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(54) **Title:** USPA1 AND USPA2 ANTIGENS OF *MORAXELLA CATARRHALIS*

(57) **Abstract**

The present invention discloses the existence of two novel proteins UspA1 and UspA2, and their respective genes *uspA1* and *uspA2*. Each protein encompasses a region that is conserved between the two proteins and comprises an epitope that is recognized by MAb 17C7. One or more than one of these species may aggregate to form the very high molecular weight form (i.e. greater than 200 kDa) of the UspA antigen. Compositions and both diagnostic and therapeutic methods for the treatment and study of *M. catarrhalis* are disclosed.

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DESCRIPTION

USPA1 AND USPA2 ANTIGENS OF *MORAXELLA CATARRHALIS*

BACKGROUND OF THE INVENTION

I. Field of the Invention

The present invention relates generally to the fields of microbiology, and clinical bacteriology. More particularly, it concerns sequences of the *uspA1* and *uspA2* genes which encode the proteins UspA1 and UspA2, respectively, both of which encode an epitope reactive with monoclonal antibody (MAb) 17C7 and provide useful epitopes for immunodiagnosis and immunoprophylaxis.

II. Description of Related Art

It was previously thought that *Moraxella catarrhalis*, previously known as *Branhamella catarrhalis* or *Neisseria catarrhalis,* was a harmless saprophyte of the upper respiratory tract (Catlin, 1990; Berk, 1990). However, during the previous decade, it has been determined that this organism is an important human pathogen. Indeed, it has been established that this Gram-negative diplococcus is the cause of a number of human infections (Murphy, 1989). *M. catarrhalis* is now known to be the third most common cause of both acute and chronic otitis media (Catlin, 1990; Faden *et al.*. 1990; 1991; Marchant, 1990), the most common disease for which infants and children receive health care according to the 1989 Consensus Report. This organism also causes acute maxillary sinusitis, generalized infections of the lower respiratory tract (Murphy and Loeb, 1989) and is an important cause of bronchopulmonary infections in patients with underlying chronic lung disease and, less frequently, of systemic infections in immunocompromised patients (Melendez and Johnson, 1990; Sarubbi *et al.*, 1990; Schonheyder and Ejlertsen, 1989; Wright and Wallace, 1989).

The 1989 Consensus Report further concluded that prevention of otitis media is an important health care goal due to both its occurrence in infants and children, as well as certain populations of all age groups. In fact, the total financial burden of otitis media has been estimated to be at least $2.5 billion annually. Vaccines were identified as the most desired approach to prevent this disease for a number of reasons. For example, it was estimated that if vaccines could reduce the incidence of otitis media by 30%, then the annual health care savings would be at least $400 million. However, while some progress has been made in the development of vaccines for 2 of the 3 common otitis media pathogens, *Streptococcus pneumoniae* and *Haemophilus influenzae*, there is no indication that similar progress has been made with respect to *M. catarrhalis*. This is particularly troublesome in that *M. catarrhalis* now accounts for approximately 17-20% of all otitis media infection (Murphy, 1989). In addition, *M. catarrhalis* is also a significant cause of sinusitis (van Cauwenberge *et al.*, 1993) and persistent cough (Gottfarb and Brauner, 1994) in children. In the elderly, it infects patients with predisposing conditions such as chronic obstructive pulmonary disease (COPD) and other chronic cardiopulmonary conditions (Boyle *et al.*, 1991; Davies and Maesen, 1988; Hager *et al.*, 1987).

Despite its recognized virulence potential, little is known about the mechanisms employed by *M. catarrhalis* in the production of disease or about host factors governing immunity to this pathogen. An antibody response to *M. catarrhalis* otitis media has been documented by means of an ELISA system using whole *M. catarrhalis* cells as antigen and acute and convalescent sera or middle ear fluid as the source of antibody (Leinonen *et al.*, 1981). The development of serum bactericidal antibody during *M. catarrhalis* infection in adults was shown to be dependent on the classical complement pathway (Chapman *et al.*, 1985). And more recently, it was reported that young children with *M. catarrhalis* otitis media develop an antibody response in the middle ear but fail to develop a systemic antibody response in a uniform manner (Faden *et al.*, 1992).

Previous attempts have been made to identify and characterize *M. catarrhalis* antigens that would serve as potentially important targets of the human immune response to infection (Murphy, 1989; Goldblatt *et al.*, 1990; Murphy *et al.*, 1990). Generally speaking, the surface of *M. catarrhalis* is composed of outer membrane proteins (OMPs), lipooligosaccharide (LOS) and fimbriae. *M. catarrhalis* appears to be somewhat distinct from other Gram-negative bacteria in that attempts to isolate the outer membrane of this organism using detergent fractionation of cell envelopes has generally proven to be unsuccessful in that the procedures did not yield consistent results (Murphy, 1989; Murphy and Loeb, 1989). Moreover, preparations were found to be contaminated with cytoplasmic membranes, suggesting an unusual characteristic of the *M. catarrhalis* cell envelope.

Passive immunization with polyclonal antisera raised against outer membrane vesicles of the *M. catarrhalis* strain 035E was also found to protect against pulmonary challenge by the heterologous *M. catarrhalis* strain TTA24. In addition, active immunization with *M. catarrhalis* outer membrane vesicles resulted in enhanced clearance of this organism from the lungs after challenge. The positive effect of immunization in pulmonary clearance indicates that antibodies play a major role in immunoprotection from this pathogen. In addition, the protection observed against pulmonary challenge with a heterologous *M. catarrhalis* strain demonstrates that one or more conserved surface antigens are targets for antibodies which function to enhance clearance of *M. catarrhalis* from the lungs.

Outer membrane proteins (OMPs) constitute major antigenic determinants of this unencapsulated organism (Bartos and Murphy, 1988) and different strains share remarkably similar OMP profiles (Bartos and Murphy, 1988; Murphy and Bartos, 1989). At least three different surface-exposed outer membrane antigens have been shown to be well-conserved among *M. catarrhalis* strains; these include the 81 kDa CopB OMP (Helminen *et al.*, 1993b), the heat-modifiable CD OMP (Murphy *et al.*, 1993) and the high-molecular weight UspA antigen (Helminen *et al.*, 1994). Of these three antigens, both the CopB protein and UspA antigen have been shown to bind antibodies which exert biological activity against *M. catarrhalis* in an animal model (Helminen *et al.*, 1994; Murphy *et al.*, 1993).

The MAb, designated 17C7, was described as binding to UspA, a very high molecular weight protein that migrated with an apparent molecular weight (in SDS-PAGE) of at least 250 kDa (Helminen *et al.*, 1994; Klingman and Murphy, 1994). MAb 17C7 enhanced pulmonary clearance of *M. catarrhalis* from the lungs of mice when used in passive immunization studies and, in colony blot radioimmunoassay analysis, bound to every isolate of *M. catarrhalis* examined. This same MAb also reacted, although less intensely, with another antigen band of approximately 100 kDa, as described in U.S. Patent No. 5,552,146 (incorporated herein by reference). A recombinant bacteriophage that contained a fragment of *M. catarrhalis* chromosomal DNA that expressed a protein product that bound MAb 17C7 was also identified and migrated at a rate similar or indistinguishable from that of the native UspA antigen from *M. catarrhalis* (Helminen *et al.*, 1994).

With the rising importance of this pathogen in respiratory tract infections, identification of the surface components of this bacterium involved in virulence expression and immunity is becoming more important. To date, there are no vaccines available, against any other OMP, LOS or fimbriae, that induce protective antibodies against *M. catarrhalis*. Thus, it is clear that there remains a need to identify and characterize useful antigens and which can be employed in the preparation of immunoprophylactic reagents. Additionally, once such an antigen or antigens is identified, there is a need for providing methods and compositions which will allow the preparation of vaccines and in quantities that will allow their use on a wide scale basis in prophylactic protocols.

SUMMARY OF THE INVENTION

It is, therefore, an object of the present invention to provide new UspA1 and UspA2 proteins and genes coding therefor. It also is an object of the present invention to provide methods of using these new proteins, for example, in the preparation of agents for the treatment and inhibition of *M. catarrhalis* infection. It also is contemplated that through the use of other technologies such as antibody treatment and immunoprophylaxis that one can inhibit or even prevent *M. catarrhalis* infections.

In satisfying these goals, there are provided epitopic core sequences of UspA1 and UspA2 which can serve as the basis for the preparation of therapeutic or prophylactic compositions or vaccines which comprise peptides of 7, 10, 20, 30, 40, 50 or even 60 amino acids in length that elicit an antigenic reaction and a pharmaceutically acceptable buffer or diluent. These peptides may be coupled to a carrier, adjuvant, another peptide or other molecule such that an effective antigenic response to *M. catarrhalis* is retained or even enhanced. Alternatively, these peptides may act as carriers themselves when coupled to another peptide or other molecule that elicits an antigenic response to *M. catarrhalis* or another pathogen. For example, UspA2 can serve as a carrier for an oligosaccharide.

In one embodiment, the epitopic core sequences of UspA1 and UspA2 comprise one or more isolated peptides of 7, 10, 20, 30, 40, 50 or even 60 amino acids in length having the amino acid sequence AQQQDQH (SEQ ID NO:17).

In another embodiment, there are provided nucleic acids, *uspA1* and *uspA2*, which encode the UspA1 and the UspA2 antigens, respectively, as well as the amino acid sequences of the UspA1 and UspA2 antigens of the *M. catarrhalis* isolates O35E, TTA24, TTA37, and O46E. It is envisioned that nucleic acid segments and fragments of the genes *uspA1* and *uspA2* and the UspA1 and UspA2 antigens will be of value in the preparation and use of therapeutic or prophylactic compositions or vaccines for treating, inhibiting or even preventing *M. catarrhalis* infections.

In another embodiment, there is provided a method for inducing an immune response in a mammal comprising the step of providing to the mammal an antigenic composition that comprises an isolated peptide of about 20 to about 60 amino acids that contains the identified epitopic core sequence and a pharmaceutically acceptable buffer or diluent.

In another embodiment, there is provided a method for diagnosing *M. catarrhalis* infection which comprises the step of determining the presence, in a sample, of an *M. catarrhalis* amino acid sequence corresponding to residues of the epitopic core sequences of either the UspA1 or UspA2 antigen. This method may comprise PCR ™ detection of the nucleotide sequences or alternatively an immunologic reactivity of an antibody to either a UspA1 or UspA2 antigen.

In a further embodiment, there is provided a method for treating an individual having an *M. catarrhalis* infection which comprises providing to the individual an isolated peptide of about 20 to about 60 amino acids that comprises at least about 10 consecutive residues of the amino acid sequence identified as an epitopic core sequence of UspA1 or UspA2.

In a still further embodiment, there is provided a method for preventing or limiting an *M. catarrhalis* infection that comprises providing to a subject an antibody that reacts immunologically with the identified epitopic core region of either UspA1 or UspA2 of *M. catarrhalis*.

In another embodiment, there is provided a method for screening a peptide for reactivity with an antibody that binds immunologically to UspA1, UspA2 or both which comprises the steps of providing the peptide and contacting the peptide with the antibody and then determining the binding of the antibody to the peptide. This method may comprise an immunoassay such as a western blot, an ELISA, an RIA or an immunoaffinity separation.

In a still further embodiment, there is provided a method for screening a UspA1 or UspA2 peptide for its ability to induce a protective immune response against *M. catarrhalis* by providing the peptide, administering it in a suitable form to an experimental animal, challenging the animal with *M. catarrhalis* and then assaying for an *M. catarrhalis* infection in the animal. It is envisioned that the animal used will be a mouse that is challenged by a pulmonary exposure to *M. catarrhalis* and that the assaying comprises assessing the degree of pulmonary clearance by the mouse.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1. Southern blot analysis of *Pvu*II-digested chromosomal DNA from strains of *M. catarrhalis* using a probe from the *uspA1* gene. Bacterial strain designations are at the top; kilobase (kb) position markers are on the left.

FIG. 2A. Proteins present in whole cell lysates of the wild-type strain O35E and the isogenic *uspA1* mutant strain. These proteins were resolved by SDS-PAGE and stained with Coomassie blue. The left lane (WT) contains the wild-type strain and right lane (MUT) contains the mutant. The arrows indicate the protein, approximately 120 kDa in size, that is present in the wild-type and missing in the mutant. Kilodalton position markers are on the left.

FIG. 2B. Western blot analysis of whole cell lysates of the wild-type strain O35E and the isogenic *uspA1* mutant strain. These proteins were resolved by SDS-PAGE and probed with MAb 17C7 in western blot analysis. The left lane (WT) contains the wild-type strain and the right lane (MUT) contains the mutant. Kilodalton position markers are on the left. It can been seen that both strains possess the very high molecular weight band reactive with MAb 17C7 whereas only the wild-type strain also has a band of approximately 120 kDa that binds this MAb.

FIG. 2C. Western blot analysis of whole cell lysate (WCL) and EDTA-extracted outer membrane vesicles (OMV) from the wild-type strain O35E (WT) and the isogenic *uspA1* mutant (MUT) using MAb 17C7. Samples were either heated at 37°C for 15 minutes (H) or at 100°C for 5 minutes (B) prior to SDS-PAGE. Molecular weight position markers (in kilodaltons) are indicated on the left. The open arrow indicates the position of the very high molecular weight form of the MAb 17C7-reactive antigen; the closed arrow indicates the position of the approximately 120 kDa protein; the open circle indicates the position of the approximately 70-80 kDa protein.

FIG. 3. Southern blot analysis of chromosomal DNA from the wild-type *M. catarrhalis* strain O35E and the isogenic *uspA1* mutant. Chromosomal DNA was digested with *Pvu*II and probed with a 0.6 kb *Bgl*II-*Pvu*II fragment from the *uspA1* gene. The wild-type strain is listed as O35E at the top of this figure and the mutant strain is listed as O35E-uspA1$^-$. Kilobase position markers are present on the left side.

FIG. 4. Western blot reactivity of proteins in *M. catarrhalis* strain O35E outer membrane vesicles (labeled O35E OMV) and the MF-4-1 GST fusion protein (labeled GST fusion protein) with MAb 17C7.

FIG. 5. PCR™ products obtained by the use of the T3 and P10 primers (middle lane - 0.9 kb product) and the T7 and P9 primers (right lane - 1.7 kb product) when used in a PCR™

amplification with chromosomal DNA from the *uspA1* mutant. A kb ladder is present in the first lane; several kb position markers are listed on the left side of this figure.

FIG. 6A-6C. SDS-PAGE and westerns of purified proteins. FIG. 6A. Coomassie blue stained gel of purified UspA2 (lane 2). FIG. 6B. Coomassie blue stained gel of purified UspA1 prepared without heating of sample (lane 4), heated for 3 min at 100°C (lane 5), heated for 5 min at 100°C (lane 6), and heated for 10 min at 100°C (lane 7). FIG. 6C. Western of the purified UspA2 (lane 9) and purified UspA1 (lane 10) probed with the 17C7 MAb. Both proteins were heated 10 min. The molecular size markers in lanes 1, 3, and 8 are as indicated in kilodaltons.

FIG. 7. Interaction of purified UspA1 and UspA2 with HEp-2 cells as determined by ELISA. HEp-2 cell monolayers cultured in 96-well plate were incubated with serially diluted UspA1 or UspA2. O35E bacterial strain was used as the positive control. The bacteria were diluted analogous to the proteins beginning with a suspension with an A_{550} of 1.0. The bound proteins or attached bacteria were detected with a 1:1 mixed antisera to UspA1 and UspA2 as described in the methods.

FIG. 8. Interaction with fibronectin and vitronectin determined by dot blot. The bound vitronectin was detected with rabbit polyclonal antibodies, the protein bound to the fibronectin was detected with pooled sera made against the UspA1 and UspA2.

FIG. 9. The levels of antibodies to the protein UspA1, UspA2 and *M. catarrhalis* O35E strain in normal human sera. Data are the $\log_{10}$ transformed end-point titers of the IgG (FIGs. 9A-9C) and IgA (FIGs. 9D-9F) antibodies determined by ELISA. The individual titers were plotted according to age group and the geometric mean titer for each age group linked by a solid line. Sera for the 2-18 month old children were consecutive samples from a group of ten children.

FIG. 10. Subclass distribution of IgG antibodies to UspA1 and UspA2 in normal human sera. FIG. 10A shows titers toward UspA1 and FIG. 10B shows titers to UspA2.

FIG. 11. Relationship of serum IgG titers to UspA1 (FIG. 11A) and UspA2 (FIG. 11B) with the bactericidal liter against the O35E strain determined by logistic regression ($p<0.05$). The solid line indicates the linear relationship between the IgG titer and bactericidal titer. Broken lines represent the 95 % confidence intervals of the linear fit.

FIG. 12. Schematic drawing showing the relative positions of decapeptides 10-24 within the region of UspA1 and UspA2 which binds to MAb 17C7.

FIG. 13. Western dot blot analysis demonstrating reactivity of decapeptides 10-24 with MAb 17C7.

