggctt ccggcaattc gcgcggccat   1740

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<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 4

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             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
     50                  55                  60

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

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
                 85                  90                  95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
            100                 105                 110

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

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
    130                 135                 140

Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285
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Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
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                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465                 470                 475                 480

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
                485                 490                 495

Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
            500                 505                 510

Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
        515                 520                 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
    530                 535                 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
545                 550                 555                 560

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<222> LOCATION: (1492)
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<222> LOCATION: (1560)
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acactgttgt ttgcaacggt tcaggcgaat gctaccgatg aagatgaaga agaagagtta 180

gaatccgtac aacgctctgt cgtagggagc attcaagcca gtatggaagg cagcggcgaa 240

ttggaaacga tatcattatc aatgactaac gacagcaagg aatttgtaga cccatacata 300

gtagttaccc tcaaagccgg cgacaacctg aaaatcaaac aaaacaccaa tgaaaacacc 360

aatgccagta gcttcaccta ctcgctgaaa aaagacctca caggcctgat caatgttgan 420

actgaaaaat tatcgtttgg cgcaaacggc aagaaagtca acatcataag cgacaccaaa 480

ggcttgaatt tcgcgaaaga aacggctggg acgaacggcg acaccacggt tcatctgaac 540

ggtatcggtt cgactttgac cgatacgctt gcgggttctt ctgcttctca cgttgatgcg 600

ggtaaccnaa gtacacatta cactcgtgca gcaagtatta aggatgtgtt gaatgcgggt 660

tggaatatta agggtgttaa annnggctca acaactggtc aatcagaaaa tgtcgatttc 720

gtccgcactt acgacacagt cgagttcttg agcgcagata cgnaaacaac gacngttaat 780

gtggaaagca aagacaacgg caagagaacc gaagttaaaa tcggtgcgaa gacttctgtt 840

attaaagaaa aagacggtaa gttggttact ggtaaaggca aaggcgagaa tggttcttct 900

acagacgaag gcgaaggctt agtgactgca aaagaagtga ttgatgcagt aaacaaggct 960

ggttggagaa tgaaaacaac aaccgctaat ggtcaaacag gtcaagctga caagtttgaa 1020

accgttacat caggcacaaa tgtaaccttt gctagtggta aaggtacaac tgcgactgta 1080

agtaaagatg atcaaggcaa catcactgtt atgtatgatg taaatgtcgg cgatgcccta 1140

aacgtcaatc agctgcaaaa cagcggttgg aatttggatt ccaaagcggt tgcaggttct 1200

tcgggcaaag tcatcagcgg caatgtttcg ccgagcaagg gaaagatgga tgaaaccgtc 1260

aacattaatg ccggcaacaa catcgagatt agccgcaacg gtaaaaatat cgacatcgcc 1320

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cgcattacca atgtcgcccc gggcgttaaa gangggatg ttacaaacgt cncacaactt 1500

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atgatggcga tcggcggcgg cacttatcgc ggcgaagccg gttacgccat cggctactcc 1680

agtatttccg acggcggaaa ttggattatc aaaggcacgg cttccggcaa ttcgcgcggc 1740

catttcggtg cttccgcatc tgtcggttat cagtggtaa 1779

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             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
     50                  55                  60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65                  70                  75                  80

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

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

Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
        115                 120                 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Xaa Thr Glu Lys Leu
    130                 135                 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
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                165                 170                 175

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

Ser Ser Ala Ser His Val Asp Ala Gly Asn Xaa Ser Thr His Tyr Thr
        195                 200                 205

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
    210                 215                 220

Gly Val Lys Xaa Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Xaa Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
465                 470                 475                 480

Arg Ile Thr Asn Val Ala Pro Gly Val Lys Xaa Gly Asp Val Thr Asn
                485                 490                 495

Val Xaa Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
            500                 505                 510

Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
        515                 520                 525

Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
    530                 535                 540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545                 550                 555                 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
                565                 570                 575
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<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 7

atgttacgtt tgactgcttt agccgtatgc accgccctcg ctttgggcgc gtgttcgccg     60

caaaattccg actctgcccc acaagccaaa gaacaggcgg tttccgccgc acaaaccgaa    120

ggcgcgtccg ttaccgtcaa aaccgcgcgc ggcgacgttc aaataccgca aaaccccgaa    180

cgcatcgccg tttacgattt gggtatgctc gacaccttga gcaaactggg cgtgaaaacc    240

ggtttgtccg tcgataaaaa ccgcctgccg tatttagagg aatatttcaa aacgacaaaa    300

cctgccggca ctttgttcga gccggattac gaaacgctca acgcttacaa accgcagctc    360

atcatcatcg gcagccgcgc cgccaaggcg tttgacaaat tgaacgaaat cgcgccgacc    420

atcgrmwtga ccgccgatac cgccaacctc aaagaaagtg ccaargaggc atcgacgctg    480

gcgcaaatct tc                                                        492


<210> SEQ ID NO 8
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (142)..(143)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 8

Met Leu Arg Leu Thr Ala Leu Ala Val Cys Thr Ala Leu Ala Leu Gly
  1               5                  10                  15

Ala Cys Ser Pro Gln Asn Ser Asp Ser Ala Pro Gln Ala Lys Glu Gln
             20                  25                  30

Ala Val Ser Ala Ala Gln Thr Glu Gly Ala Ser Val Thr Val Lys Thr
         35                  40                  45

Ala Arg Gly Asp Val Gln Ile Pro Gln Asn Pro Glu Arg Ile Ala Val
     50                  55                  60

Tyr Asp Leu Gly Met Leu Asp Thr Leu Ser Lys Leu Gly Val Lys Thr
 65                  70                  75                  80

Gly Leu Ser Val Asp Lys Asn Arg Leu Pro Tyr Leu Glu Glu Tyr Phe
                 85                  90                  95

Lys Thr Thr Lys Pro Ala Gly Thr Leu Phe Glu Pro Asp Tyr Glu Thr
            100                 105                 110

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

Lys Ala Phe Asp Lys Leu Asn Glu Ile Ala Pro Thr Ile Xaa Xaa Thr
    130                 135                 140

Ala Asp Thr Ala Asn Leu Lys Glu Ser Ala Lys Glu Ala Ser Thr Leu
145                 150                 155                 160

Ala Gln Ile Phe


<210> SEQ ID NO 9
```

-continued

<211> LENGTH: 966
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 9

atgttacgtt tgactgcttt agccgtatgc accgccctcg ctttgggcgc gtgttcgccg 60

caaaattccg actctgcccc acaagccaaa gaacaggcgg tttccgccgc acaaaccgaa 120

ggcgcgtccg ttaccgtcaa aaccgcgcgc ggcgacgttc aaataccgca aaaccccgaa 180

cgcatcgccg tttacgattt gggtatgctc gacaccttga gcaaactggg cgtgaaaacc 240

ggtttgtccg tcgataaaaa ccgcctgccg tatttagagg aatatttcaa aacgacaaaa 300

cctgccggca ctttgttcga gccggattac gaaacgctca acgcttacaa accgcagctc 360

atcatcatcg gcagccgcgc cgccaaggcg tttgacaaat tgaacgaaat cgcgccgacc 420

atcgaaatga ccgccgatac cgccaacctc aaagaaagtg ccaaagagcg catcgacgcg 480

ctggcgcaaa tcttcggcaa acaggcggaa gccgacaagc tgaaggcgga aatcgacgcg 540

tcttttgaag ccgcgaaaac tgccgcacaa ggtaagggca aaggtttggt gattttggtc 600

aacggcggca agatgtcggc tttcggcccg tcttcacgct tgggcggctg gctgcacaaa 660

gacatcggcg ttcccgctgt cgatgaatca attaaagaag gcagccacgg tcagcctatc 720

agctttgaat acctgaaaga gaaaaatccc gactggctgt ttgtccttga ccgaagcgcg 780

gccatcggcg aagagggtca ggcggcgaaa gacgtgttgg ataatccgct ggttgccgaa 840

acaaccgctt ggaaaaaagg acaggtcgtg tacctcgttc ctgaaactta tttggcagcc 900

ggtggcgcgc aagagctgct gaatgcaagc aaacaggttg ccgacgcttt taacgcggca 960

aaataa 966

<210> SEQ ID NO 10
<211> LENGTH: 321
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 10

Met Leu Arg Leu Thr Ala Leu Ala Val Cys Thr Ala Leu Ala Leu Gly
1 5 10 15

Ala Cys Ser Pro Gln Asn Ser Asp Ser Ala Pro Gln Ala Lys Glu Gln
20 25 30

Ala Val Ser Ala Ala Gln Thr Glu Gly Ala Ser Val Thr Val Lys Thr
35 40 45

Ala Arg Gly Asp Val Gln Ile Pro Gln Asn Pro Glu Arg Ile Ala Val
50 55 60

Tyr Asp Leu Gly Met Leu Asp Thr Leu Ser Lys Leu Gly Val Lys Thr
65 70 75 80

Gly Leu Ser Val Asp Lys Asn Arg Leu Pro Tyr Leu Glu Glu Tyr Phe
85 90 95

Lys Thr Thr Lys Pro Ala Gly Thr Leu Phe Glu Pro Asp Tyr Glu Thr
100 105 110

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

Lys Ala Phe Asp Lys Leu Asn Glu Ile Ala Pro Thr Ile Glu Met Thr
130 135 140

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

-continued

```
145                 150                 155                 160

Leu Ala Gln Ile Phe Gly Lys Gln Ala Glu Ala Asp Lys Leu Lys Ala
                165                 170                 175

Glu Ile Asp Ala Ser Phe Glu Ala Ala Lys Thr Ala Ala Gln Gly Lys
            180                 185                 190

Gly Lys Gly Leu Val Ile Leu Val Asn Gly Gly Lys Met Ser Ala Phe
        195                 200                 205

Gly Pro Ser Ser Arg Leu Gly Gly Trp Leu His Lys Asp Ile Gly Val
    210                 215                 220

Pro Ala Val Asp Glu Ser Ile Lys Glu Gly Ser His Gly Gln Pro Ile
225                 230                 235                 240

Ser Phe Glu Tyr Leu Lys Glu Lys Asn Pro Asp Trp Leu Phe Val Leu
                245                 250                 255

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

Leu Asp Asn Pro Leu Val Ala Glu Thr Thr Ala Trp Lys Lys Gly Gln
        275                 280                 285

Val Val Tyr Leu Val Pro Glu Thr Tyr Leu Ala Ala Gly Gly Ala Gln
    290                 295                 300

Glu Leu Leu Asn Ala Ser Lys Gln Val Ala Asp Ala Phe Asn Ala Ala
305                 310                 315                 320

Lys
```

<210> SEQ ID NO 11
<211> LENGTH: 966
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 11

```
atgttacgtt tgactgcttt agccgtatgc accgccctcg ctttgggcgc gtgttcgccg     60

caaaattccg actctgcccc acaagccaaa gaacaggcgg tttccgccgc acaatccgaa    120

ggcgtgtccg ttaccgtcaa aacggcgcgc ggcgatgttc aaataccgca aaaccccgaa    180

cgtatcgccg tttacgattt gggtatgctc gacaccttga gcaaactggg cgtgaaaacc    240

ggtttgtccg tcgataaaaa ccgcctgccg tatttagagg aatatttcaa aacgacaaaa    300

cctgccggaa ctttgttcga gccggattac gaaacgctca acgcttacaa accgcagctc    360

atcatcatcg gcagccgcgc agccaaagcg tttgacaaat tgaacgaaat cgcgccgacc    420

atcgaaatga ccgccgatac cgccaacctc aaagaaagtg ccaaagagcg tatcgacgcg    480

ctggcgcaaa tcttcggcaa aaaggcggaa gccgacaagc tgaaggcgga aatcgacgcg    540

tcttttgaag ccgcgaaaac tgccgcgcaa ggcaaaggca agggtttggt gattttggtc    600

aacggcggca agatgtccgc cttcggcccg tcttcacgac tgggcggctg gctgcacaaa    660

gacatcggcg ttcccgctgt tgacgaagcc atcaaagaag gcagccacgg tcagcctatc    720

agctttgaat acctgaaaga gaaaaatccc gactggctgt ttgtccttga ccgcagcgcg    780

gccatcggcg aagagggtca ggcggcgaaa gacgtgttga acaatccgct ggttgccgaa    840

acaaccgctt ggaaaaaagg acaagtcgtt taccttgttc ctgaaactta tttggcagcc    900

ggtggcgcgc aagagctact gaatgcaagc aaacaggttg ccgacgcttt taacgcggca    960

aaataa                                                              966
```

-continued

<210> SEQ ID NO 12
<211> LENGTH: 321
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 12

Met Leu Arg Leu Thr Ala Leu Ala Val Cys Thr Ala Leu Ala Leu Gly
1 5 10 15

Ala Cys Ser Pro Gln Asn Ser Asp Ser Ala Pro Gln Ala Lys Glu Gln
20 25 30

Ala Val Ser Ala Ala Gln Ser Glu Gly Val Ser Val Thr Val Lys Thr
35 40 45

Ala Arg Gly Asp Val Gln Ile Pro Gln Asn Pro Glu Arg Ile Ala Val
50 55 60

Tyr Asp Leu Gly Met Leu Asp Thr Leu Ser Lys Leu Gly Val Lys Thr
65 70 75 80

Gly Leu Ser Val Asp Lys Asn Arg Leu Pro Tyr Leu Glu Glu Tyr Phe
85 90 95

Lys Thr Thr Lys Pro Ala Gly Thr Leu Phe Glu Pro Asp Tyr Glu Thr
100 105 110

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

Lys Ala Phe Asp Lys Leu Asn Glu Ile Ala Pro Thr Ile Glu Met Thr
130 135 140

Ala Asp Thr Ala Asn Leu Lys Glu Ser Ala Lys Glu Arg Ile Asp Ala
145 150 155 160

Leu Ala Gln Ile Phe Gly Lys Lys Ala Glu Ala Asp Lys Leu Lys Ala
165 170 175

Glu Ile Asp Ala Ser Phe Glu Ala Ala Lys Thr Ala Ala Gln Gly Lys
180 185 190

Gly Lys Gly Leu Val Ile Leu Val Asn Gly Gly Lys Met Ser Ala Phe
195 200 205

Gly Pro Ser Ser Arg Leu Gly Gly Trp Leu His Lys Asp Ile Gly Val
210 215 220

Pro Ala Val Asp Glu Ala Ile Lys Glu Gly Ser His Gly Gln Pro Ile
225 230 235 240

Ser Phe Glu Tyr Leu Lys Glu Lys Asn Pro Asp Trp Leu Phe Val Leu
245 250 255

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

Leu Asn Asn Pro Leu Val Ala Glu Thr Thr Ala Trp Lys Lys Gly Gln
275 280 285

Val Val Tyr Leu Val Pro Glu Thr Tyr Leu Ala Ala Gly Gly Ala Gln
290 295 300

Glu Leu Leu Asn Ala Ser Lys Gln Val Ala Asp Ala Phe Asn Ala Ala
305 310 315 320

Lys

<210> SEQ ID NO 13
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

-continued

<400> SEQUENCE: 13

atgaaacttc tgaccaccgc aatcctgtct tccgcaatcg cgctcagcag tatggctgcc 60

gccgctggca cggacaaccc cactgttgca aaaaaaaccg tcagctacgt ctgccagcaa 120

ggtaaaaaag tcaaagtaac ctacggcttc aacaaacagg gtctgaccac atacgcttcc 180

gccgtcatca acggcaaacg cgtgcaaatg cctgtcaatt tggacaaatc cgacaatgtg 240

gaaacattct acggcaaaga aggcggttat gttttgggta ccggcgtgat ggatggcaaa 300

tcctaccgca aacagcccat tatgattacc gcacctgaca accaaatcgt cttcaaagac 360

tgttccccac gttaa 375

<210> SEQ ID NO 14
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 14

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

Ser Met Ala Ala Ala Ala Gly Thr Asp Asn Pro Thr Val Ala Lys Lys
20 25 30

Thr Val Ser Tyr Val Cys Gln Gln Gly Lys Lys Val Lys Val Thr Tyr
35 40 45

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

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

Glu Thr Phe Tyr Gly Lys Glu Gly Gly Tyr Val Leu Gly Thr Gly Val
85 90 95

Met Asp Gly Lys Ser Tyr Arg Lys Gln Pro Ile Met Ile Thr Ala Pro
100 105 110

Asp Asn Gln Ile Val Phe Lys Asp Cys Ser Pro Arg
115 120

<210> SEQ ID NO 15
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 15

atgaaacttc tgaccaccgc aatcctgtct tccgcaatcg cgctcagcag tatggctgct 60

gctgccggca cgaacaaccc caccgttgcc aaaaaaaccg tcagctacgt ctgccagcaa 120

ggtaaaaaag tcaaagtaac ctacggcttt aacaaacagg gcctgaccac atacgcttcc 180

gccgtcatca acggcaaacg tgtgcaaatg cctgtcaatt tggacaaatc cgacaatgtg 240

gaaacattct acggcaaaga aggcggttat gttttgggta ccggcgtgat ggatggcaaa 300

tcctatcgca aacagcctat tatgattacc gcacctgaca accaaatcgt cttcaaagac 360

tgttccccac gttaa 375

<210> SEQ ID NO 16
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

-continued

<400> SEQUENCE: 16

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

Ser Met Ala Ala Ala Ala Gly Thr Asn Asn Pro Thr Val Ala Lys Lys
20 25 30

Thr Val Ser Tyr Val Cys Gln Gln Gly Lys Lys Val Lys Val Thr Tyr
35 40 45

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

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

Glu Thr Phe Tyr Gly Lys Glu Gly Gly Tyr Val Leu Gly Thr Gly Val
85 90 95

Met Asp Gly Lys Ser Tyr Arg Lys Gln Pro Ile Met Ile Thr Ala Pro
100 105 110

Asp Asn Gln Ile Val Phe Lys Asp Cys Ser Pro Arg
115 120

<210> SEQ ID NO 17
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (425)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (485)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (489)
<223> OTHER INFORMATION: any nucleotide

<400> SEQUENCE: 17

ggcaccgaat tcaaaaccac cctttccgga gccgacatac aggcaggggt gggtgaaaaa 60

gcccgagccg atgcgaaaat tatcctaaaa ggcatcgtta accgcatcca aaccgaagaa 120

aagctggaat ccaactcgac cgtatggcaa aagcaggccg gaagcggcag cacggttgaa 180

acgctgaagc taccgagctt tgaagggccg gcactgccta agctgaccgc tcccggcggc 240

tatatcgccg acatccccaa aggcaacctc aaaaccgaaa tcgaaaagct ggccaaacag 300

cccgaatatg cctatctgaa acagcttcag acggtcaagg acgtgaactg gaaccaagta 360

cagctcgctt acgacaaatg ggactataaa caggaaggcc taaccggagc cggagccgca 420

attancgcac tggccgttac cgtggtcacc tcaggcgcag gaaccggagc cgtattggga 480

ttaanacgng tggccgccgc cgcaaccgat gcagcattt 519

<210> SEQ ID NO 18
<211> LENGTH: 173
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (142)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (162)

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<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 18

```
Gly Thr Glu Phe Lys Thr Thr Leu Ser Gly Ala Asp Ile Gln Ala Gly
  1               5                  10                  15

Val Gly Glu Lys Ala Arg Ala Asp Ala Lys Ile Ile Leu Lys Gly Ile
             20                  25                  30

Val Asn Arg Ile Gln Thr Glu Glu Lys Leu Glu Ser Asn Ser Thr Val
         35                  40                  45

Trp Gln Lys Gln Ala Gly Ser Gly Ser Thr Val Glu Thr Leu Lys Leu
     50                  55                  60

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

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

Leu Ala Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Thr Val
            100                 105                 110

Lys Asp Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp
        115                 120                 125

Tyr Lys Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Xaa Ala Leu
    130                 135                 140

Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly
145                 150                 155                 160

Leu Xaa Arg Val Ala Ala Ala Ala Thr Asp Ala Ala Phe
                165                 170
```

<210> SEQ ID NO 19
<211> LENGTH: 1923
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 19

```
atgcaactgc tggcagccga aggcattcac caacaccaat tgaatgttca gaaaagtacc     60

cgtttcatcg gcatcaaagt gggtaaaagc aattacagca aaaacgagct gaacgaaacc    120

aaactgcccg tacgcgttat cgcccaaaca gccaaaaccc gttccggctg ggataccgta    180

ctcgaaggca ccgaattcaa aaccaccctt tccggagccg acatacaggc aggggtgggt    240

gaaaaagccc gagccgatgc gaaaattatc ctaaaaggca tcgttaaccg catccaaacc    300

gaagaaaagc tggaatccaa ctcgaccgta tggcaaaagc aggccggaag cggcagcacg    360

gttgaaacgc tgaagctacc gagctttgaa gggccggcac tgcctaagct gaccgctccc    420

ggcggctata tcgccgacat ccccaaaggc aacctcaaaa ccgaaatcga aaagctggcc    480

aaacagcccg aatatgccta tctgaaacag cttcagacgg tcaaggacgt gaactggaac    540

caagtacagc tcgcttacga caaatgggac tataaacagg aaggcctaac cggagccgga    600

gccgcaatta tcgcactggc cgttaccgtg gtcacctcag gcgcaggaac cggagccgta    660

ttgggattaa acggtgcggc cgccgccgca accgatgcag catttgcctc tttggccagc    720

caggcttccg tatcgttcat caacaacaaa ggcaatatcg gtaacaccct gaaagagctg    780

ggcagaagca gcacggtgaa aaatctgatg gttgccgtcg ctaccgcagg cgtagccgac    840

aaaatcggtg cttcggcact gaacaatgtc agcgataagc agtggatcaa caacctgacc    900

gtcaacctgg ccaatgcggg cagtgccgca ctgattaata ccgctgtcaa cggcggcagc    960
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ctgaaagaca atctggaagc gaatatcctt gcggctttgg tgaatactgc gcatggagag   1020

gcagcaagta aaatcaaaca gttggatcag cactacattg cccataagat tgcccatgcc   1080

atagcgggct gtgcggcagc ggcggcgaat aagggcaagt gtcaagatgg tgcgatcggt   1140

gcggcggtcg gtgaaatcct tggcgaaacc ctactggacg gcagagaccc tggcagcctg   1200

aatgtgaagg acagggcaaa aatcattgct aaggcgaagc tggcagcagg ggcggttgcg   1260

gcgttgagta agggggatgt gagtacggcg gcgaatgcgg ctgctgtggc ggtagagaat   1320

aattctttaa atgatataca ggatcgtttg ttgagtggaa attatgcttt atgtatgagt   1380

gcaggaggag cagaaagctt ttgtgagtct tatcgaccac tgggcttgcc acactttgta   1440

agtgtttcag gagaaatgaa attacctaat aaattcggga atcgtatggt taatggaaaa   1500

ttaattatta acactagaaa tggcaatgta tatttctctg taggtaaaat atggagtact   1560

gtaaaatcaa caaaatcaaa tataagtggg gtatctgtcg gttgggtttt aaatgtttcc   1620

cctaatgatt atttaaaaga agcatctatg aatgatttca gaaatagtaa tcaaaataaa   1680

gcctatgcag aaatgatttc ccagactttg gtaggtgaga gtgttggtgg tagtctttgt   1740

ctgacaagag cctgcttttc ggtaagttca acaatatcta aatctaaatc tccttttaaa   1800

gattcaaaaa ttattgggga aatcggtttg ggaagtggtg ttgctgcagg agtagaaaaa   1860

acaatataca taggtaacat aaaagatatt gataaattta ttagtgcaaa cataaaaaaa   1920

tag                                                                1923
```

<210> SEQ ID NO 20
<211> LENGTH: 640
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 20

```
Met Gln Leu Leu Ala Ala Glu Gly Ile His Gln His Gln Leu Asn Val
  1               5                  10                  15

Gln Lys Ser Thr Arg Phe Ile Gly Ile Lys Val Gly Lys Ser Asn Tyr
             20                  25                  30

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

Gln Thr Ala Lys Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr
     50                  55                  60

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

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

Arg Ile Gln Thr Glu Glu Lys Leu Glu Ser Asn Ser Thr Val Trp Gln
            100                 105                 110

Lys Gln Ala Gly Ser Gly Ser Thr Val Glu Thr Leu Lys Leu Pro Ser
        115                 120                 125

Phe Glu Gly Pro Ala Leu Pro Lys Leu Thr Ala Pro Gly Gly Tyr Ile
    130                 135                 140

Ala Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ala
145                 150                 155                 160

Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Thr Val Lys Asp
                165                 170                 175
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Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp Tyr Lys
            180                 185                 190

Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
        195                 200                 205

Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn
    210                 215                 220

Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
225                 230                 235                 240

Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asn Ile Gly Asn Thr
                245                 250                 255

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

Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu Asn
        275                 280                 285

Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu Ala
    290                 295                 300

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

Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn Thr
                325                 330                 335

Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His Tyr
            340                 345                 350

Ile Ala His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala Ala
        355                 360                 365

Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val Gly
    370                 375                 380

Glu Ile Leu Gly Glu Thr Leu Leu Asp Gly Arg Asp Pro Gly Ser Leu
385                 390                 395                 400

Asn Val Lys Asp Arg Ala Lys Ile Ile Ala Lys Ala Lys Leu Ala Ala
                405                 410                 415

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

Ala Ala Ala Val Ala Val Glu Asn Asn Ser Leu Asn Asp Ile Gln Asp
        435                 440                 445

Arg Leu Leu Ser Gly Asn Tyr Ala Leu Cys Met Ser Ala Gly Gly Ala
    450                 455                 460

Glu Ser Phe Cys Glu Ser Tyr Arg Pro Leu Gly Leu Pro His Phe Val
465                 470                 475                 480

Ser Val Ser Gly Glu Met Lys Leu Pro Asn Lys Phe Gly Asn Arg Met
                485                 490                 495

Val Asn Gly Lys Leu Ile Ile Asn Thr Arg Asn Gly Asn Val Tyr Phe
            500                 505                 510

Ser Val Gly Lys Ile Trp Ser Thr Val Lys Ser Thr Lys Ser Asn Ile
        515                 520                 525

Ser Gly Val Ser Val Gly Trp Val Leu Asn Val Ser Pro Asn Asp Tyr
    530                 535                 540

Leu Lys Glu Ala Ser Met Asn Asp Phe Arg Asn Ser Asn Gln Asn Lys
545                 550                 555                 560

Ala Tyr Ala Glu Met Ile Ser Gln Thr Leu Val Gly Glu Ser Val Gly
                565                 570                 575

Gly Ser Leu Cys Leu Thr Arg Ala Cys Phe Ser Val Ser Ser Thr Ile
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            580                 585                 590

Ser Lys Ser Lys Ser Pro Phe Lys Asp Ser Lys Ile Ile Gly Glu Ile
        595                 600                 605

Gly Leu Gly Ser Gly Val Ala Ala Gly Val Glu Lys Thr Ile Tyr Ile
    610                 615                 620

Gly Asn Ile Lys Asp Ile Asp Lys Phe Ile Ser Ala Asn Ile Lys Lys
625                 630                 635                 640


<210> SEQ ID NO 21
<211> LENGTH: 2291
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (149)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (238)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (426)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (679)
<223> OTHER INFORMATION: any nucleotide
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<221> NAME/KEY: misc_feature
<222> LOCATION: (863)
<223> OTHER INFORMATION: any nucleotide
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<221> NAME/KEY: misc_feature
<222> LOCATION: (971)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1336)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1388)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1837)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1909)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1939)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1941)
<223> OTHER INFORMATION: any nucleotide
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1959)
<223> OTHER INFORMATION: any nucleotide
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<220> FEATURE:
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<222> LOCATION: (2079)
<223> OTHER INFORMATION: any nucleotide
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<221> NAME/KEY: misc_feature
<222> LOCATION: (2084)..(2085)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2113)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2120)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2236)..(2238)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2242)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2244)
<223> OTHER INFORMATION: any nucleotide

<400> SEQUENCE: 21

ntgcaactgc tggcagaaga aggcatccac aagcacgagt tggatgtcca aaaaagccgc 60

cgctttatcg gcatcaaggt aggtnagagc aattacagta aaaacgaact gaacgaaacc 120

aaattgcctg tccgcgtcgt cgcccaaant gcagccaccc gttcaggctg ggataccgtg 180

ctcgaaggta ccgaattcaa aaccacgctg gccggtgccg acattcaggc aggtgtangc 240

gaaaaagccc gtgtcgatgc gaaaattatc ctcaaaggca ttgtgaaccg tatccagtcg 300

gaagaaaaat tagaaaccaa ctcaaccgta tggcagaaac aggccggacg cggcagcact 360

atcgaaacgc taaaactgcc cagcttcgaa agccctactc cgcccaaatt gtccgcaccc 420

ggcggntata tcgtcgacat tccgaaaggc aatctgaaaa ccgaaatcga aaagctgtcc 480

aaacagcccg agtatgccta tctgaaacag ctccaagtag cgaaaaacat caactggaat 540

caggtgcagc ttgcttacga cagatgggac tacaaacagg agggcttaac cgaagcaggt 600

gcggcgatta tcgcactggc cgttaccgtg gtcacctcag gcgcaggaac cggagccgta 660

ttgggattaa acggtgcgnc cgccgccgca accgatgcag cattcgcctc tttggccagc 720

caggcttccg tatcgttcat caacaacaaa ggcgatgtcg gcaaaaccct gaaagagctg 780

ggcagaagca gcacggtgaa aaatctggtg gttgccgccg ctaccgcagg cgtagccgac 840

aaaatcggcg cttcggcact gancaatgtc agcgataagc agtggatcaa caacctgacc 900

gtcaacctag ccaatgcggg cagtgccgca ctgattaata ccgctgtcaa cggcggcagc 960

ctgaaagaca ntctggaagc gaatatcctt gcggctttgg tcaataccgc gcatggagaa 1020

gcagccagta aaatcaaaca gttggatcag cactacatag tccacaagat tgcccatgcc 1080

atagcgggct gtgcggcagc ggcggcgaat aagggcaagt gtcaggatgg tgcgataggt 1140

gcggctgtgg gcgagatagt cggggaggct ttgacaaacg gcaaaaatcc tgacactttg 1200

acagctaaag aacgcgaaca gattttggca tacagcaaac tggttgccgg tacggtaagc 1260

ggtgtggtcg gcggcgatgt aaatgcggcg gcgaatgcgg ctgaggtagc ggtgaaaaat 1320

aatcagctta gcgacnaaga gggtagagaa tttgataacg aaatgactgc atgcgccaaa 1380

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cagaatantc ctcaactgtg cagaaaaaat actgtaaaaa agtatcaaaa tgttgctgat 1440

aaaagacttg ctgcttcgat tgcaatatgt acggatatat cccgtagtac tgaatgtaga 1500

acaatcagaa aacaacattt gatcgatagt agaagccttc attcatcttg ggaagcaggt 1560

ctaattggta aagatgatga atggtataaa ttattcagca aatcttacac ccaagcagat 1620

ttggctttac agtcttatca tttgaatact gctgctaaat cttggcttca atcgggcaat 1680

acaaagcctt tatccgaatg gatgtccgac caaggttata cacttatttc aggagttaat 1740

cctagattca ttccaatacc aagagggttt gtaaaacaaa atacacctat tactaatgtc 1800

aaatacccgg aaggcatcag tttcgataca aacctanaaa gacatctggc aaatgctgat 1860

ggttttagtc aagaacaggg cattaaagga gcccataacc gcaccaatnt tatggcagaa 1920

ctaaattcac gaggaggang ngtaaaatct gaaacccana ctgatattga aggcattacc 1980

cgaattaaat atgagattcc tacactagac aggacaggta aacctgatgg tggatttaag 2040

gaaatttcaa gtataaaaac tgtttataat cctaaaaant tttnngatga taaaatactt 2100

caaatggctc aanatgctgn ttcacaagga tattcaaaag cctctaaaat tgctcaaaat 2160

gaaagaacta aatcaatatc ggaaagaaaa aatgtcattc aattctcaga aacctttgac 2220

ggaatcaaat ttagannnta tntngatgta aatacaggaa gaattacaaa cattcaccca 2280

gaataattta a 2291

<210> SEQ ID NO 22
<211> LENGTH: 761
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (1)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (29)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (50)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (80)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (227)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (288)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (324)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (446)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (463)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE

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<222> LOCATION: (613)
<223> OTHER INFORMATION: unknown
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<221> NAME/KEY: SITE
<222> LOCATION: (637)
<223> OTHER INFORMATION: unknown
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<221> NAME/KEY: SITE
<222> LOCATION: (647)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (653)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (693)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (695)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (705)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (707)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (746)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (748)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 22

Xaa Gln Leu Leu Ala Glu Glu Gly Ile His Lys His Glu Leu Asp Val
1 5 10 15

Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly Xaa Ser Asn Tyr
20 25 30

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

Gln Xaa Ala Ala Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr
50 55 60

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

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

Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser Thr Val Trp Gln
100 105 110

Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu Lys Leu Pro Ser
115 120 125

Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro Gly Gly Tyr Ile
130 135 140

Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ser
145 150 155 160

Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn
165 170 175

Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys
180 185 190

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Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
        195                 200                 205

Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn
    210                 215                 220

Gly Ala Xaa Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
225                 230                 235                 240

Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp Val Gly Lys Thr
                245                 250                 255

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

Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu Xaa
        275                 280                 285

Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu Ala
    290                 295                 300

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

Leu Lys Asp Xaa Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn Thr
                325                 330                 335

Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His Tyr
            340                 345                 350

Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala Ala
        355                 360                 365

Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val Gly
    370                 375                 380

Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn Pro Asp Thr Leu
385                 390                 395                 400

Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser Lys Leu Val Ala
                405                 410                 415

Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn Ala Ala Ala Asn
            420                 425                 430

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

Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys Gln Asn Xaa Pro
    450                 455                 460

Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln Asn Val Ala Asp
465                 470                 475                 480

Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp Ile Ser Arg Ser
                485                 490                 495

Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile Asp Ser Arg Ser
            500                 505                 510

Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys Asp Asp Glu Trp
        515                 520                 525

Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp Leu Ala Leu Gln
    530                 535                 540

Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu Gln Ser Gly Asn
545                 550                 555                 560

Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly Tyr Thr Leu Ile
                565                 570                 575

Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg Gly Phe Val Lys
            580                 585                 590
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```
Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu Gly Ile Ser Phe
        595                 600                 605

Asp Thr Asn Leu Xaa Arg His Leu Ala Asn Ala Asp Gly Phe Ser Gln
    610                 615                 620

Glu Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn Xaa Met Ala Glu
625                 630                 635                 640

Leu Asn Ser Arg Gly Gly Xaa Val Lys Ser Glu Thr Xaa Thr Asp Ile
                645                 650                 655

Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr Leu Asp Arg Thr
            660                 665                 670

Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser Ile Lys Thr Val
        675                 680                 685

Tyr Asn Pro Lys Xaa Phe Xaa Asp Asp Lys Ile Leu Gln Met Ala Gln
    690                 695                 700

Xaa Ala Xaa Ser Gln Gly Tyr Ser Lys Ala Ser Lys Ile Ala Gln Asn
705                 710                 715                 720

Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val Ile Gln Phe Ser
                725                 730                 735

Glu Thr Phe Asp Gly Ile Lys Phe Arg Xaa Tyr Xaa Asp Val Asn Thr
            740                 745                 750

Gly Arg Ile Thr Asn Ile His Pro Glu
        755                 760
```

<210> SEQ ID NO 23
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 23

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cggatcgttg taggtttgcg gatttcttgc gccgtagtca ccgtagtccc aagtataacc     60

caaggctttg tcttcgcctt tcattccgat aagggatatg acgctttggt cggtatagcc    120

gtcttgggaa cctttgtcca cccaacgcat atctgcctgc ggattctcat tgccgcttct    180

tggctgctga ttttttctgcc ttcgcgtttt tcaacttcgc gcttgagggc ttcggcatat    240

ttgtcggcca acgccatttc tttcggatgc agctgcctat tgttccaatc tacattcgca    300

cccaccacag caccaccact accaccagtt gcatag                              336
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<210> SEQ ID NO 24
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 24

```
Arg Ile Val Val Gly Leu Arg Ile Ser Cys Ala Val Val Thr Val Val
  1               5                  10                  15

Pro Ser Ile Thr Gln Gly Phe Val Phe Ala Phe His Ser Asp Lys Gly
             20                  25                  30

Tyr Asp Ala Leu Val Gly Ile Ala Val Leu Gly Thr Phe Val His Pro
         35                  40                  45

Thr His Ile Cys Leu Arg Ile Leu Ile Ala Ala Ser Trp Leu Leu Ile
     50                  55                  60

Phe Leu Pro Ser Arg Phe Ser Thr Ser Arg Leu Arg Ala Ser Ala Tyr
 65                  70                  75                  80
```

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Leu Ser Ala Asn Ala Ile Ser Phe Gly Cys Ser Cys Leu Leu Phe Gln
85 90 95

Ser Thr Phe Ala Pro Thr Thr Ala Pro Pro Leu Pro Pro Val Ala
100 105 110

<210> SEQ ID NO 25
<211> LENGTH: 1716
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (496)..(1542)
<223> OTHER INFORMATION: N = Unknown
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (1673)..(1674)
<223> OTHER INFORMATION: N= Unknown

<400> SEQUENCE: 25

aagtttgact ttacctggtt tattccggcg gtaatcaaat accgccggtt gtttttttgaa 60

gtattggtgg tgtcggtggt gttgcagctg tttgcgctga ttacgcctct gtttttccaa 120

gtggtgatgg acaaggtgct ggtacatcgg ggattctcta ctttggatgt ggtgtcggtg 180

gctttgttgg tggtgtcgct gtttgagatt gtgttgggcg gtttgcggac gtatctgttt 240

gcacatacga cttcacgtat tgatgtggaa ttgggcgcgc gtttgttccg gcatctgctt 300

tccctgcctt tatcctattt cgagcacaga cgagtgggtg atacggtggc tcgggtgcgg 360

gaattggagc agattcgcaa tttcttgacc ggtcaggcgc tgacttcggt gttggatttg 420

gcgttttcgt ttatctttct ggcggtgatg tggtattaca gctccactct gacttgggtg 480

gtattggctt cgttgnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 600

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 660

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 780

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 840

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 900

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 960

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1020

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1080

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1140

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1200

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1260

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1320

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1380

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1440

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1500

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnatttgcgc caaccggacg 1560

gtgctgatta tcgcccaccg tctgtccact gttaaaacgg cacaccggat cattgccatg 1620

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gataaaggca ggattgtgga agcgggaaca cagcaggaat tgctggcgaa cgnnaacgga 1680

tattaccgct atctgtatga tttacagaac gggtag 1716

<210> SEQ ID NO 26
<211> LENGTH: 571
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (166)..(514)
<223> OTHER INFORMATION: x = Unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (558)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 26

Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg
1 5 10 15

Leu Phe Phe Glu Val Leu Val Val Ser Val Val Leu Gln Leu Phe Ala
20 25 30

Leu Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
35 40 45

His Arg Gly Phe Ser Thr Leu Asp Val Val Ser Val Ala Leu Leu Val
50 55 60

Val Ser Leu Phe Glu Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe
65 70 75 80

Ala His Thr Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
85 90 95

Arg His Leu Leu Ser Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val
100 105 110

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

Leu Thr Gly Gln Ala Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe
130 135 140

Ile Phe Leu Ala Val Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val
145 150 155 160

Val Leu Ala Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
290 295 300

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305 310 315 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
325 330 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
355 360 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385 390 395 400

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
405 410 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
420 425 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
450 455 460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
485 490 495

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
500 505 510

Xaa Xaa Ile Cys Ala Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu
515 520 525

Ser Thr Val Lys Thr Ala His Arg Ile Ile Ala Met Asp Lys Gly Arg
530 535 540

Ile Val Glu Ala Gly Thr Gln Gln Glu Leu Leu Ala Asn Xaa Asn Gly
545 550 555 560

Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln Asn Gly
565 570

<210> SEQ ID NO 27
<211> LENGTH: 2133
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 27

atgtctatcg tatccgcacc gctccccgcc ctttccgccc tcatcatcct cgcccattac 60

cacggcattg ccgccaatcc tgccgatata cagcatgaat tttgtacttc cgcacagagc 120

gatttaaatg aaacgcaatg gctgttagcc gccaaatctt tgggattgaa ggcaaaggta 180

gtccgccagc ctattaaacg tttggctatg gcgactttac ccgcattggt atggtgtgat 240

gacggcaacc atttcatttt ggccaaaaca gacggtgagg gtgagcatgc ccaatttttg 300

atacaggatt tggttacgaa taagtctgcg gtattgtctt ttgccgaatt ttctaacaga 360

tattcgggca aactgatatt ggttgcttcc cgcgcttcgg tattgggcag tttggcaaag 420

tttgacttta cctggtttat tccggcggta atcaaatacc gccggttgtt ttttgaagta 480

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ttggtggtgt cggtggtgtt gcagctgttt gcgctgatta cgcctctgtt tttccaagtg    540

gtgatggaca aggtgctggt acatcgggga ttctctactt tggatgtggt gtcggtggct    600

ttgttggtgg tgtcgctgtt tgagattgtg ttgggcggtt tgcggacgta tctgtttgca    660

catacgactt cacgtattga tgtggaattg ggcgcgcgtt tgttccggca tctgctttcc    720

ctgcctttat cctatttcga gcacagacga gtgggtgata cggtggctcg ggtgcgggaa    780

ttggagcaga ttcgcaattt cttgaccggt caggcgctga cttcggtgtt ggatttggcg    840

ttttcgttta tctttctggc ggtgatgtgg tattacagct ccactctgac ttgggtggta    900

ttggcttcgt tgcctgccta tgcgttttgg tcggcattta tcagtccgat actgcggacg    960

cgtctgaacg ataagttcgc gcgcaatgca gacaaccagt cgtttttagt agaaagcatc   1020

actgcggtgg gtacggtaaa ggcgatggcg gtggagccgc agatgacgca gcgttgggac   1080

aatcagttgg cggcttatgt ggcttcggga tttcgggtaa cgaagttggc ggtggtcggc   1140

cagcaggggg tgcagctgat tcagaagctg gtgacggtgg cgacgttgtg gattggcgca   1200

cggctggtaa ttgagagcaa gctgacggtg gggcagctga ttgcgtttaa tatgctctcg   1260

ggacaggtgg cggcgcctgt tatccgtttg gcgcagttgt ggcaggattt ccagcaggtg   1320

gggatttcgg tggcgcgttt gggggatatt ctgaatgcgc cgaccgagaa tgcgtcttcg   1380

catttggctt tgcccgatat ccgggggggag attacgttcg aacatgtcga tttccgctat   1440

aaggcggacg gcaggctgat tttgcaggat ttgaacctgc ggattcgggc gggggaagtg   1500

ctggggattg tgggacgttc ggggtcgggc aaatccacac tcaccaaatt ggtgcagcgt   1560

ctgtatgtac cggagcaggg acgggtgttg gtggacggca acgatttggc tttggccgct   1620

cctgcctggc tgcggcggca ggtcggcgtg gtcttgcagg agaatgtgct gctcaaccgc   1680

agcatacgcg acaatatcgc gctgacggat acgggtatgc cgctggaacg cattatcgaa   1740

gcagccaaac tggcgggcgc acacgagttt attatggagc tgccggaagg ctacggcacc   1800

gtggtgggcg aacaaggggc cggcttgtcg ggcggacagc ggcagcgtat tgcgattgcc   1860

cgcgcgttaa tcaccaatcc gcgcattctg atttttgatg aagccaccag cgcgctggat   1920

tatgaaagtg aacgagcgat tatgcagaac atgcaggcca tttgcgccaa ccggacggtg   1980

ctgattatcg cccaccgtct gtccactgtt aaaacggcac accggatcat tgccatggat   2040

aaaggcagga ttgtggaagc gggaacacag caggaattgc tggcgaagcc gaacggatat   2100

taccgctatc tgtatgattt acagaacggg tag                                2133
```

<210> SEQ ID NO 28
<211> LENGTH: 710
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 28

```
Met Ser Ile Val Ser Ala Pro Leu Pro Ala Leu Ser Ala Leu Ile Ile
  1               5                  10                  15

Leu Ala His Tyr His Gly Ile Ala Ala Asn Pro Ala Asp Ile Gln His
            20                  25                  30

Glu Phe Cys Thr Ser Ala Gln Ser Asp Leu Asn Glu Thr Gln Trp Leu
         35                  40                  45

Leu Ala Ala Lys Ser Leu Gly Leu Lys Ala Lys Val Val Arg Gln Pro
     50                  55                  60
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Ile Lys Arg Leu Ala Met Ala Thr Leu Pro Ala Leu Val Trp Cys Asp
 65                  70                  75                  80

Asp Gly Asn His Phe Ile Leu Ala Lys Thr Asp Gly Glu Gly Glu His
                 85                  90                  95

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

Ser Phe Ala Glu Phe Ser Asn Arg Tyr Ser Gly Lys Leu Ile Leu Val
        115                 120                 125

Ala Ser Arg Ala Ser Val Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr
    130                 135                 140

Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg Leu Phe Phe Glu Val
145                 150                 155                 160

Leu Val Val Ser Val Val Leu Gln Leu Phe Ala Leu Ile Thr Pro Leu
                165                 170                 175

Phe Phe Gln Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser
            180                 185                 190

Thr Leu Asp Val Val Ser Val Ala Leu Leu Val Val Ser Leu Phe Glu
        195                 200                 205

Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe Ala His Thr Thr Ser
    210                 215                 220

Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ser
225                 230                 235                 240

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

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

Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe Ile Phe Leu Ala Val
        275                 280                 285

Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val Val Leu Ala Ser Leu
    290                 295                 300

Pro Ala Tyr Ala Phe Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr
305                 310                 315                 320

Arg Leu Asn Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu
                325                 330                 335

Val Glu Ser Ile Thr Ala Val Gly Thr Val Lys Ala Met Ala Val Glu
            340                 345                 350

Pro Gln Met Thr Gln Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Ala
        355                 360                 365

Ser Gly Phe Arg Val Thr Lys Leu Ala Val Val Gly Gln Gln Gly Val
    370                 375                 380

Gln Leu Ile Gln Lys Leu Val Thr Val Ala Thr Leu Trp Ile Gly Ala
385                 390                 395                 400

Arg Leu Val Ile Glu Ser Lys Leu Thr Val Gly Gln Leu Ile Ala Phe
                405                 410                 415

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

Leu Trp Gln Asp Phe Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly
        435                 440                 445

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

Pro Asp Ile Arg Gly Glu Ile Thr Phe Glu His Val Asp Phe Arg Tyr
```

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465                 470                 475                 480

Lys Ala Asp Gly Arg Leu Ile Leu Gln Asp Leu Asn Leu Arg Ile Arg
                485                 490                 495

Ala Gly Glu Val Leu Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser
            500                 505                 510

Thr Leu Thr Lys Leu Val Gln Arg Leu Tyr Val Pro Glu Gln Gly Arg
        515                 520                 525

Val Leu Val Asp Gly Asn Asp Leu Ala Leu Ala Ala Pro Ala Trp Leu
    530                 535                 540

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

Ser Ile Arg Asp Asn Ile Ala Leu Thr Asp Thr Gly Met Pro Leu Glu
                565                 570                 575

Arg Ile Ile Glu Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Met
            580                 585                 590

Glu Leu Pro Glu Gly Tyr Gly Thr Val Val Gly Glu Gln Gly Ala Gly
        595                 600                 605

Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile
    610                 615                 620

Thr Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp
625                 630                 635                 640

Tyr Glu Ser Glu Arg Ala Ile Met Gln Asn Met Gln Ala Ile Cys Ala
                645                 650                 655

Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser Thr Val Lys Thr
            660                 665                 670

Ala His Arg Ile Ile Ala Met Asp Lys Gly Arg Ile Val Glu Ala Gly
        675                 680                 685

Thr Gln Gln Glu Leu Leu Ala Lys Pro Asn Gly Tyr Tyr Arg Tyr Leu
    690                 695                 700

Tyr Asp Leu Gln Asn Gly
705                 710


<210> SEQ ID NO 29
<211> LENGTH: 2133
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 29

atgtctatcg tatccgcacc gctccccgcc ctttccgccc tcatcatcct cgcccattac     60

cacggcattg ccgccaatcc tgccgatata cagcatgaat tttgtacttc cgcacagagc    120

gatttaaatg aaacgcaatg gctgttagcc gccaaatctt tgggattgaa ggcaaaggta    180

gtccgccagc ctattaaacg tttggctatg gcgactttac ccgcattggt atggtgtgat    240

gacggcaacc attttatttt ggctaaaaca gacggtgggg gtgagcatgc ccaatatcta    300

atacaggatt taactacgaa taagtctgcg gtattgtctt ttgccgaatt ttctaacaga    360

tattcgggca aactgatatt ggttgcttcc cgcgcttcgg tattgggcag tttggcaaag    420

tttgacttta cctggtttat tccggcggta atcaaatacc gccggttgtt ttttgaagta    480

ttggtggtgt cggtggtgtt gcagctgttt gcgctgatta cgcctctgtt tttccaagtg    540

gtgatggaca aggtgctggt acatcgggga ttctctactt tggatgtggt gtcggtggct    600

ttgttggtgg tgtcgctgtt tgagattgtg ttgggcggtt tgcggacgta tctgtttgca    660
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catacgactt cacgtattga tgtggaattg ggcgcgcgtt tgttccggca tctgctttcc    720

ctgcctttat cctatttcga gcacagacga gtgggtgata cggtggctcg ggtgcgggaa    780

ttggagcaga ttcgcaattt cttgaccggt caggcgctga cttcggtgtt ggatttggcg    840

ttttcgttta tctttctggc ggtgatgtgg tattacagct ccactctgac ttgggtggta    900

ttggcttcgt tgcctgccta tgcgttttgg tcggcattta tcagtccgat actgcggacg    960

cgtctgaacg ataagttcgc gcgcaatgca gacaaccagt cgtttttagt agaaagcatc   1020

actgcggtgg gtacggtaaa ggcgatggcg gtggagccgc agatgacgca gcgttgggac   1080

aatcagttgg cggcttatgt ggcttcggga tttcgggtaa cgaagttggc ggtggtcggc   1140

cagcaggggg tgcagctgat tcagaagctg gtgacggtgg cgacgttgtg gattggcgca   1200

cggctggtaa ttgagagcaa gctgacggtg gggcagctga ttgcgtttaa tatgctctcg   1260

ggacaggtgg cggcgcctgt tatccgtttg gcgcagttgt ggcaggattt ccagcaggtg   1320

gggatttcgg tggcgcgttt gggggatatt ctgaatgcgc cgaccgagaa tgcgtcttcg   1380

catttggctt tgcccgatat ccgggggggag attacgttcg aacatgtcga tttccgctat   1440

aaggcggacg gcaggctgat tttgcaggat ttgaacctgc ggattcgggc gggggaagtg   1500

ctggggattg tgggacgttc ggggtcgggc aaatccacac tcaccaaatt ggtgcagcgt   1560

ctgtatgtac cggcgcaggg acgggtgttg gtggacggca acgatttggc tttggccgct   1620

cctgcttggc tgcggcggca ggtcggcgtg gtcttgcagg agaatgtgct gctcaaccgc   1680

agcatacgcg acaatatcgc gctgacggat acgggtatgc cgctggaacg cattatcgaa   1740

gcagccaaac tggcgggcgc acacgagttt attatggagc tgccggaagg ctacggcacc   1800

gtggtgggcg aacaaggggc cggcttgtcg ggcggacagc ggcagcgtat tgcgattgcc   1860

cgcgcgttaa tcaccaatcc gcgcattctg atttttgatg aagccaccag cgcgctggat   1920

tatgaaagtg aacgagcgat tatgcagaac atgcaggcca tttgcgccaa ccggacggtg   1980

ctgattatcg cccaccgtct gtccactgtt aaaacggcac accggatcat tgccatggat   2040

aaaggcagga ttgtggaagc gggaacacag caggaattgc tggcgaagcc gaacggatat   2100

taccgctatc tgtatgattt acagaacggg tag                                2133
```

<210> SEQ ID NO 30
<211> LENGTH: 710
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 30

```
Met Ser Ile Val Ser Ala Pro Leu Pro Ala Leu Ser Ala Leu Ile Ile
  1               5                  10                  15

Leu Ala His Tyr His Gly Ile Ala Ala Asn Pro Ala Asp Ile Gln His
             20                  25                  30

Glu Phe Cys Thr Ser Ala Gln Ser Asp Leu Asn Glu Thr Gln Trp Leu
         35                  40                  45

Leu Ala Ala Lys Ser Leu Gly Leu Lys Ala Lys Val Val Arg Gln Pro
     50                  55                  60

Ile Lys Arg Leu Ala Met Ala Thr Leu Pro Ala Leu Val Trp Cys Asp
 65                  70                  75                  80

Asp Gly Asn His Phe Ile Leu Ala Lys Thr Asp Gly Gly Gly Glu His
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                85                  90                  95

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

Ser Phe Ala Glu Phe Ser Asn Arg Tyr Ser Gly Lys Leu Ile Leu Val
        115                 120                 125

Ala Ser Arg Ala Ser Val Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr
    130                 135                 140

Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg Leu Phe Phe Glu Val
145                 150                 155                 160

Leu Val Val Ser Val Val Leu Gln Leu Phe Ala Leu Ile Thr Pro Leu
                165                 170                 175

Phe Phe Gln Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser
            180                 185                 190

Thr Leu Asp Val Val Ser Val Ala Leu Leu Val Val Ser Leu Phe Glu
        195                 200                 205

Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe Ala His Thr Thr Ser
    210                 215                 220

Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ser
225                 230                 235                 240

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

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

Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe Ile Phe Leu Ala Val
        275                 280                 285

Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val Val Leu Ala Ser Leu
    290                 295                 300

Pro Ala Tyr Ala Phe Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr
305                 310                 315                 320

Arg Leu Asn Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu
                325                 330                 335

Val Glu Ser Ile Thr Ala Val Gly Thr Val Lys Ala Met Ala Val Glu
            340                 345                 350

Pro Gln Met Thr Gln Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Ala
        355                 360                 365

Ser Gly Phe Arg Val Thr Lys Leu Ala Val Val Gly Gln Gln Gly Val
    370                 375                 380

Gln Leu Ile Gln Lys Leu Val Thr Val Ala Thr Leu Trp Ile Gly Ala
385                 390                 395                 400

Arg Leu Val Ile Glu Ser Lys Leu Thr Val Gly Gln Leu Ile Ala Phe
                405                 410                 415

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

Leu Trp Gln Asp Phe Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly
        435                 440                 445

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

Pro Asp Ile Arg Gly Glu Ile Thr Phe Glu His Val Asp Phe Arg Tyr
465                 470                 475                 480

Lys Ala Asp Gly Arg Leu Ile Leu Gln Asp Leu Asn Leu Arg Ile Arg
                485                 490                 495
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Ala Gly Glu Val Leu Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser
            500                 505                 510

Thr Leu Thr Lys Leu Val Gln Arg Leu Tyr Val Pro Ala Gln Gly Arg
        515                 520                 525

Val Leu Val Asp Gly Asn Asp Leu Ala Leu Ala Ala Pro Ala Trp Leu
    530                 535                 540

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

Ser Ile Arg Asp Asn Ile Ala Leu Thr Asp Thr Gly Met Pro Leu Glu
                565                 570                 575

Arg Ile Ile Glu Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Met
            580                 585                 590

Glu Leu Pro Glu Gly Tyr Gly Thr Val Val Gly Glu Gln Gly Ala Gly
        595                 600                 605

Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile
    610                 615                 620

Thr Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp
625                 630                 635                 640

Tyr Glu Ser Glu Arg Ala Ile Met Gln Asn Met Gln Ala Ile Cys Ala
                645                 650                 655

Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser Thr Val Lys Thr
            660                 665                 670

Ala His Arg Ile Ile Ala Met Asp Lys Gly Arg Ile Val Glu Ala Gly
        675                 680                 685

Thr Gln Gln Glu Leu Leu Ala Lys Pro Asn Gly Tyr Tyr Arg Tyr Leu
    690                 695                 700

Tyr Asp Leu Gln Asn Gly
705                 710


<210> SEQ ID NO 31
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 31

atgaaatact tgatccgcac cgccttactc gcagtcgcag ccgccggcat ctacgcctgc     60

caaccgcaat ccgaagccgc agtgcaagtc aaggctgaaa acagcctgac cgctatgcgc    120

ttagccgtcg ccgacaaaca ggcagagatt gacgggttga acgcccaaak sgacgccgaa    180

atcaga                                                               186


<210> SEQ ID NO 32
<211> LENGTH: 62
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (57)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 32

Met Lys Tyr Leu Ile Arg Thr Ala Leu Leu Ala Val Ala Ala Ala Gly
  1               5                  10                  15

Ile Tyr Ala Cys Gln Pro Gln Ser Glu Ala Ala Val Gln Val Lys Ala
             20                  25                  30
```

-continued

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

Glu Ile Asp Gly Leu Asn Ala Gln Xaa Asp Ala Glu Ile Arg
50 55 60

<210> SEQ ID NO 33
<211> LENGTH: 261
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 33

atgaaatact tgatccgcac cgccttactc gcagtcgcag ccgccggcat ctacgcctgc 60

caaccgcaat ccgaagccgc agtgcaagtc aaggctgaaa acagcctgac cgctatgcgc 120

ttagccgtcg ccgacaaaca ggcagagatt gacgggttga acgcccaaat cgacgccgaa 180

atcagacaac gcgaagccga agaattgaaa gactaccgat ggatacacgg cgacgcggaa 240

gtgccggagc tggaaaaatg a 261

<210> SEQ ID NO 34
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 34

Met Lys Tyr Leu Ile Arg Thr Ala Leu Leu Ala Val Ala Ala Ala Gly
1 5 10 15

Ile Tyr Ala Cys Gln Pro Gln Ser Glu Ala Ala Val Gln Val Lys Ala
20 25 30

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

Glu Ile Asp Gly Leu Asn Ala Gln Ile Asp Ala Glu Ile Arg Gln Arg
50 55 60

Glu Ala Glu Glu Leu Lys Asp Tyr Arg Trp Ile His Gly Asp Ala Glu
65 70 75 80

Val Pro Glu Leu Glu Lys
85

<210> SEQ ID NO 35
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 35

atggttatcg gaatattact cgcatcaagc aagcatgctc ttgtcattac tctattgtta 60

aatcccgtct tccatgcatc cagttgcgta tcgcgttsgg caatacggaa taaaatctgc 120

tgttctgctt tggctaaatt tgccaaattg tttattgttt ctttaggagc agcttgctta 180

gccgccttcg ctttcgacaa cgcccccaca ggcgcttccc aagcgttgcc taccgttacc 240

gcacccgtgg cgattcccgc gcccgcttcg gcagcctga 279

<210> SEQ ID NO 36
<211> LENGTH: 92
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE

-continued

<222> LOCATION: (33)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 36

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

Thr Leu Leu Leu Asn Pro Val Phe His Ala Ser Ser Cys Val Ser Arg
20 25 30

Xaa Ala Ile Arg Asn Lys Ile Cys Cys Ser Ala Leu Ala Lys Phe Ala
35 40 45

Lys Leu Phe Ile Val Ser Leu Gly Ala Ala Cys Leu Ala Ala Phe Ala
50 55 60

Phe Asp Asn Ala Pro Thr Gly Ala Ser Gln Ala Leu Pro Thr Val Thr
65 70 75 80

Ala Pro Val Ala Ile Pro Ala Pro Ala Ser Ala Ala
85 90

<210> SEQ ID NO 37
<211> LENGTH: 312
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 37

atggcttgta caggtttgat ggtttttccg ttaatggtta tcggaatatt acttgcatca 60

agcaagcctg ctcctttcct tactctattg ttaaatcccg tcttccatgc atccagttgc 120

gtatcgcgtt gggcaatacg gaataaaatc tgctgttctg ctttggctaa atttgccaaa 180

ttgtttattg tttctttagg agcagcttgc ttagccgcct tcgctttcga caacgccccc 240

acaggcgctt cccaagcgtt gcctaccgtt accgcacccg tggcgattcc cgcgcccgct 300

tcggcagcct ga 312

<210> SEQ ID NO 38
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 38

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

Leu Leu Ala Ser Ser Lys Pro Ala Pro Phe Leu Thr Leu Leu Leu Asn
20 25 30

Pro Val Phe His Ala Ser Ser Cys Val Ser Arg Trp Ala Ile Arg Asn
35 40 45

Lys Ile Cys Cys Ser Ala Leu Ala Lys Phe Ala Lys Leu Phe Ile Val
50 55 60

Ser Leu Gly Ala Ala Cys Leu Ala Ala Phe Ala Phe Asp Asn Ala Pro
65 70 75 80

Thr Gly Ala Ser Gln Ala Leu Pro Thr Val Thr Ala Pro Val Ala Ile
85 90 95

Pro Ala Pro Ala Ser Ala Ala
100

<210> SEQ ID NO 39
<211> LENGTH: 255
<212> TYPE: DNA

-continued

<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 39

atgttcagta ttttaaatgt gtttcttcat tgtattctgg cttgtgtagt ctctggtgag 60

acgcctacta tatttggtat ccttgctctt ttttacttat tgtatctttc ttatcttgct 120

gtttttaaga ttttcttttc ttttttctta gacagagttt cactccggtc tcccaggctg 180

gagtgcaaat ggcatgaccc tttggctcac tggctcacgg ccacttctgc tattctgccg 240

cctcagcctc caggg 255

<210> SEQ ID NO 40
<211> LENGTH: 85
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 40

Met Phe Ser Ile Leu Asn Val Phe Leu His Cys Ile Leu Ala Cys Val
1 5 10 15

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

Leu Leu Tyr Leu Ser Tyr Leu Ala Val Phe Lys Ile Phe Phe Ser Phe
35 40 45

Phe Leu Asp Arg Val Ser Leu Arg Ser Pro Arg Leu Glu Cys Lys Trp
50 55 60

His Asp Pro Leu Ala His Trp Leu Thr Ala Thr Ser Ala Ile Leu Pro
65 70 75 80

Pro Gln Pro Pro Gly
85

<210> SEQ ID NO 41
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 41

gtgcggacgt ggttggtttt ttggttgcag cgtttgaaat acccgttgtt gctttggatt 60

gcggatatgt tgctgtaccg gttgttgggc ggcgcggaaa tcgaatgcgg ccgttgccct 120

gtgccgccga tgacggattg gcagcatttt ttgccggcga tgggaacggt gtcggcttgg 180

gtggcggtga tttgggcata cctgatgatt gaaagtgaaa aaaacggaag atattga 237

<210> SEQ ID NO 42
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 42

Val Arg Thr Trp Leu Val Phe Trp Leu Gln Arg Leu Lys Tyr Pro Leu
1 5 10 15

Leu Leu Trp Ile Ala Asp Met Leu Leu Tyr Arg Leu Leu Gly Gly Ala
20 25 30

Glu Ile Glu Cys Gly Arg Cys Pro Val Pro Pro Met Thr Asp Trp Gln
35 40 45

His Phe Leu Pro Ala Met Gly Thr Val Ser Ala Trp Val Ala Val Ile
50 55 60

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```
Trp Ala Tyr Leu Met Ile Glu Ser Glu Lys Asn Gly Arg Tyr
 65                  70                  75


<210> SEQ ID NO 43
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 43

gtgcggacgt ggttggtttt ttggttgcag cgtttgaaat acccgttgtt gctttgtatt     60

gcggatatgc tgctgtaccg gttgttgggc ggcgcggaaa tcgaatgcgg ccgttgccct    120

gtaccgccga tgacggattg gcagcatttt ttgccgacga tgggaacggt ggcggcttgg    180

gtggcggtga tttgggcata cctgatgatt gaaagtgaaa aaaacggaag atattga       237


<210> SEQ ID NO 44
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 44

Val Arg Thr Trp Leu Val Phe Trp Leu Gln Arg Leu Lys Tyr Pro Leu
  1               5                  10                  15

Leu Leu Cys Ile Ala Asp Met Leu Leu Tyr Arg Leu Leu Gly Gly Ala
             20                  25                  30

Glu Ile Glu Cys Gly Arg Cys Pro Val Pro Pro Met Thr Asp Trp Gln
         35                  40                  45

His Phe Leu Pro Thr Met Gly Thr Val Ala Ala Trp Val Ala Val Ile
     50                  55                  60

Trp Ala Tyr Leu Met Ile Glu Ser Glu Lys Asn Gly Arg Tyr
 65                  70                  75


<210> SEQ ID NO 45
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 45

atgtttcaaa attttgattt gggcgtgttc ctgcttgccg tcctccccgt gctgccctcc     60

attaccgtct cgcacgtggc gcgcggctat acggcgcgct actggggaga caacactgcc    120

gaacaatacg gcaggctgac actgaacccc ctgccccata tcgatttggt cggcacaatc    180

atcgtaccgc tgcttacttt gatgttcacg cccttcctgt tcggctgggc gcgtccgatt    240

cctatcgatt cgcgcaactt ccgcaacccg cgccttgcct ggcgttgcgt tgccgcgtcc    300

ggcccgctgt cgaatctagc gatggctgtw ctgtggggcg tggttttggt gctgactccg    360

tatgtcggcg gggcgtatca gatgccgttg gctcaaatgg caaactacgg tattctgatc    420

aatgcgattc tgttcgcgct caacatcatc cccatcctgc cttgggacgg cggcattttc    480

atcgacacct tcctgtcggc gaaatattcg caagcgttcc gcaaaatcga accttatggg    540

acgtggatta tcctactgct gatgctgacc sgggttttgg gtgcgtttat wgcaccgatt    600

stgcggmtgc gtgattgcrt ttgtgcagat gtwcgtctga ctggctttca gacggcataa    660


<210> SEQ ID NO 46
<211> LENGTH: 219
<212> TYPE: PRT
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<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (191)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (201)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (203)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (207)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 46

```
Met Phe Gln Asn Phe Asp Leu Gly Val Phe Leu Leu Ala Val Leu Pro
  1               5                  10                  15

Val Leu Pro Ser Ile Thr Val Ser His Val Ala Arg Gly Tyr Thr Ala
             20                  25                  30

Arg Tyr Trp Gly Asp Asn Thr Ala Glu Gln Tyr Gly Arg Leu Thr Leu
         35                  40                  45

Asn Pro Leu Pro His Ile Asp Leu Val Gly Thr Ile Ile Val Pro Leu
     50                  55                  60

Leu Thr Leu Met Phe Thr Pro Phe Leu Phe Gly Trp Ala Arg Pro Ile
 65                  70                  75                  80

Pro Ile Asp Ser Arg Asn Phe Arg Asn Pro Arg Leu Ala Trp Arg Cys
                 85                  90                  95

Val Ala Ala Ser Gly Pro Leu Ser Asn Leu Ala Met Ala Val Leu Trp
            100                 105                 110

Gly Val Val Leu Val Leu Thr Pro Tyr Val Gly Gly Ala Tyr Gln Met
        115                 120                 125

Pro Leu Ala Gln Met Ala Asn Tyr Gly Ile Leu Ile Asn Ala Ile Leu
    130                 135                 140

Phe Ala Leu Asn Ile Ile Pro Ile Leu Pro Trp Asp Gly Gly Ile Phe
145                 150                 155                 160

Ile Asp Thr Phe Leu Ser Ala Lys Tyr Ser Gln Ala Phe Arg Lys Ile
                165                 170                 175

Glu Pro Tyr Gly Thr Trp Ile Ile Leu Leu Leu Met Leu Thr Xaa Val
            180                 185                 190

