

(19) **DANMARK**



Patent- og
Varemærkestyrelsen

(10) **DK/EP 2718722 T3**

(12) Oversættelse af
europæisk patentskrift

-
- (51) Int.Cl.: **G 01 N 33/68 (2006.01)** **C 12 Q 1/04 (2006.01)** **G 01 N 33/569 (2006.01)**
- (45) Oversættelsen bekendtgjort den: **2018-01-15**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2017-10-18**
- (86) Europæisk ansøgning nr.: **12726000.8**
- (86) Europæisk indleveringsdag: **2012-06-05**
- (87) Den europæiske ansøgnings publiceringsdag: **2014-04-16**
- (86) International ansøgning nr.: **US2012040910**
- (87) Internationalt publikationsnr.: **WO2012170422**
- (30) Prioritet: **2011-06-06 US 201161493829 P**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
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- (54) Benævnelse: **PROTEOMIKBASERET DIAGNOSTISK FREMGANGSMÅDE TIL PÅVISNING AF KRONISK SINUSITIS**
- (56) Fremdragne publikationer:
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DESCRIPTION

FIELD OF INVENTION

[0001] The invention provides for a proteomic approach for identification of specific bacterial protein profiles that may be used in the development of methods for the diagnosis of bacterial chronic sinusitis. The invention provides for methods of determining the presence for pathogenic bacteria in the upper respiratory tract of a subject using protein profiles of the pathogenic bacteria. The invention also provides for methods of diagnosing a bacterial infection of the upper respiratory tract of a subject using protein profiles of the pathogenic bacteria. In addition, the invention provides for devices, immunoassays and kits for identifying pathogenic bacteria in the upper respiratory tract.

BACKGROUND

[0002] Otitis media, sinusitis, bronchitis, pharyngitis, and nonspecific upper respiratory tract infections (URTI) account for approximately 75% of outpatient antibiotic prescriptions in the United States. Antibiotic use remains high despite the fact that greater than 85% of these infections are due to viruses and resolve without complication. Nonetheless, those remaining infections that are indeed due to bacterial pathogens require more effective management than is currently available. Bacterial cultures provide limited diagnostic value because the most common bacteria responsible for URTI are also often commensal organisms in the nasopharynx.

[0003] Infections of the upper airway are the number one reason for office visits in the US (American Academy of Pediatrics. Pediatrics, 2004. 113:1451-1456, Center for Disease Control and Prevention web site, Gonzales R, et al. JAMA, 1997. 278(11):901-904, Nyquist A-C. JAMA, 1998 . 279(11): 875-877). About 52% of adults patients and 45% of pediatric patients are prescribed antibiotics when diagnosed with an upper airway infection (Gonzales R, et al. JAMA, 1997. 278(11):901-904, Nyquist A-C. JAMA, 1998. 279(11): 875-877). Upper airway infections are multifactorial and polymicrobial diseases. Infection by respiratory viruses (e.g. RSV, adenovirus, rhinovirus, parainfluenza virus) predisposes to bacterial superinfection by members of the nasopharynx normal flora: nontypeable *Haemophilus influenzae*, *Streptococcus pneumoniae* and *Moraxella catarrhalis*. While viral infections are often self-limiting, therapeutic delay of bacterial disease can lead to complications, permanent sequelae and severe morbidity and mortality.

[0004] Diagnosis is mainly based on clinical manifestations. Signs and symptoms of disease of bacterial and nonbacterial etiologies are often indistinguishable. Specific bacterial identification by traditional microbiological culture techniques often fail to detect microorganisms growing within biofilms. Contamination of specimens by resident colonizing flora often results in

laboratory culture reports of uncertain clinical value. Other methods of detection are needed.

Villaseñor-Sierra and Santos (Clinical Infectious Diseases 1999;28:267-73) investigated the presence of nontypeable NTHI subtypes by determining the outer membrane protein profiles from simultaneous cultures of nasopharyngeal exudates and middle ear fluids from children with acute otitis media.

Krasan et al. (Infection and Immunity 1999 Jan;67(1):449-54) assessed the expression of hia, and hemagglutinating pili (HMW1 and HMW2) in matched nasopharyngeal and middle ear isolates of nontypeable NTHI from children with acute otitis media and determined that the majority of isolates of nontypeable NTHI associated with acute otitis media express HMW1/HMW2-like proteins.

Indiscriminate antibiotic use modifies the commensal flora in the nasopharynx and induces the selection and emergence of microorganisms resistant to common antibiotics. Despite a decreasing trend in antibiotic prescription in recent years, unnecessary and inappropriate antibiotic therapies are common, particularly in the treatment of otitis media and sinusitis.

[0005] Upper respiratory tract infection remains as a major cause of overuse of antibiotics and, therefore, a major contributor to the widespread emergence of antibiotic resistance. Therefore, there is a need for early and rapid diagnostic tests that could discriminate between commensal and pathogenic bacteria. These tests would promote judicious use of antibiotic therapy, promote more effective choice of treatment and improve outcomes.

SUMMARY OF INVENTION

[0006] Due to unique growth characteristics, bacterial biofilms produce a distinct set of proteins may be used to distinguish between commensal and pathogenic states. Described herein are methods of identifying the protein profile of bacterial biofilms. The methodology involves detecting trace quantities of signature proteins that identify specific bacterial pathogens from typically sterile sites in the paranasal sinus cavities. As described herein, biofilms produced by nontypeable *Haemophilus influenzae* (NTHI) over 10 days generate a specific protein profile. Biofilms formed by NTHI *in vitro* release a signature set of proteins into their environment that remains identifiable for several days. Outer membrane proteins (OMPs) are predominant components of the NTHI biofilm supernatant. Of particular interest are major OMPs associated with bacterial virulence: outer membrane protein P5 (OMP P5) and outer membrane protein P2 (OMP P2). Additional OMPs include high molecular weight adhesin 1/high molecular weight adhesin 2 (HMW1/HMW2), and IgA-protease. HMW1/HMW2, OMP P5 are mediators of adhesion to epithelial cells, OMP P2 is a porin and IgA protease functions to cleave host IgA.

[0007] These studies support the development of a clinical diagnostic test and device for early and rapid identification of NTHI -associated URTIs, leading to a more effective choice of treatment and improved outcomes. NTHI was used as an example for the study but the same methods may be used to identify the presence of any pathogenic bacteria including those known to cause chronic sinusitis such as *Haemophilus influenza*, *Streptococcus pneumoniae*,

Moraxella catarrhalis, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Stenotrophomonas maltophilia*.

[0008] We also describe herein an immunoassay device that involves obtaining a sample of the secretions within the typically sterile paranasal sinus cavities, and rapidly detecting the presence of trace quantities of signature proteins that identify specific bacterial pathogens from these typically sterile sites.

[0009] Disclosed herein are methods of detecting the presence of a pathogenic bacteria in the upper respiratory tract of a subject comprising the steps of: a) obtaining a sample of secretions from the upper respiratory tract of the subject; b) generating a protein profile of the sample; c) comparing the protein profile with a reference protein profile, wherein the reference protein profile identifies a pathogenic bacteria; and d) determining whether the protein profile of the sample associates to the reference protein profile, wherein association is indicative of the presence of the pathogenic bacteria in the upper respiratory tract of the subject.

[0010] We also disclose herein methods of detecting the presence of a pathogenic bacteria in the upper respiratory tract of a subject as described above wherein the method further comprises the step of administering a therapeutic compound to reduce or eliminate the pathogenic bacteria in the upper respiratory tract of the subject. Exemplary therapeutic compounds that reduce or eliminate pathogenic bacteria in the upper respiratory tract include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate and zinc salts.

[0011] We also disclose herein methods of detecting the presence of a pathogenic bacteria in the upper respiratory tract of a subject as described above wherein the method further comprises the step of informing the subject of the presence or absence of the pathogenic bacteria in the upper respiratory tract.

[0012] We also disclose herein methods of detecting the presence of a pathogenic bacteria in the upper respiratory tract of a subject as described above wherein the method further comprises the step of diagnosing the subject with a bacterial infection, wherein the presence of the pathogenic bacteria in the upper respiratory tract of the subject is indicative of a bacterial infection.

[0013] The term "pathogenic bacteria" refers to any disease causing bacteria. The term "commensal bacteria" refers to harmless or non-disease causing bacteria. The methods described herein also may be used to distinguish the presence of commensal bacteria verses pathogenic bacteria in the upper respiratory tract of a subject.

[0014] We describe herein methods of diagnosing a bacterial infection in the upper respiratory tract of a subject comprising the steps of: a) obtaining a sample of secretions from the upper respiratory tract of the subject; b) generating a protein profile of the sample; c) comparing the protein profile of the sample with a reference protein profile, wherein the reference protein profile identifies a pathogenic bacteria; and d) determining whether the protein profile of the sample associates to the protein profile; wherein association is indicative of a bacterial infection in the upper respiratory tract of the subject.

[0015] Also described herein are methods of diagnosing a bacterial infection in the upper respiratory tract of a subject as described above wherein the method further comprises the step of the step of informing the subject of the diagnosis of a bacterial infection in the upper respiratory tract.

[0016] Methods disclosed herein also include methods of diagnosing a bacterial infection in the upper respiratory tract of a subject as described above wherein the method further comprises the step of administering a therapeutic compound to treat the bacterial infection. A treatment for a bacterial infection will reduce or alleviate the symptoms caused by the pathogenic bacteria or eliminate the bacteria from the site of infection. Exemplary therapeutic compounds that treat a bacterial infection in the upper respiratory tract include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts. The term "protein profile" refers to at least one protein that is at least partially identified or characterized so that the presence or absence of the protein in any particular sample may be monitored. The term "reference protein profile" refers to a protein profile generated for a known control or standard sample.

[0017] A protein profile of a sample associates with a reference protein profile when one or more the proteins in the reference profile are present in the sample profile at a concentration that indicates infection or pathogenicity of the bacteria. To determine if a sample protein profile associates with a reference protein profile, the profiles are scored to predict how likely the mass of a fragment that it detected is likely from the peptide sequence it is predicted it to be, and how much quantity of the peptide there is in the supernatant. Software programs that analyze mass spectrometry data may be used. For example, Mascot (Matrix Science, Boston, MA), performs mass spectrometry data analysis through a statistical evaluation of matches between observed and projected peptide fragments rather than cross correlation may be used to determine in the sample associates with a reference protein profile. See, e.g., *Electrophoresis*, 20(18) 3551-67 (1999).

[0018] The preceding methods may be carried out for any pathogenic bacteria which infects the upper respiratory tract, including *Haemophilus influenzae*, *Streptococcus pneumoniae*, *Moraxella catarrhalis*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* or *Stenotrophomonas maltophilia*.

[0019] We describe herein uses of a therapeutic compound for the preparation of a medicament to reduce or eliminate the pathogenic bacteria in the upper respiratory tract of a subject or uses to treat a bacterial infection in the upper respiratory tract of a subject, wherein the subject has a protein profile that associates to a reference protein profile, and wherein the association is indicative of the presence of the pathogenic bacteria or bacterial infection in the upper respiratory tract of the subject as determined by any of the preceding methods of detecting the presence of a pathogenic bacteria or diagnosing a bacterial infection in the upper respiratory tract of a subject.

[0020] We also describe herein therapeutic compositions for the reduction or elimination of a pathogenic bacteria in the upper respiratory tract of a subject or for the treatment of a bacterial infection in the upper respiratory tract of a subject, wherein the subject has a protein profile that associates to a reference protein profile, and wherein the association is indicative of the presence of the pathogenic bacteria or bacterial infection in the upper respiratory tract of the subject as determined by any of the preceding methods of detecting the presence of a pathogenic bacteria or diagnosing a bacterial infection in the upper respiratory tract of a subject.

[0021] Exemplary therapeutic compounds that treat a bacterial infection in the upper respiratory tract include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0022] In one aspect of the invention, the invention provides for methods of detecting the presence of Nontypeable *Haemophilus influenzae* (NTHI) bacteria in the upper respiratory tract of a subject comprising the steps of: a) obtaining a sample of secretions from the upper respiratory tract of the subject; b) detecting the presence of at least one biomarker in the sample, wherein the biomarker is OMP P5 or OMP P2 wherein the presence of at least one biomarker indicates the presence of NTHI bacteria in the upper respiratory tract of the subject. In one embodiment, the method comprises detecting the presence of OMP P2 and/or OMP P5 in the sample, wherein the presence of OMP P2 and/or OMP P5 indicates the presence of NTHI bacteria in the upper respiratory tract of the subject.