FIG. 14. Partial restriction enzyme map of the *uspA1* (FIG. 14A) and *uspA2* (FIG. 14B) genes from *M. catarrhalis* strain O35E and the mutated versions of these genes. The shaded boxes indicate the open reading frame of each gene. Relevant restriction sites are indicated. PCR™ primer sites (P1-P6) are indicated by arrows. The DNA fragments containing the partial *uspA1* and *uspA2* open reading frames that were derived from *M. catarrhalis* strain O35E chromosomal DNA by PCR™ and cloned into pBluescriptII SK+ are indicated by black bars. Dotted lines connect corresponding restriction sites on these DNA inserts and the chromosome. Open bars indicate the location of the kanamycin or chloramphenicol cassettes, respectively. The DNA probes specific for *uspA1* or *uspA2* are indicated by the appropriate cross-hatched bars and were amplified by PCR™ from *M. catarrhalis* strain O35E chromosomal DNA by the use of the oligonucleotide primer pairs

P3 (5′-GACGCTCAACAGCACTAATACG-3′) (SEQ ID NO:20)/P4
(5′-CCAAGCTGATATCACTACC-3′) (SEQ ID NO:21) and
P5 (5′-TCAATGCCTTTGATGGTC-3′) (SEQ ID NO:22)/P6
(5′-TGTATGCCGCTACTCGCAGCT-3′) (SEQ ID NO:23), respectively.

FIG. 15. Detection of the UspA1 and UspA2 proteins in wild-type and mutant strains of *M. catarrhalis* O35E. Proteins present in EDTA-extracted outer membrane vesicles from the wild-type strain (lane 1), the *uspA1* mutant strain O35E.1 (lane 2), the *uspA2* mutant strain O35E.2 (lane 3), and the isogenic*uspA1 uspA2* double mutant strain O35E.12 (lane 4) were resolved by SDS-PAGE, and either stained with Coomassie blue (FIG. 15A) or transferred to nitrocellulose and probed with MAb 17C7 followed by radioiodinated goat anti-mouse

immunoglobulin in western blot analysis. In FIG. 15A, the closed arrow indicates the very high molecular weight form of the UspA antigen which is comprised of both UspA1 and UspA2. In FIG. 15B, the bracket on the left indicates the very high molecular weight forms of the UspA1 and UspA2 proteins that bind MAb 17C7. The open arrow indicates the 120 kDa, putative monomeric form of UspA1. The closed arrow indicates the 85 kDa, putative monomeric form of UspA2. Molecular weight position markers (in kilodaltons) are present on the left.

FIG. 16. Comparison of the rate and extent of growth of the wild-type and mutant strains of *M. catarrhalis*. The wild-type strain O35E (closed squares), the *uspA1* mutant O35E.1 (open squares), the *uspA2* mutant O35E.2 (closed circles), and the *uspA1 uspA2* double mutant O35E.12 (open circles) of *M. catarrhalis* O35E from overnight broth cultures were diluted to a density of 35 Klett units in BHI broth and subsequently allowed to grow at 37° with shaking. Growth was followed by means of turbidity measurements.

FIG. 17. Susceptibility of wild-type and mutant strains of *M. catarrhalis* to killing by normal human serum. Cells of the wild-type parent strain O35E (diamonds), *uspA1* mutant O35E.1 (triangles), *uspA2* mutant O35E.2 (circles), and *uspA1 uspA2* double mutant O35E.12 (squares) from logarithmic-phase BHI broth cultures were incubated in the presence of 10% (v/v) normal human serum (closed symbols) or heat-inactivated normal human serum (open symbols). Data are presented as the percentage of the original inoculum remaining at each time point.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention relates to the identification of epitopes useful for developing potential vaccines against *M. catarrhalis*. Early work was directed at determining the molecular nature of the UspA antigen and characterize the epitope which is recognized by the MAb 17C7. Preliminary work indicated that MAb 17C7 recognizes a single antigenic epitope and it was believed that this epitope was encoded by a single gene. However, isolation of the protein which contained the epitope yielded unexpected results. MAb 17C7 recognized a single epitope, but the characteristics of the protein associated with the epitope suggested the existence of not one but two separate proteins. Further careful analyses led to a surprising discovery. A single epitope of the UspA antigen is recognized by the MAb 17C7, but this epitope is present in two different proteins, UspA1 and UspA2, which are encoded by two different genes *uspA1* and *uspA2*, respectively, and only have 43% identity to each other. The present invention provides the nucleotide sequences of the genes *uspA1* and *uspA2*, their respective protein products, UspA1 and UspA2, and the shared epitope recognized by MAb 17C7.

In addition, the present invention provides insights into the antigenic structure of the UspA protein based on the analysis of the sequences of the UspA1 and UspA2 proteins which comprise the protein. Characterization of the epitopic region of the molecule that is targeted by the MAb 17C7 permits the development of agents that will be useful in protecting against *M. catarrhalis* infections, *e.g.*, in the preparation of prophylactic reagents. Particular embodiments relate to the amino acid and nucleic acids corresponding to the UspA1 and UspA2 proteins, peptides and antigenic compositions derived therefrom, and methods for the diagnosis and treatment of *M. catarrhalis* disease.

As stated previously, *M. catarrhalis* infections present a serious health challenge, especially to the young. Thus, there is a clear need to develop compositions and methods that will aid in the treatment and diagnosis of this disease. The present invention, by virtue of new information regarding the structure of the UspA antigen of *M. catarrhalis*, and discovery of the two new and distinct proteins UspA1 and UspA2 provides such improved compositions and methods. UspA1 and UspA2 represent important antigenic determinants, as the MAb 17C7 has been shown to protect experimental animals, as measured in a pulmonary clearance model, when provided in passive immunizations.

In a first embodiment, the present invention provides for the identification of the proteins UspA1 and UspA2 from *M. catarrhalis* strain O35E. The UspA1 protein comprises about 831 amino acid residues and has a predicted mass of about 88,271 daltons (SEQ ID NO:1). The UspA2 protein comprises about 576 residues and has a predicted mass of about 62,483 daltons (SEQ ID NO:3). UspA2 is not a truncated or processed form of UspA1.

In a second embodiment, the present invention has identified the specific epitope to which MAb 17C7 binds. A common peptide sequence, designated as the "3Q" peptide, found between amino acid residues 480-502 and 582-604 of the UspA1 protein (SEQ ID NO:1) and residues 355-377 of the UspA2 protein (SEQ ID NO:3) of *M. catarrhalis* strain 035E, encompasses the region which appears to be recognized by MAb 17C7. (Note that numbering of the amino acid residues is based upon strain O35E as provided in SEQ ID NO:3.) It is envisioned that this region plays an important role in the biology of the pathogen and, from this information, one will deduce amino acids residues that are critical in MAb 17C7 antibody binding. It also is envisioned that, based upon this information, one will be able to design epitopic regions that have either a higher or lower affinity for the MAb 17C7 or other antibodies. Further embodiments of the present invention are discussed below.

In another preferred embodiment, the present invention provides DNA segments, vectors and the like comprising at least one isolated gene, DNA segment or coding region that encodes a *M. catarrhalis* UspA1 or UspA2 protein, polypeptide, domain, peptide or any fusion protein thereof. Herein are provided at least an isolated gene, DNA segment or coding region that encodes a *M. catarrhalis uspA1* gene comprising about 2493 base pairs (bp) (SEQ ID NO:2) of strain O35E, about 3381 bp (SEQ ID NO:6) of strain O46E, about 3538 bp (SEQ ID NO:10) of strain TTA24, or about 3292 bp (SEQ ID NO:14) of strain TTA37. Further provided are at least an isolated gene, DNA segment or coding region that encodes a *M. catarrhalis uspA2* gene comprising about 1728 bp (SEQ ID NO:4) of strain O35E, about 3295 bp (SEQ ID NO:8) of strain O46E, about 2673 bp (SEQ ID NO:12), or about 4228 bp (SEQ ID NO:16) of strain TTA37. It is envisioned that the *uspA1* and *uspA2* genes will be useful in the preparation of proteins, antibodies, screening assays for potential candidate drugs and the like to treat or inhibit, or even prevent, *M. catarrhalis* infections.

The present invention also provides for the use of the UspA1 or UspA2 proteins or peptides as immunogenic carriers of other agents which are useful for the treatment, inhibition or even prevention of other bacterial, viral or parasitic infections. It is envisioned that either the UspA1 or UspA2 antigen, or portions thereof, will be coupled, bonded, bound, conjugated or chemically-linked to one or more agents via linkers, polylinkers or derivatized amino acids such that a bispecific or multivalent composition or vaccine which is useful for the treatment, inhibition or even prevention of infection by *M. catarrhalis* and another pathogen(s) is prepared. It is further envisioned that the methods used in the preparation of these compositions will be familiar to those of skill in the art and, for example, similar to those used to prepare conjugates to keyhole limpet hemocyannin (KLH) or bovine serum albumin (BSA).

It is important to note that screening methods for diagnosis and prophylaxis are readily available, as set forth below. Thus, the ability to (i) test peptides, mutant peptides and antibodies for their reactivity with each other and (ii) test peptides and antibodies for the ability to prevent infections *in vivo*, provide powerful tools to develop clinically important reagents.

1.0 UspA Proteins, Peptides and Polypeptides

The present invention, in one embodiment, encompasses the two new protein sequences, UspA1 and UspA2, and the peptide sequence AQQQDQH (SEQ ID NO:17) identified as the target epitope of MAb 17C7. In addition, inspection of the amino acid sequences of the UspA1 and UspA2 proteins from four strains of *M. catarrhalis* indicated that each protein contained at least one copy of the peptide YELAQQQDQH (SEQ ID NO:18) which binds Mab 17C7 or, in one instance, a peptide nearly identical and having the amino acid sequence YDLAQQQDQH (SEQ ID NO:19).

The peptide (YELAQQQDQH, SEQ ID NO:18) occurs twice in UspA1 from strain O35E at residues 486-495 and 588-597 (SEQ ID NO:1) and once in UspA2 from strain O35E at residues 358-367 (SEQ ID NO:3). It occurs once in UspA1 from strain TTA24 at residues 497-506 (SEQ ID NO:9) and twice in UspA2 from strain TTA24 at residues 225-234 and 413-422 (SEQ ID NO:11). The peptide YDLAQQQDQH (SEQ ID NO:19) occurs once in UspA1 from strain O46E at residues 448-457 (SEQ ID NO:5) whereas the peptide YELAQQQDQH (SEQ ID NO:18) occurs once in this same protein at residues 649-658 (SEQ ID NO:5). The peptide YELAQQQDQH (SEQ ID NO:18) occurs once in UspA2 from strain O46E at residues 416-425 (SEQ ID NO:7). The peptide YELAQQQDQH (SEQ ID NO:18) occurs twice in UspA1 from strain TTA37 at residues 478-487 and 630-639 (SEQ ID NO:13) and twice in UspA2 from strain TTA37 at residues 522-531 and 681-690 (SEQ ID NO:15).

Also encompassed in the present invention are hybrid molecules containing portions from one UspA protein, for example the UspA1 protein, fused with portions of the other UspA protein, in this example the UspA2 protein, or fused with other proteins which are useful for identification, such as kanamycin-resistance, or other purposes in the screening of potential vaccines or further characterization of the UspA1 and UspA2 proteins. For example, one may fuse residues 1-350 of any UspA1 with residues 351-576 of any UspA2. Alternatively, a fusion could be generated with sequences from three, four or even five peptide regions represented in a single UspA antigen. Also encompassed are fragments of the disclosed UspA1 and UspA2 molecules, as well as insertion, deletion or replacement mutants in which non-UspA sequences are introduced, UspA sequences are removed, or UspA sequences are replaced with non-UspA sequences, respectively.

UspA1 and UspA2 proteins, according to the present invention, may be advantageously cleaved into fragments for use in further structural or functional analysis, or in the generation of reagents such as UspA-related polypeptides and UspA-specific antibodies. This can be accomplished by treating purified or unpurified UspA1 and/or UspA2 with a peptidase such as endoproteinase glu-C (Boehringer, Indianapolis, IN). Treatment with CNBr is another method by which UspA1 and/or UspA2 fragments may be produced from their natural respective proteins. Recombinant techniques also can be used to produce specific fragments of UspA1 or UspA2.

More subtle modifications and changes may be made in the structure of the encoded UspA1 or UspA2 polypeptides of the present invention and still obtain a molecule that encodes a protein or peptide with characteristics of the natural UspA antigen. The following is a discussion based upon changing the amino acids of a protein to create an equivalent, or even an improved, second-generation molecule. The amino acid changes may be achieved by changing the codons of the DNA sequence, according to the following codon table:

TABLE I

Amino acid names and abbreviations			Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

It is known that certain amino acids may be substituted for other amino acids in a protein structure in order to modify or improve its antigenic or immunogenic activity (see, *e.g.*, Kyte & Doolittle, 1982; Hopp, U.S. patent 4,554,101, incorporated herein by reference). For example, through the substitution of alternative amino acids, small conformational changes may be conferred upon a polypeptide which result in increased activity or stability. Alternatively, amino acid substitutions in certain polypeptides may be utilized to provide residues which may then be linked to other molecules to provide peptide-molecule conjugates which retain enough antigenicity of the starting peptide to be useful for other purposes. For example, a selected UspA1 or UspA2 peptide bound to a solid support might be constructed which would have particular advantages in diagnostic embodiments.

The importance of the hydropathic index of amino acids in conferring interactive biological function on a protein has been discussed generally by Kyte & Doolittle (1982), wherein it is found that certain amino acids may be substituted for other amino acids having a similar hydropathic index or core and still retain a similar biological activity. As displayed in Table II below, amino acids are assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics. It is believed that the relative hydropathic character of the amino acid determines the secondary structure of the resultant protein, which in turn defines the interaction of the protein with substrate molecules. Preferred substitutions which result in an antigenically equivalent peptide or protein will generally involve amino acids having index scores within ±2 units of one another, and more preferably within ±1 unit, and even more preferably, within ±0.5 units.

TABLE II

Amino Acid	Hydropathic Index
Isoleucine	4.5
Valine	4.2
Leucine	3.8
Phenylalanine	2.8
Cysteine/cystine	2.5
Methionine	1.9
Alanine	1.8
Glycine	-0.4
Threonine	-0.7

Table II (Continued)

Amino Acid	Hydropathic Index
Tryptophan	-0.9
Serine	-0.8
Tyrosine	-1.3
Proline	-1.6
Histidine	-3.2
Glutamic Acid	-3.5
Glutamine	-3.5
Aspartic Acid	-3.5
Asparagine	-3.5
Lysine	-3.9
Arginine	-4.5

Thus, for example, isoleucine, which has a hydropathic index of +4.5, will preferably be exchanged with an amino acid such as valine (+ 4.2) or leucine (+ 3.8). Alternatively, at the other end of the scale, lysine (- 3.9) will preferably be substituted for arginine (-4.5), and so on.

Substitution of like amino acids may also be made on the basis of hydrophilicity, particularly where the biological functional equivalent protein or peptide thereby created is intended for use in immunological embodiments. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, *i.e.* with an important biological property of the protein.

As detailed in U.S. Patent 4,554,101, each amino acid has also been assigned a hydrophilicity value. These values are detailed below in Table III.

TABLE III

Amino Acid	Hydrophilic Index
arginine	+3.0
lysine	+3.0
aspartate	+3.0 ± 1
glutamate	+3.0 ± 1
serine	+0.3
asparagine	+0.2
glutamine	+0.2
glycine	0
threonine	-0.4
alanine	-0.5
histidine	-0.5
proline	-0.5 ± 1
cysteine	-1.0
methionine	-1.3
valine	-1.5
leucine	-1.8
isoleucine	-1.8
tyrosine	-2.3
phenylalanine	-2.5
tryptophan	-3.4

It is understood that one amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

Accordingly, these amino acid substitutions are generally based on the relative similarity of R-group substituents, for example, in terms of size, electrophilic character, charge, and the like. In general, preferred substitutions which take various of the foregoing characteristics into consideration will be known to those of skill in the art and include, for example, the following combinations: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, peptides derived from these polypeptides, including peptides of at least about 6 consecutive amino acids from these sequences, are contemplated. Alternatively, such peptides may comprise about 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 or 60 consecutive residues. For example, a peptide that comprises 6 consecutive amino acid residues may comprise residues 1 to 6, 2 to 7, 3 to 8 and so on of the UspA1 or UspA2 protein. Such peptides may be represented by the formula

x to $(x + n)$ = 5' to 3' the positions of the first and last consecutive residues

where x is equal to any number from 1 to the full length of a UspA1 or UspA2 protein and n is equal to the length of the peptide minus 1. So, for UspA1, $x = 1$ to 831, for UspA2, $x = 1$ to 576. Where the peptide is 10 residues long ($n = 10-1$), the formula represents every 10-mer possible for each antigen. For example, where x is equal to 1 the peptide would comprise residues 1 to $(1 + [10-1])$, or 1 to 10. Where x is equal to 2, the peptide would comprise residues 2 to $(2 + [10-2])$, or 2 to 11, and so on.