Leu Gly Ala Phe Ile Ala Pro Ile Xaa Arg Xaa Arg Asp Cys Xaa Cys
        195                 200                 205

Ala Asp Val Arg Leu Thr Gly Phe Gln Thr Ala
    210                 215
```

<210> SEQ ID NO 47
<211> LENGTH: 639
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 47

```
atgtttcaaa attttgattt gggcgtgttt ctgcttgccg tcctgcccgt gctgctctcc     60

attaccgtca gggaggtggc gcgcggctat acggcgcgct actggggaga caacactgcc    120

gaacaatacg gcaggctgac actgaacccc ctgccccata tcgatttggt cggcacaatc    180
```

-continued

```
atcgtaccgc tgcttacttt gatgttcacg cccttcctgt tcggctgggc gcgtccgatt    240

cctatcgatt cgcgcaactt ccgcaacccg cgccttgcct ggcgttgcgt tgccgcgtcc    300

ggcccgctgt cgaatctagc gatggctgtt ctgtggggcg tggttttggt gctgactccg    360

tatgtcggcg gggcgtatca gatgccgttg gctcaaatgg caaactacgg tattctgatc    420

aatgcgattc tgttcgcgct caacatcatc cccatcctgc cttgggacgg cggcattttc    480

atcgacacct tcctgtcggc gaaatattcg caagcgttcc gcaaaatcga accttatggg    540

acgtggatta tcctactgct gatgctgacc ggggttttgg gtgcgtttat tgcaccgatt    600

gtgcggctgg tgattgcgtt tgtgcagatg ttcgtctga                           639


<210> SEQ ID NO 48
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 48

Met Phe Gln Asn Phe Asp Leu Gly Val Phe Leu Leu Ala Val Leu Pro
  1               5                  10                  15

Val Leu Leu Ser Ile Thr Val Arg Glu Val Ala Arg Gly Tyr Thr Ala
             20                  25                  30

Arg Tyr Trp Gly Asp Asn Thr Ala Glu Gln Tyr Gly Arg Leu Thr Leu
         35                  40                  45

Asn Pro Leu Pro His Ile Asp Leu Val Gly Thr Ile Ile Val Pro Leu
     50                  55                  60

Leu Thr Leu Met Phe Thr Pro Phe Leu Phe Gly Trp Ala Arg Pro Ile
 65                  70                  75                  80

Pro Ile Asp Ser Arg Asn Phe Arg Asn Pro Arg Leu Ala Trp Arg Cys
                 85                  90                  95

Val Ala Ala Ser Gly Pro Leu Ser Asn Leu Ala Met Ala Val Leu Trp
            100                 105                 110

Gly Val Val Leu Val Leu Thr Pro Tyr Val Gly Gly Ala Tyr Gln Met
        115                 120                 125

Pro Leu Ala Gln Met Ala Asn Tyr Gly Ile Leu Ile Asn Ala Ile Leu
    130                 135                 140

Phe Ala Leu Asn Ile Ile Pro Ile Leu Pro Trp Asp Gly Gly Ile Phe
145                 150                 155                 160

Ile Asp Thr Phe Leu Ser Ala Lys Tyr Ser Gln Ala Phe Arg Lys Ile
                165                 170                 175

Glu Pro Tyr Gly Thr Trp Ile Ile Leu Leu Leu Met Leu Thr Gly Val
            180                 185                 190

Leu Gly Ala Phe Ile Ala Pro Ile Val Arg Leu Val Ile Ala Phe Val
        195                 200                 205

Gln Met Phe Val
    210


<210> SEQ ID NO 49
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (312)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
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<221> NAME/KEY: misc_feature
<222> LOCATION: (328)..(330)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (353)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (420)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (426)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (473)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (506)
<223> OTHER INFORMATION: any nucleotide

<400> SEQUENCE: 49

cgcggctata cagcgcgcta ctggggtgac aacactgccg aacaatacgg caggctgaca 60

ctgaaccccc tgccccatat cgatttggtc ggcacaatca tcgtaccgct gcttactttg 120

atgtttacgc ccttcctgtt cggctgggcg cgtccgattc ctatcgattc gcgcaacttc 180

cgcaacccgc gccttgcctg gcgttgcgtt gccgcgtccg gcccgctgtc gaatctggcg 240

atggctgttc tgtggggcgt ggttttggtg ctgactccgt atgtcggtgg ggcgtatcag 300

atgccgttgg cncaaatggc aaactacnnn attctgatca atgcgattct gtncgcgctc 360

aacatcatcc ccatcctgcc ttgggacggc ggcattttca tcgacacctt cctgtcggcn 420

aaatantcgc aagcgttccg caaaatcgaa ccttatggga cgtggattat ccngctgctt 480

atgctgaccg gggttttggg tgcgtntatt gcaccgattg tgcagctggt gattgcgttt 540

gtgcagatgt tcgtctga 558

<210> SEQ ID NO 50
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (110)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (118)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (142)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (158)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (169)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 50

Arg Gly Tyr Thr Ala Arg Tyr Trp Gly Asp Asn Thr Ala Glu Gln Tyr
1 5 10 15

-continued

```
Gly Arg Leu Thr Leu Asn Pro Leu Pro His Ile Asp Leu Val Gly Thr
             20                  25                  30

Ile Ile Val Pro Leu Leu Thr Leu Met Phe Thr Pro Phe Leu Phe Gly
         35                  40                  45

Trp Ala Arg Pro Ile Pro Ile Asp Ser Arg Asn Phe Arg Asn Pro Arg
     50                  55                  60

Leu Ala Trp Arg Cys Val Ala Ala Ser Gly Pro Leu Ser Asn Leu Ala
 65                  70                  75                  80

Met Ala Val Leu Trp Gly Val Val Leu Val Leu Thr Pro Tyr Val Gly
                 85                  90                  95

Gly Ala Tyr Gln Met Pro Leu Ala Gln Met Ala Asn Tyr Xaa Ile Leu
            100                 105                 110

Ile Asn Ala Ile Leu Xaa Ala Leu Asn Ile Ile Pro Ile Leu Pro Trp
        115                 120                 125

Asp Gly Gly Ile Phe Ile Asp Thr Phe Leu Ser Ala Lys Xaa Ser Gln
    130                 135                 140

Ala Phe Arg Lys Ile Glu Pro Tyr Gly Thr Trp Ile Ile Xaa Leu Leu
145                 150                 155                 160

Met Leu Thr Gly Val Leu Gly Ala Xaa Ile Ala Pro Ile Val Gln Leu
                165                 170                 175

Val Ile Ala Phe Val Gln Met Phe Val
            180                 185
```

<210> SEQ ID NO 51
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 51

```
atgaacctga tttcacgtta catcatccgt caaatggcgg ttatggcggt ttacgcgctc     60

cttgccttcc tcgctttgta cagctttttt gaaatcctgt acgaaaccgg caacctcggc    120

aaaggcagtt acggcatatg ggaaatgctg ggctacaccg ccctcaaaat gcccgcccgc    180

gcctacgaac tgattcccct cgccgtcctt atcggcggac tggtctccct cagccagctt    240

gccgccggca gcgaactgac cgtcatcaaa gccagcggca tgagcaccaa aaagctgctg    300

ttgattctgt cgcagttcgg ttttattttt gctattgcca ccgtcgcgct cggcgaatgg    360

gttgcgccca cactgagcca aaaagccgaa aacatcaaag ccgccgccat caacggcaaa    420

atcagcaccg gcaataccgg cctttggctg aaagaaaaaa acagcgtgat caatgtgcgc    480

gaaatgttgc ccgaccat                                                  498
```

<210> SEQ ID NO 52
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 52

```
Met Asn Leu Ile Ser Arg Tyr Ile Ile Arg Gln Met Ala Val Met Ala
  1               5                  10                  15

Val Tyr Ala Leu Leu Ala Phe Leu Ala Leu Tyr Ser Phe Phe Glu Ile
             20                  25                  30

Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
         35                  40                  45
```

-continued

```
Met Leu Gly Tyr Thr Ala Leu Lys Met Pro Ala Arg Ala Tyr Glu Leu
     50                  55                  60

Ile Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Leu Ser Gln Leu
 65                  70                  75                  80

Ala Ala Gly Ser Glu Leu Thr Val Ile Lys Ala Ser Gly Met Ser Thr
                 85                  90                  95

Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
            100                 105                 110

Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
        115                 120                 125

Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
    130                 135                 140

Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Val Ile Asn Val Arg
145                 150                 155                 160

Glu Met Leu Pro Asp His
                165
```

<210> SEQ ID NO 53
<211> LENGTH: 980
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 53

```
atgaacctga tttcacgtta catcatccgt caaatggcgg ttatggcggt ttacgcgctc     60

cttgccttcc tcgctttgta cagctttttt gaaatcctgt acgaaaccgg caacctcggc    120

aaaggcagtt acggcatatg ggaaatgctg ggctacaccg ccctcaaaat gcccgcccgc    180

gcctacgaac tgattcccct cgccgtcctt atcggcggac tggtctccct cagccagctt    240

gccgccggca gcgaactgac cgtcatcaaa gccagcggca tgagcaccaa aaagctgctg    300

ttgattctgt cgcagttcgg ttttattttt gctattgcca ccgtcgcgct cggcgaatgg    360

gttgcgccca cactgagcca aaaagccgaa aacatcaaag ccgccgccat caacggcaaa    420

atcagcaccg gcaataccgg cctttggctg aaagaaaaaa acagcrtkat caatgtgcgc    480

gaaatgttgc ccgaccatac gcttttgggc atcaaaattt gggcgcgcaa cgataaaaac    540

gaattggcag aggcagtgga agccgattcc gccgttttga acagcgacgg cagttggcag    600

ttgaaaaaca tccgccgcag cacgcttggc gaagacaaag tcgaggtctc tattgcggct    660

gaagaaaact ggccgatttc cgtcaaacgc aacctgatgg acgtattgct cgtcaaaccc    720

gaccaaatgt ccgtcggcga actgaccacc tacatccgcc acctccaaaa caacagccaa    780

aacacccgaa tctacgccat cgcatggtgg cgcaaattgg tttaccccgc cgcagcctgg    840

gtgatggcgc tcgtcgcctt tgcctttacc ccgcaaacca cccgccacgg caatatgggc    900

ttaaaactct tcggcggcat ctgtstcgga ttgctgttcc accttgccgg acggctcttt    960

gggtttacca gccaactcgg                                               980
```

<210> SEQ ID NO 54
<211> LENGTH: 326
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (156)
<223> OTHER INFORMATION: unknown

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<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (309)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 54

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

Val Tyr Ala Leu Leu Ala Phe Leu Ala Leu Tyr Ser Phe Phe Glu Ile
20 25 30

Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
35 40 45

Met Leu Gly Tyr Thr Ala Leu Lys Met Pro Ala Arg Ala Tyr Glu Leu
50 55 60

Ile Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Leu Ser Gln Leu
65 70 75 80

Ala Ala Gly Ser Glu Leu Thr Val Ile Lys Ala Ser Gly Met Ser Thr
85 90 95

Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
100 105 110

Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
115 120 125

Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
130 135 140

Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Xaa Ile Asn Val Arg
145 150 155 160

Glu Met Leu Pro Asp His Thr Leu Leu Gly Ile Lys Ile Trp Ala Arg
165 170 175

Asn Asp Lys Asn Glu Leu Ala Glu Ala Val Glu Ala Asp Ser Ala Val
180 185 190

Leu Asn Ser Asp Gly Ser Trp Gln Leu Lys Asn Ile Arg Arg Ser Thr
195 200 205

Leu Gly Glu Asp Lys Val Glu Val Ser Ile Ala Ala Glu Glu Asn Trp
210 215 220

Pro Ile Ser Val Lys Arg Asn Leu Met Asp Val Leu Leu Val Lys Pro
225 230 235 240

Asp Gln Met Ser Val Gly Glu Leu Thr Thr Tyr Ile Arg His Leu Gln
245 250 255

Asn Asn Ser Gln Asn Thr Arg Ile Tyr Ala Ile Ala Trp Trp Arg Lys
260 265 270

Leu Val Tyr Pro Ala Ala Ala Trp Val Met Ala Leu Val Ala Phe Ala
275 280 285

Phe Thr Pro Gln Thr Thr Arg His Gly Asn Met Gly Leu Lys Leu Phe
290 295 300

Gly Gly Ile Cys Xaa Gly Leu Leu Phe His Leu Ala Gly Arg Leu Phe
305 310 315 320

Gly Phe Thr Ser Gln Leu
325

<210> SEQ ID NO 55
<211> LENGTH: 1071
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (148)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (153)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (172)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (260)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (669)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (770)..(772)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (907)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (951)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (961)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1001)
<223> OTHER INFORMATION: any nucleotide

<400> SEQUENCE: 55

atgaacctga tttcacgtta catcatccgt caaatggcgg ttatggcggt ttacgcgctc 60

cttgccttcc tcgctttgta cagctttttt gaaatcctgt acgaaaccgg caacctcggc 120

aaaggcagtt acggcatatg ggaaatgntg ggntacaccg ccctcaaaat gnccgcccgc 180

gcctacgaac tgatgcccct cgccgtcctt atcggcggac tggtctctnt cagccagctt 240

gccgccggca gcgaactgan cgtcatcaaa gccagcggca tgagcaccaa aaagctgctg 300

ttgattctgt cgcagttcgg ttttattttt gctattgcca ccgtcgcgct cggcgaatgg 360

gttgcgccca cactgagcca aaaagccgaa aacatcaaag ccgcggccat caacggcaaa 420

atcagtaccg gcaataccgg cctttggctg aaagaaaaaa acagcattat caatgtgcgc 480

gaaatgttgc ccgaccatac cctgctgggc attaaaatct gggcccgcaa cgataaaaac 540

gaactggcag aggcagtgga agccgattcc gccgttttga acagcgacgg cagttggcag 600

ttgaaaaaca tccgccgcag cacgcttggc gaagacaaag tcgaggtctc tattgcggct 660

gaagaaaant ggccgatttc cgtcaaacgc aacctgatgg acgtattgct cgtcaaaccc 720

gaccaaatgt ccgtcggcga actgaccacc tacatccgcc acctccaaan nnacagccaa 780

aacacccgaa tctacgccat cgcatggtgg cgcaaattgg tttaccccgc cgcagcctgg 840

gtgatggcgc tcgtcgcctt tgcctttacc ccgcaaacca cccgccacgg caatatgggc 900

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ttaaaantct tcggcggcat ctgtctcgga ttgctgttcc accttgccgg ncggctcttc 960

nggtttacca gccaactcta cggcatcccg cccttcctcg ncggcgcact acctaccata 1020

gccttcgcct tgctcgccgt ttggctgata cgcaaacagg aaaaacgcta a 1071

<210> SEQ ID NO 56
<211> LENGTH: 356
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (50)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (58)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (77)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (87)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (223)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (257)..(258)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (303)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (321)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (334)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 56

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

Val Tyr Ala Leu Leu Ala Phe Leu Ala Leu Tyr Ser Phe Phe Glu Ile
20 25 30

Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
35 40 45

Met Xaa Gly Tyr Thr Ala Leu Lys Met Xaa Ala Arg Ala Tyr Glu Leu
50 55 60

Met Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Xaa Ser Gln Leu
65 70 75 80

Ala Ala Gly Ser Glu Leu Xaa Val Ile Lys Ala Ser Gly Met Ser Thr
85 90 95

Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
100 105 110

Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
115 120 125

Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
130 135 140

-continued

```
Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Ile Ile Asn Val Arg
145                 150                 155                 160

Glu Met Leu Pro Asp His Thr Leu Leu Gly Ile Lys Ile Trp Ala Arg
                165                 170                 175

Asn Asp Lys Asn Glu Leu Ala Glu Ala Val Glu Ala Asp Ser Ala Val
            180                 185                 190

Leu Asn Ser Asp Gly Ser Trp Gln Leu Lys Asn Ile Arg Arg Ser Thr
        195                 200                 205

Leu Gly Glu Asp Lys Val Glu Val Ser Ile Ala Ala Glu Glu Xaa Trp
    210                 215                 220

Pro Ile Ser Val Lys Arg Asn Leu Met Asp Val Leu Leu Val Lys Pro
225                 230                 235                 240

Asp Gln Met Ser Val Gly Glu Leu Thr Thr Tyr Ile Arg His Leu Gln
                245                 250                 255

Xaa Xaa Ser Gln Asn Thr Arg Ile Tyr Ala Ile Ala Trp Trp Arg Lys
            260                 265                 270

Leu Val Tyr Pro Ala Ala Ala Trp Val Met Ala Leu Val Ala Phe Ala
        275                 280                 285

Phe Thr Pro Gln Thr Thr Arg His Gly Asn Met Gly Leu Lys Xaa Phe
    290                 295                 300

Gly Gly Ile Cys Leu Gly Leu Leu Phe His Leu Ala Gly Arg Leu Phe
305                 310                 315                 320

Xaa Phe Thr Ser Gln Leu Tyr Gly Ile Pro Pro Phe Leu Xaa Gly Ala
                325                 330                 335

Leu Pro Thr Ile Ala Phe Ala Leu Leu Ala Val Trp Leu Ile Arg Lys
            340                 345                 350

Gln Glu Lys Arg
        355
```

<210> SEQ ID NO 57
<211> LENGTH: 854
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 57

```
gcagtagccg aaactgccaa cagccagggc aaaggtaaac aggcaggcag ttcggtttct     60

gtttcactga aaacttcagg cgacctttgc ggcaaactca aaaccaccct taaaactttg    120

gtctgctctt tggtttccct gagtatggta ttgcctgccc atgcccaaat taccaccgac    180

aaatcagcac ctaaaaacca gcaggtcgtt atccttaaaa ccaacactgg tgccccttg     240

gtgaatatcc aaactccgaa tggacgcgga ttgagccaca accgctatac gcatttgatg    300

ttgacaacaa aggggcagtg ttaaacaacg accgtaacaa taatccgttt gtggtcaaag    360

gcagtgcgca attgattttg aacgaggtac gcggtacggc tagcaaactc aacggcatcg    420

ttaccgtagg cggtcaaaag gccgacgtga ttattgccaa ccccaacggc attaccgtta    480

atggcggcgg ctttaaaaat gtcggtcggg gcatcttaac taccggtgcg ccccaaatcg    540

gcaaagacgg tgcactgaca ggatttgatg tgcgtcaagg cacattggac cgtagragca    600

gcaggttgga atgataaagg cggagcmrmy tacaccgggg tacttgctcg tgcagttgct    660

ttgcagggga aattwmmggg taaaaactgg cggtttctac cggtcctcag aaagtagatt    720

acgccagcgg cgaaatcagt gcaggtacgg cagcgggtac gaaaccgact attgcccttg    780
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atactgccgc actgggcggt atgtacgccg acagcatcac actgattgcc aatgaaaaag 840

gcgtaggcgt ctaa 854

<210> SEQ ID NO 58
<211> LENGTH: 284
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (96)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (199)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (210)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (225)..(226)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (229)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 58

Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln Ala Gly
1 5 10 15

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

Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser Leu Ser
35 40 45

Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser Ala Pro
50 55 60

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

Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn Arg Xaa
85 90 95

Tyr Ala Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn Asp Arg
100 105 110

Asn Asn Asn Pro Phe Val Val Lys Gly Ser Ala Gln Leu Ile Leu Asn
115 120 125

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

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

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

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

Lys Ala His Trp Thr Val Xaa Ala Ala Gly Trp Asn Asp Lys Gly Gly
195 200 205

Ala Xaa Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln Gly Lys
210 215 220

Xaa Xaa Gly Lys Xaa Leu Ala Val Ser Thr Gly Pro Gln Lys Val Asp

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```
225                 230                 235                 240

Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr Lys Pro
                245                 250                 255

Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala Asp Ser
            260                 265                 270

Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val
        275                 280
```

<210> SEQ ID NO 59
<211> LENGTH: 5937
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 59

```
atgaataaag gtttacatcg cattatcttt agtaaaaagc acagcaccat ggttgcagta     60

gccgaaactg ccaacagcca gggcaaaggt aaacaggcag gcagttcggt ttctgtttca    120

ctgaaaactt caggcgacct ttgcggcaaa ctcaaaacca cccttaaaac tttggtctgc    180

tctttggttt ccctgagtat ggtattgcct gcccatgccc aaattaccac cgacaaatca    240

gcacctaaaa accagcaggt cgttatcctt aaaaccaaca ctggtgcccc cttggtgaat    300

atccaaactc cgaatggacg cggattgagc cacaaccgct atacgcagtt tgatgttgac    360

aacaaagggg cagtgttaaa caacgaccgt aacaataatc cgtttgtggt caaaggcagt    420

gcgcaattga ttttgaacga ggtacgcggt acggctagca aactcaacgg catcgttacc    480

gtaggcggtc aaaaggccga cgtgattatt gccaacccca acggcattac cgttaatggc    540

ggcggcttta aaaatgtcgg tcggggcatc ttaactaccg gtgcgcccca aatcggcaaa    600

gacggtgcac tgacaggatt tgatgtgcgt caaggcacat tgaccgtagg agcagcaggt    660

tggaatgata aaggcggagc cgactacacc ggggtacttg ctcgtgcagt tgctttgcag    720

gggaaattac agggtaaaaa cctggcggtt tctaccggtc ctcagaaagt agattacgcc    780

agcggcgaaa tcagtgcagg tacggcagcg ggtacgaaac cgactattgc ccttgatact    840

gccgcactgg gcggtatgta cgccgacagc atcacactga ttgccaatga aaaaggcgta    900

ggcgtcaaaa atgccggcac actcgaagcg gccaagcaat tgattgtgac ttcgtcaggc    960

cgcattgaaa acagcggccg catcgccacc actgccgacg gcaccgaagc ttcaccgact   1020

tatctctcca tcgaaaccac cgaaaaagga gcggcaggca catttatctc caatggtggt   1080

cggatcgaga gcaaaggctt attggttatt gagacgggag aagatatcag cttgcgtaac   1140

ggagccgtgg tgcagaataa cggcagtcgc ccagctacca cggtattaaa tgctggtcat   1200

aatttggtga ttgagagcaa aactaatgtg aacaatgcca aaggcccggc tactctgtcg   1260

gccgacggcc gtaccgtcat caaggaggcc agtattcaga ctggcactac cgtatacagt   1320

tccagcaaag gcaacgccga attaggcaat aacacacgca ttaccggggc agatgttacc   1380

gtattatcca acggcaccat cagcagttcc gccgtaatag atgccaaaga caccgcacac   1440

atcgaagcag gcaaaccgct ttctttggaa gcttcaacag ttacctccga tatccgctta   1500

aacggaggca gtatcaaggg cggcaagcag cttgctttac tggcagacga taacattact   1560

gccaaaacta ccaatctgaa tactcccggc aatctgtatg ttcatacagg taaagatctg   1620

aatttgaatg ttgataaaga tttgtctgcc gccagcatcc atttgaaatc ggataacgct   1680

gcccatatta ccggcaccag taaaaccctc actgcctcaa aagacatggg tgtggaggca   1740
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ggctcgctga atgttaccaa taccaatctg cgtaccaact cgggtaatct gcacattcag 1800

gcagccaaag gcaatattca gcttcgcaat accaagctga acgcagccaa ggctctcgaa 1860

accaccgcat tgcagggcaa tatcgtttca gacggccttc atgctgtttc tgcagacggt 1920

catgtatcct tattggccaa cggtaatgcc gactttaccg gtcacaatac cctgacagcc 1980

aaggccgatg tcaatgcagg atcggttggt aaaggccgtc tgaaagcaga caataccaat 2040

atcacttcat cttcaggaga tattacgttg gttgccggca acggtattca gcttggtgac 2100

ggaaaacaac gcaattcaat caacggaaaa cacatcagca tcaaaaacaa cggtggtaat 2160

gccgacttaa aaaaccttaa cgtccatgcc aaaagcgggg cattgaacat tcattccgac 2220

cgggcattga gcatagaaaa taccaagctg gagtctaccc ataatacgca tcttaatgca 2280

caacacgagc gggtaacgct caaccaagta gatgcctacg cacaccgtca tctaagcatt 2340

accggcagcc agatttggca aaacgacaaa ctgccttctg ccaacaagct ggtggctaac 2400

ggtgtattgg cactcaatgc gcgctattcc caaattgccg acaacaccac gctgagagcg 2460

ggtgcaatca accttactgc cggtaccgcc ctagtcaagc gcggcaacat caattggagt 2520

accgtttcga ccaaaacttt ggaagataat gccgaattaa aaccattggc cggacggctg 2580

aatattgaag caggtagcgg cacattaacc atcgaacctg ccaaccgcat cagtgcgcat 2640

accgacctga gcatcaaaac aggcggaaaa ttgctgttgt ctgcaaaagg aggaaatgca 2700

ggtgcgccta gtgctcaagt ttcctcattg gaagcaaaag gcaatatccg tctggttaca 2760

ggagaaacag atttaagagg ttctaaaatt acagccggta aaaacttggt tgtcgccacc 2820

accaaaggca agttgaatat cgaagccgta aacaactcat tcagcaatta ttttcctaca 2880

caaaaagcgg ctgaactcaa ccaaaaatcc aaagaattgg aacagcagat tgcgcagttg 2940

aaaaaaagct cgcctaaaag caagctgatt ccaaccctgc aagaagaacg cgaccgtctc 3000

gctttctata ttcaagccat caacaaggaa gttaaaggta aaaaacccaa aggcaaagaa 3060

tacctgcaag ccaagctttc tgcacaaaat attgacttga tttccgcaca aggcatcgaa 3120

atcagcggtt ccgatattac cgcttccaaa aaactgaacc ttcacgccgc aggcgtattg 3180

ccaaaggcag cagattcaga ggcggctgct attctgattg acggcataac cgaccaatat 3240

gaaattggca agcccaccta caagagtcac tacgacaaag ctgctctgaa caagccttca 3300

cgtttgaccg gacgtacagg ggtaagtatt catgcagctg cggcactcga tgatgcacgt 3360

attattatcg gtgcatccga aatcaaagct ccctcaggca gcatagacat caaagcccat 3420

agtgatattg tactggaggc tggacaaaac gatgcctata ccttcttaaa aaccaaaggt 3480

aaaagcggca aaatcatcag aaaaaccaag tttaccagca cccgcgacca cctgattatg 3540

ccagcccccg tcgagctgac cgccaacggc ataacgcttc aggcaggcgg caacatcgaa 3600

gctaatacca cccgcttcaa tgcccctgca ggtaaagtta ccctggttgc gggtgaagag 3660

ctgcaactgc tggcagaaga aggcatccac aagcacgagt tggatgtcca aaaaagccgc 3720

cgctttatcg gcatcaaggt aggcaagagc aattacagta aaaacgaact gaacgaaacc 3780

aaattgcctg tccgcgtcgt cgcccaaact gcagccaccc gttcaggctg ggataccgtg 3840

ctcgaaggta ccgaattcaa aaccacgctg gccggtgcgg acattcaggc aggtgtaggc 3900

gaaaaagccc gtgccgatgc gaaaattatc ctcaaaggca ttgtgaaccg tatccagtcg 3960

gaagaaaaat tagaaaccaa ctcaaccgta tggcagaaac aggccggacg cggcagcact 4020

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atcgaaacgc tgaaactgcc cagcttcgaa agccctactc cgcccaaact gaccgccccc 4080

ggtggctata tcgtcgacat tccgaaaggc aatttgaaaa ccgaaatcga aaagctggcc 4140

aaacagcccg agtatgccta tctgaaacag ctccaagtag cgaaaaacgt caactggaac 4200

caggtgcaac tggcttacga taaatgggac tataagcagg aaggcttaac cagagccggt 4260

gcagcgattg ttaccataat cgtaaccgca ctgacttatg gatacggcgc aaccgcagcg 4320

ggcggtgtag ccgcttcagg aagtagtaca gccgcagctg ccggaacagc cgccacaacg 4380

acagcagcag ctactaccgt ttctacagcg actgccatgc aaaccgctgc tttagcctcc 4440

ttgtatagcc aagcagctgt atccatcatc aataataaag gtgatgtcgg caaagcgttg 4500

aaagatctcg gcaccagtga tacggtcaag cagattgtca cttctgccct gacggcgggt 4560

gcattaaatc agatgggcgc agatattgcc caattgaaca gcaaggtaag aaccgaactg 4620

ttcagcagta cgggcaatca aactattgcc aaccttggag gcagactggc taccaatctc 4680

agtaatgcag gtatctcagc tggtatcaat accgccgtca acggcggcag cctgaaagac 4740

aacttaggca atgccgcatt aggagcattg gttaatagct tccaaggaga agccgccagc 4800

aaaatcaaaa caaccttcag cgacgattat gttgccaaac agttcgccca cgctttggct 4860

gggtgtgtta gcggattggt acaaggaaaa tgtaaagacg gggcaattgg cgcagcagtt 4920

ggggaaatcg tagccgactc catgcttggc ggcagaaacc ctgctacact cagcgatgcg 4980

gaaaagcata aggttatcag ttactcgaag attattgccg gcagcgtggc ggcactcaac 5040

ggcggcgatg tgaatactgc ggcgaatgcg gctgaggtgg cggtagtgaa taatgctttg 5100

aattttgaca gtacccctac caatgcgaaa aagcatcaac cgcagaagcc cgacaaaacc 5160

gcactggaaa aaattatcca aggtattatg cctgcacatg cagcaggtgc gatgactaat 5220

ccgcaggata aggatgctgc catttggata agcaatatcc gtaatggcat cacaggcccg 5280

attgtgatta ccagctatgg ggtttatgct gcaggttgga cagctccgct gatcggtaca 5340

gcgggtaaat tagctatcag cacctgcatg gctaatcctt ctggttgtac tgtcatggtc 5400

actcaggctg ccgaagcggg cgcgggaatc gccacgggtg cggtaacggt aggcaacgct 5460

tgggaagcgc ctgtgggggc gttgtcgaaa gcgaaggcgg ccaagcaggc tataccaacc 5520

cagacagtta aagaacttga tggcttacta caagaatcaa aaaatatagg tgctgtaaat 5580

acacgaatta atatagcgaa tagtactact cgatatacac caatgagaca aacgggacaa 5640

ccggtatctg ctggctttga gcatgttctt gaggggcact tccataggcc tattgcgaat 5700

aaccgttcag tttttaccat ctccccaaat gaattgaagg ttatacttca aagtaataaa 5760

gtagtttctt ctcccgtatc gatgactcct gatggccaat atatgcggac tgtcgatgta 5820

ggaaaagtta ttggtactac ttctattaaa gaaggtggac aacccacaac tacaattaaa 5880

gtatttacag ataagtcagg aaatttgatt actacatacc cagtaaaagg aaactaa 5937

<210> SEQ ID NO 60
<211> LENGTH: 1978
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 60

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
1 5 10 15

-continued

```
Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
            20                  25                  30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys
        35                  40                  45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
    50                  55                  60

Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser
65                  70                  75                  80

Ala Pro Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
                85                  90                  95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
            100                 105                 110

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
        115                 120                 125

Asp Arg Asn Asn Asn Pro Phe Val Val Lys Gly Ser Ala Gln Leu Ile
    130                 135                 140

Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
145                 150                 155                 160

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

Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
            180                 185                 190

Thr Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
        195                 200                 205

Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
    210                 215                 220

Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
225                 230                 235                 240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
                245                 250                 255

Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
            260                 265                 270

Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
        275                 280                 285

Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn
    290                 295                 300

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

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
                325                 330                 335

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

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

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val
    370                 375                 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385                 390                 395                 400

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

Ala Thr Leu Ser Ala Asp Gly Arg Thr Val Ile Lys Glu Ala Ser Ile
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            420                 425                 430

Gln Thr Gly Thr Thr Val Tyr Ser Ser Ser Lys Gly Asn Ala Glu Leu
        435                 440                 445

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

Gly Thr Ile Ser Ser Ser Ala Val Ile Asp Ala Lys Asp Thr Ala His
465                 470                 475                 480

Ile Glu Ala Gly Lys Pro Leu Ser Leu Glu Ala Ser Thr Val Thr Ser
                485                 490                 495

Asp Ile Arg Leu Asn Gly Gly Ser Ile Lys Gly Gly Lys Gln Leu Ala
            500                 505                 510

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
        515                 520                 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
    530                 535                 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala
545                 550                 555                 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met
                565                 570                 575

Gly Val Glu Ala Gly Ser Leu Asn Val Thr Asn Thr Asn Leu Arg Thr
            580                 585                 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
        595                 600                 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
    610                 615                 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
625                 630                 635                 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
                645                 650                 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly
            660                 665                 670

Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile
        675                 680                 685

Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg
    690                 695                 700

Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn
705                 710                 715                 720

Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn
                725                 730                 735

Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser
            740                 745                 750

Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn
        755                 760                 765

Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln
    770                 775                 780

Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn
785                 790                 795                 800

Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr
                805                 810                 815

Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val
            820                 825                 830
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```
Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu
        835                 840                 845

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala
    850                 855                 860

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
865                 870                 875                 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
                885                 890                 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala
            900                 905                 910

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser
        915                 920                 925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys
    930                 935                 940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr
945                 950                 955                 960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln
                965                 970                 975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr
            980                 985                 990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn
        995                1000                1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala
   1010                1015                1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu
1025                1030                1035                1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala
                1045                1050                1055

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu
            1060                1065                1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys
        1075                1080                1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly
   1090                1095                1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg
1105                1110                1115                1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
                1125                1130                1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
            1140                1145                1150

Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys
        1155                1160                1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val
   1170                1175                1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu
1185                1190                1195                1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val
                1205                1210                1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His
            1220                1225                1230
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```
Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly
       1235                1240                1245

Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val
   1250                1255                1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val
1265                1270                1275                1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln
               1285                1290                1295

Ala Gly Val Gly Glu Lys Ala Arg Ala Asp Ala Lys Ile Ile Leu Lys
           1300                1305                1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser
       1315                1320                1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu
   1330                1335                1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Thr Ala Pro
1345                1350                1355                1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile
               1365                1370                1375