[0023] We also describe herein methods of detecting the presence of NTHI bacteria in the

upper respiratory tract of a subject wherein the method further comprises the step of administering a therapeutic compound to reduce or eliminate the NTHI bacteria in the upper respiratory tract of the subject. Exemplary therapeutic compounds that reduce or eliminate the NTHI bacteria in the upper respiratory tract include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0024] The invention also provides for methods of diagnosing a NTHI infection in the upper respiratory tract of a subject comprising the steps of: a) obtaining a sample of secretions from the upper respiratory tract of the subject, b) detecting the presence of at least one biomarker in the sample, wherein the biomarkers are selected from OMP P5 and OMP P2 wherein the presence of at least one biomarker indicates an NTHI infection in the upper respiratory tract of the subject. In one embodiment, the method comprises detecting the presence of OMP P2 and/or OMP P5 in the sample, wherein the presence of OMP P2 and/or OMP P5 indicates a NTHI bacterial infection in the upper respiratory tract of the subject.

[0025] We also describe herein methods of diagnosing a NTHI infection in the upper respiratory tract of a subject as described above wherein the method further comprises the step of informing the subject of the diagnosis of a NTHI infection in the upper respiratory tract.

[0026] We describe herein methods of diagnosing NTHI infection in the upper respiratory tract of a subject as described above wherein the method further comprises the step of administering a therapeutic compound to treat the NTHI infection in the upper respiratory tract of the subject. A treatment for a NTHI infection will reduce or alleviate the symptoms caused by the NTHI bacteria or eliminate the NTHI bacteria from the site of infection. Exemplary therapeutic compounds that treat a NTHI infection in the upper respiratory tract include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0027] The term "upper respiratory tract" includes the nose or nostrils, nasal cavity, mouth, throat (pharynx), paranasal sinus cavity and voice box (larynx). The respiratory system is lined with a mucous membrane that secretes mucus or fluid. This secreted mucus and fluid is referred to herein as "secretions." In any of the preceding methods, the sample of secretions

may be collected from the paranasal sinus cavity including the middle meatus or the ethmoid infundibulum. The "paranasal sinus cavity" refers to the frontal sinuses (in the forehead), maxillary sinuses (behind the cheek bones), ethmoid sinuses (between the eyes) and the sphenoid sinuses (behind the eyes).

[0028] We describe herein the use of a therapeutic compound for the preparation of a medicament to reduce or eliminate NTHI bacteria in the upper respiratory tract of a subject or to treat a NTHi infection in the upper respiratory tract of a subject, wherein the presence of NTHI bacteria or a NTHI infection is determined by the presence of at least one biomarker selected from OMP P2 and OMP P5 as determined by any of the preceding methods of detecting the presence of a NTHI bacterial or diagnosing a NTHI infection in the upper respiratory tract of a subject method as determined by the preceding methods of detecting the presence of NTHI bacteria or diagnosing a NTHI infection in the upper respiratory tract of a subject.

[0029] We describe herein a therapeutic composition for the reduction or elimination of NTHI bacteria or for the treatment of NTHI infection in the upper respiratory tract of a subject, wherein the presence of NTHi bacteria or NTHI infection as determined by any of the preceding methods of detecting the presence of a NTHI bacterial or diagnosing a NTHI infection in the upper respiratory tract of a subject.

[0030] Any of the preceding methods, uses or therapeutic compositions may be carried out on a subject suffering from chronic sinusitis, or a subject that is prone to suffering from recurrent acute sinusitis. In addition, any of the preceding methods may be carried out on a subject suffering from Otitis media, bronchitis, pharyngitis, and nonspecific upper respiratory tract infections.

[0031] Methods, uses or therapeutic compositions for treating chronic sinusitis or a pathogenic bacterial infection of the upper respiratory tract in a subject may comprise detecting a pathogenic bacteria in the upper respiratory tract of the subject using any of the preceding methods and administering the appropriate dose of a therapeutic compound known to effectively treat the particular pathogenic bacteria detected within the upper respiratory tract of the subject. A treatment for a chronic sinusitis or a pathogenic bacterial infection will reduce or alleviate the symptoms caused by the pathogenic bacteria or eliminate the pathogenic bacteria from the site of the infection. Exemplary therapeutic compounds include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0032] Methods of treating, uses and therapeutic compositions for chronic sinusitis or a pathogenic bacterial infection of the upper respiratory tract in a subject may comprise diagnosing a pathogenic bacteria infection in the upper respiratory tract of the subject using any of the preceding methods and administering the appropriate dose of a therapeutic compound known to effectively treat the particular pathogenic bacteria detected within the upper respiratory tract of the subject. Exemplary therapeutic compounds include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone and zinc salts.

[0033] In any of the preceding methods, uses or therapeutic compositions of the invention, the sample may be collected using sterile swabs, sterile gauze, nasal washing, suction tube or a balloon catheter.

[0034] For the detecting step in any of the preceding methods of the invention, the biomarker may be detected using a monoclonal antibody. In addition, an immunoassay may be used to detect the biomarker of interest in any of the preceding methods of the invention.

[0035] In any of the preceding methods of the invention, the sample may be collected with a device comprising a substrate presenting antibodies specific for the biomarkers of interest, such as a balloon catheter wherein the substrate is threaded into the suction port of the catheter.

[0036] We describe herein immunoassays for detecting the presence of a pathogenic bacteria in the upper respiratory tract of a subject comprising the steps of a) obtaining a sample of secretions from the upper respiratory tract of the subject using a device comprising antibodies specific for at least one biomarker associated with the presence of a pathogenic bacteria in the upper respiratory tract of the subject; b) detecting the presence of at least one biomarker associated with the presence of a pathogenic bacteria in the upper respiratory tract of the subject to generate a protein profile; c) comparing the protein profile with a reference protein profile, wherein the reference protein profile identifies a pathogenic bacteria; and d) determining whether the protein profile of the sample associates to the reference protein profile, wherein association is indicative of the presence of the pathogenic bacteria in the upper respiratory tract of the subject.

[0037] The term "immunoassay" is a laboratory approach to directly or indirectly detect protein or peptide in fluid, e.g. biological fluid, by use of an immunological reaction between an antigen and an antibody.

[0038] The term "antibody" is synonymous with "immunoglobulin," and includes naturally occurring human antibodies, polyclonal antibodies, and monoclonal antibodies. The term "antibody" is meant to include both the native antibody and biologically active and synthetic derivatives of antibodies, such as, for example, Fab', F(ab')₂ or Fv as well as single-domain and single-chain antibodies. A biologically active derivative of an antibody retains the ability to bind an antigen. In particular, the invention provides for methods and immunoassays that use antibodies specific for the biomarkers of interests, such as monoclonal antibodies that specifically bind biomarkers of interest, e.g. OMP P2 and OMP P5.

[0039] In addition, the immunoassays described above may further comprising a step of diagnosing the subject with a bacterial infection wherein the presence of the pathogenic bacteria in the upper respiratory tract of the subject is indicative of a bacterial infection.

[0040] We also describe herein immunoassays further comprising the step of administering a therapeutic compound in an amount effective to treat the bacterial infection. Exemplary therapeutic compounds include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0041] In any of the preceding immunoassays, the pathogenic bacteria detected may be *Haemophilus influenzae*, *Streptococcus pneumoniae*, *Moraxella catarrhalis*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* or *Stenotrophomonas maltophilia*.

[0042] A therapeutic compound for the preparation of a medicament to reduce or eliminate NTHI bacteria in the upper respiratory tract of a subject or to treat a NTHi infection in the upper respiratory tract of a subject, may be used wherein the presence of NTHi bacterial or a NTHi infection is determined by the presence of at least one biomarker selected from OMP P2 and OMP P5 as determined by any of the preceding methods.

[0043] A therapeutic composition for the reduction or elimination of NTHI bacteria in the upper respiratory tract of a subject or for the treatment of NTHi infection in the upper airway of a subject, may be used wherein the presence of NTHi bacteria or NTHi infection is determined by the presence of at least one biomarker selected from OMP P2 and OMP P5 as determined by any of the preceding immunoassays.

[0044] We describe herein immunoassays for detecting the presence of a nontypeable NTHI bacteria in the upper respiratory tract of a subject comprising the steps of a) obtaining a sample of secretions from the upper respiratory tract of the subject using a device comprising antibodies specific for at least one biomarker associated with the presence of a NTHI bacteria

in the upper respiratory tract of the subject, wherein at least one biomarker is OMP P2 or OMP P5; b) detecting the presence of at least one biomarker associated with the presence of a NTHI bacteria in the upper respiratory tract of the subject to generate a protein profile; c) comparing the protein profile with a reference protein profile, wherein the reference protein profile identifies NTHI bacteria; and d) determining whether the protein profile of the sample associates to the reference protein profile, wherein association is indicative of the presence of the NTHI bacteria in the upper respiratory tract of the subject.

[0045] We disclose herein immunoassays for detecting the presence NTHI bacteria in the upper respiratory tract of a subject as described above further comprising a step of diagnosing the subject with a NTHI infection wherein the presence of NTHI bacteria in the upper respiratory tract of the subject is indicative of a NTHI infection.

[0046] We also describe herein immunoassays, which further comprise the step of administering a therapeutic compound in an amount effective to treat the bacterial infection. Exemplary therapeutic compounds include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0047] We describe herein immunoassays for diagnosing a NTHI infection in the upper respiratory tract of a subject comprising the steps of a) obtaining a sample of secretions from the upper respiratory tract of the subject using a device comprising antibodies specific for at least one biomarker associated with the presence of a NTHI in the upper respiratory tract of the subject, wherein the at least one biomarker is OMP P2 or OMP P5; b) detecting the presence of at least one biomarker associated with the presence of a NTHI in the upper respiratory tract of the subject to generate a protein profile; c) comparing the protein profile with a reference protein profile, wherein the reference protein profile identifies NTHI; and d) determining whether the protein profile of the sample associates to the reference protein profile, wherein association is indicative of a NTHI infection in the upper respiratory tract of the subject.

[0048] We also describe herein immunoassays further comprising the step of informing the subject of the presence of a NTHI bacteria or a NTHI infection in the upper respiratory tract of the subject. Exemplary therapeutic compounds include antibiotics such as penicillin, erythromycin, amoxicillin, thimethoprim-sulfamethoxazole, doxycycline, cefpodoxime, cefuroxime, cefdinir, clarithromycin, azithromycin, levofloxacin, gatifloxacin, and moxifloxacin, alpha-adrenergic agonists such as oxymetazoline hydrochloride, anticholinergic (parasympatholytic) agents such as ipratropium bromide, antihistamines such as chlorpheniramine maleate, beta-agonist bronchodilators, non-steroidal anti-inflammatory

drugs, camphor, menthol, Echinacea, mast cell stabilizers such as cromolyn sodium, topical nasal steroids such as fluticasone propionate, budesonide, mometasone, triamcinolone, and dexamethasone, and zinc salts.

[0049] In addition, the sample used in any of the preceding immunoassays may be obtained using a sterile swab, sterile gauze, suction tube or a balloon catheter.

[0050] In another aspect we describe herein a device for obtaining a sample of secretions from the upper respiratory tract of a subject comprising a substrate presenting antibodies specific for at least one biomarker associated with the presence of a pathogenic bacteria in the upper respiratory tract of the subject.

[0051] We also describe herein devices for carrying out any of the preceding methods of the invention or any of the preceding immunoassays of the invention which is used for obtaining a sample of secretions from the upper respiratory tract of a subject comprising a substrate presenting antibodies specific for biomarkers associated with the presence of a pathogenic bacteria in the upper respiratory tract of the subject.

[0052] In any of the preceding devices, the antibodies may be specific for OMP P2 or OMP P5, such as monoclonal antibodies that specifically bind NTHI OMP P2 or monoclonal antibodies that specifically bind NTHI OMP P5.

[0053] Disclosed herein are kits for carrying out any of the preceding methods or immunoassays. The kits may comprise a substrate presenting antibodies specific for at least one biomarker associated with the presence of a pathogenic bacteria or a bacterial infection in the upper respiratory tract of the subject. The kits may comprise devices for obtaining the sample from the sterile compartments within the upper respiratory tract of the subject and generating a protein profile associated with a pathogenic bacteria or bacterial infection in the upper respiratory tract of the subject. The kits may also comprise antibodies that specifically bind the protein biomarkers of interest and components for immunoassays to detect the protein biomarkers using these antibodies.