Syntheses of peptides are readily achieved using conventional synthetic techniques such as the solid phase method (*e.g.*, through the use of a commercially available peptide synthesizer such as an Applied Biosystems Model 430A Peptide Synthesizer). Peptides synthesized in this manner may then be aliquoted in predetermined amounts and stored in conventional manners, such as in aqueous solutions or, even more preferably, in a powder or lyophilized state pending use.

In general, due to the relative stability of peptides, they may be readily stored in aqueous solutions for fairly long periods of time if desired, *e.g.*, up to six months or more, in virtually any aqueous solution without appreciable degradation or loss of antigenic activity. However, where extended aqueous storage is contemplated it will generally be desirable to include agents including buffers such as Tris or phosphate buffers to maintain a pH of 7.0 to 7.5. Moreover, it may be desirable to include agents which will inhibit microbial growth, such as sodium azide or

Merthiolate. For extended storage in an aqueous state it will be desirable to store the solutions at 4°C, or more preferably, frozen. Of course, where the peptide(s) are stored in a lyophilized or powdered state, they may be stored virtually indefinitely, *e.g.*, in metered aliquots that may be rehydrated with a predetermined amount of water (preferably distilled, deionized) or buffer prior to use.

Of particular interest are peptides that represent epitopes that lie within the UspA antigen and are encompassed by the UspA1 and UspA2 proteins of the present invention. An "epitope" is a region of a molecule that stimulates a response from a T-cell or B-cell, and hence, elicits an immune response from these cells. An epitopic core sequence, as used herein, is a relatively short stretch of amino acids that is structurally "complementary" to, and therefore will bind to, binding sites on antibodies or T-cell receptors. It will be understood that, in the context of the present disclosure, the term "complementary" refers to amino acids or peptides that exhibit an attractive force towards each other. Thus, certain epitopic core sequences of the present invention may be operationally defined in terms of their ability to compete with or perhaps displace the binding of the corresponding UspA antigen to the corresponding UspA-directed antisera.

The identification of epitopic core sequences is known to those of skill in the art. For example U.S. Patent 4,554,101 teaches identification and preparation of epitopes from amino acid sequences on the basis of hydrophilicity, and by Chou-Fasman analyses. Numerous computer programs are available for use in predicting antigenic portions of proteins, examples of which include those programs based upon Jameson-Wolf analyses (Jameson and Wolf, 1988; Wolf *et al.*, 1988), the program PepPlot® (Brutlag *et al.*, 1990; Weinberger *et al.*, 1985), and other new programs for protein tertiary structure prediction (Fetrow & Bryant, 1993) that can be used in conjunction with computerized peptide sequence analysis programs.

In general, the size of the polypeptide antigen is not believed to be particularly crucial, so long as it is at least large enough to carry the identified core sequence or sequences. The smallest useful core sequence anticipated by the present disclosure would be on the order of about 6 amino acids in length. Thus, this size will generally correspond to the smallest peptide antigens prepared in accordance with the invention. However, the size of the antigen may be larger where desired, so long as it contains a basic epitopic core sequence.

2.0 UspA1 and UspA2 Nucleic Acids

In addition to polypeptides, the present invention also encompasses nucleic acids encoding the UspA1 (SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10 and SEQ ID NO:14) and UspA2 (SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12 and SEQ ID NO:16) proteins from the exemplary *M. catarrhalis* strains O35E, O46E, TTA24 and TTA37, respectively. Because of the degeneracy of the genetic code, many other nucleic acids also may encode a given UspA1 or UspA2 protein. For example, four different three-base codons encode the amino acids alanine, glycine, proline, threonine and valine, while six different codons encode arginine, leucine and serine. Only methionine and tryptophan are encoded by a single codon. Table I provides a list of amino acids and their corresponding codons for use in such embodiments. In order to generate any nucleic acid encoding UspA1 or UspA2, one need only refer to the codon table provided herein. Substitution of the natural codon with any codon encoding the same amino acid will result in a distinct nucleic acid that encodes UspA1 or UspA2. As a practical matter, this can be accomplished by site-directed mutagenesis of an existing *uspA1* or *uspA2* gene or *de novo* chemical synthesis of one or more nucleic acids.

These observations regarding codon selection, site-directed mutagenesis and chemical synthesis apply with equal force to the discussion of substitutional mutant UspA1 or UspA2 peptides and polypeptides, as set forth above. More specifically, substitutional mutants generated by site-directed changes in the nucleic acid sequence that are designed to alter one or more codons of a given polypeptide or epitope may provide a more convenient way of generating large numbers of mutants in a rapid fashion. The nucleic acids of the present invention provide for a simple way to generate fragments (*e.g.*, truncations) of UspA1 or UspA2, UspA1-UspA2 fusion molecules (discussed above) and UspA1 or UspA2 fusions with other molecules. For example, utilization of restriction enzymes and nuclease in the *uspA1* or *uspA2* gene permits one to manipulate the structure of these genes, and the resulting gene products.

The nucleic acid sequence information provided by the present disclosure also allows for the preparation of relatively short DNA (or RNA) sequences that have the ability to specifically hybridize to gene sequences of the selected *uspA1* or *uspA2* gene. In these aspects nucleic acid probes of an appropriate length are prepared based on a consideration of the coding sequence of the *uspA1* or *uspA2* gene, or flanking regions near the *uspA1* or *uspA2* gene, such as regions downstream and upstream in the *M. catarrhalis* chromosome. The ability of such nucleic acid probes to specifically hybridize to either *uspA1* or *uspA2* gene sequences lends them particular utility in a variety of embodiments. For example, the probes can be used in a variety of diagnostic assays for detecting the presence of pathogenic organisms in a given sample. In addition, these oligonucleotides can be inserted, in frame, into expression constructs for the purpose of screening the corresponding peptides for reactivity with existing antibodies or for the ability to generate diagnostic or therapeutic reagents.

To provide certain of the advantages in accordance with the invention, the preferred nucleic acid sequence employed for hybridization studies or assays includes sequences that are complementary to at least a 10 to 20, or so, nucleotide stretch of the sequence, although sequences of 30 to 60 or so nucleotides are also envisioned to be useful. A size of at least 9 nucleotides in length helps to ensure that the fragment will be of sufficient length to form a duplex molecule that is both stable and selective. Though molecules having complementary sequences over stretches greater than 10 bases in length are generally preferred, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of the specific hybrid molecules obtained. Thus, one will generally prefer to design nucleic acid molecules having either *uspA1* or *uspA2* gene-complementary stretches of 15 to 20 nucleotides, or even longer, such as 30 to 60, where desired. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCR™ technology of U.S. Patent 4,603,102, or by introducing selected sequences into recombinant vectors for recombinant production.

The probes that would be useful may be derived from any portion of the sequences of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. Therefore, probes are specifically contemplated that comprise nucleotides 1 to 9, or 2 to 10, or 3 to 11 and so forth up to a probe comprising the last 9 nucleotides of the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. Thus, each probe would comprise at least about 9 linear nucleotides of the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16., designated by the formula "n to n + 8," where n is an integer from 1 to the number of nucleotides in the sequence. Longer probes that hybridize to the *uspA1* or *uspA2* gene under low, medium, medium-high and high stringency conditions are also contemplated, including those that comprise the entire nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. This hypothetical may be repeated for probes having lengths of about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 and greater bases.

In that the UspA antigenic epitopes of the present invention are believed to be indicative of pathogenic *Moraxella* species as exemplified by strains O35E, O46E, TTA24 and TTA37, the probes of the present invention will find particular utility as the basis for diagnostic hybridization assays for detecting UspA1 or UspA2 DNA in clinical samples. Exemplary clinical samples that can be used in the diagnosis of infections are thus any samples which could possibly include *Moraxella* nucleic acid, including middle ear fluid, sputum, mucus, bronchoalveolar fluid, amniotic fluid or the like. A variety of hybridization techniques and systems are known which can be used in connection with the hybridization aspects of the invention, including diagnostic assays such as those described in Falkow *et al.*, U.S. Patent 4,358,535. Depending on the application envisioned, one will desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of the probe toward the target sequence. For applications requiring a high degree of selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, for example, one will select relatively low salt and/or high temperature conditions, such as provided by 0.02M-0.15M NaCl at temperatures of 50°C to 70°C. These conditions are particularly selective, and tolerate little, if any, mismatch between the probe and the template or target strand.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent hybridization conditions are called for in order to allow formation of the heteroduplex. In these circumstances, one would desire to employ conditions such as 0.15M-0.9M salt, at temperatures ranging from 20°C to 55°C. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and the method of choice will generally depend on the desired results.

In certain embodiments, one may desire to employ nucleic acid probes to isolate variants from clone banks containing mutated clones. In particular embodiments, mutant clone colonies growing on solid media which contain variants of the UspA1 and/or UspA2 sequence could be identified on duplicate filters using hybridization conditions and methods, such as those used in colony blot assays, to obtain hybridization only between probes containing sequence variants and nucleic acid sequence variants contained in specific colonies. In this manner, small hybridization probes containing short variant sequences of either the *uspA1* or *uspA2* gene may be utilized to identify those clones growing on solid media which contain sequence variants of the entire *uspA1* or *uspA2* gene. These clones can then be grown to obtain desired quantities of the variant UspA1 or UspA2 nucleic acid sequences or the corresponding UspA antigen.

In clinical diagnostic embodiments, nucleic acid sequences of the present invention are used in combination with an appropriate means, such as a label, for determining hybridization. A wide variety of appropriate indicator means are known in the art, including radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred diagnostic embodiments, one will likely desire to employ an enzyme tag such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with pathogen nucleic acid-containing samples.

In general, it is envisioned that the hybridization probes described herein will be useful both as reagents in solution hybridizations as well as in embodiments employing a solid phase. In embodiments involving a solid phase, the test DNA (or RNA) from suspected clinical samples, such as exudates, body fluids (*e.g.*, amniotic fluid, middle ear effusion, bronchoalveolar lavage fluid) or even tissues, is adsorbed or otherwise affixed to a selected matrix or surface. This fixed, single-stranded nucleic acid is then subjected to specific hybridization with selected probes under desired conditions. The selected conditions will depend on the particular circumstances based on the particular criteria required (depending, for example, on the G+C contents, type of target nucleic acid, source of nucleic acid, size of hybridization probe, etc.). Following washing of the hybridized surface so as to remove nonspecifically bound probe molecules, specific hybridization is detected, or even quantified, by means of the label.

The nucleic acid sequences which encode for the UspA1 and/or UspA2 epitopes, or their variants, may be useful in conjunction with PCR™ methodology to detect *M. catarrhalis*. In general, by applying the PCR™ technology as set out, *e.g.*, in U.S. Patent 4,603,102, one may utilize various portions of either the *uspA1* or *uspA2* sequence as oligonucleotide probes for the PCR™ amplification of a defined portion of a *uspA1* or *uspA2* nucleic acid in a sample. The amplified portion of the *uspA1* or *uspA2* sequence may then be detected by hybridization with a hybridization probe containing a complementary sequence. In this manner, extremely small concentrations of *M. catarrhalis* nucleic acid may detected in a sample utilizing *uspA1* or *uspA2* sequences.

3.0 Vectors, Host Cells and Cultures for Producing UspA1 and/or UspA2 Antigens

In order to express a UspA1 and/or UspA2 polypeptide, it is necessary to provide an *uspA1* and/or *uspA2* gene in an expression cassette. The expression cassette contains a UspA1 and/or UspA2-encoding nucleic acid under transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a gene. The phrase "under transcriptional control" means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene. Those promoters most commonly used in prokaryotic recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang *et al.*, 1978; Itakura *et al.*, 1977; Goeddel *et al.*, 1979) and a tryptophan (trp) promoter system (Goeddel *et al.*, 1980; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (EPO Appl. Publ. No. 0036776). Additional examples of useful promoters are provided in Table IV below.

TABLE IV

Promoters	References
Immunoglobulin Heavy Chain	Hanerji *et al.*, 1983; Gilles *et al.*, 1983; Grosschedl and Baltimore, 1985; Atchinson and Perry, 1986, 1987; Imler *et al.*, 1987; Weinberger *et al.*, 1988; Kiledjian *et al.*, 1988; Porton *et al.*, 1990
Immunoglobulin Light Chain	Queen and Baltimore, 1983; Picard and Schaffner, 1984
T-Cell Receptor	Luria *et al.*, 1987, Winoto and Baltimore, 1989; Redondo *et al.*, 1990
HLA DQ a and DQ ß	Sullivan and Peterlin, 1987
ß-Interferon	Goodbourn *et al.*, 1986; Fujita *et al.*, 1987; Goodbourn and Maniatis, 1985
Interleukin-2	Greene *et al.*, 1989
Interleukin-2 Receptor	Greene *et al.*, 1989; Lin *et al.*, 1990
MHC Class II 5	Koch *et al.*, 1989
MHC Class II HLA-DRa	Sherman *et al.*, 1989
ß-Actin	Kawamoto *et al.*, 1988; Ng *et al.*, 1989
Muscle Creatine Kinase	Jaynes *et al.*, 1988; Horlick and Benfield, 1989; Johnson *et al.*, 1989a
Prealbumin (Transthyretin)	Costa *et al.*, 1988
Elastase *I*	Omitz *et al.*, 1987
Metallothionein	Karin *et al.*, 1987; Culotta and Hamer, 1989
Collagenase	Pinkert *et al.*, 1987; Angel *et al.*, 1987
Albumin Gene	Pinkert *et al.*, 1987, Tronche *et al.*, 1989, 1990

TABLE IV (Continued)

Promoters	References
a-Fetoprotein	Godbout *et al.*, 1988; Campere and Tilghman, 1989
t-Globin	Bodine and Ley, 1987; Perez-Stable and Constantini, 1990
ß-Globin	Trudel and Constantini, 1987
e-fos	Cohen *et al.*, 1987
c-HA-ras	Triesman, 1986; Deschamps *et al.*, 1985
Insulin	Edlund *et al.*, 1985
Neural Cell Adhesion Molecule (NCAM)	Hirsch *et al.*, 1990
$a_{1\text{-Antitrypain}}$	Latimer *et al.*, 1990
H2B (TH2B) Histone	Hwang *et al.*, 1990
Mouse or Type I Collagen	Ripe *et al.*, 1989
Glucose-Regulated Proteins (GRP94 and GRP78)	Chang *et al.*, 1989
Rat Growth Hormone	Larsen *et al.*, 1986
Human Serum Amyloid A (SAA)	Edbrooke *et al.*, 1989
Troponin I (TN I)	Yutzey *et al.*, 1989
Platelet-Derived Growth Factor	Pech *et al.*, 1989
Duchenne Muscular Dystrophy	Klamut *et al.*, 1990
SV40	Banerji *et al.*, 1981; Moreau *et al.*, 1981; Sleigh and Lockett, 1985; Firak and Subramanian, 1986; Herr and Clarke, 1986; Imbra and Karin, 1986; Kadesch and Berg, 1986; Wang and Calame, 1986; Ondek *et al.*, 1987; Kuhl *et al.*, 1987 Schaffner *et al.*, 1988

TABLE IV (Continued)

Promoters	References
Polyoma	Swartzendruber and Lehman, 1975; Vasseur *et al.*, 1980; Katinka *et al.*, 1980, 1981; Tyndell *et al.*, 1981; Dandolo *et al.*, 1983; deVilliers *et al.*, 1984; Hen *et al.*, 1986; Satake *et al.*, 1988; Campbell and Villarreal, 1988
Retroviruses	Kriegler and Botchan, 1982, 1983; Levinson *et al.*, 1982; Kriegler *et al.*, 1983, 1984a,b, 1988; Bosze *et al.*, 1986; Miksicek *et al.*, 1986; Celander and Haseltine, 1987; Thiesen *et al.*, 1988; Celander *et al.*, 1988; Chol *et al.*, 1988; Reisman and Rotter, 1989
Papilloma Virus	Campo *et al.*, 1983; Lusky *et al.*, 1983; Spandidos and Wilkie, 1983; Spalholz *et al.*, 1985; Lusky and Botchan, 1986; Cripe *et al.*, 1987; Gloss *et al.*, 1987; Hirochika *et al.*, 1987, Stephens and Hentschel, 1987; Glue *et al.*, 1988
Hepatitis B Virus	Bulla and Siddiqui, 1986; Jameel and Siddiqui, 1986; Shaul and Ben-Levy, 1987; Spandau and Lee, 1988; Vannice and Levinson, 1988
Human Immunodeficiency Virus	Muesing *et al.*, 1987; Hauber and Cullan, 1988; Jakobovits *et al.*, 1988; Feng and Holland, 1988; Takebe *et al.*, 1988; Rowen *et al.*, 1988; Berkhout *et al.*, 1989; Laspia *et al.*, 1989; Sharp and Marciniak, 1989; Braddock *et al.*, 1989
Cytomegalovirus	Weber *et al.*, 1984; Boshart *et al.*, 1985; Foecking and Hofstetter, 1986
Gibbon Ape Leukemia Virus	Holbrook *et al.*, 1987; Quinn *et al.*, 1989

The appropriate expression cassette can be inserted into a commercially available expression vector by standard subcloning techniques. For example, the *E. coli* vectors pUC or pBluescript™ may be used according to the present invention to produce recombinant UspA1 and/or UspA2 polypeptide *in vitro*. The manipulation of these vectors is well known in the art. In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (Bolivar *et al.*, 1977). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microbial organism for expression of its own proteins.