Glu Lys Leu Ala Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
           1380                1385                1390

Val Ala Lys Asn Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys
       1395                1400                1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Arg Ala Gly Ala Ala Ile Val
   1410                1415                1420

Thr Ile Ile Val Thr Ala Leu Thr Tyr Gly Tyr Gly Ala Thr Ala Ala
1425                1430                1435                1440

Gly Gly Val Ala Ala Ser Gly Ser Ser Thr Ala Ala Ala Ala Gly Thr
               1445                1450                1455

Ala Ala Thr Thr Thr Ala Ala Ala Thr Thr Val Ser Thr Ala Thr Ala
           1460                1465                1470

Met Gln Thr Ala Ala Leu Ala Ser Leu Tyr Ser Gln Ala Ala Val Ser
       1475                1480                1485

Ile Ile Asn Asn Lys Gly Asp Val Gly Lys Ala Leu Lys Asp Leu Gly
   1490                1495                1500

Thr Ser Asp Thr Val Lys Gln Ile Val Thr Ser Ala Leu Thr Ala Gly
1505                1510                1515                1520

Ala Leu Asn Gln Met Gly Ala Asp Ile Ala Gln Leu Asn Ser Lys Val
               1525                1530                1535

Arg Thr Glu Leu Phe Ser Ser Thr Gly Asn Gln Thr Ile Ala Asn Leu
           1540                1545                1550

Gly Gly Arg Leu Ala Thr Asn Leu Ser Asn Ala Gly Ile Ser Ala Gly
       1555                1560                1565

Ile Asn Thr Ala Val Asn Gly Gly Ser Leu Lys Asp Asn Leu Gly Asn
   1570                1575                1580

Ala Ala Leu Gly Ala Leu Val Asn Ser Phe Gln Gly Glu Ala Ala Ser
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Lys Ile Lys Thr Thr Phe Ser Asp Asp Tyr Val Ala Lys Gln Phe Ala
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His Ala Leu Ala Gly Cys Val Ser Gly Leu Val Gln Gly Lys Cys Lys
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Asp Gly Ala Ile Gly Ala Ala Val Gly Glu Ile Val Ala Asp Ser Met
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Leu Gly Gly Arg Asn Pro Ala Thr Leu Ser Asp Ala Glu Lys His Lys
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Val Ile Ser Tyr Ser Lys Ile Ile Ala Gly Ser Val Ala Ala Leu Asn
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Gly Gly Asp Val Asn Thr Ala Ala Asn Ala Ala Glu Val Ala Val Val
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Asn Asn Ala Leu Asn Phe Asp Ser Thr Pro Thr Asn Ala Lys Lys His
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Gln Pro Gln Lys Pro Asp Lys Thr Ala Leu Glu Lys Ile Ile Gln Gly
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Ile Met Pro Ala His Ala Ala Gly Ala Met Thr Asn Pro Gln Asp Lys
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Asp Ala Ala Ile Trp Ile Ser Asn Ile Arg Asn Gly Ile Thr Gly Pro
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Ile Val Ile Thr Ser Tyr Gly Val Tyr Ala Ala Gly Trp Thr Ala Pro
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Leu Ile Gly Thr Ala Gly Lys Leu Ala Ile Ser Thr Cys Met Ala Asn
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Pro Ser Gly Cys Thr Val Met Val Thr Gln Ala Ala Glu Ala Gly Ala
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Gly Ile Ala Thr Gly Ala Val Thr Val Gly Asn Ala Trp Glu Ala Pro
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Val Gly Ala Leu Ser Lys Ala Lys Ala Ala Lys Gln Ala Ile Pro Thr
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Gln Thr Val Lys Glu Leu Asp Gly Leu Leu Gln Glu Ser Lys Asn Ile
               1845                1850                1855

Gly Ala Val Asn Thr Arg Ile Asn Ile Ala Asn Ser Thr Thr Arg Tyr
           1860                1865                1870

Thr Pro Met Arg Gln Thr Gly Gln Pro Val Ser Ala Gly Phe Glu His
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Val Leu Glu Gly His Phe His Arg Pro Ile Ala Asn Asn Arg Ser Val
   1890                1895                1900

Phe Thr Ile Ser Pro Asn Glu Leu Lys Val Ile Leu Gln Ser Asn Lys
1905                1910                1915                1920

Val Val Ser Ser Pro Val Ser Met Thr Pro Asp Gly Gln Tyr Met Arg
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Thr Val Asp Val Gly Lys Val Ile Gly Thr Thr Ser Ile Lys Glu Gly
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Leu Ile Thr Thr Tyr Pro Val Lys Gly Asn
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ctgaaaactt caggcgacct ttgcggcaaa ctcaaaacca cccttaaaac cttggtctgc 180

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35 40 45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
50 55 60

Leu Ser Met Xaa Xaa Xaa Xaa Xaa Xaa Gln Ile Thr Thr Asp Lys Ser
65 70 75 80

Ala Pro Lys Asn Xaa Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
85 90 95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
100 105 110

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
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Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile

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

Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
            180                 185                 190

Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
        195                 200                 205

Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
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Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
225                 230                 235                 240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
                245                 250                 255

Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
            260                 265                 270

Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
        275                 280                 285

Asp Ser Ile Thr Leu Ile Ala Xaa Glu Lys Gly Val Gly Val Lys Asn
    290                 295                 300

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

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
                325                 330                 335

Ala Ser Pro Thr Tyr Leu Xaa Ile Glu Thr Thr Glu Lys Gly Ala Xaa
            340                 345                 350

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

Val Ile Glu Thr Gly Glu Asp Ile Xaa Leu Arg Asn Gly Ala Val Val
    370                 375                 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385                 390                 395                 400

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

Xaa Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile
            420                 425                 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Xaa Leu
        435                 440                 445

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

Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His
465                 470                 475                 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser
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Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln Leu Ala
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Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
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Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
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Gly Val Glu Ala Gly Leu Leu Asn Val Thr Asn Thr Asn Leu Arg Thr
            580                 585                 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
        595                 600                 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
    610                 615                 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
625                 630                 635                 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
                645                 650                 655

Thr Leu Thr Ala Lys Ala Asp Val Xaa Ala Gly Ser Val Gly Lys Gly
            660                 665                 670

Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile
        675                 680                 685

Thr Leu Val Ala Xaa Xaa Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg
    690                 695                 700

Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn
705                 710                 715                 720

Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn
                725                 730                 735

Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser
            740                 745                 750

Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn
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Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Xaa Gly Ser Gln
    770                 775                 780

Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn
785                 790                 795                 800

Gly Val Leu Ala Xaa Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr
                805                 810                 815

Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val
            820                 825                 830

Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu
        835                 840                 845

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala
    850                 855                 860

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
865                 870                 875                 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
                885                 890                 895

Gly Gly Asn Ala Gly Ala Xaa Ser Ala Gln Val Ser Ser Leu Glu Ala
            900                 905                 910

Lys Gly Asn Ile Arg Leu Val Thr Gly Xaa Thr Asp Leu Arg Gly Ser
        915                 920                 925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys
    930                 935                 940
```

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```
Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Xaa Thr
945                 950                 955                 960

Gln Lys Xaa Xaa Xaa Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln
                965                 970                 975

Ile Ala Gln Leu Lys Lys Ser Ser Xaa Lys Ser Lys Leu Ile Pro Thr
            980                 985                 990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn
        995                1000                1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala
   1010                1015                1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu
1025                1030                1035                1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala
                1045                1050                1055

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu
            1060                1065                1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys
        1075                1080                1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly
   1090                1095                1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg
1105                1110                1115                1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
                1125                1130                1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
            1140                1145                1150

Tyr Thr Phe Leu Xaa Thr Lys Gly Lys Ser Gly Xaa Xaa Ile Arg Lys
        1155                1160                1165

Thr Lys Phe Thr Ser Thr Xaa Xaa His Leu Ile Met Pro Ala Pro Val
   1170                1175                1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu
1185                1190                1195                1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val
                1205                1210                1215

Ala Gly Glu Xaa Xaa Gln Leu Leu Ala Glu Glu Gly Ile His Lys His
            1220                1225                1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly
        1235                1240                1245

Xaa Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val
   1250                1255                1260

Arg Val Val Ala Gln Xaa Ala Ala Thr Arg Ser Gly Trp Asp Thr Val
1265                1270                1275                1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln
                1285                1290                1295

Ala Gly Val Xaa Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys
            1300                1305                1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser
        1315                1320                1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu
   1330                1335                1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro
```

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1345                1350                1355                1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile
                1365                1370                1375

Glu Lys Leu Ser Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
            1380                1385                1390

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg
        1395                1400                1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile
    1410                1415                1420

Ala Leu Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val
1425                1430                1435                1440

Leu Gly Leu Asn Gly Ala Xaa Ala Ala Ala Thr Asp Ala Ala Phe Ala
                1445                1450                1455

Ser Leu Ala Ser Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp
            1460                1465                1470

Val Gly Lys Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn
        1475                1480                1485

Leu Val Val Ala Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala
    1490                1495                1500

Ser Ala Leu Xaa Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr
1505                1510                1515                1520

Val Asn Leu Ala Asn Xaa Gly Gln Cys Arg Thr Asp
                1525                1530


<210> SEQ ID NO 63
<211> LENGTH: 1782
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (89)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (697)
<223> OTHER INFORMATION: N = Unknown
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: (862)
<223> OTHER INFORMATION: N = Unknown
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (959)..(960)
<223> OTHER INFORMATION: any nucleotide

<400> SEQUENCE: 63

cgcttcattc atgatgaagc agtcggcagc aacatcggcg gcggcaaaat gattgttgca     60

gccgggcagg atatcaatgt acgcggcana agccttattt ctgataaggg cattgtttta    120

aaagcaggac acgacatcga tatttctact gcccataatc gctataccgg caatgaatac    180

cacgagagca waaawtcagg cgtcatgggt actggcggat tgggctttac tatcggtaac    240

cggaaaacta ccgatgacac tgatcgtacc aatattgtsc atacaggcag cattataggc    300

agcctgaatg gagacaccgt tacagttgca ggaaaccgct accgacaaac cggcagtacc    360

gtctccagcc ccgaggggcg caataccgtc acagccaaaw gcatagatgt agagttcgca    420

aacaaccggt atgccactga ctacgcccat acccagggaa caaaaaggcc ttaccgtcgc    480

cctcaatgtc ccggttgtcc aagctgcaca aaacttcata caagcagccc aaaatgtggg    540
```

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caaaagtaaa aataaacgcg ttaatgccat ggctgcagcc aatgctgcat ggcagagtta 600

tcaagcaacc caacaaatgc aacaatttgc tccaagcagc agtgcgggac aaggtcaaaa 660

ctacaatcaa agccccagta tcagtgtgtc cattacntac ggcgaacaga aaagtcgtaa 720

cgagcaaaaa agacattaca ccgaagcggc agcaagtcaa attatcggca aagggcaaac 780

cacacttgcg gcaacaggaa gtggggagca gtccaatatc aatattacag gttccgatgt 840

catcggccat gcaggtactc cnctcattgc cgacaaccat atcagactcc aatctgccaa 900

acaggacggc agcgagcaaa gcaaaaacaa aagcagtggt tggaatgcag gcgtacgtnn 960

caaaataggc aacggcatca ggtttggaat taccgccgga ggaaatatcg gtaaaggtaa 1020

agagcaaggg ggaagtacta cccaccgcca cacccatgtc ggcagcacaa ccggcaaaac 1080

taccatccga agcggcgggg gataccaccc tcaaaggtgt gcagctcatc ggcaaaggca 1140

tacaggcaga tacgcgcaac ctgcatatag aaagtgttca agatactgaa acctatcaga 1200

gcaaacagca aaacggcaat gtccaagttt actgtcggtt acggattcag tgcaagcggc 1260

agttaccgcc aaagcaaagt caaagcagac catgcctccg taaccgggca aagcggtatt 1320

tatgccggag aagacggcta tcaaatyaaa gtyagagaca acacagacct yaagggcggt 1380

atcatcacgt ctagccaaag cgcagaagat aagggcaaaa acctttttca gacggccacc 1440

cttactgcca gcgacattca aaaccacagc cgctacgaag gcagaagctt cggcataggc 1500

ggcagtttcg acctgaacgg cggctgggac ggcacggtta ccgacaaaca aggcaggcct 1560

accgacagga taagcccggc agccggctac ggcagcgacg gagacagcaa aaacagcacc 1620

acccgcagcg gcgtcaacac ccacaacata cacatcaccg acgaagcggg acaacttgcc 1680

cgaacaggca ggactgcaaa agaaaccgaa gcgcgtatct acaccggcat cgacaccgaa 1740

actgcggatc aacactcagg ccatctgaaa aacagcttcg ac 1782

<210> SEQ ID NO 64
<211> LENGTH: 593
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (30)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (64)..(65)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (134)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (232)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (287)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (320)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 64

Arg Phe Ile His Asp Glu Ala Val Gly Ser Asn Ile Gly Gly Gly Lys

-continued

```
  1               5                  10                  15

Met Ile Val Ala Ala Gly Gln Asp Ile Asn Val Arg Gly Xaa Ser Leu
             20                  25                  30

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

Ser Thr Ala His Asn Arg Tyr Thr Gly Asn Glu Tyr His Glu Ser Xaa
     50                  55                  60

Xaa Ser Gly Val Met Gly Thr Gly Gly Leu Gly Phe Thr Ile Gly Asn
 65                  70                  75                  80

Arg Lys Thr Thr Asp Asp Thr Asp Arg Thr Asn Ile Val His Thr Gly
                 85                  90                  95

Ser Ile Ile Gly Ser Leu Asn Gly Asp Thr Val Thr Val Ala Gly Asn
            100                 105                 110

Arg Tyr Arg Gln Thr Gly Ser Thr Val Ser Ser Pro Glu Gly Arg Asn
        115                 120                 125

Thr Val Thr Ala Lys Xaa Ile Asp Val Glu Phe Ala Asn Asn Arg Tyr
    130                 135                 140

Ala Thr Asp Tyr Ala His Thr Gln Glu Gln Lys Gly Leu Thr Val Ala
145                 150                 155                 160

Leu Asn Val Pro Val Val Gln Ala Ala Gln Asn Phe Ile Gln Ala Ala
                165                 170                 175

Gln Asn Val Gly Lys Ser Lys Asn Lys Arg Val Asn Ala Met Ala Ala
            180                 185                 190

Ala Asn Ala Ala Trp Gln Ser Tyr Gln Ala Thr Gln Gln Met Gln Gln
        195                 200                 205

Phe Ala Pro Ser Ser Ser Ala Gly Gln Gly Gln Asn Tyr Asn Gln Ser
    210                 215                 220

Pro Ser Ile Ser Val Ser Ile Xaa Tyr Gly Glu Gln Lys Ser Arg Asn
225                 230                 235                 240

Glu Gln Lys Arg His Tyr Thr Glu Ala Ala Ala Ser Gln Ile Ile Gly
                245                 250                 255

Lys Gly Gln Thr Thr Leu Ala Ala Thr Gly Ser Gly Glu Gln Ser Asn
            260                 265                 270

Ile Asn Ile Thr Gly Ser Asp Val Ile Gly His Ala Gly Thr Xaa Leu
        275                 280                 285

Ile Ala Asp Asn His Ile Arg Leu Gln Ser Ala Lys Gln Asp Gly Ser
    290                 295                 300

Glu Gln Ser Lys Asn Lys Ser Ser Gly Trp Asn Ala Gly Val Arg Xaa
305                 310                 315                 320

Lys Ile Gly Asn Gly Ile Arg Phe Gly Ile Thr Ala Gly Gly Asn Ile
                325                 330                 335

Gly Lys Gly Lys Glu Gln Gly Gly Ser Thr Thr His Arg His Thr His
            340                 345                 350

Val Gly Ser Thr Thr Gly Lys Thr Thr Ile Arg Ser Gly Gly Asp Thr
        355                 360                 365

Thr Leu Lys Gly Val Gln Leu Ile Gly Lys Gly Ile Gln Ala Asp Thr
    370                 375                 380

Arg Asn Leu His Ile Glu Ser Val Gln Asp Thr Glu Thr Tyr Gln Ser
385                 390                 395                 400

Lys Gln Gln Asn Gly Asn Val Gln Val Thr Val Gly Tyr Gly Phe Ser
                405                 410                 415
```

-continued

```
Ala Ser Gly Ser Tyr Arg Gln Ser Lys Val Lys Ala Asp His Ala Ser
            420                 425                 430

Val Thr Gly Gln Ser Gly Ile Tyr Ala Gly Glu Asp Gly Tyr Gln Ile
        435                 440                 445

Lys Val Arg Asp Asn Thr Asp Leu Lys Gly Gly Ile Ile Thr Ser Ser
    450                 455                 460

Gln Ser Ala Glu Asp Lys Gly Lys Asn Leu Phe Gln Thr Ala Thr Leu
465                 470                 475                 480

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

Gly Ile Gly Gly Ser Phe Asp Leu Asn Gly Gly Trp Asp Gly Thr Val
            500                 505                 510

Thr Asp Lys Gln Gly Arg Pro Thr Asp Arg Ile Ser Pro Ala Ala Gly
        515                 520                 525

Tyr Gly Ser Asp Gly Asp Ser Lys Asn Ser Thr Thr Arg Ser Gly Val
    530                 535                 540

Asn Thr His Asn Ile His Ile Thr Asp Glu Ala Gly Gln Leu Ala Arg
545                 550                 555                 560

Thr Gly Arg Thr Ala Lys Glu Thr Glu Ala Arg Ile Tyr Thr Gly Ile
                565                 570                 575

Asp Thr Glu Thr Ala Asp Gln His Ser Gly His Leu Lys Asn Ser Phe
            580                 585                 590

Asp
```

<210> SEQ ID NO 65
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 65

```
acgaccggca gcctcggcgg catactggcc ggcggcggca cttcccttgc cgcaccgtat     60

ttggacaaag cggcggaaaa cctcggtccg gcgggcaaag cggcggtcaa cgcactgggc    120

ggtgcggcca tcggctatgc aactggtggt agtggtggtg ctgtggtggg tgcgaatgta    180

gattggaaca ataggcagct gcatccgaaa gaaatggcgt tggccgacaa atatgccgaa    240

gccctcaagc gcgaagttga aaaacgcgaa ggcagaaaaa tcagcagcca agaagcggca    300

atgagaatcc gcaggcagat atgcgttggg tggacaaagg ttcccaagac ggctataccg    360

accaaagcgt catatccctt atcggaatga                                     390
```

<210> SEQ ID NO 66
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 66

```
Thr Thr Gly Ser Leu Gly Gly Ile Leu Ala Gly Gly Gly Thr Ser Leu
  1               5                  10                  15

Ala Ala Pro Tyr Leu Asp Lys Ala Ala Glu Asn Leu Gly Pro Ala Gly
             20                  25                  30

Lys Ala Ala Val Asn Ala Leu Gly Gly Ala Ala Ile Gly Tyr Ala Thr
         35                  40                  45

Gly Gly Ser Gly Gly Ala Val Val Gly Ala Asn Val Asp Trp Asn Asn
```

-continued

```
     50                  55                  60

Arg Gln Leu His Pro Lys Glu Met Ala Leu Ala Asp Lys Tyr Ala Glu
 65                  70                  75                  80

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

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

Lys Val Pro Lys Thr Ala Ile Pro Thr Lys Ala Ser Tyr Pro Leu Ser
        115                 120                 125

Glu
```

<210> SEQ ID NO 67
<211> LENGTH: 960
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 67

caatgccgtc tgaaaagctc acaattttac agacggcatt tgttatgcaa gtacatatac 60

agattcccta tatactgccc agrkgcgtgc gtggctgaag acacccccta cgcttgctat 120

ttgraacagc tccaagtcac caaagacgtc aactggaacc aggtacwact ggcgtacgac 180

aaatgggact ataaacagga aggcttaacc ggagccggag cagcgattat tgcgctggct 240

gttaccgtgg ttactgcggg cgcgggagcc ggagccgcac tgggcttaaa cggcgcggcc 300

gcagcggcaa ccgatgccgc attcgcctcg ctggccagcc aggcttccgt atcgctcatc 360

aacaacaaag gcaatatcgg taacaccctg aaagagctgg gcagaagcag cacggtgaaa 420

aatctgatgg ttgccgtcgc taccgcaggc gtagccgaca aaatcggtgc ttcggcactg 480

aacaatgtca gcgataagca gtggatcaac aacctgaccg tcaacctggc caatgcgggc 540

agtgccgcac tgattaatac cgctgtcaac ggcggcagcc tgaaagacaa tctggaagcg 600

aatatccttg cggctttggt gaatactgcg catggagaag cagccagtaa aatcaaacag 660

ttggatcagc actacattac ccacaagatt gcccatgcca tagcgggctg tgcggctgcg 720

gcggcgaata agggcaagtg tcaggatggt gcgataggtg cggctgtggg cgagatagtc 780

ggggaggctt tgacaaacgg caaaaatcct gacactttga cagctaaaga acgcgaacag 840

attttggcat acagcaaact ggttgccggt acggtaagcg gtgtggtcgg cggcgatgta 900

aatgcggcgg cgaatgcggc tgaggtagcg gtgaaaaata atcagcttag cgacaaatga 960

<210> SEQ ID NO 68
<211> LENGTH: 319
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (28)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (42)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (56)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 68

-continued

```
Gln Cys Arg Leu Lys Ser Ser Gln Phe Tyr Arg Arg His Leu Leu Cys
  1               5                  10                  15

Lys Tyr Ile Tyr Arg Phe Pro Ile Tyr Cys Pro Xaa Ala Cys Val Ala
             20                  25                  30

Glu Asp Thr Pro Tyr Ala Cys Tyr Leu Xaa Gln Leu Gln Val Thr Lys
         35                  40                  45

Asp Val Asn Trp Asn Gln Val Xaa Leu Ala Tyr Asp Lys Trp Asp Tyr
     50                  55                  60

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

Val Thr Val Val Thr Ala Gly Ala Gly Ala Gly Ala Ala Leu Gly Leu
                 85                  90                  95

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

Ser Gln Ala Ser Val Ser Leu Ile Asn Asn Lys Gly Asn Ile Gly Asn
        115                 120                 125

Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Met Val
    130                 135                 140

Ala Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu
145                 150                 155                 160

Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu
                165                 170                 175

Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val Asn Gly Gly
            180                 185                 190

Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn
        195                 200                 205

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

Tyr Ile Thr His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala
225                 230                 235                 240

Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val
                245                 250                 255

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

Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser Lys Leu Val
        275                 280                 285

Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn Ala Ala Ala
    290                 295                 300

Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser Asp Lys
305                 310                 315


<210> SEQ ID NO 69
<211> LENGTH: 1860
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 69

atgcaagtaa atattcagat tccctatata ctgcccagat gcgtgcgtgc tgaagacacc     60

ccctacgctt gctatttgaa acagctccaa gtcaccaaag acgtcaactg gaaccaggta    120

caactggcgt acgacaaatg ggactataaa caggaaggct taaccggagc cggagcagcg    180

attattgcgc tggctgttac cgtggttact gcgggcgcgg gagccggagc cgcactgggc    240
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ttaaacggcg cggccgcagc ggcaaccgat gccgcattcg cctcgctggc cagccaggct    300

tccgtatcgc tcatcaacaa caaaggcaat atcggtaaca ccctgaaaga gctgggcaga    360

agcagcacgg tgaaaaatct gatggttgcc gtcgctaccg caggcgtagc cgacaaaatc    420

ggtgcttcgg cactgaacaa tgtcagcgat aagcagtgga tcaacaacct gaccgtcaac    480

ctggccaatg cgggcagtgc cgcactgatt aataccgctg tcaacggcgg cagcctgaaa    540

gacaatctgg aagcgaatat ccttgcggct ttggtgaata ctgcgcatgg agaagcagcc    600

agtaaaatca aacagttgga tcagcactac attacccaca agattgccca tgccatagcg    660

ggctgtgcgg ctgcggcggc gaataagggc aagtgtcagg atggtgcgat aggtgcggct    720

gtgggcgaga tagtcgggga ggctttgaca aacggcaaaa atcctgacac tttgacagct    780

aaagaacgcg aacagatttt ggcatacagc aaactggttg ccggtacggt aagcggtgtg    840

gtcggcggcg atgtaaatgc ggcggcgaat gcggctgagg tagcggtgaa aaataatcag    900

cttagcgaca aagagggtag agaatttgat aacgaaatga ctgcatgcgc caaacagaat    960

aatcctcaac tgtgcagaaa aaatactgta aaaaagtatc aaaatgttgc tgataaaaga   1020

cttgctgctt cgattgcaat atgtacggat atatcccgta gtactgaatg tagaacaatc   1080

agaaaacaac atttgatcga tagtagaagc cttcattcat cttgggaagc aggtctaatt   1140

ggtaaagatg atgaatggta taaattattc agcaaatctt acacccaagc agatttggct   1200

ttacagtctt atcatttgaa tactgctgct aaatcttggc ttcaatcggg caatacaaag   1260

cctttatccg aatggatgtc cgaccaaggt tatacactta tttcaggagt taatcctaga   1320

ttcattccaa taccaagagg gtttgtaaaa caaaatacac ctattactaa tgtcaaatac   1380

ccggaaggca tcagtttcga tacaaaccta aaaagacatc tggcaaatgc tgatggtttt   1440

agtcaaaaac agggcattaa aggagcccat aaccgcacca attttatggc agaactaaat   1500

tcacgaggag gacgcgtaaa atctgaaacc caaactgata ttgaaggcat tacccgaatt   1560

aaatatgaga ttcctacact agacaggaca ggtaaacctg atggtggatt taaggaaatt   1620

tcaagtataa aaactgttta taatcctaaa aaatttttctg atgataaaat acttcaaatg   1680

gctcaaaatg ctgcttcaca aggatattca aaagcctcta aaattgctca aaatgaaaga   1740

actaaatcaa tatcggaaag aaaaaatgtc attcaattct cagaaacctt tgacggaatc   1800

aaatttagat catattttga tgtaaataca ggaagaatta caaacattca cccagaataa   1860
```

<210> SEQ ID NO 70
<211> LENGTH: 619
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 70

```
Met Gln Val Asn Ile Gln Ile Pro Tyr Ile Leu Pro Arg Cys Val Arg
  1               5                  10                  15

Ala Glu Asp Thr Pro Tyr Ala Cys Tyr Leu Lys Gln Leu Gln Val Thr
             20                  25                  30

Lys Asp Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp
         35                  40                  45

Tyr Lys Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Ile Ala Leu
     50                  55                  60

Ala Val Thr Val Val Thr Ala Gly Ala Gly Ala Gly Ala Ala Leu Gly
 65                  70                  75                  80
```

-continued

```
Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu
                 85                  90                  95

Ala Ser Gln Ala Ser Val Ser Leu Ile Asn Asn Lys Gly Asn Ile Gly
            100                 105                 110

Asn Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Met
        115                 120                 125

Val Ala Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala
    130                 135                 140

Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn
145                 150                 155                 160

Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val Asn Gly
                165                 170                 175

Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val
            180                 185                 190

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

His Tyr Ile Thr His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala
    210                 215                 220

Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala
225                 230                 235                 240

Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn Pro Asp
                245                 250                 255

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

Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn Ala Ala
        275                 280                 285

Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser Asp Lys
    290                 295                 300

Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys Gln Asn
305                 310                 315                 320

Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln Asn Val
                325                 330                 335

Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp Ile Ser
            340                 345                 350

Arg Ser Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile Asp Ser
        355                 360                 365

Arg Ser Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys Asp Asp
    370                 375                 380

Glu Trp Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp Leu Ala
385                 390                 395                 400

Leu Gln Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu Gln Ser
                405                 410                 415

Gly Asn Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly Tyr Thr
            420                 425                 430

Leu Ile Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg Gly Phe
        435                 440                 445

Val Lys Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu Gly Ile
    450                 455                 460

Ser Phe Asp Thr Asn Leu Lys Arg His Leu Ala Asn Ala Asp Gly Phe
465                 470                 475                 480
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```
Ser Gln Lys Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn Phe Met
                485                 490                 495

Ala Glu Leu Asn Ser Arg Gly Gly Arg Val Lys Ser Glu Thr Gln Thr
            500                 505                 510

Asp Ile Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr Leu Asp
        515                 520                 525

Arg Thr Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser Ile Lys
    530                 535                 540

Thr Val Tyr Asn Pro Lys Lys Phe Ser Asp Asp Lys Ile Leu Gln Met
545                 550                 555                 560

Ala Gln Asn Ala Ala Ser Gln Gly Tyr Ser Lys Ala Ser Lys Ile Ala
                565                 570                 575

Gln Asn Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val Ile Gln
            580                 585                 590

Phe Ser Glu Thr Phe Asp Gly Ile Lys Phe Arg Ser Tyr Phe Asp Val
        595                 600                 605

Asn Thr Gly Arg Ile Thr Asn Ile His Pro Glu
    610                 615


<210> SEQ ID NO 71
<211> LENGTH: 1788
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (181)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (365)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (473)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (838)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (890)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1339)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1411)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1441)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1443)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1461)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1581)
<223> OTHER INFORMATION: any nucleotide
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1586)..(1587)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1615)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1622)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1738)..(1740)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1744)
<223> OTHER INFORMATION: any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1746)
<223> OTHER INFORMATION: any nucleotide

<400> SEQUENCE: 71

tatctgaaac agctccaagt agcgaaaaac atcaactgga atcaggtgca gcttgcttac 60

gacagatggg actacaaaca ggagggctta accgaagcag gtgcggcgat tatcgcactg 120

gccgttaccg tggtcacctc aggcgcagga accggagccg tattgggatt aaacggtgcg 180

nccgccgccg caaccgatgc agcattcgcc tctttggcca gccaggcttc cgtatcgttc 240

atcaacaaca aaggcgatgt cggcaaaacc ctgaaagagc tgggcagaag cagcacggtg 300

aaaaatctgg tggttgccgc cgctaccgca ggcgtagccg acaaaatcgg cgcttcggca 360

ctgancaatg tcagcgataa gcagtggatc aacaacctga ccgtcaacct agccaatgcg 420

ggcagtgccg cactgattaa taccgctgtc aacggcggca gcctgaaaga cantctggaa 480

gcgaatatcc ttgcggcttt ggtcaatacc gcgcatggag aagcagccag taaaatcaaa 540

cagttggatc agcactacat agtccacaag attgcccatg ccatagcggg ctgtgcggca 600

gcggcggcga ataagggcaa gtgtcaggat ggtgcgatag gtgcggctgt gggcgagata 660

gtcggggagg ctttgacaaa cggcaaaaat cctgacactt tgacagctaa agaacgcgaa 720

cagattttgg catacagcaa actggttgcc ggtacggtaa gcggtgtggt cggcggcgat 780

gtaaatgcgg cggcgaatgc ggctgaggta gcggtgaaaa ataatcagct tagcgacnaa 840

gagggtagag aatttgataa cgaaatgact gcatgcgcca aacagaatan tcctcaactg 900

tgcagaaaaa atactgtaaa aaagtatcaa aatgttgctg ataaaagact tgctgcttcg 960

attgcaatat gtacggatat atcccgtagt actgaatgta gaacaatcag aaaacaacat 1020

ttgatcgata gtagaagcct tcattcatct tgggaagcag gtctaattgg taaagatgat 1080

gaatggtata aattattcag caaatcttac acccaagcag atttggcttt acagtcttat 1140

catttgaata ctgctgctaa atcttggctt caatcgggca atacaaagcc tttatccgaa 1200

tggatgtccg accaaggtta tacacttatt tcaggagtta atcctagatt cattccaata 1260

ccaagagggt ttgtaaaaca aaatacacct attactaatg tcaaatacac ggaaggcatc 1320

agtttcgata caaacctana aagacatctg gcaaatgctg atggttttag tcaagaacag 1380

ggcattaaag gagcccataa ccgcaccaat nttatggcag aactaaattc acgaggagga 1440

ngngtaaaat ctgaaaccca nactgatatt gaaggcatta cccgaattaa atatgagatt 1500

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cctacactag acaggacagg taaacctgat ggtggattta aggaaatttc aagtataaaa 1560

actgtttata atcctaaaaa nttttnngat gataaaatac ttcaaatggc tcaanatgct 1620

gnttcacaag gatattcaaa agcctctaaa attgctcaaa atgaaagaac taaatcaata 1680

tcggaaagaa aaaatgtcat tcaattctca gaaacctttg acggaatcaa atttagannn 1740

tatntngatg taaatacagg aagaattaca aacattcacc cagaataa 1788

<210> SEQ ID NO 72
<211> LENGTH: 595
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (61)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (122)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (158)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (280)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (297)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (447)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (471)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (481)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (487)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (527)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (529)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (539)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (541)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (580)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (582)
<223> OTHER INFORMATION: unknown