BRIEF DESCRIPTION OF DRAWINGS

[0054]

Figure 1 depicts a silver stain of the distinct protein profile maintained over time in the NTHI biofilm supernatant.

Figure 2 depicts a Western blot analysis verifying the presence of the NTHI OMPs in NTHI biofilm supernatant.

Figure 3 depicts a Western blot analysis verifying the presence of OMP P2 and OMP P5 in the biofilm supernatant of various strains of NTHI.

DETAILED DESCRIPTION

[0055] We describe herein methods with improved sensitivity and specificity for detecting and diagnosing bacterial sinusitis. In particular, the methods comprise antibody-based bacterial detection of proteins within secretions of pathogenic biofilm located within the paranasal sinus cavities. These methods allow for the detection of trace quantities of signature proteins that identify specific bacterial pathogens from typically sterile sites in the paranasal sinus cavities. The methods avoid broad-spectrum, empiric antibiotics which are often inappropriately given treat upper viral respiratory infections due to the difficulty in diagnosing bacterial sinusitis with a high sensitivity and high specificity. The methods are an improvement over typical bacterial cultures because these cultures have very low sensitivity for detecting bacterial biofilms and low specificity for distinguishing between commensal and pathogenic organisms.

[0056] We describe herein a device that involves delivering a wire through a balloon catheter to the typically sterile paranasal sinus cavities, sampling mucus from these sites, and rapidly detecting the presence of trace quantities of signature proteins that identify specific bacterial pathogens from these typically sterile sites. Upon obtaining the sample, an immunoassay may be run to generate a protein profile that is compared to a reference protein profile generated for the pathogenic bacteria known to cause chronic sinusitis or an infection of the upper respiratory tract.

Biomarkers

[0057] The term "biomarker" refers to a naturally occurring molecule, gene, or characteristic by which a particular pathological or physiological process or disease, can be identified or characterized. The term "biomarker" may refer to a protein measured in sample whose concentration reflects the severity or presence of some disease state. Biomarkers may be measured to identify risk for, diagnosis of or progression of a pathological or physiological process, or disease. Exemplary biomarkers include proteins, hormones, prohormones, lipids, carbohydrates, DNA, RNA and combinations thereof.

[0058] For example, biomarkers for NTHI pathogenic bacteria include outer membrane protein P2 (OMP P2; SEQ ID NO: 1), high molecular weight adhesin 1 (HMW1A; SEQ ID NO: 2), putative periplasmic chelated iron binding proteins (SEQ ID NO: 3), IgA-specific serine endopeptidase (SEQ ID NO: 4), outer membrane protein P5 (OMP P5; SEQ ID NO: 5), galactose-1-phosphate uridylyltransferase (SEQ ID NO: 6), HMWA (SEQ ID NO: 7), phosphate ABC transporter phosphate-binding protein (SEQ ID NO: 8), putative adhesin B precursor FimA (SEQ ID NO: 9), high molecular weight adhesin 2 (HMW2A; SEQ ID NO: 10), outer membrane protein P5 precursor (SEQ ID NO: 11) and outer membrane protein P1 (OMP P1; SEQ ID NO:

12).

[0059] The methods may include detecting at least one biomarker, at least two biomarkers, at least three biomarkers, at least four biomarkers, at least five biomarkers or six or more biomarkers of the protein profile of a pathogenic bacteria. Detection of the protein biomarkers includes detecting full length or fragments of the protein biomarkers, including immunogenic or biologically active fragments. Methods may include detecting at least OMP P2 and OMP 5 to generate a protein profile of NTHI bacteria.

[0060] Described herein are biologically active or immunologically active variants of the amino acid sequences of the present invention; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological and/or immunogenic activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides encoded by the native polynucleotides.

[0061] We also describe herein isolated polypeptides or peptides encoded by the nucleic acid fragments or by degenerate variants of the nucleic acid fragments. The term "degenerate variant" refers to nucleotide fragments which differ from a native nucleic acid fragment (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments are the ORFs that encode proteins.

[0062] Polypeptides may contain one or more conservative amino acid substitutions that do not affect the biological and/or immunogenic activity of the polypeptide. Alternatively, the polypeptides are contemplated to have conservative amino acids substitutions which may or may not alter biological activity. The term "conservative amino acid substitution" refers to a substitution of a native amino acid residue with a nonnative residue, including naturally occurring and nonnaturally occurring amino acids, such that there is little or no effect on the polarity or charge of the amino acid residue at that position. For example, a conservative substitution results from the replacement of a non-polar residue in a polypeptide with any other non-polar residue. Further, any native residue in the polypeptide may also be substituted with alanine, according to the methods of "alanine scanning mutagenesis". Naturally occurring amino acids are characterized based on their side chains as follows: basic: arginine, lysine, histidine; acidic: glutamic acid, aspartic acid; uncharged polar: glutamine, asparagine, serine, threonine, tyrosine; and non-polar: phenylalanine, tryptophan, cysteine, glycine, alanine, valine, proline, methionine, leucine, norleucine, isoleucine. General rules for amino acid substitutions are set forth in Table 1 below.

Table 1

Amino Acid Substitutions		
Original Residues	Exemplary Substitutions	Preferred Substitutions
Ala	Val, Leu, Ile	Val
Arg	Lys, Gln, Asn	Lys
Asn	Gln	Gln
Asp	Glu	Glu
Cys	Ser, Ala	Ser
Gln	Asn	Asn
Glu	Asp	Asn
Gly	Pro, Ala	Ala
His	Asn, Gln, Lys, Arg	Arg
Ile	Leu, Val, Met, Ala, Phe,	Leu
Leu	Norleucine, Ile, Val, Met,	Leu
Lys	Arg, 1,4 Diaminobutyric	Arg
Met	Leu, Phe, Ile	Leu
Phe	Leu, Val, Ile, Ala, Tyr	Arg
Pro	Ala	Gly
Ser	Thr, Ala, Cys	Thr
Thr	Ser	Ser
Trp	Tyr, Phe	Tyr
Tyr	Trp, Phe, Thr, Ser	Phe
Val	Ile, Met, Leu, Phe, Ala,	Leu

[0063] The polypeptides may be encoded by nucleotide sequences that are substantially equivalent to the polynucleotides encoding the polypeptide biomarkers. Polynucleotides according to the invention can have, e.g., at least 65%, at least 70%, at least 75%, at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more typically at least 90%, 91%, 92%, 93%, or 94% and even more typically at least 95%, 96%, 97%, 98% or 99% sequence identity to the native polynucleotide sequences.

[0064] Nucleic acid sequence fragments may hybridize under stringent conditions to the nucleotide sequences encoding the polypeptide biomarkers or compliments thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g., 15, 17, or 20 nucleotides or more that are selective for (i.e., specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes may be capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences from other polynucleotide sequences in the same family of genes or can differentiate genes from other

bacterial genes, and are preferably based on unique nucleotide sequences.

[0065] The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Hybridization stringency is principally determined by temperature, ionic strength, and the concentration of denaturing agents such as formamide. Examples of stringent conditions for hybridization and washing are 0.015 M sodium chloride, 0.0015M sodium citrate at 65-68°C or 0.015 M sodium chloride, 0.0015M sodium citrate, and 50% formamide at 42 °C See Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2.sup.nd Ed., Cold Spring Harbor Laboratory, (Cold Spring Harbor, N.Y. 1989). More stringent conditions (such as higher temperature, lower ionic strength, higher formamide, or other denaturing agent) may also be used, however, the rate of hybridization will be affected. In instances wherein hybridization of deoxyoligonucleotides is concerned, additional exemplary stringent hybridization conditions include washing in 6x.SSC 0.05% sodium pyrophosphate at 37 °C (for 14-base oligos), 48 °C (for 17-base oligos), 55 °C (for 20-base oligos), and 60 °C. (for 23-base oligos).

[0066] Other agents may be included in the hybridization and washing buffers for the purpose of reducing non-specific and/or background hybridization. Examples are 0.1% bovine serum albumin, 0.1% polyvinyl-pyrrolidone, 0.1% sodium pyrophosphate, 0.1% sodium dodecylsulfate, NaDodSO.sub.4, (SDS), ficoll, Denhardt's solution, sonicated salmon sperm DNA (or other non-complementary DNA), and dextran sulfate, although other suitable agents can also be used. The concentration and types of these additives can be changed without substantially affecting the stringency of the hybridization conditions. Hybridization experiments are usually carried out at pH 6.8-7.4, however, at typical ionic strength conditions, the rate of hybridization is nearly independent of pH. See Anderson et al., *Nucleic Acid Hybridisation: A Practical Approach*, Ch. 4, IRL Press Limited (Oxford, England). Hybridization conditions can be adjusted by one skilled in the art in order to accommodate these variables and allow DNAs of different sequence relatedness to form hybrids.

[0067] Use for sequences may also include allelic and species variations. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package, including GAP (Devereux et al., *Nucl. Acid. Res.*, 12:387,-1984; Genetics Computer Group, University of Wisconsin, Madison, Wis.), BLASTP, BLASTN, and FASTA (Altschul et al., *J. Mol. Biol.*, 215: 403-410, 1990). The BLASTX program is publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul et al. NCB/NILM/NIH Bethesda, MD 20894; Altschul et al., *supra*). The well known Smith Waterman algorithm may also be used to determine identity.

Methods of Generating Protein Profiles

[0068] The methods of the invention involve generating a protein profile of secretion samples obtained from the upper respiratory tract of a subject and generating protein profiles of pathogenic bacteria biofilm supernatants. The known pathogenic bacteria biofilm protein

profiles may be used as reference protein profiles for use in the methods of the invention.

[0069] Separation of protein of interest from the other members of the protein profile may be accomplished by any number of techniques, such as sucrose gradient centrifugation, aqueous or organic partitioning (e.g., two-phase partitioning), non-denaturing gel electrophoresis, isoelectric focusing gel electrophoresis, capillary electrophoresis, isotachyphoresis, mass spectroscopy, chromatography (e.g., HPLC), polyacrylamide gel electrophoresis (PAGE, such as SDS-PAGE), gel permeation, ion-exchange spin columns, and the like. In these embodiments, SELDI, or other rapid analysis techniques, may be used for monitoring the purification process. Following purification, all potential biomarkers may be characterized by SDS PAGE and mass spectrometry and identified by peptide mapping and/or amino acid sequence analysis.

[0070] For example, the protein biomarkers may be separated by size or buoyant density gradient separation method, such as a discontinuous sucrose gradient, that separates the component polypeptides of the sample by the sizes of the complexes in which they participate. Sucrose gradients for the separation of proteins are well known, and may be modified as needed. Such modifications may include the use of a continuous, rather than discontinuous gradient, and different gradient conditions (for instance, different sucrose concentrations or different buffers). The length of the gradient can also be varied, with longer gradients expected to give better overall separation of proteins and protein complexes, and to provide a larger number of fractions that are then each individually analyzed using a denaturing system.

[0071] The individual protein biomarkers may be separated by electrophoresis based upon size (e.g., by SDS-PAGE or sizing gel). Other separation techniques may include aqueous two-phase partitioning and non-denaturing agarose gel electrophoresis separation. In other embodiments, separation employs denaturing system such as an isoelectric focusing (IEF) gel, capillary electrophoresis, or isotachyphoresis. Alternatively or additionally, two-dimensional electrophoretic analysis may be used (e.g., Wilkins et al., *Proteome Research: New Frontiers in Functional Genomics*, Springer-Verlag, Berlin, 1997). Proteins can be visualized on such gels using any of various stains known in the art (e.g., Trypan Blue or SyproRuby dye). Traditional buffering systems can also be used for separating proteins in the component fractionations of the described systems. The temperature, voltage, and amperage at which individual gels are run also can be modified, as can the speed and duration of gradient equilibration and centrifugation.

[0072] Purification of protein biomarkers may be performed using traditional chromatographic techniques. In an embodiment, high pressure liquid chromatography (HPLC) may be used. Also, a combination of high pressure liquid chromatography (HPLC) and sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) may be used to purify the protein. The fractions may then be assayed for the protein of interest using SELDI or other methods.