In addition, phage vectors containing replicon and control sequences that are compatible with the host microorganism can be used as a transforming vector in connection with these hosts. For example, the phage lambda GEM™-11 may be utilized in making recombinant phage vector which can be used to transform host cells, such as *E. coli* LE392.

In one embodiment, the UspA antigen is expressed as a fusion protein by using the pGEX4T-2 protein fusion system (Pharmacia LKB, Piscataway, NJ), allowing characterization of the UspA antigen as comprising both the UspA1 and UspA2 proteins. Additional examples of fusion protein expression systems are the glutathione S-transferase system (Pharmacia, Piscataway, NJ), the maltose binding protein system (NEB, Beverley, MA), the FLAG system (IBI, New Haven, CT), and the 6xHis system (Qiagen, Chatsworth, CA). Some of these fusion systems produce recombinant protein bearing only a small number of additional amino acids, which are unlikely to affect the functional capacity of the recombinant protein. For example, both the FLAG system and the 6xHis system add only short sequences, both of which are known to be poorly antigenic and which do not adversely affect folding of the protein to its native conformation. Other fusion systems produce proteins where it is desirable to excise the fusion partner from the desired protein. In another embodiment, the fusion partner is linked to the recombinant protein by a peptide sequence containing a specific recognition sequence for a protease. Examples of suitable sequences are those recognized by the Tobacco Etch Virus protease (Life Technologies, Gaithersburg, MD) or Factor Xa (New England Biolabs, Beverley, MA).

E. coli is a preferred prokaryotic host. For example, *E. coli* strain RR1 is particularly useful. Other microbial strains which may be used include *E. coli* strains such as *E. coli* LE392, *E. coli* B, and *E. coli* X 1776 (ATCC No. 31537). The aforementioned strains, as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 273325), bacilli such as *Bacillus subtilis*, or other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcescens*, and various *Pseudomonas* species may be used. These examples are, of course, intended to be illustrative rather than limiting. Recombinant bacterial cells, for example *E. coli*, are grown in any of a number of suitable media, for example LB, and the expression of the recombinant polypeptide induced by adding IPTG to the media or switching incubation to a higher temperature. After culturing the bacteria for a further period of between 2 and 24 hours, the cells are collected by centrifugation and washed to remove residual media. The bacterial cells are then lysed, for example, by disruption in a cell homogenizer and centrifuged to separate the dense inclusion bodies and cell membranes from the soluble cell components. This centrifugation can be performed under conditions whereby the dense inclusion bodies are selectively enriched by incorporation of sugars such as sucrose into the buffer and centrifugation at a selective speed.

If the recombinant protein is expressed in the inclusion bodies, as is the case in many instances, these can be washed in any of several solutions to remove some of the contaminating host proteins, then solubilized in solutions containing high concentrations of urea (*e.g.* 8M) or chaotropic agents such as guanidine hydrochloride in the presence of reducing agents such as ß-mercaptoethanol or DTT (dithiothreitol).

Under some circumstances, it may be advantageous to incubate the polypeptide for several hours under conditions suitable for the protein to undergo a refolding process into a conformation which more closely resembles that of the native protein. Such conditions generally include low protein concentrations less than 500 μg/ml, low levels of reducing agent, concentrations of urea less than 2 M and often the presence of reagents such as a mixture of reduced and oxidized glutathione which facilitate the interchange of disulfide bonds within the protein molecule.

The refolding process can be monitored, for example, by SDS-PAGE or with antibodies which are specific for the native molecule (which can be obtained from animals vaccinated with the native molecule isolated from bacteria). Following refolding, the protein can then be purified further and separated from the refolding mixture by chromatography on any of several supports including ion exchange resins, gel permeation resins or on a variety of affinity columns.

There are a variety of other eukaryotic vectors that provide a suitable vehicle in which recombinant UspA proteins can be produced. In various embodiments of the invention, the expression construct may comprise a virus or engineered construct derived from a viral genome. The ability of certain viruses to enter cells via receptor-mediated endocytosis and to integrate into host cell genome and express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, 1988; Nicolas and Rubenstein, 1988; Baichwal and Sugden, 1986; Temin, 1986). The first viruses used as vectors were DNA viruses including the papovaviruses (simian virus 40 (SV40), bovine papilloma virus, and polyoma) (Ridgeway, 1988; Baichwal and Sugden, 1986) and adenoviruses (Ridgeway, 1988; Baichwal and Sugden, 1986) and adeno-associated viruses. Retroviruses also are attractive gene transfer vehicles (Nicolas and Rubenstein, 1988; Temin, 1986) as are vaccina virus (Ridgeway, 1988) adeno-associated virus (Ridgeway, 1988) and herpes simplex virus (HSV) (Glorioso *et al.*, 1995). Such vectors may be used to (i) transform cell lines *in vitro* for the purpose of expressing proteins of interest or (ii) to transform cells *in vitro* or *in vivo* to provide therapeutic polypeptides in a gene therapy scenario.

With respect to eukaryotic vectors, the term promoter will be used here to refer to a group of transcriptional control modules that are clustered around the initiation site for RNA polymerase II. Much of the thinking about how promoters are organized derives from analyses of several viral promoters, including those for the HSV thymidine kinase (tk) and SV40 early transcription units. These studies, augmented by more recent work, have shown that promoters are composed of discrete functional modules, each consisting of approximately 7-20 bp of DNA, and containing one or more recognition sites for transcriptional activator or repressor proteins.

At least one module in each promoter functions to position the start site for RNA synthesis. The best known example of this is the TATA box, but in some promoters lacking a TATA box, such as the promoter for the mammalian terminal deoxynucleotidyl transferase gene and the promoter for the SV40 late genes, a discrete element overlying the start site itself helps to fix the place of initiation.

Additional promoter elements regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have recently been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the tk promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either cooperatively or independently to activate transcription.

The particular promoter that is employed to control the expression of a nucleic acid is not believed to be critical, so long as it is capable of expressing the nucleic acid in the targeted cell. Thus, where a human cell is targeted, it is preferable to position the nucleic acid coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a human or viral promoter. Preferred promoters include those derived from HSV, including the $\alpha4$ promoter. Another preferred embodiment is the tetracycline controlled promoter.

In various other embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter and the Rous sarcoma virus long terminal repeat can be used to obtain high-level expression of transgenes. The use of other viral or mammalian cellular or bacterial phage promoters which are well-known in the art to achieve expression of a transgene is contemplated as well, provided that the levels of expression are sufficient for a given purpose. Table IV lists several promoters which may be employed, in the context of the present invention, to regulate the expression of a transgene. This list is not intended to be exhaustive of all the possible elements involved in the promotion of transgene expression but, merely, to be exemplary thereof.

Enhancers were originally detected as genetic elements that increased transcription from a promoter located at a distant position on the same molecule of DNA. This ability to act over a large distance had little precedent in classic studies of prokaryotic transcriptional regulation. Subsequent work showed that regions of DNA with enhancer activity are organized much like promoters. That is, they are composed of many individual elements, each of which binds to one or more transcriptional proteins.

The basic distinction between enhancers and promoters is operational. An enhancer region as a whole must be able to stimulate transcription at a distance; this need not be true of a promoter region or its component elements. On the other hand, a promoter must have one or more elements that direct initiation of RNA synthesis at a particular site and in a particular orientation, whereas enhancers lack these specificities. Promoters and enhancers are often overlapping and contiguous, often seeming to have a very similar modular organization. Table V lists several enhancers, of course, this list is not meant to be limiting but exemplary.

TABLE V

Enhancer	Inducer	References
MT II	Phorbol Ester (TFA) Heavy metals	Palmiter *et al.*, 1982; Haslinger and Karin, 1985; Searle *et al.*, 1985; Stuart *et al.*, 1985; Imagawa *et al.*, 1987; Karin ®, 1987; Angel *et al.*, 1987b; McNeall *et al.*, 1989
MMTV (mouse mammary tumor virus)	Glucocorticoids	Huang *et al.*, 1981; Lee *et al.*, 1981; Majors and Varmus, 1983; Chandler *et al.*, 1983; Lee *et al.*, 1984; Fonta *et al.*, 1985; Sakai *et al.*, 1986
ß-Interferon	poly(rI)X poly(rc)	Tavernier *et al.*, 1983
Adenovirus 5 E2	Ela	Imperiale and Nevins, 1984
Collagenase	Phorbol Ester (TPA)	Angle *et al.*, 1987a
Stromelysin	Phorbol Ester (TPA)	Angle *et al.*, 1987b

TABLE V (Continued)

Enhancer	Inducer	References
SV40	Phorbol Ester (TFA)	Angel *et al.*, 1987b
Murine MX Gene	Interferon, Newcastle Disease Virus	
GRP78 Gene	A23187	Resendez *et al.*, 1988
a-2-Macroglobulin	IL-6	Kunz *et al.*, 1989
Vimentin	Serum	Rittling *et al.*, 1989
MHC Class I Gene H-2kb	Interferon	Blanar *et al.*, 1989
HSP70	Ela, SV40 Large T Antigen	Taylor *et al.*, 1989; Taylor and Kingston, 1990a,b
Proliferin	Phorbol Ester-TPA	Mordacq and Linzer, 1989
Tumor Necrosis Factor	FMA	Hensel *et al.*, 1989
Thyroid Stimulating Hormone a Gene	Thyroid Hormone	Chatterjee *et al.*, 1989

Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of a transgene. Use of a T3, T7 or SP6 cytoplasmic expression system is another possible embodiment. Eukaryotic cells can support cytoplasmic transcription from certain bacterial promoters if the appropriate bacterial polymerase is provided, either as part of the delivery complex or as an additional genetic expression construct.

Host cells include eukaryotic microbes, such as yeast cultures may also be used. *Saccharomyces cerevisiae*, or common baker's yeast is the most commonly used among eukaryotic microorganisms, although a number of other strains are commonly available. For expression in *Saccharomyces*, the plasmid YRp7, for example, is commonly used (Stinchcomb *et al.*, 1979; Kingsman *et al.*, 1979; Tschemper *et al.*, 1980). This plasmid already contains the *trp*l gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the *trp*l lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzeman *et al.*, 1980) or other glycolytic enzymes (Hess *et al.*, 1968; Holland *et al.*, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. In constructing suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination. Other promoters, which have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing a yeast-compatible promoter, origin of replication and termination sequences is suitable.

In addition to eukaryotic microorganisms, cultures of cells derived from multicellular organisms may also be used as hosts. In principle, any such cell culture is workable, whether from vertebrate or invertebrate culture. However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure in recent years (*Tissue Culture*, 1973). Examples of such useful host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, and W138, BHK, COS-7, 293 and MDCK cell lines. Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located in front of the gene to be expressed, along with any necessary ribosome binding sites, RNA splice sites, polyadenylation site, and transcriptional terminator sequences.

4.0 Preparation of Antibodies to UspA Proteins

Antibodies to UspA1 or UspA2 peptides or polypeptides may be readily prepared through use of well-known techniques, such as those exemplified in U.S. Patent 4,196,265. Typically, this technique involves immunizing a suitable animal with a selected immunogen composition, *e.g.*, purified or partially purified protein, synthetic protein or fragments thereof, as discussed in the section on vaccines. Animals to be immunized are mammals such as cats, dogs and horses, although there is no limitation other than that the subject be capable of mounting an immune response of some kind. The immunizing composition is administered in a manner effective to stimulate antibody producing cells. Rodents such as mice and rats are preferred animals, however, the use of rabbit, sheep or frog cells is possible. The use of rats may provide certain advantages, but mice are preferred, with the BALB/c mouse being most preferred as the most routinely used animal and one that generally gives a higher percentage of stable fusions.

For generation of monoclonal antibodies (MAbs), following immunization, somatic cells with the potential for producing antibodies, specifically B lymphocytes (B cells), are selected for use in the MAb generating protocol. These cells may be obtained from biopsied spleens, tonsils or lymph nodes, or from a peripheral blood sample. Spleen cells and peripheral blood cells are preferred, the former because they are a rich source of antibody-producing cells that are in the dividing plasmablast stage, and the latter because peripheral blood is easily accessible. Often, a panel of animals will have been immunized and the spleen of the animal with the highest antibody titer removed. Spleen lymphocytes are obtained by homogenizing the spleen with a syringe. Typically, a spleen from an immunized mouse contains approximately 5×10^7 to 2×10^8 lymphocytes.

The antibody-producing B cells from the immunized animal are then fused with cells of an immortal myeloma cell line, generally one of the same species as the animal that was immunized. Myeloma cell lines suited for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells, called "hybridomas."

Any one of a number of myeloma cells may be used and these are known to those of skill in the art. For example, where the immunized animal is a mouse, one may use P3-X63/Ag8, X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XX0 Bul; for rats, one may use R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210; and U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6 are all useful in connection with human cell fusions.

One preferred murine myeloma cell line is the NS-1 myeloma cell line (also termed P3-NS-1-Ag4-1), which is readily available from the NIGMS Human Genetic Mutant Cell Repository by requesting cell line repository number GM3573. Another mouse myeloma cell line that may be used is the 8-azaguanine-resistant mouse murine myeloma SP2/0 non-producer cell line.

Methods for generating hybrids of antibody-producing spleen or lymph node cells and myeloma cells usually comprise mixing somatic cells with myeloma cells in a 2:1 proportion, though the proportion may vary from about 20:1 to about 1:1, respectively, in the presence of an agent or agents (chemical or electrical) that promote the fusion of cell membranes. Fusion methods using Sendai virus have been described by Kohler & Milstein (1975; 1976), and those using polyethylene glycol (PEG), such as 37% (v/v) PEG, by Gefter *et al.* (1977). The use of electrically induced fusion methods is also appropriate.

Fusion procedures usually produce viable hybrids at low frequencies, about 1×10^{-6} to 1×10^{-8}. This does not pose a problem, however, as the viable, fused hybrids are differentiated from the parental, unfused cells (particularly the unfused myeloma cells that would normally continue to divide indefinitely) by culture in a selective medium. The selective medium generally is one that contains an agent that blocks the *de novo* synthesis of nucleotides in the tissue culture media. Exemplary and preferred agents are aminopterin, methotrexate and azaserine. Aminopterin and methotrexate block *de novo* synthesis of both purines and pyrimidines, whereas azaserine blocks only purine synthesis. Where aminopterin or methotrexate is used, the media is supplemented with hypoxanthine and thymidine as a source of nucleotides (HAT medium). Where azaserine is used, the media is supplemented with hypoxanthine.

The preferred selection medium is HAT. Only cells capable of operating nucleotide salvage pathways are able to survive in HAT medium. The myeloma cells are defective in key enzymes of the salvage pathway, *e.g.*, hypoxanthine phosphoribosyl transferase (HPRT), and they cannot survive. The B cells can operate this pathway, but they have a limited life span in culture and generally die within about two weeks. Therefore, the only cells that can survive in the selective media are those hybrids formed from myeloma and B cells.

This culturing provides a population of hybridomas from which specific hybridomas are selected. Typically, selection of hybridomas is performed by single-clone dilution in microtiter plates, followed by testing the individual clonal supernatants (after about two to three weeks) for the desired reactivity. The assay should be sensitive, simple and rapid, such as radioimmunoassays, enzyme immunoassays, cytotoxicity assays, plaque assays, dot immunobinding assays, and the like.

The selected hybridomas are then serially diluted and cloned into individual antibody-producing cell lines, which clones can then be propagated indefinitely to provide MAbs. The cell lines may be exploited for MAb production in two basic ways. A sample of the hybridoma can be injected, usually in the peritoneal cavity, into a histocompatible animal of the type that was used to provide the somatic and myeloma cells for the original fusion. The injected animal develops tumors secreting the specific monoclonal antibody produced by the fused cell hybrid. The body fluids of the animal, such as serum or ascites fluid, can then be tapped to provide MAbs in high concentration. The individual cell lines could also be cultured *in vitro*, where the MAbs are naturally secreted into the culture medium from which they can be readily obtained in high concentrations. MAbs produced by either means may be further purified, if desired, using filtration, centrifugation and various chromatographic methods such as HPLC or affinity chromatography.

Monoclonal antibodies of the present invention also include anti-idiotypic antibodies produced by methods well-known in the art. Monoclonal antibodies according to the present invention also may be monoclonal heteroconjugates, *i.e.*, hybrids of two or more antibody molecules. In another embodiment, monoclonal antibodies according to the invention are chimeric monoclonal antibodies. In one approach, the chimeric monoclonal antibody is engineered by cloning recombinant DNA containing the promoter, leader, and variable-region sequences from a mouse antibody producing cell and the constant-region exons from a human antibody gene. The antibody encoded by such a recombinant gene is a mouse-human chimera. Its antibody specificity is determined by the variable region derived from mouse sequences. Its isotype, which is determined by the constant region, is derived from human DNA.