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<400> SEQUENCE: 72

```
Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn Ile Asn Trp Asn Gln Val
  1               5                  10                  15

Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu
             20                  25                  30

Ala Gly Ala Ala Ile Ile Ala Leu Ala Val Thr Val Val Thr Ser Gly
         35                  40                  45

Ala Gly Thr Gly Ala Val Leu Gly Leu Asn Gly Ala Xaa Ala Ala Ala
     50                  55                  60

Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser Gln Ala Ser Val Ser Phe
 65                  70                  75                  80

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

Ser Ser Thr Val Lys Asn Leu Val Val Ala Ala Ala Thr Ala Gly Val
            100                 105                 110

Ala Asp Lys Ile Gly Ala Ser Ala Leu Xaa Asn Val Ser Asp Lys Gln
        115                 120                 125

Trp Ile Asn Asn Leu Thr Val Asn Leu Ala Asn Ala Gly Ser Ala Ala
    130                 135                 140

Leu Ile Asn Thr Ala Val Asn Gly Gly Ser Leu Lys Asp Xaa Leu Glu
145                 150                 155                 160

Ala Asn Ile Leu Ala Ala Leu Val Asn Thr Ala His Gly Glu Ala Ala
                165                 170                 175

Ser Lys Ile Lys Gln Leu Asp Gln His Tyr Ile Val His Lys Ile Ala
            180                 185                 190

His Ala Ile Ala Gly Cys Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys
        195                 200                 205

Gln Asp Gly Ala Ile Gly Ala Ala Val Gly Glu Ile Val Gly Glu Ala
    210                 215                 220

Leu Thr Asn Gly Lys Asn Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu
225                 230                 235                 240

Gln Ile Leu Ala Tyr Ser Lys Leu Val Ala Gly Thr Val Ser Gly Val
                245                 250                 255

Val Gly Gly Asp Val Asn Ala Ala Ala Asn Ala Ala Glu Val Ala Val
            260                 265                 270

Lys Asn Asn Gln Leu Ser Asp Xaa Glu Gly Arg Glu Phe Asp Asn Glu
        275                 280                 285

Met Thr Ala Cys Ala Lys Gln Asn Xaa Pro Gln Leu Cys Arg Lys Asn
    290                 295                 300

Thr Val Lys Lys Tyr Gln Asn Val Ala Asp Lys Arg Leu Ala Ala Ser
305                 310                 315                 320

Ile Ala Ile Cys Thr Asp Ile Ser Arg Ser Thr Glu Cys Arg Thr Ile
                325                 330                 335

Arg Lys Gln His Leu Ile Asp Ser Arg Ser Leu His Ser Ser Trp Glu
            340                 345                 350

Ala Gly Leu Ile Gly Lys Asp Asp Glu Trp Tyr Lys Leu Phe Ser Lys
        355                 360                 365

Ser Tyr Thr Gln Ala Asp Leu Ala Leu Gln Ser Tyr His Leu Asn Thr
    370                 375                 380

Ala Ala Lys Ser Trp Leu Gln Ser Gly Asn Thr Lys Pro Leu Ser Glu
```

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385 390 395 400

Trp Met Ser Asp Gln Gly Tyr Thr Leu Ile Ser Gly Val Asn Pro Arg
405 410 415

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

Asn Val Lys Tyr Pro Glu Gly Ile Ser Phe Asp Thr Asn Leu Xaa Arg
435 440 445

His Leu Ala Asn Ala Asp Gly Phe Ser Gln Glu Gln Gly Ile Lys Gly
450 455 460

Ala His Asn Arg Thr Asn Xaa Met Ala Glu Leu Asn Ser Arg Gly Gly
465 470 475 480

Xaa Val Lys Ser Glu Thr Xaa Thr Asp Ile Glu Gly Ile Thr Arg Ile
485 490 495

Lys Tyr Glu Ile Pro Thr Leu Asp Arg Thr Gly Lys Pro Asp Gly Gly
500 505 510

Phe Lys Glu Ile Ser Ser Ile Lys Thr Val Tyr Asn Pro Lys Xaa Phe
515 520 525

Xaa Asp Asp Lys Ile Leu Gln Met Ala Gln Xaa Ala Xaa Ser Gln Gly
530 535 540

Tyr Ser Lys Ala Ser Lys Ile Ala Gln Asn Glu Arg Thr Lys Ser Ile
545 550 555 560

Ser Glu Arg Lys Asn Val Ile Gln Phe Ser Glu Thr Phe Asp Gly Ile
565 570 575

Lys Phe Arg Xaa Tyr Xaa Asp Val Asn Thr Gly Arg Ile Thr Asn Ile
580 585 590

His Pro Glu
595

<210> SEQ ID NO 73
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 73

atggcaatca ttacattgta ttattctgtc aatggtattt taaatgtatg tgcaaaagca 60

aaaaatattc aagtagttgc caataataag aatatggttc tttttgggtt tttggsmrgc 120

atcatcggcg gttcaaccaa tgccatgtct cccatattgt taatattttt gcttagcgaa 180

acagaaaata aaaatcgtat cgtaaaatca agcaatctat gctatctttt ggcgaaaatt 240

gttcaaatat atatgctaag agaccagtat tggttattaa ataagagtga atacgdttta 300

atatttttac tgtccgtatt gtctgttatt ggattgtatg ttggaattcg gttaaggact 360

aagattagcc caaatttttt taaaatgtta atttttattg ttttattggt attggctctg 420

aaaatcgggc attcgggttt aatcaaactt taa 453

<210> SEQ ID NO 74
<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (39)..(40)
<223> OTHER INFORMATION: unknown
<220> FEATURE:
<221> NAME/KEY: SITE

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<222> LOCATION: (99)
<223> OTHER INFORMATION: unknown

<400> SEQUENCE: 74

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

Cys Ala Lys Ala Lys Asn Ile Gln Val Val Ala Asn Asn Lys Asn Met
20 25 30

Val Leu Phe Gly Phe Leu Xaa Xaa Ile Ile Gly Gly Ser Thr Asn Ala
35 40 45

Met Ser Pro Ile Leu Leu Ile Phe Leu Leu Ser Glu Thr Glu Asn Lys
50 55 60

Asn Arg Ile Val Lys Ser Ser Asn Leu Cys Tyr Leu Leu Ala Lys Ile
65 70 75 80

Val Gln Ile Tyr Met Leu Arg Asp Gln Tyr Trp Leu Leu Asn Lys Ser
85 90 95

Glu Tyr Xaa Leu Ile Phe Leu Leu Ser Val Leu Ser Val Ile Gly Leu
100 105 110

Tyr Val Gly Ile Arg Leu Arg Thr Lys Ile Ser Pro Asn Phe Phe Lys
115 120 125

Met Leu Ile Phe Ile Val Leu Leu Val Leu Ala Leu Lys Ile Gly His
130 135 140

Ser Gly Leu Ile Lys Leu
145 150

<210> SEQ ID NO 75
<211> LENGTH: 768
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 75

atgcaagaaa taatgcaatc tatcgttttt gttgctgccg caatactgca cggaattaca 60

ggcatgggat ttccgatgct cggtacaacc gcattggctt ttatcatgcc attgtctaag 120

gttgttgcct tggtggcatt accaagcctg ttaatgagct tgttggttct atgcagcaat 180

aacaaaaagg gtttttggca agagattgtt tattatttaa aaacctataa attgcttgct 240

atcggcagcg tcgttggcag cattttgggg gtgaagttgc ttttgatact tccagtgtct 300

tggctgcttt tactgatggc aatcattaca ttgtattatt ctgtcaatgg tattttaaat 360

gtatgtgcaa aagcaaaaaa tattcaagta gttgccaata ataagaatat ggttcttttt 420

gggtttttgg caggcatcat cggcggttca accaatgcca tgtctcccat attgttaata 480

tttttgctta gcgaaacaga aaataaaaat cgtatcgtaa aatcaagcaa tctatgctat 540

cttttggcga aaattgttca aatatatatg ctaagagacc agtattggtt attaaataag 600

agtgaatacg gtttaatatt tttactgtcc gtattgtctg ttattggatt gtatgttgga 660

attcggttaa ggactaagat tagcccaaat ttttttaaaa tgttaatttt tattgtttta 720

ttggtattgg ctctgaaaat cgggcattcg ggtttaatca aactttaa 768

<210> SEQ ID NO 76
<211> LENGTH: 255
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 76

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Met Gln Glu Ile Met Gln Ser Ile Val Phe Val Ala Ala Ala Ile Leu
  1               5                  10                  15

His Gly Ile Thr Gly Met Gly Phe Pro Met Leu Gly Thr Thr Ala Leu
            20                  25                  30

Ala Phe Ile Met Pro Leu Ser Lys Val Val Ala Leu Val Ala Leu Pro
         35                  40                  45

Ser Leu Leu Met Ser Leu Leu Val Leu Cys Ser Asn Asn Lys Lys Gly
     50                  55                  60

Phe Trp Gln Glu Ile Val Tyr Tyr Leu Lys Thr Tyr Lys Leu Leu Ala
 65                  70                  75                  80

Ile Gly Ser Val Val Gly Ser Ile Leu Gly Val Lys Leu Leu Leu Ile
                85                  90                  95

Leu Pro Val Ser Trp Leu Leu Leu Leu Met Ala Ile Ile Thr Leu Tyr
            100                 105                 110

Tyr Ser Val Asn Gly Ile Leu Asn Val Cys Ala Lys Ala Lys Asn Ile
        115                 120                 125

Gln Val Val Ala Asn Asn Lys Asn Met Val Leu Phe Gly Phe Leu Ala
    130                 135                 140

Gly Ile Ile Gly Gly Ser Thr Asn Ala Met Ser Pro Ile Leu Leu Ile
145                 150                 155                 160

Phe Leu Leu Ser Glu Thr Glu Asn Lys Asn Arg Ile Val Lys Ser Ser
                165                 170                 175

Asn Leu Cys Tyr Leu Leu Ala Lys Ile Val Gln Ile Tyr Met Leu Arg
            180                 185                 190

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

Leu Ser Val Leu Ser Val Ile Gly Leu Tyr Val Gly Ile Arg Leu Arg
    210                 215                 220

Thr Lys Ile Ser Pro Asn Phe Phe Lys Met Leu Ile Phe Ile Val Leu
225                 230                 235                 240

Leu Val Leu Ala Leu Lys Ile Gly His Ser Gly Leu Ile Lys Leu
                245                 250                 255
```

<210> SEQ ID NO 77
<211> LENGTH: 768
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 77

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atgcaagaaa taatgcaatc tatcgttttt gttgctgccg caatactgca cggaattaca     60

ggcatgggat ttccgatgct cggtacaacc gcattggctt ttatcatgcc attgtctaag    120

gttgttgcct tggtggcatt accaagcctg ttaatgagct tgttggttct atgcagcaat    180

aacaaaaagg gtttttggca agagattgtt tattatttaa aaacctataa attgcttgct    240

atcggcagcg tcgttggcag cattttgggg gtgaagttgc ttttgatact tccagtgtct    300

tggctgcttt tactgatggc aatcattaca ttgtattatt ctgtcaatgg tattttaaat    360

gtatgtgcaa aagcaaaaaa tattcaagta gttgccaata ataagaatat ggttcttttt    420

gggtttttgg caggcatcat cggcggttca accaatgcca tgtctcccat attgttaata    480

tttttgctta gcgaaacaga gaataaaaat cgtatcgcaa aatcaagcaa tctatgctat    540

cttttggcaa aaattgttca aatatatatg ctaagagacc agtattggtt attaaataag    600
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agtgaatacg gtttaatatt tttactgtcc gtattgtctg ttattggatt gtatgttgga 660

attcggttaa ggactaagat tagcccaaat ttttttaaaa tgttaatttt tattgtttta 720

ttggtattgg ctctgaaaat cgggtattca ggtttaatca aactttaa 768

<210> SEQ ID NO 78
<211> LENGTH: 255
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 78

Met Gln Glu Ile Met Gln Ser Ile Val Phe Val Ala Ala Ala Ile Leu
1 5 10 15

His Gly Ile Thr Gly Met Gly Phe Pro Met Leu Gly Thr Thr Ala Leu
20 25 30

Ala Phe Ile Met Pro Leu Ser Lys Val Val Ala Leu Val Ala Leu Pro
35 40 45

Ser Leu Leu Met Ser Leu Leu Val Leu Cys Ser Asn Asn Lys Lys Gly
50 55 60

Phe Trp Gln Glu Ile Val Tyr Tyr Leu Lys Thr Tyr Lys Leu Leu Ala
65 70 75 80

Ile Gly Ser Val Val Gly Ser Ile Leu Gly Val Lys Leu Leu Leu Ile
85 90 95

Leu Pro Val Ser Trp Leu Leu Leu Leu Met Ala Ile Ile Thr Leu Tyr
100 105 110

Tyr Ser Val Asn Gly Ile Leu Asn Val Cys Ala Lys Ala Lys Asn Ile
115 120 125

Gln Val Val Ala Asn Asn Lys Asn Met Val Leu Phe Gly Phe Leu Ala
130 135 140

Gly Ile Ile Gly Gly Ser Thr Asn Ala Met Ser Pro Ile Leu Leu Ile
145 150 155 160

Phe Leu Leu Ser Glu Thr Glu Asn Lys Asn Arg Ile Ala Lys Ser Ser
165 170 175

Asn Leu Cys Tyr Leu Leu Ala Lys Ile Val Gln Ile Tyr Met Leu Arg
180 185 190

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

Leu Ser Val Leu Ser Val Ile Gly Leu Tyr Val Gly Ile Arg Leu Arg
210 215 220

Thr Lys Ile Ser Pro Asn Phe Phe Lys Met Leu Ile Phe Ile Val Leu
225 230 235 240

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

<210> SEQ ID NO 79
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 79

atgagacata tgaaaataca aaattattta ctagtattta tagttttaca tatagccttg 60

atagtaatta atatagtgtt tggttatttt gtttttctat ttgatttttt tgcgtttttg 120

ttttttgcaa acgtctttct tgctgtaaat ttattatttt tagaaaaaaa cataaaaaac 180

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aaattattgt ttttattgcc gatttctatt attatatgga tggtaattca tattagtatg 240

ataaatataa aattttataa atttgagcat caaataaagg aacaaaatat atcctcgatt 300

actggggtga taaaaccaca tgatagttat aattatgttt atgactcaaa tggatatgct 360

aaattaaaag ataatcatag atatggtagg gtaattagag aaacacctta tattgatgta 420

gttgcatctg atgttaaaaa taaatccata agattaagct tggtttgtgg tattcattca 480

tatgctccat gtgccaattt tataaaattt gtcagg 516

<210> SEQ ID NO 80
<211> LENGTH: 172
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 80

Met Arg His Met Lys Ile Gln Asn Tyr Leu Leu Val Phe Ile Val Leu
1 5 10 15

His Ile Ala Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
20 25 30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
35 40 45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
50 55 60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
65 70 75 80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
85 90 95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
100 105 110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
115 120 125

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

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
145 150 155 160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Val Arg
165 170

<210> SEQ ID NO 81
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 81

atgagacata tgaaaaataa aaattattta ctagtattta tagttttaca tatagccttg 60

atagtaatta atatagtgtt tggttatttt gtttttctat ttgatttttt tgcgtttttg 120

ttttttgcaa acgtctttct tgctgtaaat ttattatttt tagaaaaaaa cataaaaaac 180

aaattattgt ttttattgcc gatttctatt attatatgga tggtaattca tattagtatg 240

ataaatataa aattttataa atttgagcat caaataaagg aacaaaatat atcctcgatt 300

actggggtga taaaaccaca tgatagttat aattatgttt atgactcaaa tggatatgct 360

aaattaaaag ataatcatag atatggtagg gtaattagag aaacacctta tattgatgta 420

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gttgcatctg atgttaaaaa taaatccata agattaagct tggtttgtgg tattcattca 480

tatgctccat gtgccaattt tataaaattt gcaaaaaaac ctgttaaaat ttatttttat 540

aatcaacctc aaggagattt tatagataat gtaatatttg aaattaatga tggaaacaaa 600

agtttgtact tgttagataa gtataaaaca ttttttctta ttgaaaacag tgtttgtatc 660

gtattaatta ttttatattt aaaatttaat ttgcttttat ataggactta cttcaatgag 720

ttggaatag 729

<210> SEQ ID NO 82
<211> LENGTH: 242
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 82

Met Arg His Met Lys Asn Lys Asn Tyr Leu Leu Val Phe Ile Val Leu
1 5 10 15

His Ile Ala Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
20 25 30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
35 40 45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
50 55 60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
65 70 75 80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
85 90 95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
100 105 110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
115 120 125

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

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
145 150 155 160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Ala Lys Lys Pro Val Lys
165 170 175

Ile Tyr Phe Tyr Asn Gln Pro Gln Gly Asp Phe Ile Asp Asn Val Ile
180 185 190

Phe Glu Ile Asn Asp Gly Asn Lys Ser Leu Tyr Leu Leu Asp Lys Tyr
195 200 205

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

Leu Tyr Leu Lys Phe Asn Leu Leu Leu Tyr Arg Thr Tyr Phe Asn Glu
225 230 235 240

Leu Glu

<210> SEQ ID NO 83
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 83

atgagacata tgaaaaataa aaattattta ctagtattta tagttttaca tataaccttg 60

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atagtaatta atatagtgtt tggttatttt gtttttctat ttgatttttt tgcgtttttg 120

ttttttgcaa acgtctttct tgctgtaaat ttattatttt tagaaaaaaa cataaaaaac 180

aaattattgt ttttattgcc gatttctatt attatatgga tggtaattca tattagtatg 240

ataaatataa aattttataa atttgagcat caaataaagg aacaaaatat atcctcgatt 300

actggggtga taaaaccaca tgatagttat aattatgttt atgactcaaa tggatatgct 360

aaattaaaag ataatcatag atatggtagg gtaattagag aaacacctta tattgatgta 420

gttgcatctg atgttaaaaa taaatccata agattaagct tggtttgtgg tattcattca 480

tatgctccat gtgccaattt tataaaattt gcaaaaaaac ctgttaaaat ttatttttat 540

aatcaacctc aaggagattt tatagataat gtaatatttg aaattaatga tggaaaaaaa 600

agtttgtact tgttagataa gtataaaaca ttttttctta ttgaaaacag tgtttgtatc 660

gtattaatta ttttatattt aaaatttaat ttgcttttat ataggactta cttcaatgag 720

ttggaatag 729

<210> SEQ ID NO 84
<211> LENGTH: 242
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 84

Met Arg His Met Lys Asn Lys Asn Tyr Leu Leu Val Phe Ile Val Leu
1 5 10 15

His Ile Thr Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
20 25 30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
35 40 45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
50 55 60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
65 70 75 80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
85 90 95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
100 105 110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
115 120 125

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

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
145 150 155 160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Ala Lys Lys Pro Val Lys
165 170 175

Ile Tyr Phe Tyr Asn Gln Pro Gln Gly Asp Phe Ile Asp Asn Val Ile
180 185 190

Phe Glu Ile Asn Asp Gly Lys Lys Ser Leu Tyr Leu Leu Asp Lys Tyr
195 200 205

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

Leu Tyr Leu Lys Phe Asn Leu Leu Leu Tyr Arg Thr Tyr Phe Asn Glu

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225 230 235 240

Leu Glu

<210> SEQ ID NO 85
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 85

acccccaaca gcgtgaccgt cttgccgtct ttcggcggat tcgggcgtac cggcgcgacc 60

atcaatgcag caggcggggt cggcatgact gccttttcga caaccttaat ttccgtagcc 120

gagggcgcgg ttgtagagct gcaggccgtg agagccaaag ccgtcaatgc aaccgccgct 180

tgcattttta cggtcttgag taaggacatt ttcgatttcc tttttatttt ccgttttcag 240

acggctgact tccgcctgta ttttcgccaa agccatgccg acagcgtgcg ccttgacttc 300

atatttaaaa gcttccgcgc gtgccagttc cagttcgcgc gcatagtttt gagccgacaa 360

cagcagggct tgcgccttgt cgcgctccat cttgtcgatg accgcctgca gcttcgcaaa 420

tgccgacttg tagccttgat ggtgcgacac agccaagccc gtgccgacaa gcgcgataat 480

ggcaatcggt tgccagtaat tcgccagcag tttcacgaga ttcattctcg acctcctgac 540

gcttcacgct ga 552

<210> SEQ ID NO 86
<211> LENGTH: 183
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 86

Thr Pro Asn Ser Val Thr Val Leu Pro Ser Phe Gly Gly Phe Gly Arg
1 5 10 15

Thr Gly Ala Thr Ile Asn Ala Ala Gly Gly Val Gly Met Thr Ala Phe
20 25 30

Ser Thr Thr Leu Ile Ser Val Ala Glu Gly Ala Val Val Glu Leu Gln
35 40 45

Ala Val Arg Ala Lys Ala Val Asn Ala Thr Ala Ala Cys Ile Phe Thr
50 55 60

Val Leu Ser Lys Asp Ile Phe Asp Phe Leu Phe Ile Phe Arg Phe Gln
65 70 75 80

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

Arg Leu Asp Phe Ile Phe Lys Ser Phe Arg Ala Cys Gln Phe Gln Phe
100 105 110

Ala Arg Ile Val Leu Ser Arg Gln Gln Gln Gly Leu Arg Leu Val Ala
115 120 125

Leu His Leu Val Asp Asp Arg Leu Gln Leu Arg Lys Cys Arg Leu Val
130 135 140

Ala Leu Met Val Arg His Ser Gln Ala Arg Ala Asp Lys Arg Asp Asn
145 150 155 160

Gly Asn Arg Leu Pro Val Ile Arg Gln Gln Phe His Glu Ile His Ser
165 170 175

Arg Pro Pro Asp Ala Ser Arg
180

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<210> SEQ ID NO 87
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 87

atgactgcct tttcgacaac cttaatttcc gtagccgagg gcgcggttgt agagctgcag 60

gccgtgagag ccaaagccgt caatgcaacc gccgcttgca tttttacggt cttgagtaag 120

gacattttcg atttcctttt tattttccgt tttcagacgg ctgacttccg cctgtttttt 180

cgccaaagcc atgccgacag cgtgcgcctt gacttcatat tttttagctt ccgcgcgtgc 240

cagttccagt tcgcgcgcat agttttgagc cgacaacagc agggcttgcg ccttgtcgcg 300

ctccatcttg tcgatgaccg cctgctgctt cgcaaatgcc gacttgtagc cttgatggtg 360

cgacacagcc aagcccgtgc cgacaagcgc gataatggca atcggttgcc agttattcgc 420

cagcagtttc acgagattca ttctcgacct cctgacgctt cacgctga 468

<210> SEQ ID NO 88
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 88

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

Val Glu Leu Gln Ala Val Arg Ala Lys Ala Val Asn Ala Thr Ala Ala
20 25 30

Cys Ile Phe Thr Val Leu Ser Lys Asp Ile Phe Asp Phe Leu Phe Ile
35 40 45

Phe Arg Phe Gln Thr Ala Asp Phe Arg Leu Phe Phe Arg Gln Ser His
50 55 60

Ala Asp Ser Val Arg Leu Asp Phe Ile Phe Phe Ser Phe Arg Ala Cys
65 70 75 80

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

Arg Leu Val Ala Leu His Leu Val Asp Asp Arg Leu Leu Leu Arg Lys
100 105 110

Cys Arg Leu Val Ala Leu Met Val Arg His Ser Gln Ala Arg Ala Asp
115 120 125

Lys Arg Asp Asn Gly Asn Arg Leu Pro Val Ile Arg Gln Gln Phe His
130 135 140

Glu Ile His Ser Arg Pro Pro Asp Ala Ser Arg
145 150 155

<210> SEQ ID NO 89
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 89

atgaccgcct tttcgacaac cttaatttcc gtagccgagg gcgcgcttgt agagctgcaa 60

gccgtgatgg ccaaagccgt caatacaacc gccgcctgca tttttacggt cttgagtaag 120

gacattttcg atttcctttt tattttccgt tttcagacgg ctgacttccg cctgtttttt 180

-continued

cgccaaagcc atgccgacgg cgtgcgcctt gacttcatat tttttagctt ccgcacgcgc 240

ctgttccagt tcgcgggcgt agttttgagc cgacaacagc agggcttgcg ccttgtcgcg 300

cttcattttc tcaatgaccg cctgctgctt cgcaaaagcc gacttgtagc cttgatggtg 360

cgacaccgcc aaacccgtgc cgacaagcgc gatgatggca atcggttgcc agttattcgc 420

cagcagtttc acgagattca ttctcgacct cctgacgttt ga 462

<210> SEQ ID NO 90
<211> LENGTH: 153
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 90

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

Val Glu Leu Gln Ala Val Met Ala Lys Ala Val Asn Thr Thr Ala Ala
20 25 30

Cys Ile Phe Thr Val Leu Ser Lys Asp Ile Phe Asp Phe Leu Phe Ile
35 40 45

Phe Arg Phe Gln Thr Ala Asp Phe Arg Leu Phe Phe Arg Gln Ser His
50 55 60

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

Leu Phe Gln Phe Ala Gly Val Val Leu Ser Arg Gln Gln Gln Gly Leu
85 90 95

Arg Leu Val Ala Leu His Phe Leu Asn Asp Arg Leu Leu Leu Arg Lys
100 105 110

Ser Arg Leu Val Ala Leu Met Val Arg His Arg Gln Thr Arg Ala Asp
115 120 125

Lys Arg Asp Asp Gly Asn Arg Leu Pro Val Ile Arg Gln Gln Phe His
130 135 140

Glu Ile His Ser Arg Pro Pro Asp Val
145 150

<210> SEQ ID NO 91
<211> LENGTH: 592
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 91

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
1 5 10 15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
50 55 60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
65 70 75 80

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

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

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Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
        115                 120                 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
    130                 135                 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

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

Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr
        195                 200                 205

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
    210                 215                 220

Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
465                 470                 475                 480

Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
                485                 490                 495

Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
            500                 505                 510
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Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
        515                 520                 525

Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
    530                 535                 540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545                 550                 555                 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
                565                 570                 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 92
<211> LENGTH: 594
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 92

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
     50                  55                  60

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

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

Arg Val Leu Lys Ala Gly Ala Ile Thr Leu Lys Ala Gly Asp Asn Leu
            100                 105                 110

Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Asp Ser Ser Phe Thr
        115                 120                 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
    130                 135                 140

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

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
                165                 170                 175

Pro Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
            180                 185                 190

Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
        195                 200                 205

Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
    210                 215                 220

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

Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
                245                 250                 255

Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
            260                 265                 270

Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
        275                 280                 285
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Lys Leu Val Thr Gly Lys Gly Lys Asp Glu Asn Gly Ser Ser Thr Asp
    290                 295                 300

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

Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
                325                 330                 335

Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe
            340                 345                 350

Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
        355                 360                 365

Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
    370                 375                 380

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

Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
                405                 410                 415

Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
            420                 425                 430

Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln
        435                 440                 445

Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
    450                 455                 460

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

Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
                485                 490                 495

Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg
            500                 505                 510

Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
        515                 520                 525

Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
    530                 535                 540

Ala Ile Gly Gly Asp Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545                 550                 555                 560

Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
                565                 570                 575

Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
            580                 585                 590

Gln Trp
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<210> SEQ ID NO 93
<211> LENGTH: 594
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 93

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Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45
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Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
     50                  55                  60

Thr Ala Pro Val Leu Ser Phe His Ala Asp Ser Glu Gly Thr Gly Glu
 65                  70                  75                  80

Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys
                85                  90                  95

Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu
            100                 105                 110

Lys Ile Lys Gln Asn Thr Asp Glu Asn Thr Asn Ala Ser Ser Phe Thr
        115                 120                 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
    130                 135                 140

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

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
                165                 170                 175

Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
            180                 185                 190

Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
        195                 200                 205

Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
    210                 215                 220

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

Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
                245                 250                 255

Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
            260                 265                 270

Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
        275                 280                 285

Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp
    290                 295                 300

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

Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
                325                 330                 335

Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe
            340                 345                 350

Ala Ser Gly Asn Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
        355                 360                 365

Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
    370                 375                 380

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

Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
                405                 410                 415

Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
            420                 425                 430

Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln
        435                 440                 445
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Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
    450                 455                 460

Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
465                 470                 475                 480

Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
                485                 490                 495

Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
            500                 505                 510

Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
        515                 520                 525

Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
    530                 535                 540

Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545                 550                 555                 560

Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
                565                 570                 575

Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
            580                 585                 590

Gln Trp


<210> SEQ ID NO 94
<211> LENGTH: 594
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 94

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
     50                  55                  60

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

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

Arg Val Leu Lys Ala Gly Ala Ile Thr Leu Lys Ala Gly Asp Asn Leu
            100                 105                 110

Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Asp Ser Ser Phe Thr
        115                 120                 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
    130                 135                 140

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

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
                165                 170                 175

Pro Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
            180                 185                 190

Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
        195                 200                 205
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Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
    210                 215                 220

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

Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
                245                 250                 255

Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
            260                 265                 270

Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
        275                 280                 285

Lys Leu Val Thr Gly Lys Gly Lys Asp Glu Asn Gly Ser Ser Thr Asp
    290                 295                 300

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

Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
                325                 330                 335

Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe
            340                 345                 350

Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
        355                 360                 365

Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
    370                 375                 380

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

Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
                405                 410                 415

Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
            420                 425                 430

Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln
        435                 440                 445

Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
    450                 455                 460

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

Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
                485                 490                 495

Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg
            500                 505                 510

Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
        515                 520                 525

Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
    530                 535                 540

Ala Ile Gly Gly Asp Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545                 550                 555                 560

Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
                565                 570                 575

Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
            580                 585                 590

Gln Trp
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<210> SEQ ID NO 95

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<211> LENGTH: 591
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 95

```
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Glu Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
     50                  55                  60

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

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
                 85                  90                  95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
            100                 105                 110

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

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
    130                 135                 140

Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
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    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465                 470                 475                 480

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
                485                 490                 495

Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
            500                 505                 510

Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
        515                 520                 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
    530                 535                 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
545                 550                 555                 560

Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
                565                 570                 575

Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 96
<211> LENGTH: 591
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 96

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
     50                  55                  60

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

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
                 85                  90                  95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
            100                 105                 110

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

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
    130                 135                 140
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Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465                 470                 475                 480

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
                485                 490                 495

Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
            500                 505                 510

Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
        515                 520                 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
    530                 535                 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
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545                 550                 555                 560

Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
                565                 570                 575

Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 97
<211> LENGTH: 595
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 97

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Glu Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Thr Asp Glu Asp Asp Glu Leu Glu Pro Val Val
     50                  55                  60

Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
 65                  70                  75                  80

Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp
                 85                  90                  95

His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
            100                 105                 110

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

Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr
    130                 135                 140

Glu Glu Leu Ser Phe Gly Ala Asn Gly Asn Lys Val Asn Ile Thr Ser
145                 150                 155                 160

Asp Thr Lys Gly Leu Asn Phe Ala Lys Lys Thr Ala Gly Thr Asn Gly
                165                 170                 175

Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr
            180                 185                 190

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

His Tyr Thr Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp
    210                 215                 220

Asn Ile Lys Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn
225                 230                 235                 240

Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp
                245                 250                 255

Thr Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg
            260                 265                 270

Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp
        275                 280                 285

Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr
    290                 295                 300

Asp Glu Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val
305                 310                 315                 320
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Asn Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr
                325                 330                 335

Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr
            340                 345                 350

Phe Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln
        355                 360                 365

Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn
    370                 375                 380

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

Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys
                405                 410                 415

Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu
            420                 425                 430

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

Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu
    450                 455                 460

Ser Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn
465                 470                 475                 480

Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp
                485                 490                 495

Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn
            500                 505                 510

His Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala
        515                 520                 525

Ile Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met
    530                 535                 540

Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile
545                 550                 555                 560

Gly Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr
                565                 570                 575

Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly
            580                 585                 590

Tyr Gln Trp
        595


<210> SEQ ID NO 98
<211> LENGTH: 592
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 98

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
     50                  55                  60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65                  70                  75                  80
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Leu Glu Thr Ile Ser Leu Ser Met Thr Asn Asp Ser Lys Glu Phe Val
                 85                  90                  95

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

Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
        115                 120                 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
    130                 135                 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

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

Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr
        195                 200                 205

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
    210                 215                 220

Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
465                 470                 475                 480
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Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
                485                 490                 495

Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
            500                 505                 510

Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
        515                 520                 525

Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
    530                 535                 540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545                 550                 555                 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
                565                 570                 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 99
<211> LENGTH: 594
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 99

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
     50                  55                  60

Thr Ala Pro Val Leu Ser Phe His Ala Asp Ser Glu Gly Thr Gly Glu
 65                  70                  75                  80

Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys
                 85                  90                  95

Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu
            100                 105                 110

Lys Ile Lys Gln Asn Thr Asp Glu Asn Thr Asn Ala Ser Ser Phe Thr
        115                 120                 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
    130                 135                 140

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

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
                165                 170                 175

Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
            180                 185                 190

Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
        195                 200                 205

Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
    210                 215                 220

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

Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
                245                 250                 255
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Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
            260                 265                 270

Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
        275                 280                 285

Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp
    290                 295                 300

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

Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
                325                 330                 335

Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe
            340                 345                 350

Ala Ser Gly Asn Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
        355                 360                 365

Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
    370                 375                 380

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

Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
                405                 410                 415

Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
            420                 425                 430

Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln
        435                 440                 445

Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
    450                 455                 460

Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
465                 470                 475                 480

Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
                485                 490                 495

Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
            500                 505                 510

Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
        515                 520                 525

Ala Thr Ala Ser Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
    530                 535                 540

Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545                 550                 555                 560

Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
                565                 570                 575

Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
            580                 585                 590