[0073] A variety of methods may be used to generate the protein profile such as certain Matrix Assisted Laser Desorption Ionization (MALDI) Mass Spectrometry technology, Surface

Enhanced Laser Desorption/Ionization (SELDI) and Protein Chip Mass Spectrometry.

[0074] The methods may include steps for analyzing the protein profile. In an embodiment, analysis of the protein profile comprises a statistical analysis and other data manipulation techniques (e.g., signal processing, removal of noise). In some embodiments, techniques for analysis comprise computer statistical and data processing software. For example, analysis of the protein profile may comprise a determination of at least one of the molecular weight (mass), net charge, and or amount of the proteins in the sample.

[0075] The method may also comprise the step of comparing the protein profile for the subject's sample to a reference protein profile. In addition to biofilm protein profiles generated for known strains of bacteria, the reference profile may be from a healthy control subject who does not exhibit symptoms of the disease of interest (i.e., a negative control). The reference profile may be from a subject who has a disease of interest (i.e., a positive control). Also, the sample protein profile may be compared to a reference protein profile isolated from the same subject, but at a different point in time (e.g., to monitor progression or remission of the disease). The sample protein profile may be compared to a plurality of a reference protein profiles, as for example, reference profiles generated as diagnostic of a particular disease or disease subtype. In this way, it may be possible to determine whether the sample protein profile matches a particular protein or proteins of interest that are typical of any one disease or disease subtype.

Kits and Devices

[0076] Kits may be used for carrying out the methods and immunoassays of the invention. The kits may comprise devices for obtaining the secretion sample from the sterile compartments within the upper respiratory tract of the subject. The kits may also comprise antibodies that specifically bind the protein biomarkers of interest and components for immunoassays to detect the protein biomarkers using these antibodies. In addition, the kits may comprise substrates presenting antibodies specific for the protein biomarkers of interest. Furthermore, the kits may comprise instructions for carrying out the any of the methods or immunoassays of the invention.

[0077] In one embodiment, secretions from the upper respiratory tract may be obtained using sterile swabs or gauze. In another embodiment of the invention, the secretion sample may be collected using nasal washing methods. Alternatively, the secretion sample may be collected using a suction tube attached to an electric pump and a catheter inserted into the nasopharynx of the subject.

[0078] In another embodiment, the device for obtaining the secretion sample is a modified balloon catheter Seldinger technique that allows for collection of secretions from the sterile compartments within the upper respiratory tract of the subject. The balloon catheter may have a substrate presenting antibodies specific for the protein biomarkers of interest threaded into

the catheter. A modified distal chip bronchoesophagoscope or transnasal esophagoscope may be used in which a substrate presenting antibodies specific for the protein biomarkers of interest is threaded into the suction port of the device.

[0079] The invention provides for an immunoassay for detecting the at least one biomarker in the methods. For example, antibodies specific for two or more biomarkers within the protein profile are presented or absorbed to a solid substrate, and the secretion sample obtained from the upper airway of the respiratory tract of a subject are contacted with the solid substrate and binding of the antibody to the substrate is detected.

[0080] Any type of immunoassay system known in the art may be used to detect the biomarkers of the protein profiles. Exemplary methods include, but not limited to: radioimmunoassays, ELISA assays, sandwich assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, fluorescent immunoassays, protein A immunoassays and immunoelectrophoresis assays and any other methods of generating a protein profile described herein. The immunoassays may be a sandwich assay in which the target analyte (biomarker of interest) is "sandwiched" between a labeled antibody and an antibody immobilized on the solid substrate. The immunoassay is read by observing the presence and amount of antigen-labeled antibody complex bound to the immobilized antibody. Another immunoassay may also be a "competition" type immunoassay, wherein an antibody immobilized on a solid surface is contacted with a sample (e.g., secretions from the upper respiratory tract) containing both an unknown quantity of antigen analyte (biomarker of interest) and with labeled antigen of the same type. The amount of labeled antigen bound on the solid substrate is then determined to provide an indirect measure of the amount of antigen analyte (biomarker of interest) in the sample. Such immunoassays are readily performed in a "dipstick" or other test device format (e.g., a flow-through or migratory dipstick or other test device design) for convenient use. For example, numerous types of dipstick immunoassays are described in U.S. Pat. No. 5,656,448.

[0081] The immune assays may be carried out on sheets, e.g. strips or sheets of nitrocellulose or polyvinylidene difluoride (PVDF) or other membranes, dipstick, wells e.g. 96-well plastic plates, or in tubes.

[0082] A device used in the methods and immunoassays of the invention can, for example, provide a color indication when the biomarker of interest is within the secretion sample from the upper respiratory tract of a subject. The device could be used in a clinical setting to quickly determine if a subject has a pathological bacteria or a bacterial infection in the upper respiratory tract. Alternatively, the methods and immunoassays of the present invention may be used in combination with a densitometer or generally a device for measuring light intensity, transmittance, reflection or refraction, or for measuring the wavelength of light as a measure of assay result. The densitometer or other device can provide rapid measurement of the optical density of the substrate within the device that have been contacted with the secretions sample. In one embodiment, a change in color, density, or other parameter can be read by the naked eye.

[0083] The invention also may be carried out using a lateral-flow immunoassay which contains a device within the assay to extract the sample for analysis, and antibodies specific for the proteins within the protein profile of a pathogenic bacteria of interest. An immunoassay device, for example, such as those described in US Patent Nos. 5,415,994 and 5,763,262, may comprise a protein profile identified for a particular pathogenic bacteria using any of the methods of the invention. In particular, the invention provides for colorimetric immunoassays that allow for visual detection of the biomarkers of interest within the secretion sample. Visual detection allows for a rapid result which can be incorporated into a treatment plan for the infection.

[0084] A reference or standard protein profile may be used in the methods of the invention to compare the sample protein profile generated by the methods, immunoassays or kits of the invention. The reference or standard protein profile provides the concentration of a biomarker known to be present in the biofilm secretion of a pathogenic bacteria within the upper respiratory tract during an infection. A "calibrator" refers to immunoassays that detect known amounts of biomarkers of interest to generate a calibration curve to quantify the concentration of the biomarker in an unknown biological fluid.

[0085] The term "standard" or "reference" refers to immunoassays that measure biomarkers of interest from biological fluids known to be collected from a subject having a bacterial infection of the upper respiratory tract in a suitable quantitative form to control the quality of reagents contained in an immunoassay kit of the present invention. Other aspects and advantages of the present invention will be understood upon consideration of the following illustrative examples.

EXAMPLES

Example 1

Determination of Signature Protein Profile for Pathogenic Bacteria

[0086] Supernatants from Nontypeable *H. influenzae* (NTHI) biofilm were analyzed to determine the NTHI signature protein profile. NTHI strain 86-028NP was cultured in eight-well chamber slides for 10 days and the resulting supernatants were collected at 24 hours intervals. The proteins in the supernatants collected from NTHI biofilm cultures were separated by SDS-PAGE and silver stain revealed a distinct protein profile maintained over time as shown in Figure 1.

[0087] The proteins isolated from NTHI biofilm supernatants were analyzed by nano-liquid

chromatography/tandem mass spectrometry (LC-MS/MS). The molecular weights of the identified proteins were compared to the molecular weights of the known protein profile for the NTHI strain 86-028NP ((Bakaletz et al. Infection and Immunity, 56(2): 331-335, 1988), and the identified proteins were scored based on their association to the 86-028NP protein profile using Mascot (Matrix Science, Boston MA) according to the manufacturer's instructions. The results of this comparison are set out in Table 2 below. Several NTHI outer membrane proteins (OMPs) were identified (in bold), with predominance of major OMPs (bold italics): high molecular weight adhesins 1 and 2 (HMW1/HMW2), OMP P5, OMP P2, OMP P1, and IgA-protease.

[0088] In order to verify the presence of the NTHI OMPs in NTHI biofilm supernatants, Western blot analysis was carried out with antiserum against total OMPs, OMP P5 and OMP P2 (chinchilla polyclonal antibodies), as well as HMW1 and HMW2 proteins (monoclonal antibodies). This analysis verified the presence of multiple NTHI- specific OMPs in biofilm supernatants (see Figure 2).

Table 2:

IDENTIFIED PROTEIN	Score	Mass (kDa)	Accession #	SEQ ID NO:
<i>Outer membrane protein P2</i>	1227	39.9	<i>gi 68248747</i>	1
<i>HMW1A</i> , high molecular weight adhesin 1	1205	154.5	<i>gi 68250281</i>	2
putative periplasmic chelated iron binding protein	1089	32.4	<i>gi 301169065</i>	3
<i>IgA-specific serine endopeptidase</i>	948	197.5	<i>gi 68249575</i>	4
<i>Outer membrane protein P5</i>	886	38.4	<i>gi 68249712</i>	5
galactose-1-phosphate uridylyltransferase	791	34.0	<i>gi 145640927</i>	6
HMWA	720	160.5	<i>gi 68249817</i>	7
phosphate ABC transporter phosphate-binding protein	703	36.6	<i>gi 16273649</i>	8
putative adhesin B precursor FimA	402	35.0	<i>gi 3003012</i>	9
<i>HMW2A</i> , high molecular weight adhesin 2	326	160.7	<i>gi 68249817</i>	10
HMWA	321	160.5	<i>gi 5929966</i>	11
<i>Outer membrane protein P5; Precursor</i>	283	37.7	<i>gi 585614</i>	12
<i>Outer membrane protein P1</i>	215	49.7	<i>gi 9716607</i>	13

[0089] One example of a signature protein profile of pathogenic NTHI biofilm is OMP P5, OMP P2, HMW1 and HMW2. Therefore, detection of these protein biomarkers in a secretion sample obtained from the upper respiratory tract is indicative of NTHI infection. Precise diagnosis of

pathogenic bacterial infection, such as NTHI infection, in patients with upper airway infection will facilitate the selection of appropriate therapy and promote judicious prescription of antibiotics in order to achieve an early recovery in patients and to reduce the emergence of antibiotic-resistant infections in the community.

Example 2

Detection of NTHI Biofilm-Specific Proteins in Paranasal Sinus Infection

[0090] In order to determine the protein profile of a human patient suffering from sinusitis, secretion samples are obtained from the upper respiratory tract of the patients. These samples are analyzed as described in Example 1 for the presence of OMP P5, OMP P2, HMW1 and HMW2. The protein profile of the patients is compared with the reference protein profile generated from the supernatants of *in vitro* NTHI biofilms as described above.

Example 3

Identification of Protein Biomarkers Associated with other Bacteria Species

[0091] The methods described in Example 1 are carried out with the supernatants from biofilms of other pathogenic bacteria species such as *Streptococcus pneumonia*, *Moraxella catarrhalis*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Stenotrophomonas maltophilia*.

Example 4

Further Analysis of Determination of Signature Protein Profile for Pathogenic Bacteria

[0092] Supernatants from biofilm obtained from multiple stains of Nontypeable *H. influenzae* (NTHI) were analyzed to define the NTHI signature protein profile. NTHI strains 86-028NP, 1128MEE, 1714, 1748, 1885MEE and 2019 were cultured in eight-well chamber slides for 10 days and the resulting supernatants were collected at 24 hours intervals. The proteins in the supernatants collected from NTHI biofilm cultures were separated by SDS-PAGE and silver staining revealed a distinct protein profile maintained over time. Figure 3 depicts a Western blot using chinchilla anti-OMP P2 or anti-OMP P5 antibodies, which demonstrates that OMP P2 and OMP P5 are present in high levels in the biofilms of all NTHI strains tested.

[0093] The proteins isolated from NTHI biofilm supernatants were analyzed by nano-liquid chromatography/tandem mass spectrometry (LC-MS/MS). The molecular weights of the identified proteins were compared to the molecular weights of the known protein profile for the NTHI strain 86-028NP ((Bakaletz et al. Infection and Immunity, 56(2): 331-335, 1988), and the identified proteins were scored based on their association to the 86-028NP protein profile using Mascot (Matrix Science, Boston MA) according to the manufacturer's instructions. The results of this comparison are set out in Table 3 below. These studies demonstrate that a preferred NTHI biofilm protein profile comprises OMP P2 and OMP P5.