In another embodiment, the monoclonal antibody according to the present invention is a "humanized" monoclonal antibody, produced by techniques well-known in the art. That is, mouse complementary determining regions ("CDRs") are transferred from heavy and light V-chains of the mouse Ig into a human V-domain, followed by the replacement of some human residues in the framework regions of their murine counterparts. "Humanized" monoclonal antibodies in accordance with this invention are especially suitable for use in *in vivo* diagnostic and therapeutic methods for treating *Moraxella* infections.

As stated above, the monoclonal antibodies and fragments thereof according to this invention can be multiplied according to *in vitro* and *in vivo* methods well-known in the art. Multiplication *in vitro* is carried out in suitable culture media such as Dulbecco's modified Eagle medium or RPMI 1640 medium, optionally replenished by a mammalian serum such as fetal calf serum or trace elements and growth-sustaining supplements, *e.g.*, feeder cells, such as normal mouse peritoneal exudate cells, spleen cells, bone marrow macrophages or the like. *In vitro* production provides relatively pure antibody preparations and allows scale-up to give large amounts of the desired antibodies. Techniques for large scale hybridoma cultivation under tissue culture conditions are known in the art and include homogenous suspension culture, *e.g.*, in an airlift reactor or in a continuous stirrer reactor or immobilized or entrapped cell culture.

Large amounts of the monoclonal antibody of the present invention also may be obtained by multiplying hybridoma cells *in vivo*. Cell clones are injected into mammals which are histocompatible with the parent cells, *e.g.*, syngeneic mice, to cause growth of antibody-producing tumors. Optionally, the animals are primed with a hydrocarbon, especially oils such as Pristane (tetramethylpentadecane) prior to injection.

In accordance with the present invention, fragments of the monoclonal antibody of the invention can be obtained from monoclonal antibodies produced as described above, by methods which include digestion with enzymes such as pepsin or papain and/or cleavage of disulfide bonds by chemical reduction. Alternatively, monoclonal antibody fragments encompassed by the present invention can be synthesized using an automated peptide synthesizer, or they may be produced manually using techniques well known in the art.

The monoclonal conjugates of the present invention are prepared by methods known in the art, *e.g.*, by reacting a monoclonal antibody prepared as described above with, for instance, an enzyme in the presence of a coupling agent such as glutaraldehyde or periodate. Conjugates with fluorescein markers are prepared in the presence of these coupling agents, or by reaction with an isothiocyanate. Conjugates with metal chelates are similarly produced. Other moieties to which antibodies may be conjugated include radionuclides such as ^{3}H, ^{125}I, ^{131}I ^{32}P, ^{35}S, ^{14}C, ^{51}Cr, ^{36}Cl, ^{57}Co, ^{58}Co, ^{59}Fe, ^{75}Se, ^{152}Eu, and ^{99}mTc, are other useful labels which can be conjugated to antibodies. Radio-labeled monoclonal antibodies of the present invention are produced according to well-known methods in the art. For instance, monoclonal antibodies can be iodinated by contact with sodium or potassium iodide and a chemical oxidizing agent such as sodium hypochlorite, or an enzymatic oxidizing agent, such as lactoperoxidase. Monoclonal antibodies according to the invention may be labeled with technetium-^{99}m by ligand exchange process, for example, by reducing pertechnate with stannous solution, chelating the reduced technetium onto a Sephadex column and applying the antibody to this column or by direct labeling techniques, *e.g.*, by incubating pertechnate, a reducing agent such as $SNCl_2$, a buffer solution such as sodium-potassium phthalate solution, and the antibody.

5.0 Use of Peptides and Monoclonal Antibodies in Immunoassays

It is proposed that the monoclonal antibodies of the present invention will find useful application in standard immunochemical procedures, such as ELISA and western blot methods, as well as other procedures which may utilize antibodies specific to CopB epitopes. While ELISAs are preferred, it will be readily appreciated that such assays include RIAs and other non-enzyme linked antibody binding assays or procedures. Additionally, it is proposed that monoclonal antibodies specific to the particular UspA epitope may be utilized in other useful applications. For example, their use in immunoabsorbent protocols may be useful in purifying native or recombinant UspA proteins or variants thereof.

It also is proposed that the disclosed UspA1 and UspA2 peptides of the invention will find use as antigens for raising antibodies and in immunoassays for the detection of anti-UspA antigen-reactive antibodies. In a variation on this embodiment, UspA1 and UspA2 mutant peptides may be screened, in immunoassay format, for reactivity against UspA1- or UspA2-specific antibodies, such as MAb 17C7. In this way, a mutational analysis of various epitopes may be performed. Results from such analyses may then be used to determine which additional UspA1 or UspA2 epitopes may be recognized by antibodies and useful in the preparation of potential vaccines for *Moraxella.*

Diagnostic immunoassays include direct culturing of bodily fluids, either in liquid culture or on a solid support such as nutrient agar. A typical assay involves collecting a sample of bodily fluid from a patient and placing the sample in conditions optimum for growth of the pathogen. The determination can then be made as to whether the microbe exists in the sample. Further analysis can be carried out to determine the hemolyzing properties of the microbe.

Immunoassays encompassed by the present invention include, but are not limited to those described in U.S. Patent No. 4,367,110 (double monoclonal antibody sandwich assay) and U.S. Patent No. 4,452,901 (western blot). Other assays include immunoprecipitation of labeled ligands and immunocytochemistry, both *in vitro* and *in vivo.*

Immunoassays, in their most simple and direct sense, are binding assays. Certain preferred immunoassays are the various types of enzyme linked immunosorbent assays (ELISAs) and radioimmunoassays (RIAs) known in the art. Immunohistochemical detection using tissue sections is also particularly useful. However, it will be readily appreciated that detection is not limited to such techniques, and western blotting, dot blotting, FACS analyses, and the like may also be used.

In one exemplary ELISA, the anti-UspA antibodies of the invention are immobilized onto a selected surface exhibiting protein affinity, such as a well in a polystyrene microtiter plate. Then, a test composition suspected of containing the desired antigen, such as a clinical sample, is added to the wells. After binding and washing to remove non-specifically bound immune complexes, the bound antigen may be detected. Detection is generally achieved by the addition of another antibody, specific for the desired antigen, that is linked to a detectable label. This type of ELISA is a simple "sandwich ELISA". Detection may also be achieved by the addition of a second antibody specific for the desired antigen, followed by the addition of a third antibody that has binding affinity for the second antibody, with the third antibody being linked to a detectable label.

In another exemplary ELISA, the samples suspected of containing the UspA antigen are immobilized onto the well surface and then contacted with the anti-UspA antibodies. After binding and appropriate washing, the bound immune complexes are detected. Where the initial antigen specific antibodies are linked to a detectable label, the immune complexes may be detected directly. Again, the immune complexes may be detected using a second antibody that has binding affinity for the first antigen specific antibody, with the second antibody being linked to a detectable label.

Further methods include the detection of primary immune complexes by a two step approach. A second binding ligand, such as an antibody, that has binding affinity for the primary antibody is used to form secondary immune complexes, as described above. After washing, the secondary immune complexes are contacted with a third binding ligand or antibody that has binding affinity for the second antibody, again under conditions effective and for a period of time sufficient to allow the formation of immune complexes (tertiary immune complexes). The third ligand or antibody is linked to a detectable label, allowing detection of the tertiary immune complexes thus formed. This system may provide for signal amplification if desired.

Competition ELISAs are also possible in which test samples compete for binding with known amounts of labeled antigens or antibodies. The amount of reactive species in the unknown sample is determined by mixing the sample with the known labeled species before or during incubation with coated wells. (Antigen or antibodies may also be linked to a solid support, such as in the form of beads, dipstick, membrane or column matrix, and the sample to be analyzed applied to the immobilized antigen or antibody.) The presence of reactive species in the sample acts to reduce the amount of labeled species available for binding to the well and thus reduces the ultimate signal.

Irrespective of the format employed, ELISAs have certain features in common, such as coating, incubating or binding, washing to remove non-specifically bound species, and detecting the bound immune complexes. These are described below.

In coating a plate with either antigen or antibody, one will generally incubate the wells of the plate with a solution of the antigen or antibody, either overnight or for a specified period. The wells of the plate will then be washed to remove incompletely adsorbed material. Any remaining available surfaces of the wells are then "coated" with a nonspecific protein that is antigenically neutral with regard to the test antisera. These include bovine serum albumin (BSA), casein and solutions of milk powder. The coating allows for blocking of nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific binding of antisera onto the surface.

After binding of antigenic material to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the antisera or clinical or biological extract to be tested in a manner conducive to immune complex (antigen/antibody) formation. Such conditions preferably include diluting the antisera with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline (PBS)/Tween. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from 2 to 4 hours, at temperatures preferably on the order of 25° to 27°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A preferred washing procedure includes washing with a solution such as PBS/Tween, or borate buffer.

Following formation of specific immunocomplexes between the test sample and the bound antigen, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody having specificity for the first. Of course, in that the test sample will typically be of human origin, the second antibody will preferably be an antibody having specificity in general for human IgG. To provide a detecting means, the second antibody will preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the antisera-bound surface with a urease or peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (*e.g.*, incubation for 2 hours at room temperature in a PBS-containing solution such as PBS-Tween).

After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethyl-benzthiazoline-6-sulfonic acid [ABTS] and H_2O_2, in the case of peroxidase as the enzyme label. Quantification is then achieved by measuring the degree of color generation, *e.g.*, using a visible spectra spectrophotometer. Alternatively, the label may be a chemilluminescent one. The use of such labels is described in U.S. Patent Nos. 5,310,687, 5,238,808 and 5,221,605.

6.0 Prophylactic Use of UspA Peptides and UspA-Specific Antibodies

In a further embodiment of the present invention, there are provided methods for active and passive immunoprophylaxis. Active immunoprophylaxis will be discussed first, followed by a discussion on passive immunoprophylaxis. It should be noted that the discussion of formulating vaccine compositions in the context of active immunotherapy is relevant to the raising antibodies in experimental animals for passive immunotherapy and for the generation of diagnostic methods.

6.1 Active Immunotherapy

According to the present invention, UspA1 or UspA2 polypeptides or UspA1- or UspA2-derived peptides, as discussed above, may be used as vaccine formulations to generate protective anti-*M. catarrhalis* antibody responses *in vivo*. By protective, it is only meant that the immune system of a treated individual is capable of generating a response that reduces, to any extent, the clinical impact of the bacterial infection. This may range from a minimal decrease in bacterial burden to outright prevention of infection. Ideally, the treated subject will not exhibit the more serious clinical manifestations of *M. catarrhalis* infection.

Generally, immunoprophylaxis involves the administration, to a subject at risk, of a vaccine composition. In the instant case, the vaccine composition will contain a UspA1 and/or UspA2 polypeptide or immunogenic derivative thereof in a pharmaceutically acceptable carrier, diluent or excipient. As stated above, those of skill in the art are able, through a variety of mechanisms, to identify appropriate antigenic characteristics of UspA1 and UspA2 and , in so doing, develop vaccines that will achieve generation of immune responses against *M. catarrhalis*.

The stability and immunogenicity of UspA1 and UspA2 antigens may vary and, therefore, it may be desirable to couple the antigen to a carrier molecule. Exemplary carriers are KLH, BSA, human serum albumin, myoglobin, β-galactosidase, penicillinase, CRM_{197} and bacterial toxoids, such as diphtheria toxoid and tetanus toxoid. Those of skill in the art are aware of proper methods by which peptides can be linked to carriers without destroying their immunogenic value. Synthetic carriers such as multi-poly-DL-alanyl-poly-L-lysine and poly-L-lysine also are contemplated. Coupling generally is accomplished through amino or carboxyl-terminal residues of the antigen, thereby affording the peptide or polypeptide the greatest chance of assuming a relatively "native" conformation following coupling.

It is recognized that other protective agents could be coupled with either a UspA1 or UspA2 antigen such that the UspA1 or UspA2 antigen acts as the carrier molecule. For example, agents which protect against other pathogenic organisms, such as bacteria, viruses or parasites, could be coupled to either a UspA1 or UspA2 antigen to produce a multivalent vaccine or pharmaceutical composition which would be useful for the treatment or inhibition of both *M. catarrhalis* infection and other pathogenic infections. In particular, it is envisioned that either UspA1 or UspA2 proteins or peptides could serve as immunogenic carriers for other vaccine components, for example, saccharides of pneumococcus, menigococcus or hemophylus influenza and could even be covalently coupled to these other components.

It also may be desirable to include in the composition any of a number of different substances referred to as adjuvants, which are known to stimulate the appropriate portion of the immune system of the vaccinated animal. Suitable adjuvants for the vaccination of subjects (including experimental animals) include, but are not limited to oil emulsions such as Freund's complete or incomplete adjuvant (not suitable for livestock use), Marcol 52:Montanide 888 (Marcol is a Trademark of Esso, Montanide is a Trademark of SEPPIC, Paris), squalane or squalene, Adjuvant 65 (containing peanut oil, mannide monooleate and aluminum monostearate), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research Inc., Hamilton, Utah), Stimulon™ (QS-21; Aquila Biopharmaceuticals Inc., Wooster, MA), mineral gels such as aluminum hydroxide, aluminum phosphate, calcium phosphate and alum, surfactants such as hexadecylamine, octadecylamine, lysolecithin, dimethyl-dioctadecylammonium bromide, N,N-dioctadecyl-N,N'-bis(2-hydroxyethyl)-propanediamine, methoxyhexadecylglycerol and pluronic polyols, polyanions such as pyran, dextran sulfate, polyacrylic acid and carbopol, peptides and amino acids such as muramyl dipeptide, dimethylglycine, tuftsin and trehalose dimycolate. Agents include synthetic polymers of sugars (Carbopol), emulsion in physiologically acceptable oil vehicles such as mannide mono-oleate (Aracel A) or emulsion with 20 percent solution of a perfluorocarbon (Fluosol-DA) also may be employed.

The preparation of vaccines which contain peptide sequences as active ingredients is generally well understood in the art, as exemplified by U.S. Patents 4,608,251; 4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4.578,770, all incorporated herein by reference. Typically, such vaccines are prepared as injectables. Either as liquid solutions or suspensions: Solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants which enhance the effectiveness of the vaccines.

The vaccine preparations of the present invention also can be administered following incorporation into non-toxic carriers such as liposomes or other microcarrier substances, or after conjugation to polysaccharides, proteins or polymers or in combination with Quil-A to form "iscoms" (immunostimulating complexes). These complexes can serve to reduce the toxicity of the antigen, delay its clearance from the host and improve the immune response by acting as an adjuvant. Other suitable adjuvants for use this embodiment of the present invention include INF, IL-2, IL-4, IL-8, IL-12 and other immunostimulatory compounds. Further, conjugates comprising the immunogen together with an integral membrane protein of prokaryotic origin, such as TraT (see PCT/AU87/00107) may prove advantageous.

The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkalene glycols or triglycerides: such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10-95% of active ingredient, preferably 25-70%.

The peptides may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, including, *e.g.*, the capacity of the individual's immune system to synthesize antibodies, and the degree of protection desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner. However, suitable dosage ranges are of the order of several hundred micrograms active ingredient per vaccination. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by subsequent inoculations or other administrations.

The manner of application may be varied widely. Any of the conventional methods for administration of a vaccine are applicable. These are believed to include oral application on a solid physiologically acceptable base or in a physiologically acceptable dispersion, parenterally, by injection or the like. The dosage of the vaccine will depend on the route of administration and will vary according to the size of the host.

In many instances, it will be desirable to have multiple administrations of the vaccine, usually not exceeding six vaccinations, more usually not exceeding four vaccinations and preferably one or more, usually at least about three vaccinations. The vaccinations will normally be at from two to twelve week intervals, more usually from three to five week intervals. Periodic boosters at intervals of 1-5 years, usually three years, will be desirable to maintain protective levels of the antibodies. The course of the immunization may be followed by assays for antibodies for the supernatant antigens. The assays may be performed by labeling with conventional labels, such as radionuclides, enzymes, fluorescers, and the like. These techniques are well known and may be found in a wide variety of patents, such as U.S. Patent Nos. 3,791,932; 4,174,384 and 3,949,064, as illustrative of these types of assays.

6.2 Passive Immunotherapy

Passive immunity is defined, for the purposes of this application, as the transfer to an organism of an immune response effector that was generated in another organism. The classic example of establishing passive immunity is to transfer antibodies produced in one organism into a second, immunologically compatible animal. By "immunologically compatible," it is meant that the antibody can perform at least some of its immune functions in the new host animal. More recently, as a better understanding of cellular immune functions has evolved, it has become possible to accomplish passive immunity by transferring other effectors, such as certain kinds of lymphocytes, including cytotoxic and helper T cells, NK cells and other immune effector cells. The present invention contemplates both of these approaches.