Gln Trp
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<210> SEQ ID NO 100
<211> LENGTH: 599
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 100

```
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15
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```
Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
            20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
        35                  40                  45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Pro Val Val
    50                  55                  60

Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
65                  70                  75                  80

Glu Asn Glu Ser Thr Gly Asn Ile Gly Trp Ser Ile Tyr Tyr Asp Asn
                85                  90                  95

His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
            100                 105                 110

Leu Lys Ile Lys Gln Asn Thr Asn Lys Asn Thr Asn Glu Asn Thr Asn
        115                 120                 125

Asp Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr
    130                 135                 140

Ser Val Glu Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Asn Lys Val
145                 150                 155                 160

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

Gly Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr
            180                 185                 190

Leu Thr Asp Thr Leu Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn
        195                 200                 205

Asp Asn Val Thr Asp Asp Lys Lys Lys Arg Ala Ala Ser Val Lys Asp
    210                 215                 220

Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr
225                 230                 235                 240

Ala Ser Asp Asn Val Asp Phe Val His Thr Tyr Asp Thr Val Glu Phe
                245                 250                 255

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

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

Lys Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu Asn
    290                 295                 300

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

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

Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly
            340                 345                 350

Thr Asn Val Thr Phe Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser
        355                 360                 365

Lys Asp Asp Gln Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly
    370                 375                 380

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

Ser Lys Ala Val Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val
                405                 410                 415
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```
Ser Pro Ser Lys Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly
            420                 425                 430

Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr
        435                 440                 445

Ser Met Thr Pro Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp
    450                 455                 460

Ala Pro Thr Leu Ser Val Asp Asp Lys Gly Ala Leu Asn Val Gly Ser
465                 470                 475                 480

Lys Asp Ala Asn Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val
                485                 490                 495

Lys Glu Gly Asp Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln
            500                 505                 510

Asn Leu Asn Asn Arg Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly
        515                 520                 525

Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro
    530                 535                 540

Gly Lys Ser Met Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala
545                 550                 555                 560

Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile
                565                 570                 575

Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser
            580                 585                 590

Ala Ser Val Gly Tyr Gln Trp
        595


<210> SEQ ID NO 101
<211> LENGTH: 598
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 101

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
     50                  55                  60

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

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

Arg Val Leu Lys Ala Gly Ala Ile Thr Leu Lys Ala Gly Asp Asn Leu
            100                 105                 110

Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Glu Asn Thr Asn Asp
        115                 120                 125

Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser
    130                 135                 140

Val Glu Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Asn Lys Val Asn
145                 150                 155                 160

Ile Thr Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly
                165                 170                 175
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Thr Asn Gly Asp Pro Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu
            180                 185                 190

Thr Asp Thr Leu Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp
        195                 200                 205

Asn Val Thr Asp Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val
    210                 215                 220

Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala
225                 230                 235                 240

Ser Asp Asn Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu
                245                 250                 255

Ser Ala Asp Thr Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn
            260                 265                 270

Gly Lys Lys Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys
        275                 280                 285

Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Asp Glu Asn Gly
    290                 295                 300

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

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

Gly Gln Thr Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr
            340                 345                 350

Lys Val Thr Phe Ala Ser Gly Asn Gly Thr Thr Ala Thr Val Ser Lys
        355                 360                 365

Asp Asp Gln Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp
    370                 375                 380

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

Lys Ala Val Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser
                405                 410                 415

Pro Ser Lys Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn
            420                 425                 430

Asn Ile Glu Ile Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser
        435                 440                 445

Met Thr Pro Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala
    450                 455                 460

Pro Thr Leu Ser Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys
465                 470                 475                 480

Asp Ala Asn Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys
                485                 490                 495

Glu Gly Asp Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn
            500                 505                 510

Leu Asn Asn Arg Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile
        515                 520                 525

Ala Gln Ala Ile Ala Thr Ala Gly Leu Ala Gln Ala Tyr Leu Pro Gly
    530                 535                 540

Lys Ser Met Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly
545                 550                 555                 560

Tyr Ala Ile Gly Tyr Ser Ser Ile Ser Asp Thr Gly Asn Trp Val Ile
                565                 570                 575
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```
Lys Gly Thr Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala
            580                 585                 590

Ser Val Gly Tyr Gln Trp
        595
```

<210> SEQ ID NO 102
<211> LENGTH: 594
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 102

```
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
     50                  55                  60

Thr Ala Pro Val Leu Ser Phe His Ala Asp Ser Glu Gly Thr Gly Glu
 65                  70                  75                  80

Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys
                 85                  90                  95

Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu
            100                 105                 110

Lys Ile Lys Gln Asn Thr Asp Glu Asn Thr Asn Ala Ser Ser Phe Thr
        115                 120                 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
    130                 135                 140

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

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
                165                 170                 175

Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
            180                 185                 190

Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
        195                 200                 205

Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
    210                 215                 220

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

Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
                245                 250                 255

Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
            260                 265                 270

Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
        275                 280                 285

Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp
    290                 295                 300

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

Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
                325                 330                 335
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```
Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe
            340                 345                 350

Ala Ser Gly Asn Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
        355                 360                 365

Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
    370                 375                 380

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

Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
                405                 410                 415

Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
            420                 425                 430

Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln
        435                 440                 445

Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
    450                 455                 460

Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
465                 470                 475                 480

Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
                485                 490                 495

Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
            500                 505                 510

Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
        515                 520                 525

Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
    530                 535                 540

Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545                 550                 555                 560

Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
                565                 570                 575

Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
            580                 585                 590

Gln Trp


<210> SEQ ID NO 103
<211> LENGTH: 591
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 103

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
     50                  55                  60

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

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
                 85                  90                  95
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```
Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
            100                 105                 110

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

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
    130                 135                 140

Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn His
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465                 470                 475                 480

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
                485                 490                 495
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```
Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
            500                 505                 510

Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
        515                 520                 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
    530                 535                 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
545                 550                 555                 560

Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
                565                 570                 575

Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 104
<211> LENGTH: 591
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 104

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
     50                  55                  60

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

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
                85                  90                  95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
            100                 105                 110

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

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
    130                 135                 140

Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270
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Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465                 470                 475                 480

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
                485                 490                 495

Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
            500                 505                 510

Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
        515                 520                 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
    530                 535                 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
545                 550                 555                 560

Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
                565                 570                 575

Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 105
<211> LENGTH: 591
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 105

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
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         35                  40                  45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
     50                  55                  60

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

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
                85                  90                  95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
            100                 105                 110

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

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
    130                 135                 140

Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445
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```
Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465                 470                 475                 480

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
                485                 490                 495

Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
            500                 505                 510

Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
        515                 520                 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
    530                 535                 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
545                 550                 555                 560

Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
                565                 570                 575

Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 106
<211> LENGTH: 592
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 106

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
     50                  55                  60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65                  70                  75                  80

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

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

Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
        115                 120                 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
    130                 135                 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

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

Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr
        195                 200                 205

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
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```
    210                 215                 220

Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
465                 470                 475                 480

Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
                485                 490                 495

Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
            500                 505                 510

Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
        515                 520                 525

Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
    530                 535                 540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545                 550                 555                 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
                565                 570                 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590
```

<210> SEQ ID NO 107
<211> LENGTH: 592
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

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<400> SEQUENCE: 107

```
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
     50                  55                  60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65                  70                  75                  80

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

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

Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
        115                 120                 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
    130                 135                 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

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

Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr
        195                 200                 205

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
    210                 215                 220

Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
465                 470                 475                 480

Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
                485                 490                 495

Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
            500                 505                 510

Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
        515                 520                 525

Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
    530                 535                 540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545                 550                 555                 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
                565                 570                 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 108
<211> LENGTH: 589
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 108

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Thr Asp Glu Asp Glu Glu Leu Glu Ser Val Val
     50                  55                  60

Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
 65                  70                  75                  80

Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp
                 85                  90                  95

His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
            100                 105                 110

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

Glu Leu Lys Asp Leu Thr Ser Val Glu Thr Glu Lys Leu Ser Phe Gly
    130                 135                 140

Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys Gly Leu Asn
145                 150                 155                 160
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Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Pro Thr Val His Leu
                165                 170                 175

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

Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr Arg Ala Ala
        195                 200                 205

Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys
    210                 215                 220

Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr
225                 230                 235                 240

Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr Thr Thr Val
                245                 250                 255

Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly
            260                 265                 270

Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly
        275                 280                 285

Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu
    290                 295                 300

Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala Gly Trp Arg
305                 310                 315                 320

Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe
                325                 330                 335

Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe Ala Ser Gly Asn Gly
            340                 345                 350

Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile Thr Val Lys
        355                 360                 365

Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln Leu Gln Asn
    370                 375                 380

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

Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met Asp Glu Thr
                405                 410                 415

Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys
            420                 425                 430

Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser Ser Val Ser
        435                 440                 445

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

Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val Arg Ile Thr
465                 470                 475                 480

Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val Ala Gln
                485                 490                 495

Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn Val Asp
            500                 505                 510

Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu
        515                 520                 525

Ala Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly Gly Gly
    530                 535                 540

Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser
545                 550                 555                 560

Asp Thr Gly Asn Trp Val Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg
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               565                 570                 575

Gly His Phe Gly Thr Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585


<210> SEQ ID NO 109
<211> LENGTH: 589
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 109

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Thr Asp Glu Asp Glu Glu Leu Glu Ser Val Val
     50                  55                  60

Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
 65                  70                  75                  80

Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp
                 85                  90                  95

His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
            100                 105                 110

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

Glu Leu Lys Asp Leu Thr Ser Val Glu Thr Glu Lys Leu Ser Phe Gly
    130                 135                 140

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

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

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

Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr Arg Ala Ala
        195                 200                 205

Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys
    210                 215                 220

Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr
225                 230                 235                 240

Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr Thr Thr Val
                245                 250                 255

Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly
            260                 265                 270

Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly
        275                 280                 285

Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu
    290                 295                 300

Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala Gly Trp Arg
305                 310                 315                 320

Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe
                325                 330                 335
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Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe Ala Ser Gly Asn Gly
            340                 345                 350

Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile Thr Val Lys
        355                 360                 365

Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln Leu Gln Asn
    370                 375                 380

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

Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met Asp Glu Thr
                405                 410                 415

Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys
            420                 425                 430

Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser Ser Val Ser
        435                 440                 445

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

Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val Arg Ile Thr
465                 470                 475                 480

Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val Ala Gln
                485                 490                 495

Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn Val Asp
            500                 505                 510

Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu
        515                 520                 525

Ala Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly Gly Gly
    530                 535                 540

Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser
545                 550                 555                 560

Asp Thr Gly Asn Trp Val Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg
                565                 570                 575

Gly His Phe Gly Thr Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585


<210> SEQ ID NO 110
<211> LENGTH: 592
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 110

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
     50                  55                  60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65                  70                  75                  80

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

Asp Pro Tyr Ile Val Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile
            100                 105                 110
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Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
        115                 120                 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
    130                 135                 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
145                 150                 155                 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
                165                 170                 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Met Leu Leu Asn
            180                 185                 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
        195                 200                 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
    210                 215                 220

Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225                 230                 235                 240

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
                245                 250                 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
            260                 265                 270

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
        275                 280                 285

Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
    290                 295                 300

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

Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
                325                 330                 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
            340                 345                 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
        355                 360                 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
    370                 375                 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
                405                 410                 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
            420                 425                 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
        435                 440                 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
    450                 455                 460

Asp Lys Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
465                 470                 475                 480

Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
                485                 490                 495

Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
            500                 505                 510
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Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
        515                 520                 525

Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
    530                 535                 540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545                 550                 555                 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
                565                 570                 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
            580                 585                 590


<210> SEQ ID NO 111
<211> LENGTH: 600
<212> TYPE: PRT
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 111

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ile Ala Leu Asn Ala Trp
  1               5                  10                  15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
             20                  25                  30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Gln
         35                  40                  45

Ala Asn Ala Thr Asp Glu Glu Asp Asn Glu Asp Leu Glu Pro Val Val
     50                  55                  60

Arg Thr Ala Pro Val Leu Ser Phe His Ser Asp Lys Glu Gly Thr Gly
 65                  70                  75                  80

Glu Lys Glu Glu Val Gly Ala Ser Ser Asn Leu Thr Val Tyr Phe Asp
                 85                  90                  95

Lys Asn Arg Val Leu Lys Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp
            100                 105                 110

Asn Leu Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Glu Asn Thr
        115                 120                 125

Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Gly Leu
    130                 135                 140

Ile Asn Val Glu Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Lys Lys
145                 150                 155                 160

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

Ala Gly Thr Asn Gly Asp Pro Thr Val His Leu Asn Gly Ile Gly Ser
            180                 185                 190

Thr Leu Thr Asp Thr Leu Ala Gly Ser Ser Ala Ser His Val Asp Ala
        195                 200                 205

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

Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Thr Gly Ser Thr Thr
225                 230                 235                 240

Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu
                245                 250                 255

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

Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val
        275                 280                 285
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Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu
    290                 295                 300

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

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

Ala Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser
            340                 345                 350

Gly Thr Lys Val Thr Phe Ala Ser Gly Asn Gly Thr Thr Ala Thr Val
        355                 360                 365

Ser Lys Asp Asp Gln Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val
    370                 375                 380

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

Asp Ser Lys Ala Val Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn
                405                 410                 415

Val Ser Pro Ser Lys Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala
            420                 425                 430

Gly Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala
        435                 440                 445

Thr Ser Met Thr Pro Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala
    450                 455                 460

Asp Ala Pro Thr Leu Ser Val Asp Asp Glu Gly Ala Leu Asn Val Gly
465                 470                 475                 480

Ser Lys Asp Ala Asn Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly
                485                 490                 495

Val Lys Glu Gly Asp Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala
            500                 505                 510

Gln Asn Leu Asn Asn Arg Ile Asp Asn Val Asp Gly Asn Ala Arg Ala
        515                 520                 525

Gly Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu
    530                 535                 540

Pro Gly Lys Ser Met Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu
545                 550                 555                 560

Ala Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp
                565                 570                 575

Ile Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala
            580                 585                 590

Ser Ala Ser Val Gly Tyr Gln Trp
        595                 600


<210> SEQ ID NO 112
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 112

cgcggatccc atatgtcgcc gcaaaattcc ga                                  32


<210> SEQ ID NO 113
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis
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<400> SEQUENCE: 113

cccgctcgag ttttgccgcg ttaaaagc 28

<210> SEQ ID NO 114
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 114

cgcggatccc atatgaccgt gaagaccgcc 30

<210> SEQ ID NO 115
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 115

cccgctcgag ccactgataa ccgacaga 28

<210> SEQ ID NO 116
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 116

cgcggatccc atatgtattt gaaacagctc caag 34

<210> SEQ ID NO 117
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 117

cccgctcgag ttctgggtga atgtta 26

<210> SEQ ID NO 118
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 118

gcggatccca tatgggcacg gacaacccc 29

<210> SEQ ID NO 119
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 119

cccgctcgag acgtggggaa cagtct 26

<210> SEQ ID NO 120
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 120

gcggatccca tatgaaaaat attcaagtag ttgc 34

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<210> SEQ ID NO 121
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 121

cccgctcgag aagtttgatt aaacccg 27

<210> SEQ ID NO 122
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 122

cgcggatccc atatgtgcca accgcaatcc g 31

<210> SEQ ID NO 123
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 123

cccgctcgag tttttccagc tccggca 27

<210> SEQ ID NO 124
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 124

gcggatccca tatggttatc ggaatattac tcg 33

<210> SEQ ID NO 125
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 125

cccgctcgag ggctgcagaa gctgg 25

<210> SEQ ID NO 126
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 126

cgcggatccc atatgcggac gtggttggtt tt 32

<210> SEQ ID NO 127
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 127

cccgctcgag atatcttccg tttttttcac 30

<210> SEQ ID NO 128
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 128

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cgcggatccg ctagcgtaaa tttattattt ttagaa 36

<210> SEQ ID NO 129
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 129

cccgctcgag ttccaactca ttgaagta 28

<210> SEQ ID NO 130
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 130

cgcggatccc atatgaataa aggtttacat cgcat 35

<210> SEQ ID NO 131
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 131

cccgctcgag aatcgctgca ccggct 26

<210> SEQ ID NO 132
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 132

cgcggatccc atatgactgc cttttcgaca 30

<210> SEQ ID NO 133
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 133

cccgctcgag gcgtgaagcg tcagga 26

<210> SEQ ID NO 134
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: BamHI - NdeI

<400> SEQUENCE: 134

cgcggatccc atatg 15

<210> SEQ ID NO 135
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: BamHI - NheI

<400> SEQUENCE: 135

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cgcggatccg ctagc 15

<210> SEQ ID NO 136
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: EcoRI - NheI

<400> SEQUENCE: 136

ccggaattct agctagc 17

<210> SEQ ID NO 137
<211> LENGTH: 10
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: XhoI

<400> SEQUENCE: 137

cccgctcgag 10

<210> SEQ ID NO 138
<211> LENGTH: 291
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF40a
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (6)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (130)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (193)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (218)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (245)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 138

Ser Ala Leu Asn Ala Xaa Val Ala Val Ser Glu Leu Thr Arg Asn His
1 5 10 15

Thr Lys Arg Ala Ser Ala Thr Val Lys Thr Ala Val Leu Ala Thr Leu
20 25 30

Leu Phe Ala Thr Val Gln Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu
35 40 45

Glu Leu Glu Ser Val Gln Arg Ser Val Val Gly Ser Ile Gln Ala Ser
50 55 60

Met Glu Gly Ser Gly Glu Leu Glu Thr Ile Ser Leu Ser Met Thr Asn
65 70 75 80

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

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```
Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala
            100                 105                 110

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

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

Ile Ile Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly
145                 150                 155                 160

Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu
                165                 170                 175

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

Xaa Ser Thr His Tyr Thr Arg Ala Ala Ser Ile Lys Asp Val Leu Asn
        195                 200                 205

Ala Gly Trp Asn Ile Lys Gly Val Lys Xaa Gly Ser Thr Thr Gly Gln
    210                 215                 220

Ser Glu Asn Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu
225                 230                 235                 240

Ser Ala Asp Thr Xaa Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn
                245                 250                 255

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

Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu Asn Gly
        275                 280                 285

Ser Ser Thr
    290
```

<210> SEQ ID NO 139
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 139

```
Thr Leu Leu Phe Ala Thr Val Gln Ala Asn Ala Thr Asp Glu Asp Glu
  1               5                  10                  15

Glu Leu Asp Pro Val Val Arg Thr Ala Pro Val Leu Ser Phe His Ser
             20                  25                  30

Asp Lys Glu Gly Thr Gly Glu Lys Glu Val Thr Glu Asn Ser Asn Trp
         35                  40                  45

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

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

Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp
                 85                  90                  95

Leu Thr Ser Val Ala Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Asp
            100                 105                 110

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

Gly Asn Gly Asn Val His Leu Asn Gly Leu Asp Ser Thr Leu Pro Asp
    130                 135                 140
```

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```
Ala Val Thr Asn Thr Gly Val Leu Ser Ser Ser Ser Phe Thr Pro Asn
145                 150                 155                 160

Asp Val Glu Lys Thr Arg Ala Ala Thr Val Lys Asp Val Leu Asn Ala
                165                 170                 175

Gly Trp Asn Ile Lys Gly Ala Lys Thr Ala Gly Gly Asn Val Glu Ser
            180                 185                 190

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

Lys Asn Thr Leu Asp Val Val Leu Thr Ala Lys Glu Asn Gly Lys Thr
    210                 215                 220

Thr Glu Val Lys Phe Thr Pro Lys Thr Ser Val Ile Lys Glu Lys Asp
225                 230                 235                 240


<210> SEQ ID NO 140
<211> LENGTH: 251
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: overlap
      identity
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (10)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (12)..(13)
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<400> SEQUENCE: 140

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Thr Leu Leu Phe Ala Thr Val Gln Ala Xaa Ala Xaa Xaa Glu Xaa Xaa
  1               5                  10                  15

Glu Xaa Xaa Xaa Xaa Leu Asp Pro Val Xaa Arg Thr Xaa Xaa Val Leu
             20                  25                  30

Xaa Xaa Xaa Ser Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
         35                  40                  45

Xaa Asn Ser Xaa Trp Xaa Xaa Tyr Phe Xaa Xaa Lys Gly Val Leu Xaa
     50                  55                  60

Ala Xaa Xaa Ile Thr Xaa Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln
 65                  70                  75                  80

Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Thr Tyr Ser Leu Lys
                 85                  90                  95

Lys Asp Leu Thr Asp Leu Thr Ser Val Xaa Thr Glu Lys Leu Ser Phe
            100                 105                 110

Xaa Ala Asn Gly Xaa Lys Val Xaa Ile Thr Ser Asp Xaa Xaa Gly Leu
        115                 120                 125

Xaa Xaa Ala Lys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Val His
    130                 135                 140

Leu Asn Gly Xaa Xaa Ser Thr Leu Xaa Asp Xaa Xaa Xaa Asn Thr Gly
145                 150                 155                 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Lys Xaa
                165                 170                 175

Arg Ala Ala Xaa Val Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
            180                 185                 190
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```
Gly Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asp Xaa Val Xaa
        195                 200                 205

Xaa Tyr Xaa Xaa Val Glu Phe Xaa Xaa Xaa Asp Xaa Xaa Thr Xaa Xaa
    210                 215                 220

Val Xaa Xaa Xaa Xaa Lys Xaa Asn Gly Lys Xaa Thr Glu Val Lys Xaa
225                 230                 235                 240

Xaa Xaa Lys Thr Ser Val Ile Lys Glu Lys Asp
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<210> SEQ ID NO 141
<211> LENGTH: 36
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF40a

<400> SEQUENCE: 141

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Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
  1               5                  10                  15

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
             20                  25                  30

Ala Asn Ala Thr
         35
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<210> SEQ ID NO 142
<211> LENGTH: 36
<212> TYPE: PRT
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<220> FEATURE:
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<222> LOCATION: (19)
<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 142

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Val Xaa Val Ser Glu Leu Thr Arg Xaa His Thr Lys Arg Ala Ser Ala
  1               5                  10                  15

Thr Val Xaa Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
             20                  25                  30