Table 3:

P2 Fragment		
Score	Description	Organism
2927	Outer membrane protein P2	<i>H. influenzae</i>
771	Outer membrane protein P5	<i>H. influenzae</i>
688	Spermidine/putrescine-binding periplasmic protein 1	<i>H. influenzae</i>
352	Keratin, type II cytoskeletal 2 epidermal	<i>Homo sapiens</i>
335	Trypsin	<i>Sus scrofa</i>
292	Protein mrp homolog	<i>H. influenzae</i>
165	3-dehydroquinate synthase	<i>H. influenzae</i>
143	Phenylalanyl-tRNA synthetase alpha chain	<i>H. influenzae</i>
105	Glutamate 5-kinase	<i>H. influenzae</i>
100	Aspartate-semialdehyde dehydrogenase	<i>H. influenzae</i>
P5 Fragment		
Score	Description	Organism
1512	Lipoprotein E	<i>H. influenzae</i>
1105	Outer membrane protein P2	<i>H. influenzae</i>
718	Hybrid peroxiredoxin hyPrx5	<i>H. influenzae</i>
361	Outer membrane protein P5	<i>H. influenzae</i>
354	Trypsin OS=Sus scrofa	<i>Sus scrofa</i>
255	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	<i>H. influenzae</i>
168	Putative glutamine amidotransferase HI_1037	<i>H. influenzae</i>
167	Phosphate import ATP-binding protein PstB	<i>H. influenzae</i>
124	Dihydrodipicolinate reductase	<i>H. influenzae</i>
118	Ig kappa chain C region	<i>M. musculus</i>

[0094] The isolated proteins were also purified using cationic and gel chromatography. The purified OMP P2 and OMP P5 protein will be used to generate monoclonal antibodies for use in the methods, immunoassays and devices of the invention. It is critical that the antibodies used in the methods, immunoassays and devices of the invention be highly specific. The currently available chinchilla polyclonal antibodies do not exhibit the specificity necessary for carrying out the methods of the invention.

Example 5

Generation of Monoclonal Antibodies

[0095] The purified OMP P2 and OMP P5 proteins described in Example 4 are used to generate monoclonal antibodies for use in the methods, immunoassays and devices of the invention using standard techniques well known in the art.

[0096] For example, a mouse is immunized intraperitoneally with the purified OMP P2 protein or purified OMP P5 protein. Four days later, the mouse is sacrificed and spleen cells are fused with murine myeloma cells using methods standard in the art. For example, hybridoma technology is described in Kohler et al., *Nature* 256: 495, the human B-cell hybridoma technique is described in Kozbor et al., *Immunol. Today* 4, 72 (1983), the EBV-hybridoma technique to produce human monoclonal antibodies is described in Cole et al. *Monoclonal Antibodies in Cancer Therapy* (1985) Allen R. Bliss, Inc., pages 77-96, and methods of screening combinatorial antibody libraries is described in Huse et al., *Science* 246, 1275 (1989).

[0097] The fused cells are cloned in a 96-well plate for single colony selection. Seven to ten days after fusion, culture supernatants from each well with colonies are assayed for the presence of anti-OMP P2 or anti-OMP P5 antibodies. Two to four weeks after cloning, supernatants from single cell colonies are screen for the presence of anti-OMP P2 or anti-OMP P5 antibodies again. Wells with positive reactions are further expanded into larger wells and eventually expanded into flasks to harvest more supernatant for further testing.

[0098] Hybridoma cells from the positive clones are injected into pristine mice for production of ascites. The monoclonal antibodies are purified from the ascites, and the specificity of the purified monoclonal antibodies is tested using standard assays known in the art.

Example 6

Immunoassays of the Invention

[0099] Anti-OMP P2 and OPM P5 monoclonal antibodies, as described in Example 5, are used in order to determine the protein profile of a human patient suffering from sinusitis. Secretion samples are obtained from the upper respiratory tract of the patients. These samples are analyzed as described in Example 1 for the presence of at least OMP P5, OMP P2, HMW1 or HMW2. The protein profile of the patients is compared with the reference protein profile generated from the supernatants of *in vitro* NTHI biofilms as described above

[0100] The sensitivity and specificity parameters for the use of anti-OMP P2 and anti-OPM P5 monoclonal antibodies, as described in Example 5, are determined against a gold-standard real-time PCR assay using hpd as a primer for the detection of non-typeable *Haemophilus influenzae* that has been shown to be 100% specific and sensitive for the detection of NTHI strains 86-028NP, 1128MEE, 1714, 1748, 1885MEE and 2019 and several clinical isolates of *Moraxella catarrhalis*.

SEQUENCE LISTING

[0101]

<110> Das, et al.

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<130> 28335/46294A

<150> 61/493,829

<151> 2011-06-06

<160> 13

<170> PatentIn version 3.5

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Gly Ser	Thr Pro Gln Pro	Arg	Ser Arg Arg Thr	Arg	Arg Ser Ala
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Gln Asn	Ser Tyr Glu Pro	Val	Glu Leu His Thr	Glu	Asn Ala Glu
1475		1480		1485	
Asn Pro	Gln Ser Gly Asn	Asp	Val Ala Thr Gln	Leu	Val Leu Arg
1490		1495		1500	
Asp Leu	Thr Ser Thr Asn	Thr	Asn Ala Val Ile	Ser	Asp Ala Met
1505		1510		1515	
Ala Lys	Ala Gln Phe Val	Ala	Leu Asn Val Gly	Lys	Ala Val Ser
1520		1525		1530	
Gln His	Ile Ser Gln Leu	Glu	Met Asn Asn Glu	Gly	Gln Tyr Asn
1535		1540		1545	
Val Trp	Val Ser Asn Thr	Ser	Met Lys Glu Asn	Tyr	Ser Ser Ser
1550		1555		1560	
Gln Tyr	Arg His Phe Ser	Ser	Lys Ser Ala Gln	Thr	Gln Leu Gly
1565		1570		1575	
Trp Asp	Gln Thr Ile Ser	Ser	Asn Val Gln Leu	Gly	Gly Val Phe
1580		1585		1590	

Thr Tyr Val Arg Asn Ser Asn Asn Phe Asp Lys Ala Ser Ser Lys
1595 1600 1605

Asn Thr Leu Ala Gln Ala Asn Leu Tyr Ser Lys Tyr Tyr Met Asp
1610 1615 1620

Asn His Trp Tyr Leu Ala Val Asp Leu Gly Tyr Gly Asn Phe Gln
1625 1630 1635

Ser Asn Leu Gln Thr Asn His Asn Ala Lys Phe Ala Arg His Thr
1640 1645 1650

Ala Gln Phe Gly Leu Thr Ala Gly Lys Ala Phe Asn Leu Gly Asn
1655 1660 1665

Phe Ala Val Lys Pro Thr Val Gly Val Arg Tyr Ser Tyr Leu Ser
1670 1675 1680

Asn Ala Asn Phe Ala Leu Ala Lys Asp Arg Ile Lys Val Asn Pro
1685 1690 1695

Ile Ser Val Lys Thr Ala Phe Ala Gln Val Asp Leu Ser Tyr Thr
1700 1705 1710

Tyr His Leu Gly Glu Phe Ser Ile Thr Pro Ile Leu Ser Ala Arg
1715 1720 1725

Tyr Asp Ala Asn Gln Gly Ser Gly Lys Ile Asn Val Asp Arg Tyr
1730 1735 1740

Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln Gln Tyr Asn Ala Gly
1745 1750 1755

Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser Leu Ile Gly Gly
1760 1765 1770

Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr Ala Glu Val
1775 1780 1785

Lys Leu Ser Phe Ser Phe
1790

<210> 5

<211> 359

<212> PRT

<213> Haemophilus influenzae

<400> 5

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

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

Lys Ala Gly Gln Gly Ser Phe His Asp Gly Ile Asn Asn Asn Gly Ala
35 40 45 50 55

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

340

345

350

Ile Ala Val Asn Gly Thr Lys
355

<210> 6

<211> 317

<212> PRT

<213> Haemophilus influenzae

<400> 6

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

Ser Phe Ala Ala Asp Asn Arg Ile Gly Val Thr Ile Tyr Lys Tyr Asp
20 25 30

Asp Asn Phe Met Ser Leu Met Arg Lys Glu Ile Asp Lys Glu Ala Lys
35 40 45

Val Val Gly Gly Ile Lys Leu Leu Met Asn Asp Ser Gln Asn Ala Gln
50 55 60

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

Ala Leu Ala Ile Asn Leu Val Asp Pro Ala Ala Ala Pro Thr Ile Ile
85 90 95

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

Pro Gly Ala Lys Ala Ile Gly Ser Tyr Glu Gln Ala Tyr Tyr Val Gly
115 120 125

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

Gln Trp Lys Ala Asn Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile
145 150 155 160

Gln Phe Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Val
165 170 175

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

Glu Gln Leu Phe Ile Asp Thr Gly Met Trp Asp Ala Ala Met Ala Lys
195 200 205

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

Val Ile Ile Ser Asn Asn Asp Gly Met Ala Leu Gly Ala Leu Glu Ala
225 230 235 240

Thr Lys Ala His Gly Lys Lys Leu Pro Ile Phe Gly Val Asp Ala Leu
245 250 255

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

Leu Asn Asp Ser Val Asn Gln Gly Lys Ala Val Val Gln Leu Ser Asn
275 280 285

Asn Leu Ala Gln Gly Lys Ser Ala Thr Glu Gly Thr Lys Met Gly Ile
290 295 300

Lys Arg Pro Cys Cys Thr His Ser Leu Cys Trp Cys Gly
305 310 315

<210> 7

<211> 1542

<212> PRT

<213> Haemophilus influenzae

<400> 7

Met Asn Lys Ile Tyr Arg Leu Lys Phe Ser Lys Arg Leu Asn Ala Leu
1 5 10 15

Val Ala Val Ser Glu Leu Thr Arg Gly Cys Asp His Ser Thr Glu Lys
20 25 30

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

Pro Leu Ser Ala Ile Leu Leu Ser Leu Gly Met Ala Ser Ile Pro Gln
50 55 60

Ser Val Leu Ala Ser Gly Leu Gln Gly Met Ser Val Val His Gly Thr
65 70 75 80

Ala Thr Met Gln Val Asp Gly Asn Lys Thr Thr Ile Arg Asn Ser Val
85 90 95

Asn Ala Ile Ile Asn Trp Lys Gln Phe Asn Ile Asp Gln Asn Glu Met
100 105 110

Val Gln Phe Leu Gln Glu Asn Asn Asn Ser Ala Val Phe Asn Arg Val
115 120 125

Thr Ser Asp Gln Ile Ser Gln Leu Lys Gly Ile Leu Asp Ser Asn Gly
130 135 140

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

Ile Ile Asn Thr Asn Gly Phe Thr Ala Ser Thr Leu Asp Ile Ser Asn
165 170 175

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

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Ala Leu Ala Glu Ile Val Asn His Gly Leu Ile Thr Val Gly Lys Asp
    195                      200                      205

Gly Ser Val Asn Leu Ile Gly Gly Lys Val Lys Asn Glu Gly Val Ile
    210                      215                      220

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

Ile Ser Asp Ile Ile Asn Pro Thr Ile Thr Tyr Ser Ile Ala Ala Pro
                      245                      250                      255

Glu Asn Glu Ala Ile Asn Leu Gly Asp Ile Phe Ala Lys Gly Gly Asn
                      260                      265                      270

Ile Asn Val Arg Ala Ala Thr Ile Arg Asn Lys Gly Lys Leu Ser Ala
                      275                      280                      285

Asp Ser Val Ser Lys Asp Lys Ser Gly Asn Ile Ile Leu Ser Ala Lys
    290                      295                      300

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

Ala Lys Gly Gly Lys Leu Met Ile Thr Gly Asp Lys Val Thr Leu Lys
                      325                      330                      335

Thr Gly Ala Val Ile Asp Leu Ser Gly Lys Glu Gly Gly Glu Thr Tyr
                      340                      345                      350

Leu Gly Gly Asp Glu Arg Gly Glu Gly Lys Asn Gly Ile Gln Leu Ala
                      355                      360                      365

Lys Lys Thr Ser Leu Glu Lys Gly Ser Thr Ile Asn Val Ser Gly Lys
    370                      375                      380

Glu Lys Gly Gly Arg Ala Ile Val Trp Gly Asp Ile Ala Leu Ile Asp
    385                      390                      395                      400

Gly Asn Ile Asn Ala Gln Gly Ser Asp Ile Ala Lys Thr Gly Gly Phe
                      405                      410                      415

Val Glu Thr Ser Gly His Tyr Leu Ser Ile Asp Ser Asn Ala Ile Val
                      420                      425                      430