Antibodies, antisera and immune effector cells are raised using standard vaccination regimes in appropriate animals, as discussed above. The primary animal is vaccinated with at least a microbe preparation or one bacterial product or by-product according to the present invention, with or without an adjuvant, to generate an immune response. The immune response may be monitored, for example, by measurement of the levels of antibodies produced, using standard ELISA methods.

Once an adequate immune response has been generated, immune effector cells can be collected on a regular basis, usually from blood draws. The antibody fraction can be purified from the blood by standard means, *e.g.*, by protein A or protein G chromatography. In an alternative preferred embodiment, monoclonal antibody-producing hybridomas are prepared by standard means (Coligan *et al.*, 1991). Monoclonal antibodies are then prepared from the hybridoma cells by standard means. If the primary host's monoclonal antibodies are not compatible with the animal to be treated, it is possible that genetic engineering of the cells can be employed to modify the antibody to be tolerated by the animal to be treated. In the human context, murine antibodies, for example, may be "humanized" in this fashion.

Antibodies, antisera or immune effector cells, prepared as set forth above, are injected into hosts to provide passive immunity against microbial infestation. For example, an antibody composition is prepared by mixing, preferably homogeneously mixing, at least one antibody with at least one pharmaceutically or veterinarally acceptable carrier, diluent, or excipient using standard methods of pharmaceutical or veterinary preparation. The amount of antibody required to produce a single dosage form will vary depending upon the microbial species being vaccinated against, the individual to be treated and the particular mode of administration. The specific dose level for any particular individual will depend upon a variety of factors including the age, body weight, general health, sex, and diet of the individual, time of administration, route of administration, rate of excretion, drug combination and the severity of the microbial infestation.

The antibody composition may be administered intravenously, subcutaneously, intranasally, orally, intramuscularly, vaginally, rectally, topically or via any other desired route. Repeated dosings may be necessary and will vary, for example, depending on the clinical setting, the particular microbe, the condition of the patient and the use of other therapies.

6.3 DNA Immunization HC

The invention also relates to a vaccine comprising a nucleic acid molecule encoding a UspA1, UspA2 protein or a peptide comprsing SEQ ID NO:17 wherein said UspA1, UspA2 protein or peptide retains immunogenicity and, when incorporated into an immunogenic composition or vaccine and administered to a vertebrate, provides protection without inducing enhanced disease upon subsequent infection of the vertebrate with *M. catarrhalis*, and a physiologically acceptable vehicle. Such a vaccine is referred to herein as a nucleic acid vaccine or DNA vaccine and is useful for the genetic immunization of vertebrates.

The term, “genetic immunization”, as used herein, refers to inoculation of a vertebrate, particularly a mammal such as a mouse or human, with a nucleic acid vaccine directed against a pathogenic agent, particularly *M. catarrhalis*, resulting in protection of the vertebrate against *M.*

catarrhalis. A "nucleic acid vaccine" or "DNA vaccine" as used herein, is a nucleic acid construct comprising a nucleic acid molecule encoding UspA1, UspA2 or an immunogenic epitope comprising SEQ ID NO:17. The nucleic acid construct can also include transcriptional promoter elements, enhancer elements, splicing signals, termination and polyadenylation signals, and other nucleic acid sequences.

The nucleic acid vaccine can be produced by standard methods. For example, using known methods, a nucleic acid (*e.g.*, DNA) encoding UspA1 or UspA2 can be inserted into an expression vector to construct a nucleic acid vaccine (see Maniatis *et al.*, 1989). The individual vertebrate is inoculated with the nucleic acid vaccine (*i.e.*, the nucleic acid vaccine is administered), using standard methods. The vertebrate can be inoculated subcutaneously, intravenously, intraperitoneally, intradermally, intramuscularly, topically, orally, rectally, nasally, buccally, vaginally, by inhalation spray, or via an implanted reservoir in dosage formulations containing conventional non-toxic, physiologically acceptable carriers or vehicles. Alternatively, the vertebrate is inoculated with the nucleic acid vaccine through the use of a particle acceleration instrument (a "gene gun"). The form in which it is administered (*e.g.*, capsule, tablet, solution, emulsion) will depend in part on the route by which it is administered. For example, for mucosal administration, nose drops, inhalants or suppositories can be used.

The nucleic acid vaccine can be administered in conjunction with any suitable adjuvant. The adjuvant is administered in a sufficient amount, which is that amount that is sufficient to generate an enhanced immune response to the nucleic acid vaccine. The adjuvant can be administered prior to (*e.g.*, 1 or more days before) inoculation with the nucleic acid vaccine; concurrently with (*e.g.*, within 24 hours of) inoculation with the nucleic acid vaccine; contemporaneously (simultaneously) with the nucleic acid vaccine (*e.g.*, the adjuvant is mixed with the nucleic acid vaccine, and the mixture is administered to the vertebrate); or after (*e.g.*, 1 or more days after) inoculation with the nucleic acid vaccine. The adjuvant can also be administered at more than one time (*e.g.*, prior to inoculation with the nucleic acid vaccine and also after inoculation with the nucleic acid vaccine). As used herein, the term "in conjunction with" encompasses any time period, including those specifically described herein and combinations of the time periods specifically described herein, during which the adjuvant can be administered so as to generate an enhanced immune response to the nucleic acid vaccine (*e.g.*, an increased antibody titer to the antigen encoded by the nucleic acid vaccine, or an increased antibody titer to *M. catarrhalis*). The adjuvant and the nucleic acid vaccine can be administered at approximately the same location on the vertebrate; for example, both the adjuvant and the nucleic acid vaccine are administered at a marked site on a limb of the vertebrate.

In a particular embodiment, the nucleic acid construct is co-administered with a transfection-facilitating agent. In a preferred embodiment, the transfection-facilitating agent is dioctylglycylspermine (DOGS) (as exemplified in published PCT application publication no. WO 96/21356 and incorporated herein by reference). In another embodiment, the transfection-facilitating agent is bupivicaine (as exemplified in U.S. Patent 5,593,972 and incorporated herein by reference).

6.4 Animal Model for Testing Efficacy of Therapies

The evaluation of the functional significance of antibodies to surface antigens of *M. catarrhalis* has been hampered by the lack of a suitable animal model. The relative lack of virulence of this organism for animals rendered identification of an appropriate model system difficult (Doern, 1986). Attempts to use rodents, including chinchillas, to study middle ear infections caused by *M. catarrhalis* were unsuccessful, likely because this organism cannot grow or survive in the middle ear of these hosts (Doyle, 1989).

Murine short-term pulmonary clearance models have now been developed (Unhanand *et al.*, 1992; Verghese *et al.*, 1990) which permit an evaluation of the interaction of *M. catarrhalis* with the lower respiratory tract as well as assessment of pathologic changes in the lungs. This model reproducibly delivers an inoculum of bacteria to a localized peripheral segment of the murine lung. Bacteria multiply within the lung, but are eventually cleared as a result of (i) resident defense mechanisms, (ii) the development of an inflammatory response, and/or (iii) the development of a specific immune response. Using this model, it has been demonstrated that serum IgG antibody can enter the alveolar spaces in the absence of an inflammatory response and enhance pulmonary clearance of nontypable *H. influenzae* (McGehee *et al.*, 1989), a pathogen with a host range and disease spectrum nearly identical to those of *M. catarrhalis*.

7.0 Screening Assays

In still further embodiments, the present invention provides methods for identifying new *M. catarrhalis* inhibitory compounds, which may be termed as "candidate substances," by screening for immunogenic activity with peptides that include one or more mutations to the identified immunogenic epitopic region. It is contemplated that such screening techniques will prove useful in the general identification of any compound that will serve the purpose of inhibiting, or even killing, *M. catarrhalis*, and in preferred embodiments, will provide candidate vaccine compounds.

It is further contemplated that useful compounds in this regard will in no way be limited to proteinaceous or peptidyl compounds. In fact, it may prove to be the case that the most useful pharmacological compounds for identification through application of the screening assays will be non-peptidyl in nature and, *e.g.*, which will serve to inhibit bacterial protein transcription through a tight binding or other chemical interaction. Candidate substances may be obtained from libraries of synthetic chemicals, or from natural samples, such as rain forest and marine samples.

To identify a *M. catarrhalis* inhibitor, one would simply conduct parallel or otherwise comparatively controlled immunoassays and identify a compound that inhibits the phenotype of *M. catarrhalis*. Those of skill in the art are familiar with the use of immunoassays for competitive screenings (for example refer to Sambrook *et al.* 1989).

Once a candidate substance is identified, one would measure the ability of the candidate substance to inhibit *M. catarrhalis* in the presence of the candidate substance. In general, one will desire to measure or otherwise determine the activity of *M. catarrhalis* in the absence of the added candidate substance relative to the activity in the presence of the candidate substance in order to assess the relative inhibitory capability of the candidate substance.

7.1 Mutagenesis

Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent proteins or peptides, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art. as will be appreciated, the technique typically employs a bacteriophage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage vectors are commercially available and their use is generally well known to those skilled in the art. Double stranded plasmids are also routinely employed in site directed mutagenesis, which eliminates the step of transferring the gene of interest from a phage to a plasmid.

In general, site-directed mutagenesis is performed by first obtaining a single-stranded vector, or melting of two strands of a double stranded vector which includes within its sequence a DNA sequence encoding the desired protein. An oligonucleotide primer bearing the desired mutated sequence is synthetically prepared. This primer is then annealed with the single-stranded DNA preparation, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected that include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected gene using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting, as there are other ways in which sequence variants of genes may be obtained. For example, recombinant vectors encoding the desired gene may be treated with mutagenic agents, such as hydrox ylamine, to obtain sequence variants.

7.2 Second Generation Inhibitors

In addition to the inhibitory compounds initially identified, the inventor also contemplates that other sterically similar compounds may be formulated to mimic the key portions of the structure of the inhibitors. Such compounds, which may include peptidomimetics of peptide inhibitors, may be used in the same manner as the initial inhibitors.

Certain mimetics that mimic elements of protein secondary structure are designed using the rationale that the peptide backbone of proteins exists chiefly to orientate amino acid side chains in such a way as to facilitate molecular interactions. A peptide mimetic is thus designed to permit molecular interactions similar to the natural molecule.

Some successful applications of the peptide mimetic concept have focused on mimetics of β-turns within proteins, which are known to be highly antigenic. Likely β-turn structure within a polypeptide can be predicted by computer-based algorithms, as discussed herein. Once the component amino acids of the turn are determined, mimetics can be constructed to achieve a similar spatial orientation of the essential elements of the amino acid side chains.

The generation of further structural equivalents or mimetics may be achieved by the techniques of modeling and chemical design known to those of skill in the art. The art of computer-based chemical modeling is now well known. Using such methods, a chemical that specifically inhibits viral transcription elongation can be designed, and then synthesized, following the initial identification of a compound that inhibits RNA elongation, but that is not specific or sufficiently specific to inhibit viral RNA elongation in preference to human RNA elongation. It will be understood that all such sterically similar constructs and second generation molecules fall within the scope of the present invention.

8.0 Diagnosing *M. catarrhalis* Infections

8.1 Amplification and PCR™

Nucleic acid sequence used as a template for amplification is isolated from cells contained in the biological sample, according to standard methodologies (Sambrook *et al.*, 1989). The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to convert the RNA to a cDNA.

Pairs of primers that selectively hybridize to nucleic acids corresponding to UspA1 or UspA2 protein or a mutant thereof are contacted with the isolated nucleic acid under conditions that permit selective hybridization. The term "primer", as defined herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process. Typically, primers are oligonucleotides from ten to twenty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded or single-stranded form, although the single-stranded form is preferred.

Once hybridized, the nucleic acid:primer complex is contacted with one or more enzymes that facilitate template-dependent nucleic acid synthesis. Multiple rounds of amplification, also referred to as "cycles," are conducted until a sufficient amount of amplification product is produced.

Next, the amplification product is detected. In certain applications, the detection may be performed by visual means. Alternatively, the detection may involve indirect identification of the product *via* chemiluminescence, radioactive scintigraphy of incorporated radiolabel or fluorescent label or even *via* a system using electrical or thermal impulse signals (Affymax technology).

A number of template dependent processes are available to amplify the marker sequences present in a given template sample. One of the best known amplification methods is the polymerase chain reaction (referred to as PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, and each incorporated herein by reference in entirety.

Briefly, in PCR™, two primer sequences are prepared that are complementary to regions on opposite complementary strands of the marker sequence. An excess of deoxynucleoside triphosphates are added to a reaction mixture along with a DNA polymerase, *e.g.*, *Taq* polymerase. If the marker sequence is present in a sample, the primers will bind to the marker and the polymerase will cause the primers to be extended along the marker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the marker to form reaction products, excess primers will bind to the marker and to the reaction products and the process is repeated.

A reverse transcriptase PCR™ (RT-PCR™) amplification procedure may be performed in order to quantify the amount of mRNA amplified or to prepare cDNA from the desired mRNA. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989. Alternative methods for reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These methods are described in WO 90/07641, filed December 21, 1990, incorporated herein by reference. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction ("LCR"), disclosed in EPA No. 320 308, incorporated herein by reference in its entirety. In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR™, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U.S. Patent 4,883,750 describes a method similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase, described in PCT Application No. PCT/US87/00880, incorporated herein by reference, may also be used as still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5′-[alpha-thio]-triphosphates in one strand of a restriction site may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand displacement and synthesis, *i.e.*, nick translation. A similar method, called Repair Chain Reaction (RCR), involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy detection. A similar approach is used in SDA. Target specific sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having 3′ and 5′ sequences of non-specific DNA and a middle sequence of specific RNA is hybridized to DNA that is present in a sample. Upon hybridization, the reaction is treated with RNase H, and the products of the probe identified as distinctive products that are released after digestion. The original template is annealed to another cycling probe and the reaction is repeated.

Still another amplification methods described in GB Application No. 2 202 328, and in PCT Application No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCR™-like, template- and enzyme-dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.*, biotin) and/or a detector moiety (*e.g.*, enzyme). In the latter application, an excess of labeled probes are added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS), including nucleic acid sequence based amplification (NASBA) and 3SR Gingeras *et al.*, PCT Application WO 88/10315, incorporated herein by reference. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a clinical sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer which has target specific sequences. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target specific primer, followed by polymerization. The double-stranded DNA molecules are then multiply transcribed by an RNA polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNA's are reverse transcribed into single stranded DNA, which is then converted to double stranded DNA, and then transcribed once again with an RNA polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target specific sequences.

Davey *et al.*, EPA No. 329 822 (incorporated herein by reference in its entirety) disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from the resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in duplex with either DNA or RNA). The resultant ssDNA is a template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5′ to its homology to the template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of *E. coli* DNA polymerase I), resulting in a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

Miller *et al.*, PCT Application WO 89/06700 (incorporated herein by reference in its entirety) disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic, *i.e.*, new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" and "one-sided PCR" (Frohman, 1990, incorporated by reference).

Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, may also be used in the amplification step of the present invention.

Following any amplification, it may be desirable to separate the amplification product from the template and the excess primer for the purpose of determining whether specific amplification has occurred. In one embodiment, amplification products are separated by agarose, agarose-acrylamide or polyacrylamide gel electrophoresis using standard methods. See Sambrook *et al.*, 1989.

Alternatively, chromatographic techniques may be employed to effect separation. There are many kinds of chromatography which may be used in the present invention: adsorption, partition, ion-exchange and molecular sieve, and many specialized techniques for using them including column, paper, thin-layer and gas chromatography.

Amplification products must be visualized in order to confirm amplification of the marker sequences. One typical visualization method involves staining of a gel with ethidium bromide and visualization under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the amplification products can then be exposed to x-ray film or visualized under the appropriate stimulating spectra, following separation.

In one embodiment, visualization is achieved indirectly. Following separation of amplification products, a labeled, nucleic acid probe is brought into contact with the amplified marker sequence. The probe preferably is conjugated to a chromophore but may be radiolabeled. In another embodiment, the probe is conjugated to a binding partner, such as an antibody or biotin, and the other member of the binding pair carries a detectable moiety.

In one embodiment, detection is by Southern blotting and hybridization with a labeled probe. The techniques involved in Southern blotting are well known to those of skill in the art and can be found in many standard books on molecular protocols. See Sambrook *et al.*, 1989. Briefly, amplification products are separated by gel electrophoresis. The gel is then contacted with a membrane, such as nitrocellulose, permitting transfer of the nucleic acid and non-covalent binding. Subsequently, the membrane is incubated with a chromophore-conjugated probe that is capable of hybridizing with a target amplification product. Detection is by exposure of the membrane to x-ray film or ion-emitting detection devices.

One example of the foregoing is described in U.S. Patent No. 5,279,721, incorporated by reference herein, which discloses an apparatus and method for the automated electrophoresis and transfer of nucleic acids. The apparatus permits electrophoresis and blotting without external manipulation of the gel and is ideally suited to carrying out methods according to the present invention.

All the essential materials and reagents required for detecting P-TEFb or kinase protein markers in a biological sample may be assembled together in a kit. This generally will comprise preselected primers for specific markers. Also included may be enzymes suitable for amplifying nucleic acids including various polymerases (RT, Taq, *etc.*), deoxynucleotides and buffers to provide the necessary reaction mixture for amplification.