Ala Asn Ala Thr
         35
```

<210> SEQ ID NO 143
<211> LENGTH: 36
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 143

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Val Val Val Ser Glu Leu Thr Arg Thr His Thr Lys Arg Ala Ser Ala
  1               5                  10                  15
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Thr Val Glu Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
20 25 30

Ala Asn Ala Thr
35

<210> SEQ ID NO 144
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Orf40a

<400> SEQUENCE: 144

Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asn
1 5 10 15

Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu
20 25 30

Thr Gly Leu Ile Asn Val
35

<210> SEQ ID NO 145
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: homology
<220> FEATURE:
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<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 145

Xaa Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Xaa
1 5 10 15

Glu Xaa Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu
20 25 30

Thr Xaa Leu Xaa Xaa Val
35

<210> SEQ ID NO 146
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 146

Ile Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asp
1 5 10 15

-continued

Glu Ser Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu
20 25 30

Thr Asp Leu Thr Ser Val
35

<210> SEQ ID NO 147
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Orf40a

<400> SEQUENCE: 147

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

Ile Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr
20 25

<210> SEQ ID NO 148
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: homology
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<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: absent or positive
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<223> OTHER INFORMATION: absent or positive
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<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 148

Val Xaa Xaa Lys Leu Ser Xaa Gly Xaa Asn Gly Xaa Lys Val Asn Ile
1 5 10 15

Xaa Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Xaa Xaa
20 25

<210> SEQ ID NO 149
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 149

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

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Thr Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Asp Ser
20 25

<210> SEQ ID NO 150
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF40a

<400> SEQUENCE: 150

Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu
1 5 10 15

Thr Asp Thr Leu Ala Gly Ser Ser Ala Ser His Val Asp Ala Gly Asn
20 25 30

<210> SEQ ID NO 151
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: absent or positive
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<223> OTHER INFORMATION: absent or positive
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<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 151

Thr Xaa Xaa Asp Xaa Xaa Xaa His Leu Asn Gly Ile Xaa Ser Thr Leu
1 5 10 15

Thr Asp Thr Leu Xaa Xaa Ser Xaa Ala Xaa Xaa Xaa Xaa Xaa Gly Asn
20 25 30

<210> SEQ ID NO 152
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 152

Thr Gly Asp Asp Ala Asn Ile His Leu Asn Gly Ile Ala Ser Thr Leu
1 5 10 15

Thr Asp Thr Leu Leu Asn Ser Gly Ala Thr Thr Asn Leu Gly Gly Asn
20 25 30

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<210> SEQ ID NO 153
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF40a

<400> SEQUENCE: 153

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

Gly Val Lys

<210> SEQ ID NO 154
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: homology
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<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 154

Arg Ala Ala Ser Xaa Lys Asp Val Leu Asn Ala Gly Trp Asn Xaa Xaa
1 5 10 15

Gly Val Lys

<210> SEQ ID NO 155
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 155

Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn Val Arg
1 5 10 15

Gly Val Lys

<210> SEQ ID NO 156
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF40a

<400> SEQUENCE: 156

Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr Tyr Asp
1 5 10 15

Thr Val Glu Phe Leu Ser Ala Asp Thr Thr Thr Thr
20 25

<210> SEQ ID NO 157
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: homology
<220> FEATURE:

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<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive
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<222> LOCATION: (25)..(26)
<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 157

Ser Xaa Xaa Xaa Gln Xaa Glu Asn Xaa Asp Phe Val Xaa Thr Tyr Asp
1 5 10 15

Thr Val Xaa Phe Xaa Ser Xaa Asp Xaa Xaa Thr Thr
20 25

<210> SEQ ID NO 158
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Hsf

<400> SEQUENCE: 158

Ser Ala Asn Asn Gln Val Glu Asn Ile Asp Phe Val Ala Thr Tyr Asp
1 5 10 15

Thr Val Asp Phe Val Ser Gly Asp Lys Asp Thr Thr
20 25

<210> SEQ ID NO 159
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF38a

<400> SEQUENCE: 159

Met Leu Arg Leu Thr Ala Leu Ala Val Cys Thr Ala Leu Ala Leu Gly
1 5 10 15

Ala Cys Ser Pro Gln Asn Ser Asp Ser Ala Pro Gln Ala Lys Glu Gln
20 25 30

Ala Val Ser Ala Ala Gln Ser Glu Gly Val Ser Val Thr Val Lys Thr
35 40 45

Ala Arg Gly Asp Val Gln Ile Pro Gln Asn Pro Glu Arg Ile Ala Val

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     50                  55                  60

Tyr Asp Leu Gly Met Leu Asp Thr Leu Ser Lys Leu Gly Val Lys Thr
 65                  70                  75                  80

Gly Leu Ser Val Asp Lys Asn Arg Leu Pro Tyr Leu Glu Glu Tyr Phe
                 85                  90                  95

Lys Thr Thr Lys Pro Ala Gly Thr Leu Phe Glu Pro Asp Tyr Glu Thr
            100                 105                 110

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

Lys Ala Phe Asp Lys Leu Asn Glu Ile Ala Pro Thr Ile Glu Met Thr
    130                 135                 140

Ala Asp Thr Ala Asn Leu Lys Glu Ser Ala Lys Glu Arg Ile Asp Ala
145                 150                 155                 160

Leu Ala Gln Ile Phe Gly Lys Lys Ala Glu Ala Asp Lys Leu Lys Ala
                165                 170                 175

Glu Ile Asp Ala Ser Phe Glu Ala Ala Lys Thr Ala Ala Gln Gly Lys
            180                 185                 190

Gly Lys Gly Leu Val Ile Leu Val Asn Gly Gly Lys Met Ser Ala Phe
        195                 200                 205

Gly Pro Ser Ser Arg Leu Gly Gly Trp Leu His Lys Asp Ile Gly Val
    210                 215                 220

Pro Ala Val Asp Glu Ala Ile Lys Glu Gly Ser His Gly Gln Pro Ile
225                 230                 235                 240


<210> SEQ ID NO 160
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF38

<400> SEQUENCE: 160

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

Pro Gln Asn Pro Glu Arg Ile Ala Val Tyr Asp Leu Gly Met Leu Asp
             20                  25                  30

Thr Leu Ser Lys Leu Gly Val Lys Thr Gly Leu Ser Val Asp Lys Asn
         35                  40                  45

Arg Leu Pro Tyr Leu Glu Glu Tyr Phe Lys Thr Thr Lys Pro Ala Gly
     50                  55                  60

Thr Leu Phe Glu Pro Asp Tyr Glu Thr Leu Asn Ala Tyr Lys Pro Gln
 65                  70                  75                  80

Leu Ile Ile Ile Gly Ser Arg Ala Ala Lys Ala Phe Asp Lys
                 85                  90


<210> SEQ ID NO 161
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: overlap
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<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive
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<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive

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<400> SEQUENCE: 161

Glu Gly Xaa Ser Xaa Xaa Val Lys Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
1 5 10 15

Pro Xaa Asn Pro Xaa Xaa Xaa Xaa Xaa Xaa Asp Leu Gly Xaa Leu Asp
20 25 30

Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa
35 40 45

Xaa Xaa Leu Pro Xaa Xaa Xaa Xaa Xaa Phe Lys Xaa Xaa Xaa Xaa Xaa
50 55 60

Gly Xaa Xaa Xaa Xaa Xaa Asp Xaa Glu Xaa Xaa Asn Ala Xaa Lys Pro
65 70 75 80

Xaa Leu Ile Ile Ile Xaa Xaa Arg Xaa Xaa Lys Xaa Xaa Asp Lys Leu
85 90 95

<210> SEQ ID NO 162
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Lipo

<400> SEQUENCE: 162

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

Pro Lys Asn Pro Ser Lys Val Val Ile Leu Asp Leu Gly Ile Leu Asp
20 25 30

Thr Phe Asp Ala Leu Lys Leu Asn Asp Lys Val Ala Gly Val Pro Ala
35 40 45

Lys Asn Leu Pro Lys Tyr Leu Gln Gln Phe Lys Asn Lys Pro Ser Val
50 55 60

Gly Gly Val Gln Gln Val Asp Phe Glu Ala Ile Asn Ala Leu Lys Pro
65 70 75 80

Asp Leu Ile Ile Ile Ser Gly Arg Gln Ser Lys Phe Tyr Asp Lys Leu
85 90 95

<210> SEQ ID NO 163
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF44

<400> SEQUENCE: 163

Thr Val Ser Tyr Val Cys Gln Gln Gly Lys Lys Val Lys Val Thr Tyr
1 5 10 15

Gly Phe Asn Lys Gln Gly Leu Thr Thr Tyr Ala Ser Ala Val Ile Asn
20 25 30

Gly Lys Arg Val Gln Met Pro Val Asn Leu Asp Lys Ser Asp Asn Val
35 40 45

Glu Thr Phe Tyr Gly Lys Glu Gly Gly Tyr Val Leu Gly Thr Gly Val
50 55 60

Met Asp Gly Lys Ser Tyr Arg Lys Gln Pro Ile Met Ile Thr Ala Pro
65 70 75 80

Asp Asn Gln Ile Val Phe Lys Asp Cys Ser Pro
85 90

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<210> SEQ ID NO 164
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: overlap identity
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (1)
<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
<222> LOCATION: (3)
<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
<222> LOCATION: (10)..(13)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
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<222> LOCATION: (15)
<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
<222> LOCATION: (17)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
<222> LOCATION: (23)..(24)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
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<222> LOCATION: (26)
<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
<222> LOCATION: (33)..(38)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (40)
<223> OTHER INFORMATION: absent or positive
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<222> LOCATION: (43)..(44)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (49)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (51)..(56)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (59)
<223> OTHER INFORMATION: absent or positive
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<222> LOCATION: (61)
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<223> OTHER INFORMATION: absent or positive

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<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (67)..(69)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (72)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (74)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (76)..(78)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (81)..(82)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (84)..(86)
<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 164

Xaa Val Xaa Tyr Val Cys Gln Gln Gly Xaa Xaa Xaa Xaa Val Xaa Tyr
1 5 10 15

Xaa Phe Asn Xaa Xaa Gly Xaa Xaa Thr Xaa Ala Xaa Xaa Xaa Xaa Asn
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asn Leu Xaa Xaa Ser Asp Asn Val
35 40 45

Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr Xaa Leu Xaa Thr Xaa Xaa
50 55 60

Met Asp Xaa Xaa Xaa Tyr Arg Xaa Gln Xaa Ile Xaa Xaa Xaa Ala Pro
65 70 75 80

Xaa Xaa Gln Xaa Xaa Xaa Lys Asp Cys Ser Pro
85 90

<210> SEQ ID NO 165
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: LecA

<400> SEQUENCE: 165

Ser Val Ala Tyr Val Cys Gln Gln Gly Arg Arg Leu Asn Val Asn Tyr
1 5 10 15

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

Asn Arg Asn Leu Arg Leu Pro Tyr Asn Leu Ser Ala Ser Asp Asn Val
35 40 45

Asp Thr Val Phe Ser Ala Asn Gly Tyr Arg Leu Thr Thr Asn Ala Met
50 55 60

Asp Ser Ala Asn Tyr Arg Ser Gln Asp Ile Ile Val Ser Ala Pro Asn
65 70 75 80

Gly Gln Met Leu Tyr Lys Asp Cys Ser Pro
85 90

<210> SEQ ID NO 166
<211> LENGTH: 240

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF49a
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (18)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (48)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (195)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 166

Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val Arg Val Val Ala
1 5 10 15

Gln Xaa Ala Ala Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr
20 25 30

Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln Ala Gly Val Xaa
35 40 45

Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys Gly Ile Val Asn
50 55 60

Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser Thr Val Trp Gln
65 70 75 80

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

Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro Gly Gly Tyr Ile
100 105 110

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

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

Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys
145 150 155 160

Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
165 170 175

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

Gly Ala Xaa Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
195 200 205

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

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

<210> SEQ ID NO 167
<211> LENGTH: 540
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF49a
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (1)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:

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<221> NAME/KEY: SITE
<222> LOCATION: (29)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (50)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (80)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (227)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (288)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (324)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (446)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (463)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 167

Xaa Gln Leu Leu Ala Glu Glu Gly Ile His Lys His Glu Leu Asp Val
  1   5   10   15

Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly Xaa Ser Asn Tyr
             20   25   30

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

Gln Xaa Ala Ala Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr
     50   55   60

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

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

Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser Thr Val Trp Gln
            100   105   110

Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu Lys Leu Pro Ser
        115   120   125

Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro Gly Gly Tyr Ile
    130   135   140

Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ser
145   150   155   160

Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn
                165   170   175

Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys
            180   185   190

Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
        195   200   205

Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn
    210   215   220

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Gly Ala Xaa Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
225                 230                 235                 240

Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp Val Gly Lys Thr
                245                 250                 255

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

Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu Xaa
        275                 280                 285

Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu Ala
    290                 295                 300

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

Leu Lys Asp Xaa Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn Thr
                325                 330                 335

Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His Tyr
            340                 345                 350

Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala Ala
        355                 360                 365

Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val Gly
    370                 375                 380

Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn Pro Asp Thr Leu
385                 390                 395                 400

Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser Lys Leu Val Ala
                405                 410                 415

Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn Ala Ala Ala Asn
            420                 425                 430

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

Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys Gln Asn Xaa Pro
    450                 455                 460

Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln Asn Val Ala Asp
465                 470                 475                 480

Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp Ile Ser Arg Ser
                485                 490                 495

Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile Asp Ser Arg Ser
            500                 505                 510

Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys Asp Asp Glu Trp
        515                 520                 525

Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp
    530                 535                 540


<210> SEQ ID NO 168
<211> LENGTH: 540
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF49-1

<400> SEQUENCE: 168

Met Gln Leu Leu Ala Ala Glu Gly Ile His Gln His Gln Leu Asn Val
  1               5                  10                  15

Gln Lys Ser Thr Arg Phe Ile Gly Ile Lys Val Gly Lys Ser Asn Tyr
             20                  25                  30
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Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val Arg Val Ile Ala
         35                  40                  45

Gln Thr Ala Lys Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr
     50                  55                  60

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

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

Arg Ile Gln Thr Glu Glu Lys Leu Glu Ser Asn Ser Thr Val Trp Gln
            100                 105                 110

Lys Gln Ala Gly Ser Gly Ser Thr Val Glu Thr Leu Lys Leu Pro Ser
        115                 120                 125

Phe Glu Gly Pro Ala Leu Pro Lys Leu Thr Ala Pro Gly Gly Tyr Ile
    130                 135                 140

Ala Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ala
145                 150                 155                 160

Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Thr Val Lys Asp
                165                 170                 175

Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp Tyr Lys
            180                 185                 190

Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
        195                 200                 205

Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn
    210                 215                 220

Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
225                 230                 235                 240

Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asn Ile Gly Asn Thr
                245                 250                 255

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

Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu Asn
        275                 280                 285

Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu Ala
    290                 295                 300

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

Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn Thr
                325                 330                 335

Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His Tyr
            340                 345                 350

Ile Ala His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala Ala
        355                 360                 365

Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val Gly
    370                 375                 380

Glu Ile Leu Gly Glu Thr Leu Leu Asp Gly Arg Asp Pro Gly Ser Leu
385                 390                 395                 400

Asn Val Lys Asp Arg Ala Lys Ile Ile Ala Lys Ala Lys Leu Ala Ala
                405                 410                 415

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

Ala Ala Ala Val Ala Val Glu Asn Asn Ser Leu Asn Asp Ile Gln Asp
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        435                 440                 445

Arg Leu Leu Ser Gly Asn Tyr Ala Leu Cys Met Ser Ala Gly Gly Ala
    450                 455                 460

Glu Ser Phe Cys Glu Ser Tyr Arg Pro Leu Gly Leu Pro His Phe Val
465                 470                 475                 480

Ser Val Ser Gly Glu Met Lys Leu Pro Asn Lys Phe Gly Asn Arg Met
                485                 490                 495

Val Asn Gly Lys Leu Ile Ile Asn Thr Arg Asn Gly Asn Val Tyr Phe
            500                 505                 510

Ser Val Gly Lys Ile Trp Ser Thr Val Lys Ser Thr Lys Ser Asn Ile
        515                 520                 525

Ser Gly Val Ser Val Gly Trp Val Leu Asn Val Ser
    530                 535                 540


<210> SEQ ID NO 169
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF39
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (166)..(193)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 169

Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg
  1               5                  10                  15

Leu Phe Phe Glu Val Leu Val Val Ser Val Val Leu Gln Leu Phe Ala
             20                  25                  30

Leu Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
         35                  40                  45

His Arg Gly Phe Ser Thr Leu Asp Val Val Ser Val Ala Leu Leu Val
     50                  55                  60

Val Ser Leu Phe Glu Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe
 65                  70                  75                  80

Ala His Thr Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
                 85                  90                  95

Arg His Leu Leu Ser Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val
            100                 105                 110

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

Leu Thr Gly Gln Ala Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe
    130                 135                 140

Ile Phe Leu Ala Val Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val
145                 150                 155                 160

Val Leu Ala Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                165                 170                 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            180                 185                 190

Xaa Ile Cys Ala Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser
        195                 200                 205

Thr Val
    210
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<210> SEQ ID NO 170
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF39a

<400> SEQUENCE: 170

Ala Val Leu Ser Phe Ala Glu Phe Ser Asn Arg Tyr Ser Gly Lys Leu
1 5 10 15

Ile Leu Val Ala Ser Arg Ala Ser Val Leu Gly Ser Leu Ala Lys Phe
20 25 30

Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg Leu Phe
35 40 45

Phe Glu Val Leu Val Val Ser Val Val Leu Gln Leu Phe Ala Leu Ile
50 55 60

Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val His Arg
65 70 75 80

Gly Phe Ser Thr Leu Asp Val Val Ser Val Ala Leu Leu Val Val Ser
85 90 95

Leu Phe Glu Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe Ala His
100 105 110

Thr Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe Arg His
115 120 125

Leu Leu Ser Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val Gly Asp
130 135 140

Thr Val Ala Arg Val Arg Glu Leu Glu Gln Ile Arg Asn Phe Leu Thr
145 150 155 160

Gly Gln Ala Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe Ile Phe
165 170 175

Leu Ala Val Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val Val Leu
180 185 190

Ala Ser Leu Pro Ala Tyr Ala Phe Trp Ser Ala Phe Ile Ser Pro Ile
195 200 205

Leu Arg Thr Arg Leu Asn Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln
210 215 220

Ser Phe Leu Val Glu Ser Ile Thr Ala Val Gly Thr Val Lys Ala Met
225 230 235 240

<210> SEQ ID NO 171
<211> LENGTH: 690
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF39a
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (29)..(40)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (137)..(153)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (173)..(187)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 171

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Tyr His Gly Ile Ala Ala Asn Pro Ala Asp Ile Gln His Glu Phe Cys
  1               5                  10                  15

Thr Ser Ala Gln Ser Asp Leu Asn Glu Thr Gln Trp Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Val Arg Gln Pro Ile Lys Arg
         35                  40                  45

Leu Ala Met Ala Thr Leu Pro Ala Leu Val Trp Cys Asp Asp Gly Asn
     50                  55                  60

His Phe Ile Leu Ala Lys Thr Asp Gly Gly Gly Glu His Ala Gln Tyr
 65                  70                  75                  80

Leu Ile Gln Asp Leu Thr Thr Asn Lys Ser Ala Val Leu Ser Phe Ala
                85                  90                  95

Glu Phe Ser Asn Arg Tyr Ser Gly Lys Leu Ile Leu Val Ala Ser Arg
            100                 105                 110

Ala Ser Val Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
        115                 120                 125

Pro Ala Val Ile Lys Tyr Arg Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Thr Pro Leu Phe Phe Gln
145                 150                 155                 160

Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Xaa Xaa Xaa Xaa
                165                 170                 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Glu Ile Val Leu
            180                 185                 190

Gly Gly Leu Arg Thr Tyr Leu Phe Ala His Thr Thr Ser Arg Ile Asp
        195                 200                 205

Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ser Leu Pro Leu
    210                 215                 220

Ser Tyr Phe Glu His Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg
225                 230                 235                 240

Glu Leu Glu Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser
                245                 250                 255

Val Leu Asp Leu Ala Phe Ser Phe Ile Phe Leu Ala Val Met Trp Tyr
            260                 265                 270

Tyr Ser Ser Thr Leu Thr Trp Val Val Leu Ala Ser Leu Pro Ala Tyr
        275                 280                 285

Ala Phe Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn
    290                 295                 300

Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser
305                 310                 315                 320

Ile Thr Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met
                325                 330                 335

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

Arg Val Thr Lys Leu Ala Val Val Gly Gln Gln Gly Val Gln Leu Ile
        355                 360                 365

Gln Lys Leu Val Thr Val Ala Thr Leu Trp Ile Gly Ala Arg Leu Val
    370                 375                 380

Ile Glu Ser Lys Leu Thr Val Gly Gln Leu Ile Ala Phe Asn Met Leu
385                 390                 395                 400
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Ser Gly Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln
                405                 410                 415

Asp Phe Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly Asp Ile Leu
            420                 425                 430

Asn Ala Pro Thr Glu Asn Ala Ser Ser His Leu Ala Leu Pro Asp Ile
        435                 440                 445

Arg Gly Glu Ile Thr Phe Glu His Val Asp Phe Arg Tyr Lys Ala Asp
    450                 455                 460

Gly Arg Leu Ile Leu Gln Asp Leu Asn Leu Arg Ile Arg Ala Gly Glu
465                 470                 475                 480

Val Leu Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr
                485                 490                 495

Lys Leu Val Gln Arg Leu Tyr Val Pro Ala Gln Gly Arg Val Leu Val
            500                 505                 510

Asp Gly Asn Asp Leu Ala Leu Ala Ala Pro Ala Trp Leu Arg Arg Gln
        515                 520                 525

Val Gly Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg Ser Ile Arg
    530                 535                 540

Asp Asn Ile Ala Leu Thr Asp Thr Gly Met Pro Leu Glu Arg Ile Ile
545                 550                 555                 560

Glu Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Met Glu Leu Pro
                565                 570                 575

Glu Gly Tyr Gly Thr Val Val Gly Glu Gln Gly Ala Gly Leu Ser Gly
            580                 585                 590

Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile Thr Asn Pro
        595                 600                 605

Arg Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser
    610                 615                 620

Glu Arg Ala Ile Met Gln Asn Met Gln Ala Ile Cys Ala Asn Arg Thr
625                 630                 635                 640

Val Leu Ile Ile Ala His Arg Leu Ser Thr Val Lys Thr Ala His Arg
                645                 650                 655

Ile Ile Ala Met Asp Lys Gly Arg Ile Val Glu Ala Gly Thr Gln Gln
            660                 665                 670

Glu Leu Leu Ala Lys Pro Asn Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu
        675                 680                 685

Gln Asn
    690


<210> SEQ ID NO 172
<211> LENGTH: 690
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: homology
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (3)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (6)
<223> OTHER INFORMATION: absent or positive
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (9)..(12)
<223> OTHER INFORMATION: absent or positive
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<220> FEATURE:
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Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Thr Xaa Trp Xaa Xaa Xaa Xaa
             20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Ile Xaa Arg
         35                  40                  45

Leu Ala Xaa Xaa Xaa Leu Pro Ala Leu Val Trp Xaa Xaa Asp Gly Xaa
     50                  55                  60

His Phe Ile Leu Xaa Lys Xaa Asp Xaa Xaa Xaa Glu Xaa Xaa Xaa Tyr
 65                  70                  75                  80

Leu Ile Xaa Asp Leu Xaa Thr Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Ala
                 85                  90                  95

Glu Phe Xaa Xaa Xaa Tyr Xaa Gly Lys Leu Ile Leu Val Ala Ser Arg
            100                 105                 110

Ala Ser Xaa Xaa Gly Xaa Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
        115                 120                 125

Pro Ala Val Ile Lys Tyr Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Thr Pro Leu Phe Phe Gln
145                 150                 155                 160

Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Xaa Xaa Xaa Xaa
                165                 170                 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Glu Ile Val Leu
            180                 185                 190

Xaa Gly Leu Arg Thr Tyr Xaa Phe Ala His Xaa Thr Ser Arg Ile Asp
        195                 200                 205

Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Xaa Leu Pro Xaa
    210                 215                 220

Ser Tyr Phe Glu Xaa Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg
225                 230                 235                 240

Glu Leu Xaa Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser
                245                 250                 255

Val Leu Asp Leu Xaa Phe Ser Phe Ile Phe Xaa Ala Val Met Trp Tyr
            260                 265                 270

Tyr Ser Xaa Xaa Leu Thr Xaa Val Xaa Leu Xaa Ser Leu Pro Xaa Tyr
        275                 280                 285

Xaa Xaa Trp Ser Xaa Phe Ile Ser Pro Ile Leu Arg Xaa Arg Leu Xaa
    290                 295                 300

Xaa Lys Phe Ala Arg Xaa Ala Asp Asn Gln Ser Phe Leu Val Glu Ser
305                 310                 315                 320

Xaa Thr Ala Xaa Xaa Thr Xaa Lys Ala Xaa Ala Val Xaa Pro Gln Met
                325                 330                 335

Thr Xaa Xaa Trp Asp Xaa Gln Leu Ala Xaa Tyr Val Xaa Xaa Gly Phe
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Arg Val Thr Xaa Leu Ala Xaa Xaa Gly Gln Gln Gly Val Gln Xaa Ile
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Gln Lys Xaa Val Xaa Val Xaa Thr Leu Trp Xaa Gly Ala Xaa Leu Val
    370                 375                 380

Ile Xaa Xaa Xaa Leu Xaa Xaa Gly Gln Leu Ile Ala Phe Asn Met Leu
385                 390                 395                 400

Ser Gly Gln Val Xaa Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln
                405                 410                 415

Asp Phe Gln Gln Val Gly Ile Ser Val Xaa Arg Leu Gly Asp Xaa Leu
            420                 425                 430

Asn Xaa Pro Thr Glu Xaa Xaa Xaa Xaa Xaa Leu Ala Leu Pro Xaa Ile
        435                 440                 445

Xaa Gly Xaa Ile Thr Phe Xaa Xaa Xaa Xaa Phe Arg Tyr Lys Xaa Asp
    450                 455                 460

Xaa Xaa Xaa Ile Leu Xaa Asp Xaa Asn Leu Xaa Ile Xaa Xaa Gly Glu
465                 470                 475                 480

Val Xaa Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr
                485                 490                 495

Lys Leu Xaa Gln Arg Xaa Tyr Xaa Pro Xaa Xaa Gly Xaa Val Leu Xaa
            500                 505                 510

Asp Gly Xaa Asp Leu Ala Leu Ala Xaa Pro Xaa Trp Leu Arg Arg Gln
        515                 520                 525

Val Gly Val Val Leu Gln Xaa Asn Val Leu Leu Asn Arg Ser Ile Arg
    530                 535                 540

Asp Asn Ile Ala Leu Xaa Asp Xaa Gly Met Pro Xaa Glu Xaa Ile Xaa
545                 550                 555                 560

Xaa Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Xaa Glu Leu Xaa
                565                 570                 575

Glu Gly Tyr Xaa Thr Xaa Val Gly Glu Gln Gly Ala Gly Leu Ser Gly
            580                 585                 590

Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Xaa Xaa Asn Pro
        595                 600                 605

Xaa Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser
    610                 615                 620

Glu Xaa Xaa Ile Met Xaa Asn Met Xaa Xaa Ile Cys Xaa Xaa Arg Thr
625                 630                 635                 640

Val Xaa Ile Ile Ala His Arg Leu Ser Thr Val Lys Xaa Ala Xaa Arg
                645                 650                 655

Ile Ile Xaa Met Xaa Lys Gly Xaa Ile Val Glu Xaa Gly Xaa Xaa Xaa
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Glu Leu Leu Ala Xaa Pro Asn Gly Xaa Tyr Xaa Tyr Leu Xaa Xaa Leu
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Gln Xaa
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<400> SEQUENCE: 173

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Leu Glu Gly Lys Gly Leu Asp Leu Thr Ala Trp Leu Leu Ala Ala Lys
             20                  25                  30

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

Ala Phe Ile Ala Leu Pro Ala Leu Val Trp Arg Glu Asp Gly Lys His
     50                  55                  60

Phe Ile Leu Thr Lys Ile Asp Asn Glu Ala Lys Lys Tyr Leu Ile Phe
 65                  70                  75                  80

Asp Leu Glu Thr His Asn Pro Arg Ile Leu Glu Gln Ala Glu Phe Glu
                 85                  90                  95

Ser Leu Tyr Gln Gly Lys Leu Ile Leu Val Ala Ser Arg Ala Ser Ile
            100                 105                 110

Val Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val
        115                 120                 125

Ile Lys Tyr Arg Lys Ile Phe Ile Glu Thr Leu Ile Val Ser Ile Phe
    130                 135                 140

Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val Met
145                 150                 155                 160

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

Val Ala Leu Ala Ile Val Val Leu Phe Glu Ile Val Leu Asn Gly Leu
            180                 185                 190

Arg Thr Tyr Ile Phe Ala His Ser Thr Ser Arg Ile Asp Val Glu Leu
        195                 200                 205

Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Ile Ser Tyr Phe
    210                 215                 220

Glu Asn Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg Glu Leu Asp
225                 230                 235                 240

Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu Asp
                245                 250                 255

Leu Met Phe Ser Phe Ile Phe Phe Ala Val Met Trp Tyr Tyr Ser Pro
            260                 265                 270

Lys Leu Thr Leu Val Ile Leu Gly Ser Leu Pro Phe Tyr Met Gly Trp
        275                 280                 285

Ser Ile Phe Ile Ser Pro Ile Leu Arg Arg Arg Leu Asp Glu Lys Phe
    290                 295                 300

Ala Arg Gly Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Val Thr Ala
305                 310                 315                 320

Ile Asn Thr Ile Lys Ala Leu Ala Val Thr Pro Gln Met Thr Asn Thr
                325                 330                 335

Trp Asp Lys Gln Leu Ala Ser Tyr Val Ser Ala Gly Phe Arg Val Thr
            340                 345                 350

Thr Leu Ala Thr Ile Gly Gln Gln Gly Val Gln Phe Ile Gln Lys Val
        355                 360                 365

Val Met Val Ile Thr Leu Trp Leu Gly Ala His Leu Val Ile Ser Gly
    370                 375                 380

Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met Leu Ser Gly Gln
385                 390                 395                 400
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Val Ile Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe Gln
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Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val Leu Asn Ser Pro
            420                 425                 430

Thr Glu Ser Tyr Gln Gly Lys Leu Ala Leu Pro Glu Ile Lys Gly Asp
        435                 440                 445

Ile Thr Phe Arg Asn Ile Arg Phe Arg Tyr Lys Pro Asp Ala Pro Val
    450                 455                 460

Ile Leu Asn Asp Val Asn Leu Ser Ile Gln Gln Gly Glu Val Ile Gly
465                 470                 475                 480

Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr Lys Leu Ile
                485                 490                 495

Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu Ile Asp Gly His
            500                 505                 510

Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg Gln Val Gly Val
        515                 520                 525

Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile Arg Asp Asn Ile
    530                 535                 540

Ala Leu Ala Asp Pro Gly Met Pro Met Glu Lys Ile Val His Ala Ala
545                 550                 555                 560

Lys Leu Ala Gly Ala His Glu Phe Ile Ser Glu Leu Arg Glu Gly Tyr
                565                 570                 575

Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly Gly Gln Arg
            580                 585                 590

Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn Pro Lys Ile Leu
        595                 600                 605

Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser Glu His Ile
    610                 615                 620

Ile Met Arg Asn Met His Gln Ile Cys Lys Gly Arg Thr Val Ile Ile
625                 630                 635                 640

Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg Ile Ile Val
                645                 650                 655

Met Glu Lys Gly Gln Ile Val Glu Gln Gly Lys His Lys Glu Leu Leu
            660                 665                 670

Ala Asp Pro Asn Gly Leu Tyr His Tyr Leu His Gln Leu Gln Ser
        675                 680                 685


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<400> SEQUENCE: 174
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Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg
  1               5                  10                  15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
         35                  40                  45

His Arg Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     50                  55                  60

Xaa Xaa Xaa Phe Glu Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe
 65                  70                  75                  80

Ala His Thr Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
                85                  90                  95

Arg His Leu Leu Ser Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val
            100                 105                 110

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

Leu Thr Gly Gln Ala Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe
    130                 135                 140

Ile Phe Leu Ala Val Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val
145                 150                 155                 160

Val Leu Ala Ser Leu Ile Cys Ile Cys Ala Asn Arg Thr Val Leu Ile
                165                 170                 175

Ile Ala His Arg Leu Ser Thr Val Lys Thr Ala His Arg Ile Ile Ala
            180                 185                 190

Met Asp Lys Gly Arg Ile Val Glu Ala Gly Thr Gln Gln Glu Leu Leu
        195                 200                 205

Ala Asn Xaa Asn Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln
    210                 215                 220


<210> SEQ ID NO 175
<211> LENGTH: 222
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<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive
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<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: absent or positive

<400> SEQUENCE: 175

Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
35 40 45

His Arg Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Phe Glu Ile Xaa Leu Gly Gly Leu Arg Thr Tyr Xaa Phe
65 70 75 80

Ala His Xaa Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
85 90 95

Arg His Leu Leu Xaa Leu Pro Xaa Ser Tyr Phe Glu Xaa Arg Arg Val
100 105 110

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

Leu Thr Gly Gln Ala Leu Thr Ser Xaa Leu Asp Leu Xaa Phe Ser Phe
130 135 140

Ile Phe Xaa Ala Val Met Trp Tyr Tyr Ser Xaa Xaa Leu Thr Xaa Val
145 150 155 160

Val Leu Xaa Ser Leu Xaa Cys Ile Cys Xaa Asn Arg Thr Val Leu Ile
165 170 175

Ile Ala His Arg Leu Ser Thr Val Lys Xaa Ala Xaa Arg Ile Ile Xaa
180 185 190

Met Asp Lys Gly Xaa Ile Xaa Glu Xaa Gly Xaa Xaa Gln Glu Leu Leu
195 200 205

Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Tyr Leu Xaa Xaa Leu Gln
210 215 220

<210> SEQ ID NO 176
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: HlyB

<400> SEQUENCE: 176

Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Lys
1 5 10 15

Ile Phe Ile Glu Thr Leu Ile Val Ser Ile Phe Leu Gln Ile Phe Ala
20 25 30

Leu Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
35 40 45

His Arg Gly Phe Ser Thr Leu Asn Val Ile Thr Val Ala Leu Ala Ile

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     50                  55                  60

Val Val Leu Phe Glu Ile Ile Leu Gly Gly Leu Arg Thr Tyr Val Phe
 65                  70                  75                  80

Ala His Ser Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
                 85                  90                  95

Arg His Leu Leu Ala Leu Pro Ile Ser Tyr Phe Glu Ala Arg Arg Val
            100                 105                 110

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

Leu Thr Gly Gln Ala Leu Thr Ser Ile Leu Asp Leu Leu Phe Ser Phe
    130                 135                 140

Ile Phe Phe Ala Val Met Trp Tyr Tyr Ser Pro Lys Leu Thr Leu Val
145                 150                 155                 160

Val Leu Gly Ser Leu Pro Cys Ile Cys Gln Asn Arg Thr Val Leu Ile
                165                 170                 175

Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg Ile Ile Val
            180                 185                 190

Met Asp Lys Gly Glu Ile Ile Glu Gln Gly Lys His Gln Glu Leu Leu
        195                 200                 205

Lys Asp Glu Lys Gly Leu Tyr Ser Tyr Leu His Gln Leu Gln
    210                 215                 220


<210> SEQ ID NO 177
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF112a
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<221> NAME/KEY: SITE
<222> LOCATION: (223)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 177

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

Val Tyr Ala Leu Leu Ala Phe Leu Ala Leu Tyr Ser Phe Phe Glu Ile
             20                  25                  30

Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
         35                  40                  45

Met Xaa Gly Tyr Thr Ala Leu Lys Met Xaa Ala Arg Ala Tyr Glu Leu
     50                  55                  60

Met Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Xaa Ser Gln Leu
 65                  70                  75                  80
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Ala Ala Gly Ser Glu Leu Xaa Val Ile Lys Ala Ser Gly Met Ser Thr
                85                  90                  95

Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
            100                 105                 110

Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
        115                 120                 125

Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
    130                 135                 140

Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Ile Ile Asn Val Arg
145                 150                 155                 160

Glu Met Leu Pro Asp His Thr Leu Leu Gly Ile Lys Ile Trp Ala Arg
                165                 170                 175

Asn Asp Lys Asn Glu Leu Ala Glu Ala Val Glu Ala Asp Ser Ala Val
            180                 185                 190

Leu Asn Ser Asp Gly Ser Trp Gln Leu Lys Asn Ile Arg Arg Ser Thr
        195                 200                 205

Leu Gly Glu Asp Lys Val Glu Val Ser Ile Ala Ala Glu Glu Xaa Trp
    210                 215                 220

Pro Ile Ser Val Lys Arg Asn Leu Met Asp Val Leu Leu Val Lys Pro
225                 230                 235                 240


<210> SEQ ID NO 178
<211> LENGTH: 360
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF114a
<220> FEATURE:
<221> NAME/KEY: SITE
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<223> OTHER INFORMATION: place-holder
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<221> NAME/KEY: SITE
<222> LOCATION: (85)
<223> OTHER INFORMATION: place-holder
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<223> OTHER INFORMATION: place-holder
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<223> OTHER INFORMATION: place-holder
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<221> NAME/KEY: SITE
<222> LOCATION: (352)
<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 178

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
  1               5                  10                  15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
             20                  25                  30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys
         35                  40                  45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
     50                  55                  60

Leu Ser Met Xaa Xaa Xaa Xaa Xaa Xaa Gln Ile Thr Thr Asp Lys Ser
 65                  70                  75                  80
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```
Ala Pro Lys Asn Xaa Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
                 85                  90                  95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
            100                 105                 110

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
        115                 120                 125

Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile
    130                 135                 140

Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
145                 150                 155                 160

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

Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
            180                 185                 190

Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
        195                 200                 205

Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
    210                 215                 220

Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
225                 230                 235                 240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
                245                 250                 255

Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
            260                 265                 270

Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
        275                 280                 285

Asp Ser Ile Thr Leu Ile Ala Xaa Glu Lys Gly Val Gly Val Lys Asn
    290                 295                 300

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

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
                325                 330                 335

Ala Ser Pro Thr Tyr Leu Xaa Ile Glu Thr Thr Glu Lys Gly Ala Xaa
            340                 345                 350

Gly Thr Phe Ile Ser Asn Gly Gly
        355                 360


<210> SEQ ID NO 179
<211> LENGTH: 1574
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF114-1

<400> SEQUENCE: 179

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
  1               5                  10                  15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
             20                  25                  30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys
         35                  40                  45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
     50                  55                  60
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```
Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser
 65                  70                  75                  80

Ala Pro Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
                85                  90                  95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
            100                 105                 110

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
        115                 120                 125

Asp Arg Asn Asn Asn Pro Phe Val Val Lys Gly Ser Ala Gln Leu Ile
    130                 135                 140

Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
145                 150                 155                 160

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

Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
            180                 185                 190

Thr Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
        195                 200                 205

Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
    210                 215                 220

Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
225                 230                 235                 240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
                245                 250                 255

Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
            260                 265                 270

Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
        275                 280                 285

Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn
    290                 295                 300

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

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
                325                 330                 335

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

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

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val
    370                 375                 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385                 390                 395                 400

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

Ala Thr Leu Ser Ala Asp Gly Arg Thr Val Ile Lys Glu Ala Ser Ile
            420                 425                 430

Gln Thr Gly Thr Thr Val Tyr Ser Ser Ser Lys Gly Asn Ala Glu Leu
        435                 440                 445

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

Gly Thr Ile Ser Ser Ser Ala Val Ile Asp Ala Lys Asp Thr Ala His
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465                 470                 475                 480

Ile Glu Ala Gly Lys Pro Leu Ser Leu Glu Ala Ser Thr Val Thr Ser
                485                 490                 495

Asp Ile Arg Leu Asn Gly Gly Ser Ile Lys Gly Gly Lys Gln Leu Ala
            500                 505                 510

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
        515                 520                 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
    530                 535                 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala
545                 550                 555                 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met
                565                 570                 575

Gly Val Glu Ala Gly Ser Leu Asn Val Thr Asn Thr Asn Leu Arg Thr
            580                 585                 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
        595                 600                 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
    610                 615                 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
625                 630                 635                 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
                645                 650                 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly
            660                 665                 670

Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile
        675                 680                 685

Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg
    690                 695                 700

Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn
705                 710                 715                 720

Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn
                725                 730                 735

Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser
            740                 745                 750

Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn
        755                 760                 765

Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln
    770                 775                 780

Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn
785                 790                 795                 800

Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr
                805                 810                 815

Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val
            820                 825                 830

Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu
        835                 840                 845

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala
    850                 855                 860

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
865                 870                 875                 880
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```
Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
               885                 890                 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala
           900                 905                 910

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser
        915                 920                 925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys
    930                 935                 940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr
945                 950                 955                 960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln
               965                 970                 975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr
           980                 985                 990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn
        995                1000                1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala
   1010                1015                1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu
1025               1030                1035                1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala
               1045                1050                1055

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu
           1060                1065                1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys
       1075                1080                1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly
   1090                1095                1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg
1105               1110                1115                1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
               1125                1130                1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
           1140                1145                1150

Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys
       1155                1160                1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val
   1170                1175                1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu
1185               1190                1195                1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val
               1205                1210                1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His
           1220                1225                1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly
       1235                1240                1245

Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val
   1250                1255                1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val
1265               1270                1275                1280
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Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln
              1285                1290                1295

Ala Gly Val Gly Glu Lys Ala Arg Ala Asp Ala Lys Ile Ile Leu Lys
          1300                1305                1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser
       1315                1320                1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu
   1330                1335                1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Thr Ala Pro
1345                1350                1355                1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile
              1365                1370                1375

Glu Lys Leu Ala Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
          1380                1385                1390

Val Ala Lys Asn Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys
       1395                1400                1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Arg Ala Gly Ala Ala Ile Val
   1410                1415                1420

Thr Ile Ile Val Thr Ala Leu Thr Tyr Gly Tyr Gly Ala Thr Ala Ala
1425                1430                1435                1440

Gly Gly Val Ala Ala Ser Gly Ser Ser Thr Ala Ala Ala Ala Gly Thr
              1445                1450                1455

Ala Ala Thr Thr Thr Ala Ala Ala Thr Thr Val Ser Thr Ala Thr Ala
          1460                1465                1470

Met Gln Thr Ala Ala Leu Ala Ser Leu Tyr Ser Gln Ala Ala Val Ser
       1475                1480                1485

Ile Ile Asn Asn Lys Gly Asp Val Gly Lys Ala Leu Lys Asp Leu Gly
   1490                1495                1500

Thr Ser Asp Thr Val Lys Gln Ile Val Thr Ser Ala Leu Thr Ala Gly
1505                1510                1515                1520

Ala Leu Asn Gln Met Gly Ala Asp Ile Ala Gln Leu Asn Ser Lys Val
              1525                1530                1535

Arg Thr Glu Leu Phe Ser Ser Thr Gly Asn Gln Thr Ile Ala Asn Leu
          1540                1545                1550

Gly Gly Arg Leu Ala Thr Asn Leu Ser Asn Ala Gly Ile Ser Ala Gly
       1555                1560                1565

Ile Asn Thr Ala Val Asn
   1570


<210> SEQ ID NO 180
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF114
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (29)..(51)
<223> OTHER INFORMATION: place-holder
<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (96)
<223> OTHER INFORMATION: place-holder
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<221> NAME/KEY: SITE
<222> LOCATION: (199)
<223> OTHER INFORMATION: place-holder
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<220> FEATURE:
<221> NAME/KEY: SITE
<222> LOCATION: (210)
<223> OTHER INFORMATION: place-holder
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Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln Ala Gly
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Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser Ala Pro
50 55 60

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

Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn Arg Xaa
85 90 95

Tyr Ala Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn Asp Arg
100 105 110

Asn Asn Asn Pro Phe Val Val Lys Gly Ser Ala Gln Leu Ile Leu Asn
115 120 125

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

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

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

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

Lys Ala His Trp Thr Val Xaa Ala Ala Gly Trp Asn Asp Lys Gly Gly
195 200 205

Ala Xaa Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln Gly Lys
210 215 220

Xaa Xaa Gly Lys Xaa Leu Ala Val Ser Thr Gly Pro Gln Lys Val Asp
225 230 235 240

Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr Lys Pro
245 250 255

Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala Asp Ser
260 265 270

Ile Thr Leu Ile Ala Asn Glu Lys Gly
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<400> SEQUENCE: 181

Ala Val Ala Glu Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa Xaa Gln Xaa Xaa
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Xaa Xaa Xaa Ser Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Ala Xaa Ala Xaa Xaa Ile Xaa Xaa
50 55 60

Asp Lys Ser Ala Pro Lys Asn Gln Gln Xaa Val Ile Leu Xaa Thr Xaa
65 70 75 80

Xaa Gly Xaa Pro Xaa Val Asn Ile Gln Thr Pro Xaa Xaa Xaa Gly Xaa
85 90 95

Ser Xaa Asn Arg Xaa Xaa Xaa Phe Asp Val Asp Xaa Lys Gly Xaa Xaa
100 105 110

Leu Asn Asn Xaa Arg Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Asn Pro Xaa Xaa Xaa Xaa Gly Xaa Ala Xaa Xaa Ile Xaa Asn
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Leu Asn Gly Xaa Xaa Xaa Val
145 150 155 160

Gly Gly Xaa Xaa Ala Xaa Val Xaa Xaa Ala Asn Pro Xaa Gly Ile Xaa
165 170 175

Val Asn Gly Gly Gly Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Leu Thr Xaa
180 185 190

Gly Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Thr Gly Phe Asp Val
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Asp Xaa Xaa
210 215 220

Xaa Ala Xaa Tyr Thr Xaa Xaa Leu Xaa Arg Ala Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Xaa Gly Lys Xaa Xaa Xaa Val Xaa Xaa Gly Xaa Xaa Lys Xaa
245 250 255

Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa
260 265 270

Xaa Xaa Xaa Xaa Pro Thr Xaa Ala Xaa Asp Thr Ala Xaa Leu Gly Gly
275 280 285

Met Tyr Ala Asp Xaa Ile Thr Leu Ile Xaa Xaa Xaa Xaa Gly
290 295 300

<210> SEQ ID NO 182
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<400> SEQUENCE: 182

Ala Val Ala Glu Asn Val His Arg Asp Gly Lys Ser Met Gln Asp Ser

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Glu Ala Ala Ser Val Arg Val Thr Gly Ala Ala Ser Val Ser Ser Ala
             20                  25                  30

Arg Ala Ala Phe Gly Phe Arg Met Ala Ala Phe Ser Val Met Leu Ala
         35                  40                  45

Leu Gly Val Ala Ala Phe Ser Pro Ala Pro Ala Ser Gly Ile Ile Ala
     50                  55                  60

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

Asn Gly Leu Pro Gln Val Asn Ile Gln Thr Pro Ser Ser Gln Gly Val
                 85                  90                  95

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

Leu Asn Asn Ser Arg Ser Asn Thr Gln Thr Gln Leu Gly Gly Trp Ile
        115                 120                 125

Gln Gly Asn Pro His Leu Ala Arg Gly Glu Ala Arg Val Ile Val Asn
    130                 135                 140

Gln Ile Asp Ser Ser Asn Pro Ser Leu Leu Asn Gly Tyr Ile Glu Val
145                 150                 155                 160

Gly Gly Lys Arg Ala Glu Val Val Val Ala Asn Pro Ser Gly Ile Arg
                165                 170                 175

Val Asn Gly Gly Gly Leu Ile Asn Ala Ala Ser Val Thr Leu Thr Ser
            180                 185                 190

Gly Val Pro Val Leu Asn Asn Gly Asn Leu Thr Gly Phe Asp Val Ser
        195                 200                 205

Ser Gly Lys Val Val Ile Gly Gly Lys Gly Leu Asp Thr Ser Asp Ala
    210                 215                 220

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

Trp Gly Lys Asp Val Lys Val Val Ser Gly Lys Asn Lys Leu Asp Phe
                245                 250                 255

Asp Gly Ser Leu Ala Lys Thr Ala Ser Ala Pro Ser Ser Ser Asp Ser
            260                 265                 270

Val Thr Pro Thr Val Ala Ile Asp Thr Ala Thr Leu Gly Gly Met Tyr
        275                 280                 285

Ala Asp Lys Ile Thr Leu Ile Ser Thr Asp Asn Gly
    290                 295                 300


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<400> SEQUENCE: 183

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
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Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
             20   25   30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Xaa Xaa
         35   40   45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     50   55   60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Ile Thr Thr Asp Lys Ser
 65   70   75   80

Ala Pro Lys Asn Xaa Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
                 85   90   95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
            100   105   110

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
        115   120   125

Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile
    130   135   140

Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
145   150   155   160

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

Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
            180   185   190

Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
        195   200   205

Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
    210   215   220

Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
225   230   235   240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
                245   250   255

Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
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Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
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Asp Ser Ile Thr Leu Ile Ala Xaa Glu Lys Gly Val Gly Val Lys Asn
    290                 295                 300

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

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
                325                 330                 335

Ala Ser Pro Thr Tyr Leu Xaa Ile Glu Thr Thr Glu Lys Gly Ala Xaa
            340                 345                 350

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

Val Ile Glu Thr Gly Glu Asp Ile Xaa Leu Arg Asn Gly Ala Val Val
    370                 375                 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385                 390                 395                 400

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

Xaa Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile
            420                 425                 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Xaa Leu
        435                 440                 445

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

Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His
465                 470                 475                 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser
                485                 490                 495

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

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
        515                 520                 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
    530                 535                 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala
545                 550                 555                 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met
                565                 570                 575

Gly Val Glu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            580                 585                 590

Xaa Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
        595                 600                 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
    610                 615                 620

Gln Gly Asn Ile
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<210> SEQ ID NO 184
<211> LENGTH: 663
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Met Xaa Ala Val Ala Glu Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa Xaa Gln
             20                  25                  30

Xaa Xaa Xaa Xaa Xaa Ser Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
         35                  40                  45

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
 65                  70                  75                  80

Xaa Xaa Asp Lys Ser Ala Pro Lys Asn Xaa Gln Xaa Val Ile Leu Xaa
                 85                  90                  95

Thr Xaa Xaa Gly Xaa Pro Xaa Val Asn Ile Gln Thr Pro Xaa Xaa Xaa
            100                 105                 110

Gly Xaa Ser Xaa Asn Arg Xaa Xaa Gln Phe Asp Val Asp Xaa Lys Gly
        115                 120                 125

Xaa Xaa Leu Asn Asn Xaa Arg Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140

Xaa Xaa Xaa Xaa Asn Pro Xaa Leu Xaa Xaa Gly Xaa Ala Xaa Xaa Ile
145                 150                 155                 160

Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Leu Asn Gly Xaa Xaa
                165                 170                 175

Xaa Val Gly Gly Xaa Xaa Ala Xaa Val Xaa Xaa Ala Asn Pro Xaa Gly
            180                 185                 190

Ile Xaa Val Asn Gly Gly Gly Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Leu
        195                 200                 205

Thr Xaa Gly Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Thr Gly Phe
    210                 215                 220

Asp Val Xaa Xaa Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Gly Xaa Xaa Asp
225                 230                 235                 240
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Xaa Xaa Xaa Ala Asp Tyr Thr Xaa Xaa Leu Xaa Arg Ala Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa Xaa Xaa Val Xaa Xaa Gly Xaa Xaa
260 265 270

Lys Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa
275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Pro Thr Xaa Ala Xaa Asp Thr Ala Xaa Leu
290 295 300

Gly Gly Met Tyr Ala Asp Xaa Ile Thr Leu Ile Xaa Xaa Xaa Xaa Gly
305 310 315 320

Xaa Xaa Xaa Xaa Asn Xaa Gly Xaa Xaa Xaa Ala Ala Xaa Xaa Xaa Xaa
325 330 335

Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Asn Ser Gly Xaa Ile Xaa Xaa
340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr
355 360 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ile
370 375 380

Xaa Ser Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa
385 390 395 400

Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Xaa Xaa Xaa Xaa Xaa
405 410 415

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa
420 425 430

Asn Asn Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa
435 440 445

Xaa Xaa Xaa Xaa Xaa Asn Asp Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Val
450 455 460

Xaa Ser Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa
465 470 475 480

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa
485 490 495

Xaa Xaa Ile Xaa Ala Xaa Asp Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
500 505 510

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Arg Xaa Xaa Xaa
515 520 525

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
530 535 540

Ile Thr Xaa Xaa Xaa Xaa Xaa Ala Lys Xaa Xaa Asn Xaa Xaa Thr Xaa
545 550 555 560

Gly Xaa Xaa Tyr Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp
565 570 575

Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Ala
580 585 590

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa
595 600 605

Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
610 615 620

Ser Gly Xaa Leu His Ile Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
625 630 635 640

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Gln Xaa Xaa Asn Thr Xaa Leu Xaa Asn Xaa Xaa Xaa Ala Xaa Glu Xaa
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Xaa Xaa Xaa Xaa Gly Asn Ile
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Met Met Ala Val Ala Glu Asn Val His Arg Asp Gly Lys Ser Met Gln
             20                  25                  30

Asp Ser Glu Ala Ala Ser Val Arg Val Thr Gly Ala Ala Ser Val Ser
         35                  40                  45

Ser Ala Arg Ala Ala Phe Gly Phe Arg Met Ala Ala Phe Ser Val Met
     50                  55                  60

Leu Ala Leu Gly Val Ala Ala Phe Ser Pro Ala Pro Ala Ser Gly Ile
 65                  70                  75                  80

Ile Ala Asp Lys Ser Ala Pro Lys Asn Gln Gln Ala Val Ile Leu Gln
                 85                  90                  95

Thr Ala Asn Gly Leu Pro Gln Val Asn Ile Gln Thr Pro Ser Ser Gln
            100                 105                 110

Gly Val Ser Val Asn Arg Phe Lys Gln Phe Asp Val Asp Glu Lys Gly
        115                 120                 125

Val Ile Leu Asn Asn Ser Arg Ser Asn Thr Gln Thr Gln Leu Gly Gly
    130                 135                 140

Trp Ile Gln Gly Asn Pro His Leu Ala Arg Gly Glu Ala Arg Val Ile
145                 150                 155                 160

Val Asn Gln Ile Asp Ser Ser Asn Pro Ser Leu Leu Asn Gly Tyr Ile
                165                 170                 175

Glu Val Gly Gly Lys Arg Ala Glu Val Val Val Ala Asn Pro Ser Gly
            180                 185                 190

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

Thr Ser Gly Val Pro Val Leu Asn Asn Gly Asn Leu Thr Gly Phe Asp
    210                 215                 220

Val Ser Ser Gly Lys Val Val Ile Gly Gly Lys Gly Leu Asp Thr Ser
225                 230                 235                 240

Asp Ala Asp Tyr Thr Arg Ile Leu Ser Arg Ala Ala Glu Ile Asn Ala
                245                 250                 255

Gly Val Trp Gly Lys Asp Val Lys Val Val Ser Gly Lys Asn Lys Leu
            260                 265                 270

Asp Phe Asp Gly Ser Leu Ala Lys Thr Ala Ser Ala Pro Ser Ser Ser
        275                 280                 285

Asp Ser Val Thr Pro Thr Val Ala Ile Asp Thr Ala Thr Leu Gly Gly
    290                 295                 300

Met Tyr Ala Asp Lys Ile Thr Leu Ile Ser Thr Asp Asn Gly Ala Val
305                 310                 315                 320
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Ile Arg Asn Lys Gly Arg Ile Phe Ala Ala Thr Gly Gly Val Thr Leu
                325                 330                 335

Ser Ala Asp Gly Lys Leu Ser Asn Ser Gly Ser Ile Asp Ala Ala Glu
            340                 345                 350

Ile Thr Ile Ser Ala Gln Thr Val Asp Asn Arg Gln Gly Phe Ile Arg
        355                 360                 365

Ser Gly Lys Gly Ser Val Leu Lys Val Ser Asp Gly Ile Asn Asn Gln
    370                 375                 380

Ala Gly Leu Ile Gly Ser Ala Gly Leu Leu Asp Ile Arg Asp Thr Gly
385                 390                 395                 400

Lys Ser Ser Leu His Ile Asn Asn Thr Asp Gly Thr Ile Ile Ala Gly
                405                 410                 415

Lys Asp Val Ser Leu Gln Ala Lys Ser Leu Asp Asn Asp Gly Ile Leu
            420                 425                 430

Thr Ala Ala Arg Asp Val Ser Val Ser Leu His Asp Asp Phe Ala Gly
        435                 440                 445

Lys Arg Asp Ile Glu Ala Gly Arg Thr Leu Thr Phe Ser Thr Gln Gly
    450                 455                 460

Arg Leu Lys Asn Thr Arg Ile Ile Gln Ala Gly Asp Thr Val Ser Leu
465                 470                 475                 480

Thr Ala Ala Gln Ile Asp Asn Thr Val Ser Gly Lys Ile Gln Ser Gly
                485                 490                 495

Asn Arg Thr Gly Leu Asn Gly Lys Asn Gly Ile Thr Asn Arg Gly Leu
            500                 505                 510

Ile Asn Ser Asn Gly Ile Thr Leu Leu Gln Thr Glu Ala Lys Ser Asp
        515                 520                 525

Asn Ala Gly Thr Gly Arg Ile Tyr Gly Ser Arg Val Ala Val Glu Ala
    530                 535                 540

Asp Thr Leu Leu Asn Arg Glu Glu Thr Val Asn Gly Glu Thr Lys Ala
545                 550                 555                 560

Ala Val Ile Ala Ala Arg Glu Arg Leu Asp Ile Gly Ala Arg Glu Ile
                565                 570                 575

Glu Asn Arg Glu Ala Ala Leu Leu Ser Ser Ser Gly Asp Leu His Ile
            580                 585                 590

Gly Ser Ala Leu Asn Gly Ser Arg Gln Val Gln Gly Ala Asn Thr Ser
        595                 600                 605

Leu His Asn Arg Ser Ala Ala Ile Glu Ser Ser Gly Asn Ile
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Leu Gln Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro
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Gln Lys Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala
20 25 30

Gly Thr Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met
35 40 45

Tyr Ala Asp Ser Ile Thr Leu Ile Ala Xaa Glu Lys Gly Val Gly Val
50 55 60

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

Ser Gly Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly
85 90 95

Thr Glu Ala Ser Pro Thr Tyr Leu Xaa Ile Glu Thr Thr Glu Lys Gly
100 105 110

Ala Xaa Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly
115 120 125

Leu Leu Val Ile Glu Thr Gly Glu Asp Ile Xaa Leu Arg Asn Gly Ala
130 135 140

Val Val Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala
145 150 155 160

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

Gly Ser Xaa Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala
180 185 190

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

Xaa Leu Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu
210 215 220

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

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

Ala Ser Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln
260 265 270

Leu Ala Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu
275 280 285

Asn Thr Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu
290 295 300

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Asn Val Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp
305                 310                 315                 320

Asn Ala Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys
                325                 330                 335

Asp Met Gly Val Glu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            340                 345                 350

Xaa Xaa Xaa Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile
        355                 360                 365

Gln Leu Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr
    370                 375                 380

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


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<223> OTHER INFORMATION: absent or positive

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             20                  25                  30

Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa
         35                  40                  45

Xaa Xaa Xaa Ser Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
     50                  55                  60

Xaa Asn Xaa Gly Xaa Xaa Xaa Ala Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa
 65                  70                  75                  80

Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Thr Ala
                 85                  90                  95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Thr Xaa
            100                 105                 110

Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Gly Gly Xaa Ile Xaa
        115                 120                 125

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa
    130                 135                 140

Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa
145                 150                 155                 160

Xaa Xaa Xaa Gly Xaa Asn Leu Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa
                165                 170                 175

Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Leu Xaa
            180                 185                 190

Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Ala Gly Xaa
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Gly
    210                 215                 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa
                245                 250                 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            260                 265                 270

Thr Xaa Xaa Ser Xaa Xaa Xaa Xaa Asn Asn Xaa Xaa Xaa Lys Xaa Xaa
        275                 280                 285

Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Asn Xaa Xaa Xaa Lys Xaa Xaa
    290                 295                 300

Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Asp
305                 310                 315                 320

Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Ser Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Thr
            340                 345                 350

Xaa Thr Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Gly Xaa Xaa
        355                 360                 365

Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    370                 375                 380
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385                 390                 395                 400

Xaa Xaa Xaa Asn Thr Xaa Xaa Xaa Ala Xaa Xaa Ala Xaa Xaa Xaa Xaa
                405                 410                 415

Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Ala
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Asp Ile Thr Asn Thr Gly Ser Ile Gly Ala Glu Asn Ala Leu Leu Leu
             20                  25                  30

Lys Ala Ser Asn Asn Ile Glu Ser Arg Ser Glu Thr Arg Ser Asn Gln
         35                  40                  45

Asn Glu Gln Gly Ser Val Arg Asn Ile Gly Arg Val Ala Gly Ile Tyr
     50                  55                  60

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

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

Thr Val Leu Asn Ala Gly Gly Asp Ile Arg Ser Asp Thr Thr Gly Ile
            100                 105                 110

Ser Arg Asn Gln Asn Thr Ile Phe Asp Ser Asp Asn Tyr Val Ile Arg
        115                 120                 125

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

Ser Leu Asn Ala Lys Gly Asp Ile Arg Ile Arg Ala Ala Glu Val Gly
145                 150                 155                 160

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

Glu Ala Gly Lys Ala His Thr Glu Thr Glu Asp Ala Leu Lys Tyr Thr
            180                 185                 190

Gly Arg Ser Gly Gly Gly Ile Lys Gln Lys Met Thr Arg His Leu Lys
        195                 200                 205

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

Ile Leu Val Ser Gly Arg Asp Ile Thr Val Thr Gly Ser Asn Ile Ile
225                 230                 235                 240

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

Ala Ala Glu Thr Arg Ser Arg Ser Ala Glu Met Asn Lys Lys Glu Lys
            260                 265                 270

Ser Gly Leu Met Gly Ser Gly Gly Ile Gly Phe Thr Ala Gly Ser Lys
        275                 280                 285

Lys Asp Thr Gln Thr Asn Arg Ser Glu Thr Val Ser His Thr Glu Ser
    290                 295                 300
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Val Val Gly Ser Leu Asn Gly Asn Thr Leu Ile Ser Ala Gly Lys His
305                 310                 315                 320

Tyr Thr Gln Thr Gly Ser Thr Ile Ser Ser Pro Gln Gly Asp Val Gly
                325                 330                 335

Ile Ser Ser Gly Lys Ile Ser Ile Asp Ala Ala Gln Asn Arg Tyr Ser
            340                 345                 350

Gln Glu Ser Lys Gln Val Tyr Glu Gln Lys Gly Val Thr Val Ala Ile
        355                 360                 365

Ser Val Pro Val Val Asn Thr Val Met Gly Ala Val Asp Ala Val Lys
    370                 375                 380

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

Ala Ala
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Glu Ala Val Gly Ser Asn Ile Gly Gly Gly Lys Met Ile Val Ala Ala
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Gly Gln Asp Ile Asn Val Arg Gly Xaa Ser Leu Ile Ser Asp Lys Gly
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Ile Val Leu Lys Ala Gly His Asp Ile Asp Ile Ser Thr Ala His Asn
         35                  40                  45

Arg Tyr Thr Gly Asn Glu Tyr His Glu Ser Xaa Xaa Xaa Xaa Xaa Xaa
     50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Arg Lys Xaa Xaa Xaa
 65                  70                  75                  80

Xaa Xaa Xaa Arg Thr Asn Ile Val His Thr Gly Ser Ile Ile Gly Ser
                 85                  90                  95

Leu Asn Gly Asp Thr Val Thr Val Ala Gly Asn Arg Tyr Arg Gln Thr
            100                 105                 110

Gly Ser Thr Val Ser Ser Pro Glu Gly Arg Asn Thr Val Thr Ala Lys
        115                 120                 125

Xaa Ile Asp Val Glu Phe Ala Asn Asn Arg Tyr Ala Thr Asp Tyr Ala
    130                 135                 140

His Thr Gln Glu Gln Lys Gly Leu Thr Val Ala Leu Asn Val Pro Xaa
145                 150                 155                 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Lys
                165                 170                 175

Ser Lys Asn Lys Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp
            180                 185                 190

Gln Ser Tyr Gln Ala Thr Gln Gln Met Gln Gln Phe Ala Pro Ser Ser
        195                 200                 205

Ser Ala Gly Gln Gly Gln Asn Tyr Asn Gln Ser Pro Ser Ile Ser Val
    210                 215                 220

Ser Ile Xaa Tyr Gly Glu Gln Lys Ser Arg Asn Glu Gln Lys Arg His
225                 230                 235                 240

Tyr Thr Glu Ala Ala Ala Ser Gln Ile Ile Gly Lys Gly Gln Thr Thr
                245                 250                 255

Leu Ala Ala Thr Gly Ser Gly Glu Gln Ser Asn Ile Asn Ile Thr Gly
            260                 265                 270

Ser Asp Val Ile Gly His Ala Gly Thr Xaa Leu Ile Ala Asp Asn His
        275                 280                 285

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

Lys Ser Ser Gly Trp Asn Ala Gly Val Arg Xaa Lys Ile Gly Asn Gly
305                 310                 315                 320

Ile Arg Phe Gly Ile Thr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Xaa Xaa Ser Thr Thr His Arg His Thr His Val Gly Ser Thr Thr
            340                 345                 350

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

Gln Leu Ile Gly Lys Gly Ile Gln Ala Asp Thr Arg Asn Leu His Ile
    370                 375                 380

Glu Ser Val Gln Asp Thr Glu Thr Tyr Gln Ser Lys Gln Gln Asn Gly
385                 390                 395                 400

Asn Val Gln Val Thr Val Gly Tyr Gly Phe Ser Ala Ser Gly Ser Tyr
                405                 410                 415

Arg Gln Ser Lys Val Lys Ala Asp His Ala Ser Val Thr Gly Gln Ser
            420                 425                 430

Gly Ile Tyr Ala Gly Glu Asp Gly Tyr Gln Ile Lys Val Arg Asp Asn
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        435                 440                 445

Thr Asp Leu Lys Gly Gly Ile Ile Thr Ser Ser Gln Ser Ala Glu Asp
    450                 455                 460

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

Gln Asn His Ser Arg Tyr Glu Gly Arg Ser Phe Gly Ile Gly Gly Ser
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Phe
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<400> SEQUENCE: 190

Xaa Ala Val Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Ile Xaa Xaa Xaa
1 5 10 15

Gly Xaa Asp Ile Xaa Val Xaa Gly Xaa Xaa Xaa Ile Xaa Asp Xaa Xaa
20 25 30

Xaa Xaa Leu Xaa Ala Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Ala Xaa Xaa
35 40 45

Arg Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Thr Xaa Ser Xaa Xaa Gly Ser
85 90 95

Leu Asn Gly Xaa Thr Xaa Xaa Xaa Ala Gly Xaa Xaa Tyr Xaa Gln Thr
100 105 110

Gly Ser Thr Xaa Ser Ser Pro Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Ile Xaa Xaa Xaa Xaa Ala Xaa Asn Arg Tyr Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Glu Gln Lys Gly Xaa Thr Val Ala Xaa Xaa Val Pro Xaa

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145                 150                 155                 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                165                 170                 175

Xaa Gly Lys Ser Lys Asn Xaa Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            180                 185                 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala
        195                 200                 205

Xaa Xaa Pro Xaa Xaa Xaa Ala Gly Gln Gly Xaa Xaa Xaa Xaa Xaa Xaa
    210                 215                 220

Xaa Xaa Ile Ser Val Ser Xaa Xaa Tyr Gly Glu Gln Lys Xaa Xaa Xaa
225                 230                 235                 240

Glu Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Gly
                245                 250                 255

Xaa Gly Xaa Xaa Xaa Leu Xaa Ala Xaa Gly Xaa Gly Xaa Xaa Ser Xaa
            260                 265                 270

Ile Xaa Ile Thr Gly Ser Asp Val Xaa Gly Xaa Xaa Gly Thr Xaa Leu
        275                 280                 285

Xaa Ala Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Gln Xaa Xaa Xaa
    290                 295                 300

Glu Xaa Ser Xaa Asn Lys Ser Xaa Gly Xaa Asn Ala Gly Val Xaa Xaa
305                 310                 315                 320

Xaa Ile Xaa Xaa Gly Ile Xaa Phe Gly Xaa Thr Ala Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Arg Xaa Xaa His
            340                 345                 350

Xaa Gly Ser Xaa Xaa Xaa Xaa Thr Xaa Ile Xaa Ser Gly Gly Asp Thr
        355                 360                 365

Xaa Xaa Lys Gly Xaa Gln Leu Xaa Gly Lys Gly Xaa Xaa Xaa Xaa Xaa
    370                 375                 380

Xaa Xaa Leu His Ile Glu Ser Xaa Gln Asp Thr Xaa Xaa Xaa Xaa Xaa
385                 390                 395                 400

Lys Gln Xaa Asn Xaa Xaa Xaa Gln Val Thr Val Gly Tyr Gly Phe Ser
                405                 410                 415

Xaa Xaa Gly Ser Tyr Xaa Xaa Ser Lys Xaa Xaa Xaa Asp Xaa Ala Ser
            420                 425                 430

Val Xaa Xaa Gln Ser Gly Ile Xaa Ala Gly Xaa Asp Gly Tyr Xaa Ile
        435                 440                 445

Xaa Val Xaa Xaa Xaa Thr Xaa Leu Xaa Gly Xaa Xaa Xaa Xaa Ser Xaa
    450                 455                 460

Xaa Xaa Xaa Xaa Asp Lys Xaa Lys Asn Leu Xaa Xaa Thr Xaa Xaa Xaa
465                 470                 475                 480

Xaa Xaa Xaa Asp Ile Gln Asn His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                485                 490                 495

Gly Xaa Xaa Gly Xaa Phe
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<210> SEQ ID NO 191
<211> LENGTH: 491
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: pspA

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<400> SEQUENCE: 191

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

Gly Arg Asp Ile Thr Val Thr Gly Ser Asn Ile Ile Ala Asp Asn His
             20                  25                  30

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

Arg Ser Arg Ser Ala Glu Met Asn Lys Lys Glu Lys Ser Gly Leu Met
     50                  55                  60

Gly Ser Gly Gly Ile Gly Phe Thr Ala Gly Ser Lys Lys Asp Thr Gln
 65                  70                  75                  80

Thr Asn Arg Ser Glu Thr Val Ser His Thr Glu Ser Val Val Gly Ser
                 85                  90                  95

Leu Asn Gly Asn Thr Leu Ile Ser Ala Gly Lys His Tyr Thr Gln Thr
            100                 105                 110

Gly Ser Thr Ile Ser Ser Pro Gln Gly Asp Val Gly Ile Ser Ser Gly
        115                 120                 125

Lys Ile Ser Ile Asp Ala Ala Gln Asn Arg Tyr Ser Gln Glu Ser Lys
    130                 135                 140

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

Val Asn Thr Val Met Gly Ala Val Asp Ala Val Lys Ala Val Gln Thr
                165                 170                 175

Val Gly Lys Ser Lys Asn Ser Arg Val Asn Ala Met Ala Ala Ala Asn
            180                 185                 190

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

Arg Asn Pro Lys Lys Ala Ala Gly Gln Gly Ile Ser Val Ser Val Thr
    210                 215                 220

Tyr Gly Glu Gln Lys Asn Thr Ser Glu Ser Arg Ile Lys Gly Thr Gln
225                 230                 235                 240

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

Ser Gly Ala Gly Lys Asp Ser Arg Ile Thr Ile Thr Gly Ser Asp Val
            260                 265                 270

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

Glu Ala Ala Arg Gln Thr His Gln Glu Arg Ser Glu Asn Lys Ser Ala
    290                 295                 300

Gly Phe Asn Ala Gly Val Ala Ile Ala Ile Asn Lys Gly Ile Ser Phe
305                 310                 315                 320

Gly Phe Thr Ala Gly Ala Asn Tyr Gly Lys Gly Tyr Gly Asn Gly Asp
                325                 330                 335

Glu Thr Ala Tyr Arg Asn Ser His Ile Gly Ser Lys Asp Ser Gln Thr
            340                 345                 350

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

Gly Lys Gly Val Gly Val Thr Ala Glu Ser Leu His Ile Glu Ser Leu
    370                 375                 380

Gln Asp Thr Ala Val Phe Lys Gly Lys Gln Glu Asn Val Ser Ala Gln
385                 390                 395                 400
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Val Thr Val Gly Tyr Gly Phe Ser Val Gly Gly Ser Tyr Asn Arg Ser
                405                 410                 415

Lys Ser Ser Ser Asp Tyr Ala Ser Val Asn Glu Gln Ser Gly Ile Phe
            420                 425                 430

Ala Gly Gly Asp Gly Tyr Arg Ile Arg Val Asn Gly Lys Thr Gly Leu
        435                 440                 445

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

Lys Thr Ser Glu Ile Trp His Lys Asp Ile Gln Asn His Ala Ser Ala
465                 470                 475                 480

Ala Ala Ser Ala Leu Gly Leu Ser Gly Gly Phe
                485                 490


<210> SEQ ID NO 192
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 192

Tyr Arg Arg His Leu Leu Cys Lys Tyr Ile Tyr Arg Phe Pro Ile Tyr
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Cys Pro Xaa Ala Cys Val Ala Glu Asp Thr Pro Tyr Ala Cys Tyr Leu
             20                  25                  30

Xaa Gln Leu Gln Val Thr Lys Asp Val Asn Trp Asn Gln Val Xaa Leu
         35                  40                  45

Ala Tyr Asp Lys Trp Asp Tyr Lys Gln Glu Gly Leu Thr Gly Ala Gly
     50                  55                  60

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

Ala Gly Ala Ala Leu Gly Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp
                 85                  90                  95

Ala Ala Phe Ala Ser Leu Ala Ser Gln Ala Ser Val Ser Leu Ile Asn
            100                 105                 110

Asn Lys Gly Asn Ile Gly Asn Thr Leu Lys Glu Leu Gly Arg Ser Ser
        115                 120                 125

Thr Val Lys Asn Leu Met Val Ala Val Ala Thr Ala Gly Val Ala Asp
    130                 135                 140

Lys Ile Gly Ala Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile
145                 150                 155                 160

Asn Asn Leu Thr Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile
                165                 170                 175

Asn Thr Ala Val Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn
            180                 185                 190
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Ile Leu Ala Ala Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys
        195                 200                 205

Ile Lys Gln Leu Asp Gln His Tyr Ile Thr His Lys Ile Ala His Ala
    210                 215                 220

Ile Ala Gly Cys Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp
225                 230                 235                 240

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

Asn Gly Lys Asn Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile
            260                 265                 270

Leu Ala Tyr Ser Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly
        275                 280                 285

Gly Asp Val Asn Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn
    290                 295                 300

Asn Gln Leu Ser Asp Lys
305                 310


<210> SEQ ID NO 193
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF41a
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<223> OTHER INFORMATION: place-holder

<400> SEQUENCE: 193

Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn Ile Asn Trp Asn Gln Val
  1               5                  10                  15

Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu
             20                  25                  30

Ala Gly Ala Ala Ile Ile Ala Leu Ala Val Thr Val Val Thr Ser Gly
         35                  40                  45

Ala Gly Thr Gly Ala Val Leu Gly Leu Asn Gly Ala Xaa Ala Ala Ala
     50                  55                  60

Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser Gln Ala Ser Val Ser Phe
 65                  70                  75                  80

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

Ser Ser Thr Val Lys Asn Leu Val Val Ala Ala Ala Thr Ala Gly Val
            100                 105                 110
```