Lys Thr Lys Glu Trp Leu Leu Asp Pro Asp Asn Val Thr Ile Glu Ala
    435                      440                      445

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

Gly Asp Gly Thr Glu Asn Ser Pro Lys Lys Asn Ala Asp Lys Thr Ile
    465                      470                      475                      480

Leu Thr Asn Glu Thr Ile Ser Asn Phe Leu Gln Asn Ala Lys Val Met
    485                      490                      495

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

Ser His Asn Arg Asn Ser Asn Ala Phe Glu Ile Lys Lys Asp Leu Thr
 785 790 795 800
 Ile Asn Ala Thr Asn Ser Lys Phe Ser Leu Lys Gln Thr Lys Asp Leu
 805 810 815
 Phe Glu Asn Gln Tyr Thr Gly Asp Ala Ile Asn Ser Thr Arg Asn Leu
 820 825 830
 Thr Ile Leu Gly Gly Asn Val Thr Leu Gly Gly Glu Asn Ser Ser Ser
 835 840 845
 Asn Ile Thr Gly Asn Ile Thr Ile Ala Ala Glu Ala Asn Val Thr Leu
 850 855 860
 Gln Ala Tyr Ala Asp Asn Ser Ile Lys Gly His Lys Lys Lys Thr Leu
 865 870 875 880
 Thr Leu Gly Asn Val Ser Thr Ser Gly Asn Leu Ser Leu Thr Gly Ser
 885 890 895
 Lys Val Glu Val Lys Gly Asp Leu Ala Val Leu Asn Gly Ala Thr Phe
 900 905 910
 Lys Gly Glu Thr Asn Asp Ser Leu Asn Ile Thr Gly Thr Phe Thr Asn
 915 920 925
 Asn Gly Thr Ala Asp Ile Asn Ile Lys Arg Gly Val Val Asn Ile Gln
 930 935 940
 Gly Asp Ile Thr Asn Lys Gly Gly Leu Asn Ile Thr Thr Asn Ala Gln
 945 950 955 960
 Lys Asn Gln Lys Thr Ile Ile Asn Gly Asn Ile Thr Asn Lys Lys Gly
 965 970 975
 Asn Leu Asn Ile Thr Asn Asn Gly Asn Asp Thr Glu Ile Gln Ile Gly
 980 985 990
 Gly Asn Ile Ser Gln Lys Glu Gly Asn Leu Thr Ile Ser Ser Asp Lys
 995 1000 1005
 Val Asn Ile Thr Lys Gln Ile Thr Ile Lys Ala Gly Val Asp Glu
 1010 1015 1020
 Lys Asp Ser Ser Ser Ser Thr Ala Ser Asp Ala Asn Leu Thr Ile
 1025 1030 1035
 Lys Thr Lys Glu Leu Lys Leu Val Glu Asp Leu Asn Ile Ser Gly
 1040 1045 1050
 Phe Asn Lys Ala Glu Ile Thr Ala Lys Asp Gly Ser Asp Leu Thr
 1055 1060 1065
 Ile Gly Asn Thr Asn Ser Ala Asp Gly Thr Asn Ala Lys Lys Val
 1070 1075 1080

Thr Phe	Asn Gln Val Lys Asp	Ser Lys Ile Ser Ala	Asn Asp His
1085	1090	1095	
Asn Val	Thr Leu Asn Ser Lys	Val Glu Thr Ser Gly	Asn Thr Asp
1100	1105	1110	
Asn Thr	Gly Asp Gly Ser Gly	Asn Asn Ala Gly Leu	Thr Ile Ala
1115	1120	1125	
Ala Lys	Asn Val Glu Val Lys	Asn Asn Ile Thr Ser	Asn Lys Thr
1130	1135	1140	
Val Asn	Ile Thr Ala Ser Glu	Lys Leu Thr Thr Lys	Ala Asp Ala
1145	1150	1155	
Thr Ile	Asn Ala Thr Thr Gly	Asn Val Glu Val Thr	Ala Lys Thr
1160	1165	1170	
Gly Asp	Ile Lys Gly Glu Val	Lys Ser Thr Ser Gly	Asn Val Asn
1175	1180	1185	
Ile Thr	Ala Asn Gly Asp Thr	Leu Asn Val Ser Asn	Val Ser Gly
1190	1195	1200	
Asn Ala	Val Thr Ile Thr Ala	Asp Lys Gly Lys Leu	Thr Thr Gln
1205	1210	1215	
Glu Ser	Ser Thr Ile Ser Gly	Thr Glu Ser Val Thr	Thr Ser Ser
1220	1225	1230	
Gln Ser	Gly Asp Ile Gly Gly	Ala Ile Ser Gly Asn	Thr Val Ser
1235	1240	1245	
Val Lys	Ala Thr Asn Asp Leu	Ile Thr Lys Ala Asn	Ser Lys Ile
1250	1255	1260	
Glu Ala	Lys Thr Gly Glu Ala	Asn Val Thr Ser Ala	Thr Gly Ile
1265	1270	1275	
Ile Gly	Gly Thr Ile Ser Gly	Asn Thr Val Asn Val	Thr Ala Asn
1280	1285	1290	
Thr Gly	Ser Leu Thr Ile Lys	Gly Gly Ala Lys Val	Asp Ala Thr
1295	1300	1305	
Asn Gly	Ala Ala Thr Leu Thr	Ala Glu Ser Gly Lys	Leu Thr Thr
1310	1315	1320	
Gln Ala	Gly Ser Thr Ile Thr	Ser Asn Asn Gly Gln	Thr Thr Leu
1325	1330	1335	
Thr Ala	Lys Asp Gly Ser Ile	Ala Gly Ser Ile Asp	Ala Ala Asn
1340	1345	1350	
Val Thr	Leu Asn Thr Thr Gly	Thr Leu Thr Thr Val	Val Gly Ser
1355	1360	1365	