Such kits generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each marker primer pair. Preferred pairs of primers for amplifying nucleic acids are selected to amplify the sequences specified in SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16 such that, for example, nucleic acid fragments are prepared that include a contiguous stretch of nucleotides identical to for example about 15, 20, 25, 30, 35, *etc.*; 48, 49, 50, 51, *etc.*; 75, 76, 77, 78, 79, 80 *etc.*; 100, 101, 102, 103 *etc.*; 118, 119, 120, 121 *etc.*; 127, 128, 129, 130, 131, *etc.*; 316, 317, 318, 319, *etc.*; 322, 323, 324, 325, 326, *etc.*; 361, 362, 363, 364, *etc.*; 372, 373, 374, 375, *etc.* of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID

NO:16, so long as the selected contiguous stretches are from spatially distinct regions. Similar fragments may be prepared which are identical or complimentary to, for example, SEQ ID NO:1 such that the fragments do not hybridize to, for example, SEQ ID NO:3.

In another embodiment, such kits will comprise hybridization probes specific for UspA1 or UspA2 proteins chosen from a group including nucleic acids corresponding to the sequences specified in SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16 or to intermediate lengths of the sequences specified. Such kits generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each marker hybridization probe.

8.2 Other Assays

Other methods for genetic screening to accurately detect *M. catarrhalis* infections that alter normal cellular production and processing, in genomic DNA, cDNA or RNA samples may be employed, depending on the specific situation.

For example, one method of screening for genetic variation is based on RNase cleavage of base pair mismatches in RNA/DNA and RNA/RNA heteroduplexes. As used herein, the term "mismatch" is defined as a region of one or more unpaired or mispaired nucleotides in a double-stranded RNA/RNA, RNA/DNA or DNA/DNA molecule. This definition thus includes mismatches due to insertion/deletion mutations, as well as single and multiple base point mutations.

U.S. Patent No. 4,946,773 describes an RNase A mismatch cleavage assay that involves annealing single-stranded DNA or RNA test samples to an RNA probe, and subsequent treatment of the nucleic acid duplexes with RNase A. After the RNase cleavage reaction, the RNase is inactivated by proteolytic digestion and organic extraction, and the cleavage products are denatured by heating and analyzed by electrophoresis on denaturing polyacrylamide gels. For the detection of mismatches, the single-stranded products of the RNase A treatment, electrophoretically separated according to size, are compared to similarly treated control duplexes. Samples containing smaller fragments (cleavage products) not seen in the control duplex are scored as +.

Currently available RNase mismatch cleavage assays, including those performed according to U.S. Patent No. 4,946,773, require the use of radiolabeled RNA probes. Myers and Maniatis in U.S. Patent No. 4,946,773 describe the detection of base pair mismatches using RNase A. Other investigators have described the use of *E. coli* enzyme, RNase I, in mismatch assays. Because it has broader cleavage specificity than RNase A, RNase I would be a desirable enzyme to employ in the detection of base pair mismatches if components can be found to decrease the extent of non-specific cleavage and increase the frequency of cleavage of mismatches. The use of RNase I for mismatch detection is described in literature from Promega Biotech. Promega markets a kit containing RNase I that is shown in their literature to cleave three out of four known mismatches, provided the enzyme level is sufficiently high.

The RNase protection assay was first used to detect and map the ends of specific mRNA targets in solution. The assay relies on being able to easily generate high specific activity radiolabeled RNA probes complementary to the mRNA of interest by *in vitro* transcription. Originally, the templates for *in vitro* transcription were recombinant plasmids containing bacteriophage promoters. The probes are mixed with total cellular RNA samples to permit hybridization to their complementary targets, then the mixture is treated with RNase to degrade excess unhybridized probe. Also, as originally intended, the RNase used is specific for single-stranded RNA, so that hybridized double-stranded probe is protected from degradation. After inactivation and removal of the RNase, the protected probe (which is proportional in amount to the amount of target mRNA that was present) is recovered and analyzed on a polyacrylamide gel.

The RNase Protection assay was adapted for detection of single base mutations. In this type of RNase A mismatch cleavage assay, radiolabeled RNA probes transcribed *in vitro* from wild type sequences, are hybridized to complementary target regions derived from test samples. The test target generally comprises DNA (either genomic DNA or DNA amplified by cloning in plasmids or by PCR^{TM}), although RNA targets (endogenous mRNA) have occasionally been used. If single nucleotide (or greater) sequence differences occur between the hybridized probe and target, the resulting disruption in Watson-Crick hydrogen bonding at that position ("mismatch") can be recognized and cleaved in some cases by single-strand specific ribonuclease. To date, RNase A has been used almost exclusively for cleavage of single-base mismatches, although RNase I has recently been shown as useful also for mismatch cleavage. There are recent descriptions of using the MutS protein and other DNA-repair enzymes for detection of single-base mismatches.

9.0 Examples

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLE I: Sequence Analysis and Characterization of *uspA1*

Bacterial strains and culture conditions. M. *catarrhalis* strains 035E, 046E, TTA24, 012E, FR2682, and B21 have been previously described (Helminen *et al.*, 1993a; Helminen *et al.*, 1994; Unhanand *et al.*, 1992). *M. catarrhalis* strains FR3227 and FR2336 were obtained from Richard Wallace, University of Texas Health Center, Tyler, TX. *M. catarrhalis* strain B6 was obtained from Elliot Juni, University of Michigan, Ann Arbor, MI. *M. catarrhalis* strain TTA1 was obtained from Steven Berk, East Tennessee State University, Johnson City, TN. *M. catarrhalis* strain 25240 was obtained from the American Type Culture Collection, Rockville, MD. *M. catarrhalis* strains were routinely cultured in Brain Heart Infusion (BHI) broth (Difco Laboratories, Detroit, MI) at 37°C or on BHI agar plates in an atmosphere of 95% air-5% CO_2. *Escherichia coli* strains LE392 and XL1-Blue MRF′ (Stratagene, La Jolla, CA) were grown on Lubria-Bertani medium (Maniatis *et al.*, 1982) supplemented with maltose (0.2% w/v) and 10 mM $MgSO_4$ at 37°C, with antimicrobial supplementation as necessary.

Monoclonal antibodies (MAbs). MAb 17C7 is a murine IgG antibody reactive with the UspA proteinaceous material of all *M. catarrhalis* strains tested to date (Helminen *et al.*, 1994). Additional MAbs specific for UspA material (*i.e.*, 16A7, 17B1, and 5C12) were produced for this study by fusing spleen cells from mice immunized with outer membrane vesicles from

M. catarrhalis 035E with the SP2/0-Ag14 plasmacytoma cell line, as described (Helminen *et al.*, 1993a). These MAbs were used in the form of hybridoma culture supernatant fluid in western blot and dot blot analyses.

Cloning vectors. Plasmid and bacteriophage cloning vectors utilized in this work and the recombinant derivatives of these vectors are listed in Table VI.

TABLE VI

Bacteriophages And Plasmids

Bacteriophage or plasmid	Description	Source
Bacteriophage		
LambdaGEM-11	Cloning vector	Promega Corp. (Madison, WI)
MEH200	LambdaGEM-11 containing an 11 kb insert of *M. catarrhalis* strain 035E DNA encoding the UspA proteinaceous material	(Helminen *et al.*, 1994)
ZAP Express	Cloning vector	Stratagene
USP100	ZAP Express with a 2.7 kb fragment of DNA (containing the *uspA1*) amplified from the chromosome of *M. catarrhalis* strain 035E	This study
Plasmids		
pBluescript II SK+ (pBS)	Cloning vector, Amp^R	Stratagene
pJL501.6	pBS containing the 1.6 kb *Bgl*II-*Eco*RI fragment from MEH200	This study
pJL500.5	pBS containing the 600-bp *Bgl*II fragment from MEH200	This study

MEH200, the original recombinant bacteriophage clone that produced plaques reactive with the UspA-specific MAb 17C7, has been described previously (Helminen *et al.,* 1994).

Genetic techniques. Standard recombinant DNA techniques including plasmid isolation, restriction enzyme digestions, DNA modifications, ligation reactions and transformation of *E. coli* are familiar to those of skill in the art and were performed as previously described (Maniatis *et al.,* 1982; Sambrook *et al.,* 1989).

Polymerase Chain Reaction (PCR™). PCR™ was performed using the GeneAmp kit (Perkin-Elmer, Branchberg, NJ). All reaction were carried out according to the manufacturer's instructions. To amplify products from total genomic DNA, 1 μg of *M. catarrhalis* chromosomal DNA and 100 ng of each primer were used in each 100 μl reaction.

Nucleotide sequence analysis. Nucleotide sequence analysis of DNA fragments in recombinant plasmids, in bacteriophage, or derived by PCR™ was performed using an Applied Biosystems Model 373A automated DNA sequencer (Applied Biosystems, Foster City, CA). DNA sequence information was analyzed using the Intelligenetics suite package and programs from the University of Wisconsin Genetics Computer Group software analysis package (Devereux *et al.,* 1984). Analysis of protein hydrophilicity using the method of Kyte and Doolittle (1982) and analysis of repeated amino acid sequences within the UspA protein was performed using the MacVector™ software protein matrix analysis package (Eastman Kodak Company, Rochester, NY).

Identification of recombinant bacteriophage. Lysates were generated from *E. coli* cells infected with recombinant bacteriophage by using the plate lysis method as described (Helminen *et al.,* 1994). MAb-based screening of plaques formed by recombinant ZAP Express bacteriophage on *E. coli* XL1-Blue MRF' cells was performed according to the manufacturer's instructions (Stratagene, La Jolla, CA). Briefly, nitrocellulose filters soaked in 10 mM IPTG were applied to the surface of agar plates five hours after bacteriophage infection of the bacterial lawn. After overnight incubation at 37°C, the nitrocellulose pads were removed, washed with PBS containing 0.5% (v/v) Tween 20 and 5% (w/v) skim milk (PBS-T) and incubated with hybridoma culture supernatant containing the MAb for 4 hours at room temperature. After four washes with PBS-T, PBS-T containing ^{125}I-labeled goat anti-mouse

IgG was applied to each pad. After overnight incubation at 4°C, the pads were washed four times with PBS-T, blotted dry, and exposed to film.

Characterization of *M. catarrhalis* protein antigens. Outer membrane vesicles were prepared from BHI broth-grown *M. catarrhalis* cells by the EDTA-buffer method (Murphy and Loeb, 1989). Proteins present in these vesicles were resolved by sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis (PAGE) using 7.5% (w/v) polyacrylamide separating gels. These SDS-PAGE-resolved proteins were electrophoretically transferred to nitrocellulose and western blot analysis was performed as described using MAb 17C7 as the primary antibody (Kimura *et al.,* 1985). For western blot analysis of proteins encoded by DNA inserts in recombinant bacteriophage, one part of a lysate from bacteriophage-infected *E. coli* cells was mixed with one part SDS-digestion buffer (Kimura *et al.,* 1985) and this mixture was incubated at 37°C for 15 minutes prior to SDS-PAGE.

Features of the *uspA1* gene and its encoded protein product. The nucleotide sequence of the *M. catarrhalis* 035E *uspA1* gene and the deduced amino acid sequence of the UspA1 protein are provided in SEQ ID NO:2 and SEQ ID NO:1, respectively. The open reading frame (ORF), containing 2,493 nucleotides , encoded a protein product of 831 amino acids , with a calculated molecular mass of 88,271 daltons.

The predicted protein product of the *uspA1* ORF had a pI or 4.7, was highly hydrophilic, and was characterized by extensively repeated motifs. The first motif consists of the consensus sequence NXAXXYSXIGGGXN (SEQ ID NO:24), which is extensively repeated between amino acid residues 80 and 170. The second region, from amino acid residues 320 to 460, contains a long sequence which is repeated three times in its entirety, but which also contains smaller units which are repeated several times themselves. This "repeat within a repeat" arrangement is also true of the third region, which extends from amino acid residues 460 to 600 . This last motif consists of many repeats of the small motif QADI (SEQ ID NO:25) and two large repeats which contain the QADI (SEQ ID NO:25) motif within themselves.

Similarity of UspA1 to other proteins. A BLAST-X search (Altschul *et al.,* 1990; Gish and States, 1993) of the available databases for proteins with significant homology to UspA1 indicated that the prokaryotic proteins that were most similar to this *M. catarrhalis* antigen were a putative adhesin of *H. influenzae* Rd (GenBank accession number U32792) (Fleischmann *et al.*, 1995), the Hia adhesin from nontypable *H. influenzae* (GenBank accession number U38617) (Barenkamp and St. Geme III, 1996), and the YadA invasin of *Yersinia enterocolitica* (Skurnik and Wolf-Watz, 1989) (SwissProt:P31489). When the GAP alignment program (Devereux *et al.*, 1984) was used to compare the UspA1 sequence to that of these and closely related bacterial adhesins, UspA1 proved to be 25% identical and 47% similar to the *E. coli* AIDA-I adhesin from enteropathogenic *E. coli* (Benz and Schmidt, 1989; Benz and Schmidt, 1992b), 23% identical and 46% similar to Hia (Barenkamp and St. Geme III, 1996), and 24% identical and 43% similar to YadA (Skurnik and Wolf-Watz, 1989). Other proteins retrieved from database searches as having homology with UspA1 included myosin heavy chains from a number of species.

EXAMPLE II: Two Genes Encode the Proteins UspA1 and UspA2

MAb 17C7 binds to a very high molecular weight proteinaceous material of *M. catarrhalis*, designated UspA, that migrates with an apparent molecular weight (in SDS-PAGE) of at least 250 kDa. This same MAb also reacts with another antigen band of approximately 100 kDa, as described in U.S. Patent No. 5,552,146 and incorporated herein by reference, and it is bound by a phage lysate from *E. coli* infected by a recombinant bacteriophage that contained a fragment of *M. catarrhalis* chromosomal DNA. The *M. catarrhalis* proteinaceous material in the phage lysate that binds this MAb migrates at a rate similar or indistinguishable from that of the native UspA material (Helminen *et al.*, 1994).

Analysis of *uspA1.* Nucleotide sequence analysis of the *M. catarrhalis* strain O35E gene expressed by the recombinant bacteriophage, designated *uspA1*, revealed the presence of an ORF encoding a predicted protein product with a molecular mass of 88,271 (SEQ ID NO:1). The use of the *uspA1* ORF in an *in vitro* DNA-directed protein expression system revealed that the protein encoded by the *uspA1* gene migrated in SDS-PAGE with an apparent molecular weight of about 120 kDa. (Those of skill in the art will be aware that denaturing processes, such as SDS-PAGE, can alter the migration rate of proteins such that the apparent molecular weight of the denatured protein is somewhat different than the predicted molecular weight of the non-denatured protein.) In addition, when the *uspA1* ORF was introduced into a bacteriophage vector, the recombinant *E. coli* strain containing this recombinant phage expressed a protein that migrated in SDS-PAGE apparently at the same rate as the native UspA protein from *M. catarrhalis*.

Southern blot analysis of chromosomal DNA from several *M. catarrhalis* strains, using a 0.6 kb *Bgl*II-*Pvu*II fragment derived from the cloned *uspA1* gene as the probe, revealed that, with several strains, there were two distinct restriction fragments that bound this *uspA1*-derived probe (FIG. 1), indicating that *M. catarrhalis* possessed a second gene had some similarity to the *uspA1* gene.

Native very high molecular weight UspA proteinaceous material from *M. catarrhalis* strain O35E was resolved by SDS PAGE, electroeluted, and digested with a protease. N-terminal acid sequence analysis of some of the resultant peptides revealed that the amino acid sequences of several peptides did not match that of the deduced amino acid sequence of UspA1. Other peptides obtained from this experiment were similar to those present in the deduced amino acid sequence but not identical.

Protease and cyanogen bromide (CNBr) Cleavage of High Molecular Weight UspA Proteinaceous Material: Three tenths (0.3) mg of purified very high molecular weight UspA proteinaceous material (at the time of the purification this material was thought to be a single protein) was precipitated with 90% ethanol and the pellet was resuspended in 100 ml of 88% formic acid containing 12M urea. Following resuspension, 100 ml of 88% formic acid containing 2M CNBr was added and the mixture was incubated in the dark overnight at room temperature. One ml (2.0 mg) of purified UspA material was added directly to a vial containing 25 mg of either trypsin or chymotrypsin. The reaction mixtures were incubated for ~48 hours. at 37°C. One ml (2.0 mg) of purified UspA material was added directly to a vial containing 15 mg of endoproteinase Lys-C. The reaction mixtures were incubated for about 48 hours at 37°C.