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Ala Asp Lys Ile Gly Ala Ser Ala Leu Xaa Asn Val Ser Asp Lys Gln
        115                 120                 125

Trp Ile Asn Asn Leu Thr Val Asn Leu Ala Asn Ala Gly Ser Ala Ala
    130                 135                 140

Leu Ile Asn Thr Ala Val Asn Gly Gly Ser Leu Lys Asp Xaa Leu Glu
145                 150                 155                 160

Ala Asn Ile Leu Ala Ala Leu Val Asn Thr Ala His Gly Glu Ala Ala
                165                 170                 175

Ser Lys Ile Lys Gln Leu Asp Gln His Tyr Ile Val His Lys Ile Ala
            180                 185                 190

His Ala Ile Ala Gly Cys Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys
        195                 200                 205

Gln Asp Gly Ala Ile Gly Ala Ala Val Gly Glu Ile Val Gly Glu Ala
    210                 215                 220

Leu Thr Asn Gly Lys Asn Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu
225                 230                 235                 240

Gln Ile Leu Ala Tyr Ser Lys Leu Val Ala Gly Thr Val Ser Gly Val
                245                 250                 255

Val Gly Gly Asp Val Asn Ala Ala Ala Asn Ala Ala Glu Val Ala Val
            260                 265                 270

Lys Asn Asn Gln Leu Ser Asp Xaa Glu Gly Arg Glu Phe Asp Asn Glu
        275                 280                 285

Met Thr Ala Cys Ala Lys Gln Asn Xaa Pro Gln Leu Cys Arg Lys Asn
    290                 295                 300

Thr Val Lys Lys Tyr Gln Asn Val Ala Asp Lys Arg Leu Ala Ala Ser
305                 310                 315                 320

Ile Ala Ile Cys Thr Asp Ile Ser Arg Ser
                325                 330


<210> SEQ ID NO 194
<211> LENGTH: 180
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF51a

<400> SEQUENCE: 194

Tyr Lys Leu Leu Ala Ile Gly Ser Val Val Gly Ser Ile Leu Gly Val
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Lys Leu Leu Leu Ile Leu Pro Val Ser Trp Leu Leu Leu Leu Met Ala
             20                  25                  30

Ile Ile Thr Leu Tyr Tyr Ser Val Asn Gly Ile Leu Asn Val Cys Ala
         35                  40                  45

Lys Ala Lys Asn Ile Gln Val Val Ala Asn Asn Lys Asn Met Val Leu
     50                  55                  60

Phe Gly Phe Leu Ala Gly Ile Ile Gly Gly Ser Thr Asn Ala Met Ser
 65                  70                  75                  80

Pro Ile Leu Leu Ile Phe Leu Leu Ser Glu Thr Glu Asn Lys Asn Arg
                 85                  90                  95

Ile Ala Lys Ser Ser Asn Leu Cys Tyr Leu Leu Ala Lys Ile Val Gln
            100                 105                 110

Ile Tyr Met Leu Arg Asp Gln Tyr Trp Leu Leu Asn Lys Ser Glu Tyr
        115                 120                 125
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```
Gly Leu Ile Phe Leu Leu Ser Val Leu Ser Val Ile Gly Leu Tyr Val
    130                 135                 140

Gly Ile Arg Leu Arg Thr Lys Ile Ser Pro Asn Phe Phe Lys Met Leu
145                 150                 155                 160

Ile Phe Ile Val Leu Leu Val Leu Ala Leu Lys Ile Gly Tyr Ser Gly
                165                 170                 175

Leu Ile Lys Leu
            180


<210> SEQ ID NO 195
<211> LENGTH: 180
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: ORF82a

<400> SEQUENCE: 195

Met Arg His Met Lys Asn Lys Asn Tyr Leu Leu Val Phe Ile Val Leu
  1               5                  10                  15

His Ile Thr Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
             20                  25                  30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
         35                  40                  45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
     50                  55                  60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
 65                  70                  75                  80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
                85                  90                  95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
            100                 105                 110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
        115                 120                 125

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

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
145                 150                 155                 160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Ala Lys Lys Pro Val Lys
                165                 170                 175

Ile Tyr Phe Tyr
            180
```

1-17. (canceled)

18. An isolated polypeptide comprising a member selected from the group consisting of

(a) the amino acid sequence of SEQ ID NO: 4; and

(b) an immunogenic fragment of at least 15 contiguous amino acids of SEQ ID NO: 4, wherein the immunogenic fragment, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell meditated immune response that recognizes the isolated polypeptide SEQ ID NO: 4.

19. The isolated polypeptide of claim 18, wherein the polypeptide is according to (a).

20. The isolated polypeptide of claim 18, wherein the polypeptide is according to (b).

21. The isolated polypeptide of claim 18, wherein the immunogenic fragment of (b) comprises at least 20 contiguous amino acids of SEQ ID NO:4; wherein the immunogenic fragment, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell meditated immune response that recognizes the polypeptide SEQ ID NO: 4.

22. The isolated polypeptide of claim 18, wherein the isolated polypeptide consists of SEQ ID NO: 4.

23. A fusion protein comprising the isolated polypeptide of claim 18.

24. An immunogenic composition comprising the polypeptide of claim 18, and a pharmaceutically acceptable carrier.

25. The isolated polypeptide of claim 18, wherein the isolated polypeptide is a recombinant polypeptide.

26. The isolated polypeptide of claim 19, wherein the isolated polypeptide is a recombinant polypeptide.

27. The isolated polypeptide of claim 20, wherein the isolated polypeptide is a recombinant polypeptide.

28. An immunogenic composition comprising the isolated polypeptide of claim 19.

29. An immunogenic composition comprising the isolated polypeptide of claim 20.

30. A fusion protein comprising the isolated polypeptide of claim 19.

31. A fusion protein comprising the isolated polypeptide of claim 20.

* * * * *