Ser Ile Asn Ala Asn Glu Gly Thr Leu Val Ile Asn Ala Gln Asp
1370 1375 1380

Ala Thr Leu Asn Gly Asp Ala Ser Gly Asp Arg Thr Glu Val Asn
1385 1390 1395

Ala Val Asn Ala Ser Gly Ser Gly Ser Val Thr Ala Val Thr Ser
1400 1405 1410

Ser Ser Val Asn Ile Thr Gly Asp Leu Ser Thr Ile Asn Gly Leu
1415 1420 1425

Asn Ile Ile Ser Lys Asn Gly Lys Asn Thr Val Val Leu Lys Gly
1430 1435 1440

Ala Glu Ile Asp Val Lys Tyr Ile Gln Pro Gly Val Ala Ser Ala
1445 1450 1455

Glu Glu Val Ile Glu Ala Lys Arg Ala Leu Glu Lys Val Lys Asp
1460 1465 1470

Leu Ser Asp Glu Glu Arg Glu Thr Leu Ala Lys Leu Gly Val Ser
1475 1480 1485

Ala Val Arg Phe Val Glu Pro Asn Asn Ala Ile Thr Val Asn Thr
1490 1495 1500

Gln Asn Glu Phe Thr Thr Arg Pro Ser Ser Gln Val Thr Ile Ser
1505 1510 1515

Glu Gly Lys Ala Cys Phe Ser Ser Gly Asp Gly Ala Ala Val Cys
1520 1525 1530

Thr Asn Val Ala Asp Asp Gly Gln Gln
1535 1540

<210> 8

<211> 334

<212> PRT

<213> Haemophilus influenzae

<400> 8

Met Lys Lys Lys Ser Tyr Tyr Val Leu Thr Leu Gly Thr Leu Pro Phe
1 5 10 15

Ala Gln Ala Asn Ser Ile Thr Gly Ala Gly Ala Ser Phe Pro Tyr Pro
20 25 30

Ile Tyr Ala Lys Trp Ala Ser Leu Tyr Glu Lys Glu Thr Gly Asn Lys
35 40 45

Val Asn Tyr Gln Ser Ile Gly Ser Gly Gly Gly Gln Gln Gln Ile Ile
50 55 60

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

<210> 9

<211> 311

<212> PRT

<213> Haemophilus influenzae

<400> 9

Val Leu Ala Ser Val Lys Pro Leu Gly Phe Ile Asp Ser Ser Ile Ala
 1 5 10 15

Asp Gly Val Thr Gly Thr Gln Val Leu Val Pro Ala Gly Ala Ser Pro
 20 25 30

His Asp Tyr Asn Leu Lys Leu Ser Asp Ile Gln Lys Val Lys Ser Ala
 35 40 45

Asp Leu Val Val Trp Ile Gly Glu Asp Ile Asp Ser Phe Leu Asp Lys
 50 55 60

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

Ala Asp Val Lys Pro Leu Leu Ser Lys Ala His His Glu His Phe His
 85 90 95

Glu Asp Gly Asp His Asp His Asp His Lys Asp Glu His Lys His Asp
 100 105 110

His Lys His Asp His Lys His Glu His Lys His Glu His Lys His Asp
 115 120 125

His Glu His His Asp His Asp His His Glu Gly Leu Thr Thr Asn Trp
 130 135 140

His Val Trp Tyr Ser Pro Ala Ile Ser Lys Ile Val Ala Gln Lys Val
 145 150 155 160

Ala Asp Lys Leu Thr Ala Gln Phe Pro Asp Lys Lys Ala Leu Ile Ala
 165 170 175

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

Ile Thr Ala Gln Leu Ala Asn Val Lys Asp Lys Gly Phe Tyr Val Phe
 195 200 205

His Asp Ala Tyr Gly Tyr Phe Asn Asp Ala Tyr Gly Leu Lys Gln Thr
 210 215 220

Gly Tyr Phe Thr Ile Asn Pro Leu Val Ala Pro Gly Ala Lys Thr Leu
 225 230 235 240

Ala His Ile Lys Glu Glu Ile Asp Glu His Lys Val Asn Cys Leu Phe
 245 250 255

Ala Glu Pro Gln Phe Thr Pro Lys Val Ile Glu Ser Leu Ala Lys Asn
 260 265 270

Thr Lys Val Asn Val Gly Gln Leu Asp Pro Ile Gly Asp Lys Val Thr
 275 280 285

Leu Gly Lys Asn Ser Tyr Ala Thr Phe Leu Gln Ser Thr Ala Asp Ser
 290 295 300

Tyr Met Glu Cys Leu Ala Lys
 305 310

<210> 10

<211> 1542

<212> PRT

<213> Haemophilus influenzae

<400> 10

Met Asn Lys Ile Tyr Arg Leu Lys Phe Ser Lys Arg Leu Asn Ala Leu
 1 5 10 15

Val Ala Val Ser Glu Leu Thr Arg Gly Cys Asp His Ser Thr Glu Lys
 20 25 30

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

Pro Leu Ser Ala Ile Leu Leu Ser Leu Gly Met Ala Ser Ile Pro Gln
 50 55 60

Ser Val Leu Ala Ser Gly Leu Gln Gly Met Ser Val Val His Gly Thr
 65 70 75 80

Ala Thr Met Gln Val Asp Gly Asn Lys Thr Thr Ile Arg Asn Ser Val
 85 90 95

Asn Ala Ile Ile Asn Trp Lys Gln Phe Asn Ile Asp Gln Asn Glu Met
 100 105 110

Val Gln Phe Leu Gln Glu Asn Asn Asn Ser Ala Val Phe Asn Arg Val
 115 120 125

Thr Ser Asp Gln Ile Ser Gln Leu Lys Gly Ile Leu Asp Ser Asn Gly
 130 135 140

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

Ile Ile Asn Thr Asn Gly Phe Thr Ala Ser Thr Leu Asp Ile Ser Asn
 165 170 175

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

Ala Leu Ala Glu Ile Val Asn His Gly Leu Ile Thr Val Gly Lys Asp
 195 200 205

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

515					520					525					
Gly	Val	Gln	Ile	Asp	Gly	Asp	Ile	Thr	Ser	Glu	Gly	Gly	Asn	Leu	Thr
530					535					540					
Ile	Asn	Ser	Gly	Gly	Trp	Val	Asp	Val	His	Lys	Asn	Ile	Thr	Leu	Gly
545					550					555					560
Thr	Gly	Phe	Leu	Asn	Ile	Thr	Ala	Gly	Gly	Ser	Val	Ala	Phe	Glu	Lys
				565					570					575	
Gly	Gly	Asn	Asn	Ala	Arg	Asn	Ala	Thr	Asp	Ala	Gln	Ile	Thr	Ala	Gln
			580					585					590		
Gly	Thr	Ile	Thr	Val	Asn	Lys	Asp	Asp	Lys	Gln	Phe	Arg	Phe	Asn	Asn
	595						600					605			
Val	Ser	Ile	Asn	Gly	Thr	Gly	Glu	Gly	Leu	Lys	Phe	Ile	Ala	Asn	Gln
	610					615					620				
Asn	Asn	Phe	Thr	His	Lys	Phe	Asp	Gly	Glu	Ile	Asn	Ile	Ser	Gly	Ile
625					630					635					640
Val	Thr	Ile	Asn	Gln	Thr	Thr	Lys	Lys	Asp	Ala	Lys	Tyr	Trp	His	Ala
			645						650					655	
Ser	Lys	Asp	Ser	Tyr	Trp	Asn	Val	Ser	Ser	Leu	Thr	Leu	Asn	Asp	Asp
			660					665					670		
Ala	Lys	Phe	Thr	Phe	Ile	Lys	Phe	Val	Asp	Ser	Gly	Ser	Asn	Ser	Gln
		675					680					685			
Asp	Leu	Arg	Ser	Ala	Arg	Arg	Arg	Phe	Ala	Gly	Val	His	Phe	Asn	Gly
	690					695					700				
Thr	Gly	Gly	Lys	Thr	Asn	Phe	Asn	Ile	Gly	Ala	Asn	Ala	Lys	Ala	Leu
705					710					715					720
Phe	Lys	Leu	Lys	Pro	Asn	Ala	Ala	Thr	Asp	Pro	Lys	Lys	Glu	Leu	Pro
				725					730					735	
Ile	Thr	Phe	Asn	Ala	Asn	Ile	Thr	Ala	Thr	Gly	Ser	Ser	Asp	Ser	Ser
			740					745					750		
Val	Met	Phe	Asp	Ile	His	Ala	Asn	Leu	Thr	Ser	Arg	Ala	Ala	Ser	Ile
	755						760					765			
Asn	Met	Asp	Ser	Ile	Asn	Ile	Thr	Gly	Gly	Leu	Asp	Phe	Ser	Ile	Thr
	770					775					780				
Ser	His	Asn	Arg	Asn	Ser	Asn	Ala	Phe	Glu	Ile	Lys	Lys	Asp	Leu	Thr
785				790					795						800
Ile	Asn	Ala	Thr	Asn	Ser	Lys	Phe	Ser	Leu	Lys	Gln	Thr	Lys	Asp	Leu
			805						810					815	
Phe	Glu	Asn	Gln	Tyr	Thr	Gly	Asp	Ala	Ile	Asn	Ser	Thr	Arg	Asn	Leu
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820	825	830
Thr Ile Leu Gly Gly Asn Val	Thr Leu Gly Gly Glu Asn Ser Ser Ser	
835	840	845
Asn Ile Thr Gly Asn Ile Thr Ile Ala Ala Glu Ala Asn Val Thr Leu		
850	855	860
Gln Ala Tyr Ala Asp Asn Ser Ile Lys Gly His Lys Lys Lys Thr Leu		
865	870	875
880		
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Lys Val Glu Val Lys Gly Asp Leu Ala Val Leu Asn Gly Ala Thr Phe		
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960		
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Val Asn 1145	Ile Thr Ala Ser Glu 1150	Lys Leu Thr Thr Lys Ala Asp Ala 1155
Thr Ile 1160	Asn Ala Thr Thr Gly 1165	Asn Val Glu Val Thr Ala Lys Thr 1170
Gly Asp 1175	Ile Lys Gly Glu Val 1180	Lys Ser Thr Ser Gly Asn Val Asn 1185
Ile Thr 1190	Ala Asn Gly Asp Thr 1195	Leu Asn Val Ser Asn Val Ser Gly 1200
Asn Ala 1205	Val Thr Ile Thr Ala 1210	Asp Lys Gly Lys Leu Thr Thr Gln 1215
Glu Ser 1220	Ser Thr Ile Ser Gly 1225	Thr Glu Ser Val Thr Thr Ser Ser 1230
Gln Ser 1235	Gly Asp Ile Gly Gly 1240	Ala Ile Ser Gly Asn Thr Val Ser 1245
Val Lys 1250	Ala Thr Asn Asp Leu 1255	Ile Thr Lys Ala Asn Ser Lys Ile 1260
Glu Ala 1265	Lys Thr Gly Glu Ala 1270	Asn Val Thr Ser Ala Thr Gly Ile 1275
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Thr Gly 1295	Ser Leu Thr Ile Lys 1300	Gly Gly Ala Lys Val Asp Ala Thr 1305
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Gln Ala 1325	Gly Ser Thr Ile Thr 1330	Ser Asn Asn Gly Gln Thr Thr Leu 1335
Thr Ala 1340	Lys Asp Gly Ser Ile 1345	Ala Gly Ser Ile Asp Ala Ala Asn 1350
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Ala Thr 1385	Leu Asn Gly Asp Ala 1390	Ser Gly Asp Arg Thr Glu Val Asn 1395

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Gln Asn Glu Phe Thr Thr Arg Pro Ser Ser Gln Val Thr Ile Ser
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<211> 1557

<212> PRT

<213> Haemophilus influenzae

<400> 11

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

Pro Leu Ser Ala Ile Leu Leu Ser Leu Gly Met Ala Ser Ile Pro Gln
50 55 60

Ser Val Leu Ala Ser Gly Leu Gln Gly Met Ser Val Val His Gly Thr
65 70 75 80

Ala Thr Met Gln Val Asp Gly Asn Lys Thr Thr Ile Arg Asn Ser Val
85 90 95

Asn Ala Ile Ile Asn Tyr Lys Gln Phe Asn Ile Asn Gln Asn Glu Met

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Asn Ala Ile Ile Asn Asp Lys Gln Phe Asn Ile Asp Gln Asn Glu Met
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Val Gln Phe Leu Gln Glu Ser Ser Asn Ser Ala Val Phe Asn Arg Val
115                      120                      125

Thr Ser Asp Gln Ile Ser Gln Leu Lys Gly Ile Leu Asp Ser Asn Gly
130                      135                      140

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

Ile Ile Asn Thr Asn Gly Phe Thr Ala Ser Thr Leu Asp Ile Ser Asn
165                      170                      175

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

Ala Leu Ala Glu Ile Val Asn His Gly Leu Ile Thr Val Gly Lys Asp
195                      200                      205

Gly Ser Val Asn Leu Ile Gly Gly Lys Val Lys Asn Glu Gly Val Ile
210                      215                      220

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

Ile Ser Asp Ile Ile Asn Pro Thr Ile Thr Tyr Ser Ile Ala Ala Pro
245                      250                      255

Glu Asn Glu Ala Ile Asn Leu Gly Asp Ile Phe Ala Lys Gly Gly Asn
260                      265                      270

Ile Asn Val Arg Ala Ala Asn Ile Arg Asn Gln Gly Lys Leu Ser Ala
275                      280                      285

Asp Ser Val Ser Lys Asp Lys Ser Gly Asn Ile Val Leu Ser Ala Lys
290                      295                      300

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

Ala Lys Gly Gly Lys Leu Met Ile Thr Gly Asp Lys Val Thr Leu Lys
325                      330                      335

Thr Gly Ala Val Ile Asp Leu Ser Gly Lys Glu Gly Gly Glu Thr Tyr
340                      345                      350

Leu Gly Gly Asp Glu Arg Gly Glu Gly Lys Asn Gly Ile Gln Leu Ala
355                      360                      365

Lys Lys Thr Ser Leu Glu Lys Gly Ser Thr Ile Asn Val Ser Gly Lys
370                      375                      380

Glu Lys Gly Gly Arg Ala Ile Val Trp Gly Asp Ile Ala Leu Ile Asp
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Gly Asn Ile Asn Ala Gln Gly Lys Asp Ile Ala Lys Thr Gly Gly Phe

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Val Glu Thr Ser Gly His Tyr Leu Ser Ile Gly Asn Asp Ala Ala Val		
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Gly Asn Asp Asp Gln Ser Gln Leu Lys Asp Asp Arg Gly Asp Ser Pro		
450	455	460
Asn Lys Ile Leu Ala Asp Asn Lys His Thr Val Asn Asn Lys Thr Leu		
465	470	475
Ser Thr Ala Leu Ala Lys Gly Ile Gly Val Asn Ile Ser Ala Lys Lys		
485	490	495
Lys Val Asn Val Thr Ala Asp Ile Asn Val His Asn Gly Thr Leu Thr		
500	505	510
Leu His Ser Glu Gln Gly Gly Val Glu Ile Asn Gly Asp Ile Thr Ser		
515	520	525
Glu Gln Asn Gly Asn Leu Thr Ile Lys Ala Gly Ser Trp Val Asp Val		
530	535	540
His Lys Asn Ile Thr Ile Gly Thr Gly Phe Leu Asn Ile Thr Ala Gly		
545	550	555
Gly Ser Val Ala Phe Glu Lys Ala Gly Gly Asp Lys Gly Arg Ala Ala		
565	570	575
Ser Asp Ala Lys Ile Val Ala Gln Gly Val Ile Thr Ala Gly Ser Gly		
580	585	590
Gln Asp Phe Arg Phe Asn Asn Val Ser Leu Asn Gly Thr Gly Arg Gly		
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Leu Lys Phe Ile Thr Ala Lys Gly Asn Lys Gly Asn Phe Ser Ala Lys		
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Phe Asp Gly Val Leu Asn Ile Ser Gly Asn Ile Ser Ile Asn His Thr		
625	630	635
Ala Asn Asn Gln Leu Ser Tyr Phe His Arg Gln Gly Tyr Thr Tyr Trp		
645	650	655
Asn Leu Thr Gln Leu Asn Val Asp Ser Asp Ser Ser Phe Ser Leu Thr		
660	665	670
Ser Ile Lys Asp Ala Ile Lys Val Gly Gly Tyr Asp Asn Ala Lys Asp		
675	680	685
Lys Lys Asn Thr Gly Gly Ile Gly Phe Thr Arg Asp Thr Ile Phe Asn		
690	695	700

Val Lys Gln Gly Ala Arg Val Asp Ile Ser Tyr Thr Leu Pro Ile Ser
705 710 715 720

Pro Val Lys Asn Ser Arg Ile Ala Ala Val Asn Phe Asp Gly Asn Ile
725 730 735

Thr Val Lys Gly Gly Gly Val Val Asn Leu Lys Phe Asn Ala Leu Ser
740 745 750

Asn Asn Tyr Lys Thr Pro Gly Val Asn Ile Ser Ser Arg Phe Ile Asn
755 760 765

Val Thr Glu Gly Ser Gln Leu Asn Ile Thr Gly Ser Met Pro Ser Thr
770 775 780

Thr Leu Phe Asn Val Ala Asn Asp Leu Ile Ile Asn Ala Thr Asn Ser
785 790 795 800

Phe Val Ser Ile Lys Glu Ile Glu Gly Thr Asp Thr His Leu Asp Thr
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Gly Leu Lys Val Asn Gly Asn Val Thr Ile Lys Gly Gly Asn Val Thr
820 825 830

Leu Gly Ser Asn Lys Ala Lys Thr Lys Phe Asp Lys Asn Val Thr Val
835 840 845

Glu Lys Gly Ala Asn Leu Thr Leu Ala Ser Ala Asn Phe Gly Asn His
850 855 860

Lys Gly Ala Leu Thr Val Ala Gly Asn Ile Asn Thr Gln Gly Lys Leu
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Val Ala Thr Gly Asp Thr Ile Asp Val Ser Gly Asp Phe Thr Val Gly
885 890 895

Asn Asp Ala Thr Phe Asn Gly Asn Thr Asn Asn Asn Leu Asn Ile Thr
900 905 910

Gly Asn Phe Thr Asn Asn Gly Thr Ser Ile Ile Asp Val Lys Lys Gly
915 920 925

Ala Ala Lys Leu Gly Asn Ile Thr Asn Glu Gly Ser Leu Asn Ile Thr
930 935 940

Thr His Ala Asn Thr Asn Gln Lys Thr Ile Ile Thr Gly Asn Ile Thr
945 950 955 960

Asn Lys Lys Gly Asp Leu Asn Ile Arg Asp Asn Lys Asn Asn Ala Glu
965 970 975

Ile Gln Ile Gly Gly Asn Ile Ser Gln Lys Glu Gly Asn Leu Thr Ile
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Ala Gln	Lys Val Ile Phe	Asp	Lys Val Lys Asp Ser	Lys Ile Ser
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Ala Gly	Asn His Asn Val	Thr	Leu Asn Ser Glu Val	Glu Thr Ser
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Gly Leu	Thr Ile Ser Ala	Lys	Asp Val Ala Val Asn	Asn Asn Ile
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Thr Ser	His Lys Thr Ile	Asn	Ile Ser Ala Thr Thr	Gly Asn Val
1130		1135		1140
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1145		1150		1155
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Gly Thr	Leu Thr Thr Lys	Ala	Asp Ser Thr Ile Lys	Gly Thr Gly
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Ser Val	Thr Thr Leu Ser	Gln	Ser Gly Asp Ile Gly	Gly Thr Ile
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Ser Gly	Lys Thr Val Ser	Val	Thr Ala Thr Thr Asp	Ser Leu Thr
1235		1240		1245
Val Lys	Gly Gly Ala Lys	Ile	Asn Ala Thr Glu Gly	Thr Ala Thr
1250		1255		1260
Leu Thr	Ala Ser Ser Gly	Lys	Leu Thr Thr Glu Ala	Asn Ser Ala
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Ile Ser	Gly Ala Asn Gly	Val	Thr Ala Ser Ser Gln	Ser Gly Asp
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 1295 1300 1305
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<211> 353

<212> PRT

<213> Haemophilus influenzae

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Glu Lys Asn Val Gly Tyr His Arg Asn Ser Phe Thr Tyr Gly Val Phe
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Glu Tyr Gln Trp Leu Thr Arg Val Gly Lys Tyr Arg Pro Gln Asp Lys
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Ser Ile Tyr Gly Glu Met Ser Gln Val Lys Ser Ala Lys Val Ala Val

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Thr	His	Leu	Pro	Ser	Lys	Asp	Lys	Ser	Val	Val	Ser	Leu	Gln	Asp	Arg
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Ala	Ala	Trp	Gly	Phe	Gly	Trp	Asn	Ala	Gly	Val	Met	Tyr	Gln	Phe	Asn
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Lys	Tyr	Thr	His	Trp	Ser	Arg	Leu	Thr	Lys	Leu	His	Ala	Ser	Phe	Glu
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Asp	Gly	Lys	Lys	Ala	Phe	Asp	Lys	Glu	Leu	Gln	Tyr	Ser	Asn	Asn	Ser
			340					345					350		
Arg	Val	Ala	Leu	Gly	Ala	Ser	Tyr	Asn	Leu	Tyr	Glu	Lys	Leu	Thr	Leu
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Ala Asn Leu Tyr Gly Leu Asn Leu Asn Tyr Ser Phe
 450 455 460

REFERENCES CITED IN THE DESCRIPTION

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Patentkrav

1. Fremgangsmåde til påvisning af tilstedeværelse af ikke-typebestemmelige *Haemophilus influenzae* (NTHI)-bakterier i de øvre luftveje hos en person, som omfatter trinene:
- 5 a) modtagelse af en prøve af sekreter fra de øvre luftveje hos personen; og
- b) påvisning af tilstedeværelse af mindst én biomarkør i prøven, hvor biomarkøren er OMP P2 eller OMP P5,
- 10 hvor tilstedeværelse af mindst én biomarkør indikerer tilstedeværelse af NTHI-bakterier i de øvre luftveje hos personen.
2. Fremgangsmåde til diagnosticering af ikke-typebestemmelig *Haemophilus influenzae* (NTHI)-infektion i de øvre luftveje hos en person, som omfatter trinene:
- 15 a) modtagelse af en prøve af sekreter fra de øvre luftveje hos personen; og
- b) påvisning af tilstedeværelse af mindst én biomarkør i prøven, hvor biomarkørerne er valgt blandt OMP P2 og OMP P5,
- 20 hvor tilstedeværelse af mindst én biomarkør indikerer en NTHI-infektion i de øvre luftveje hos personen.
3. Fremgangsmåde ifølge krav 1 eller krav 2, hvor prøven er udtaget fra næsen eller næseborene, næsehulen, munden, pharynx, næsebihulerne eller larynx.
- 25
4. Fremgangsmåde ifølge krav 3, hvor prøven er udtaget fra midterste meatus.
- 30
5. Fremgangsmåde ifølge et hvilket som helst af kravene 1-4, hvor biomarkøren påvises ved anvendelse af et antistof, der er specifikt for OMP P2 eller OMP P5.
- 35
6. Fremgangsmåde ifølge et hvilket som helst af kravene 1-5, hvor personen lider af bakteriel sinusitis.
7. Fremgangsmåde ifølge et hvilket som helst af kravene 1-6,

hvor prøven er udtaget ved anvendelse af sterile pødepinde, steril gaze, næseskylning, en sugeslange eller et ballonkateter.

- 5 8. Fremgangsmåde ifølge et hvilket som helst af kravene 1-7, hvor biomarkøren påvises ved anvendelse af et monoklonalt antistof.
9. Fremgangsmåde ifølge et hvilket som helst af kravene 1-8, 10 hvor et immunoassay anvendes til påsning af biomarkøren.
10. Fremgangsmåde ifølge et hvilket som helst af kravene 1-9, hvor prøven er udtaget med en anordning, der omfatter et substrat, som fremviser antistoffer, der er specifikke for 15 biomarkørerne.
11. Fremgangsmåde ifølge krav 10, hvor anordningen er et ballonkateter, og substratet er indsat i sugeporten på kateteret.

DRAWINGS

Figure 1

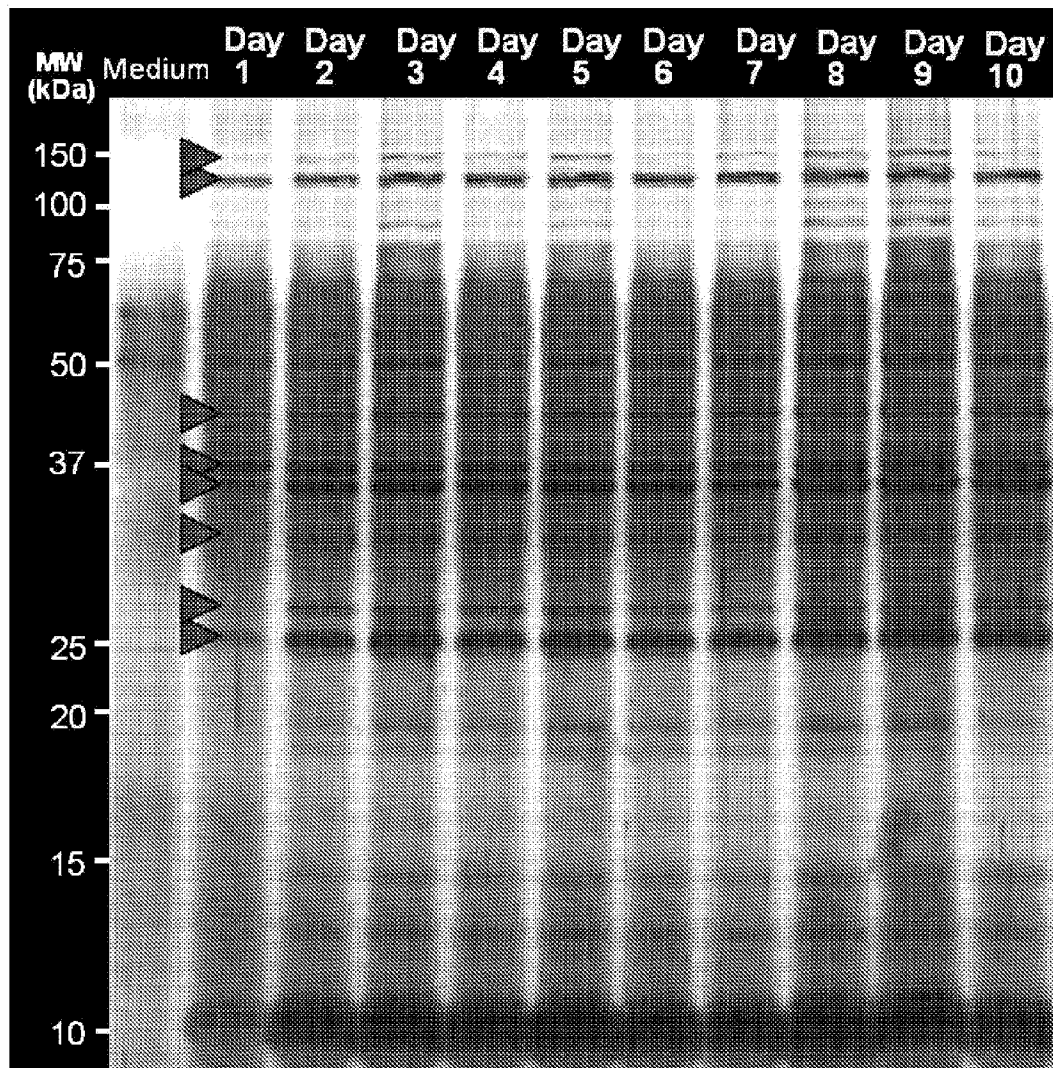


Figure 2

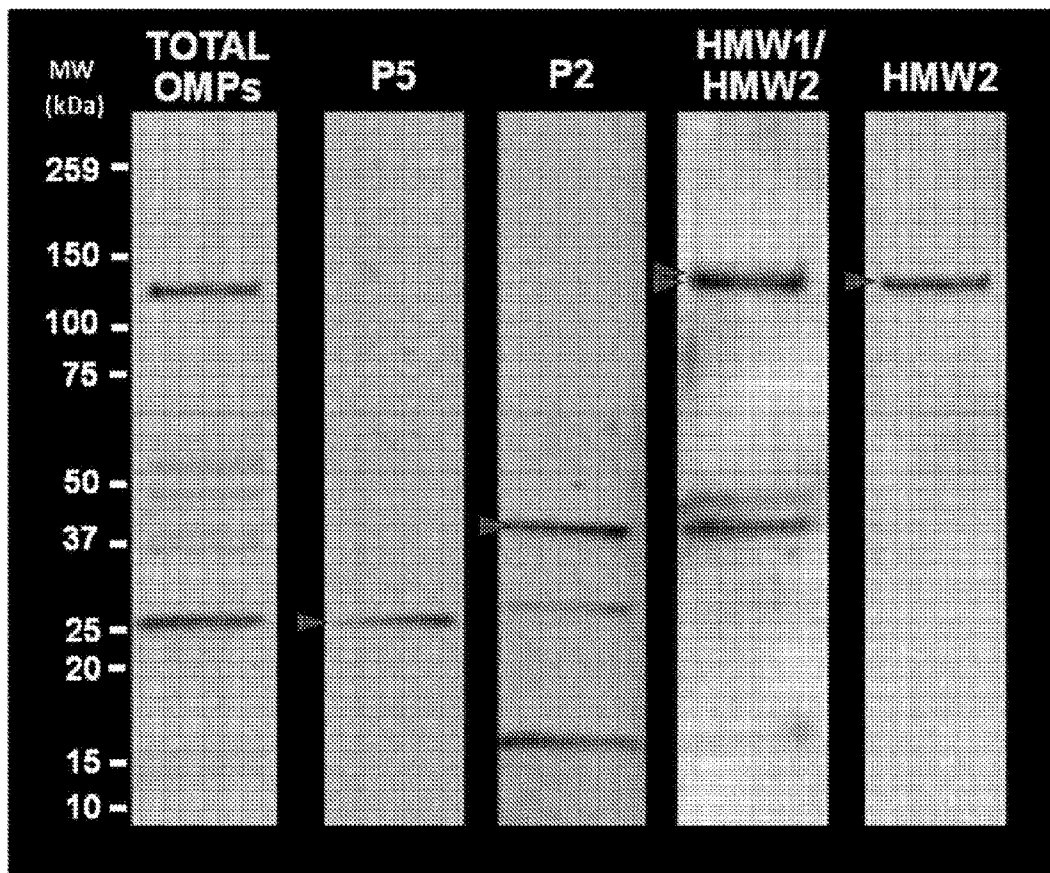


Figure 3