The cleavage reaction mixtures were clarified by centrifugation in an Eppendorf™ centrifuge at 12,000 rpm for 5 minutes. The clarified supernatant was loaded directly onto a Vydac C4 HPLC column using a mobile phase of 0.1% (v/v) aqueous trifluoroacetic acid (Solvent A) and acetonitrile:H_2O:trifluoroacetic acid, 80:20:0.1 (v/v/v) (Solvent B) at a flow rate of 1.0 ml/min. The reaction mixtures were washed onto the column with 100% Solvent A followed by elution of cleavage fragments using a 30 minutes linear gradient (0-100%) of Solvent B. Fractions were collected manually, dried overnight in a Speed-Vac and resuspended in House Pure Water. The resuspended HPLC-separated fractions were subjected to SDS-PAGE analysis using 10-18% gradient gels in a Tris-Tricine buffer system. The fractions which exhibited a single peptide band were submitted for direct N-terminal sequence analysis. Fractions displaying multiple peptide bands were transferred from SDS-PAGE onto a PVDF membrane and individual bands excised and submitted for N-terminal sequence analysis.

The N-terminal amino acid sequences of these fragments then were determined using an Applied Biosystems Model 477A PTH Analyzer (Applied Biosystems, Foster City, CA, U.S.A.). A summary of these sequences is given in Table VII. About half of the sequences were found to match the sequence deduced from the *uspA1* gene, while the other half did not. Attempts at shifting the reading frame of the *uspA1* gene sequence failed to account for the non-matching peptide sequences, indicating that the high molecular weight UspA protein may comprise either a multimer of more than one distinct protein or distinct multimers of two different proteins.

TABLE VII

Summary of the N-terminal Sequences of Internal Peptide Fragments

Digest	Sequence[a]
CNBr	AAQAALSGLFVPYSVGKFNATAALGGYGSK SEQ ID NO:26 GKITKNAARQENG SEQ ID NO:27
LysC Digest #1	VIGDLGRKV SEQ ID NO:28 ALEXNVEEGL SEQ ID NO:29 ALESNVEEGLXXLS SEQ ID NO:30 ALEFNGE SEQ ID NO:31
LysC Digest #2	SITDLGXKV SEQ ID NO:32 SITDLGTIVDGFXXX SEQ ID NO:33 SITDLGTIVD SEQ ID NO:34
Trypsin	VDALXTKVNALDXKVNSDXT SEQ ID NO:35 LLAEQQLNGKTLTPV SEQ ID NO:36 AKHDAASTEKGKMD SEQ ID NO:37 ALESNVEEGLLDLSG SEQ ID NO:38
Trypsin Digest #1	NQNTLIEKTANK SEQ ID NO:39 IDKNEYSIK SEQ ID NO:40 SITDLGTK SEQ ID NO:41

TABLE VII (Continued)

Digest	Sequence[a]
Trypsin Digest #2	NQNTLIEK SEQ ID NO:42 ALHEQQLETLTK SEQ ID NO:43 NSSD SEQ ID NO:44 NKADADASFETLTK SEQ ID NO:45 FAATAIAKDK SEQ ID NO:46 KASSENTQNIAK SEQ ID NO:47 RLLDQK SEQ ID NO:48
Chymotrypsin	AATADAITKNGX SEQ ID NO:49 AKAXAANXDR SEQ ID NO:50
Digest of research grade UspA with cys-C-endopeptidase	NQADIAQNQTDIQDLAAYNELQ SEQ ID NO:51 NQADIANNINNIYELAQQQDQ SEQ ID NO:52 YNERQTEAIDALN SEQ ID NO:53 ILGDTAIVSNSQD SEQ ID NO:54

[a] Certain residues of several peptides could not be verified and these ambiguities are shown by an "X" in SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:49 and SEQ ID NO:50. In SEQ ID NO:29 the ambiguous residue is likely to be a serine; in SEQ ID NO:33, position 13 is likely to be aspartic acid, position 14 is likely to be glycine and position 15 is likely to be arginine; in SEQ ID NO:35 both positions 13 and 19 are likely to be serines; in SEQ ID NO:49 the ambiguous residue is likely to be an asparagine; and in SEQ ID NO:50 position 4 is likely to be serine and position 8 is likely to be threonine.

Additional attempts to resolve the very high molecular weight UspA protein band from *M. catarrhalis* strain O35E by SDS-PAGE, followed by electroelution and digestion with proteases or with cyanogen bromide, again yielded a number of peptides which were sequenced. Several peptides (peptides 1-6, Table VIII) were obtained. The amino acid sequence of which was identical or very similar to that deduced from the nucleotide sequence of the *uspA1* gene. However, several additional peptides, peptides 7-10, Table VIII, were not present in the deduced amino acid sequence. This finding substantiated the suggestion that a second protein was present in the UspA antigen preparation.

TABLE VIII

Matching or closely matching peptides:		
Peptide #	**Amino acid sequence**	
Peptide 1	KALESNVEEGLLDLSGR	(SEQ ID NO:55)
Peptide 2	ALESNVEEGLLELSGRTIDQR	(SEQ ID NO:56)
Peptide 3	NQAHIANNINXIYELAQQQDQK	(SEQ ID NO:57)
Peptide 4	NQADIAQNQTDIQDLAAYNELQ	(SEQ ID NO:58)
Peptide 5	ATHDYNERQTEA	(SEQ ID NO:59)
Peptide6	KASSENTQNIAK	(SEQ ID NO:60)

Nonmatching peptides:		
Peptide #	**Amino acid sequence**	
Peptide 7	MILGDTAIVSNSQDNKTQLKFYK	(SEQ ID NO:61)
Peptide 8	AGDTIIPLDDDXXP	(SEQ ID NO:62)
Peptide 9	LLHEQQLXGK	(SEQ ID NO:63)
Peptide 10	IFFNXG	(SEQ ID NO:64)

[a] Certain residues of several peptides could not be verified and these ambiguities are shown by an "X" in SEQ ID NO:57, SEQ ID NO:62, SEQ ID NO:63 and SEQ ID NO:64.

Further evidence corroborating the assertion that the high molecular weight UspA proteinaceous material was either a multimer of more than one distinct protein or distinct multimers of two different proteins was derived from earlier electrospray mass spectroscopic analysis which predicted that a monomer of the UspA material had a molecular weight of 59,500. This approximately 60 kDa protein reacted immunogenically with the MAbs 17C7, 45-2, 13-1, and 29-31, in contrast to the UspA1 protein which only cross-reacted with MAb 17C7. The fact that MAb 17C7 reacted with both isolated proteins suggested that this Mab recognized an epitope common to both proteins.

Preparation of mutant *uspA1* construct. The nucleotide sequence of the cloned *uspA1* gene was used to construct an isogenic *uspA1* mutant. Oligonucleotide primers (*Bam*HI-ended P1 and P16 in Table IX) were used to amplify a truncated version of the *uspA1* ORF from *M. catarrhalis* strain O35E chromosomal DNA; this PCR™ product was cloned into the *Bam*HI site of the plasmid vector pBluescript II SK+. A 0.6 kb *Bgl*II fragment from the middle of this cloned fragment was excised and was replaced by a *Bam*HI-ended cassette encoding kanamycin resistance. This new plasmid was grown in *E. coli* DH5α, purified by column chromatography, linearized by digestion with *Eco*RI, precipitated, and then dissolved in water. This linear DNA molecule was used to electroporate the wild-type *M. catarrhalis* strain O35E, using a technique described previously (Helminen *et al.*, 1993b). Approximately 5,000 kanamycin-resistant transformants were obtained; several picked at random were found to be still reactive with MAb 17C7. One of these kanamycin-resistant clones was randomly chosen for further examination and Southern blot analysis confirmed that this mutant was isogenic.

Analysis of products expressed by the *uspA1* mutant. When whole cell lysates of both the wild-type *M. catarrhalis* strain and this mutant were subjected to SDS-PAGE, both the wild-type strain and the mutant strain still expressed the very high-molecular-weight band originally designated as UspA. However, a protein of approximately 120 kDa was found to be missing in the mutant strain (FIG. 2A). The fact that both this mutant and the wild-type parent strain still expressed a very high molecular weight antigen reactive with MAb 17C7 (FIG. 2B) indicated that there had to be a second gene in *M. catarrhalis* strain O35E that encoded a MAb 17C7-reactive antigen. Furthermore, it should be noted that EDTA-extracted outer membrane vesicles of both the wild-type strain (FIG. 2C, lanes 5 and 7) and mutant strain (FIG. 2C, lanes 6 and 8) possessed a protein of approximately 70-80 kDa that was reactive with MAb 17C7. This approximately 70-80 kDa band likely represents one form, perhaps the monomeric form, of the product of a second gene encoding the MAb 17C7-reactive epitope.

It is important to note that, when chromosomal DNA from both the wild-type parent strain and the mutant were digested with *Pvu*II and probed in Southern blot analysis with a 0.6 kb *Bgl*II-*Pvu*II fragment derived from the *uspA1* gene, the wild-type strain exhibited a 2.6 kb band and a 2.8 kb band which bound this probe (FIG. 3). In contrast, the mutant strain had a 2.6 kb band and a 3.4 kb band that bound this probe. The presence of the 3.4 kb band was the result of the insertion of the *kan* cartridge into the deletion site in the *uspA1* gene.

EXAMPLE III: Characterization of UspA2 and *uspA2*

Construction of fusion proteins. The epitope which binds MAb 17C7 was localized by using the nucleotide sequence of the *uspA1* gene described above to construct fusion proteins. First, fusion proteins containing five peptides spanning the UspA1 protein were constructed by using the pGEX4T-2 protein fusion system (Pharmacia LKB). The oligonucleotide primers used in PCR™ to amplify the desired nucleotide sequences from *M. catarrhalis* strain O35E chromosomal DNA are listed in Table IX. Each of these had either a *Bam*HI site or a *Xho*I site at the 5′ end, thereby allowing directional in-frame cloning of the amplified product into the *Bam*HI- and *Xho*I-digested vector. When recombinant *E. coli* strains expressing each of these five fusion proteins were used in a colony blot radioimmunoassay, only fusion protein MF-4 readily bound MAb 17C7. Further analysis of the *uspA1*-derived nucleotide sequence in the MF-4 fusion construct involved the production of fusion proteins containing 79 amino acid residues (MF-4-1) and 123 amino acid residues (MF-4-2) derived from the MF-4 fusion protein (Table IX). These two fusion proteins both bound MAb 17C7 (Table IX). FIG. 4 depicts the western blot reactivity of MAb 17C7 with the MF-4-1 fusion protein. These two fusion proteins had in common only a 23-residue region NNINNIYELAQQQDQHSSDIKTL (SEQ ID NO:65), suggesting that this 23-residue region, designated as the "3Q" peptide, contains the epitope that binds MAb 17C7.

TABLE IX

PCR™ primers used for the production of *usp A1* gene fragments for use in the construction of fusion proteins and mutagenesis and the reactivity of the resulting fusion protein with MAb 17C7

Fragment Generated:	Primer Pair[a]	Reactivity with MAb 17C7
MF-3	P5-P8	-
MF-4	P6-P13	+
MF-4.1	P7-P12	+
MF-4.2	P11-P13	+

[a] primer sequences are as follows:

P5	GGTGCAGGTCAGATCAGTGAC	SEQ ID NO:66
P6	GCCACCAACCAAGCTGAC	SEQ ID NO:67
P7	AGCGGTCGCCTGCTTGATCAG	SEQ ID NO:68
P8	CTGATCAAGCAGGCGACCGCT	SEQ ID NO:69
P11	CAAGATCTGGCCGCTTACAA	SEQ ID NO:70
P12	TTGTAAGCGGCCAGATCTTG	SEQ ID NO:71
P13	TGCATGAGCCGCAAACCC	SEQ ID NO:72

Elucidation of the MAb 17C7 Epitope. It is important to note that the nucleotide sequence encoding this 23-residue polypeptide (*i.e.*, the 3Q peptide) was present in the 0.6 kb *Bgl*II-*Pvu*II fragment used in the Southern blot analysis described in Example II. This finding suggested that the epitope that bound MAb 17C7 might be encoded by DNA present in both the 2.6 and 2.8 kb *Pvu*II fragments, with the 2.8 kb *Pvu*II fragment being derived from the cloned *uspA1* gene and the 2.6 kb *Pvu*II fragment representing all or part of another gene encoding this same epitope.

A ligation-based PCR™ system was used to verify this finding. Chromosomal DNA from the mutant strain was digested to completion with *Pvu*II and was resolved by agarose gel electrophoresis. Fragments ranging in size from 2-3 kb were excised from the agarose, blunt-ended, and ligated into the *Eco*RV site in pBluescript II SK+ This ligation reaction mixture was precipitated and used in a PCR™ amplification reaction. Each PCR™ reaction contained either the T3 or T7 primer derived from the DNA encoding the 3Q peptide. This approach yielded a 1.7

kb product with the T3 and P10 primers and a 0.9 kb product from the T7 and P9 primers (FIG. 5). The sum of these two bands is the same as the 2.6 kb size of the desired DNA fragment.

Nucleotide sequence analysis of these two PCR™ products revealed two incomplete ORFs which, when joined at the region encoding the 3Q peptide, formed a 1,728-bp ORF encoding a protein with a calculated molecular weight of 62,483 daltons (SEQ ID NO:3). The amino acid sequence of this protein had 43% identity with that of UspA1. Closer examination revealed that a region extending from amino acids 278-411 in this second protein, designated UspA2, was nearly identical to the region in UspA1 between amino acids 505-638 (SEQ ID NO:1). Furthermore, these two regions both contain the 23-mer (the 3Q peptide) that likely contains the epitope that binds MAb 17C7. It should also be noted that the four peptides from Table IX (Peptides 7-10) that were not found in UspA1 were found to be identical or very similar to peptides in the deduced amino acid sequence of UspA2. In addition, the first six peptides listed in Table IX, which matched or were very similar to peptides in the deduced amino acid sequence of UspA1, also matched peptides found in the deduced amino acid sequence of UspA2.

Oligonucleotide primers P1 and P2 (Table IX) were used to amplify a 2.5-2.6 kb fragment from *M. catarrhalis* strain O35E chromosomal DNA. Nucleotide sequence analysis of this PCR™ product was used to confirm the nucleotide sequence of the *uspA2* ORF determined from the ligation-based PCR™ study. These results proved that *M. catarrhalis* strain O35E contains two different ORFs (*i.e.*, *uspA1* and *uspA2*) which encode the same peptide (*i.e.*, the 3Q peptide) which likely binds MAb 17C7. This 3Q peptide appears twice in UspA1 and once in UspA2 (SEQ ID NO:1 and SEQ ID NO:3).

The nucleotide sequences of the two DNA segments encoding these 3Q peptides in *uspA1* are nearly identical, with three nucleotides being different. These nucleotide differences did not cause a change in the amino acid sequence. The nucleotide sequence of the DNA segment encoding the 3Q peptide in *uspA2* is identical to the DNA encoding the first 3Q peptide in UspA1.

As seen in FIG. 2C, lane 7, the three dominant MAb 17C7-reactive bands present in *M. catarrhalis* strain O35E outer membrane vesicles have apparent molecular weights of greater than 200 kDa, approximately 120 kDa, and approximately 70-80 kDa. It should be noted that the existence of several MAb 17C7-reactive bands, with apparent molecular weights of greater than 200 kDa, approximately 120 kDa, and approximately 70-80 kDa was also apparent in U.S. Patent

5,552,146 (FIG. 1, lane H). Therefore, the existence of at least more than one *M. catarrhalis* antigens reactive with MAb 17C7 was apparent as early as 1991. It is now apparent that the approximately 120 kDa band likely represents the monomeric form of the UspA1 antigen and the approximately 70-80 kDa band likely represents the monomeric form of the UspA2 antigen from *M. catarrhalis* strain O35E. One or more than one of these species may aggregate to form the very high molecular weight proteinaceous material (*i.e.* greater than 200 kDa) of the UspA antigen.

A new *M. catarrhalis* strain O35E genomic library was constructed in the bacteriophage vector ZAP Express (Stratagene, La Jolla, CA). Chromosomal DNA from this strain was partially digested with *Sau*3A1 and 4-9 kb DNA fragments were ligated into the vector arms according to the instructions obtained from the manufacturer. This library was amplified in *E. coli* MRF'. An aliquot of this library was diluted and plated and the resultant plaques were screened for reactivity with MAb 17C7. Approximately 24 plaques which bound this MAb were detected; the responsible recombinant bacteriophage were purified by the single plaque isolation method, and the DNA insert from one of these bacteriophage was subjected to nucleotide sequence analysis. Nucleotide sequence of the 2.6 kb DNA fragment present in this recombinant bacteriophage revealed that, on one end, it contained an incomplete ORF that encoded the 3Q peptide. Until its truncation by the vector cloning site, the sequence of this incomplete ORF was identical or nearly identical to that of the *uspA2* ORF derived from the ligation-based PCR™ study described immediately above, providing further evidence that two genes which share a common epitope encode the UspA antigen.

EXAMPLE IV: Purification of and Immunological Properties of the Proteins UspA1 and UspA2

Materials and Methods

Bacteria. TTA24 and O35E isolates were as previously described in Example I. Additional isolates were obtained from the University of Rochester and the American Type Culture Collection (ATCC). The bacteria were routinely passaged on Mueller-Hinton agar (Difco, Detroit, Ml) incubated at 35°C with 5% carbon dioxide. The bacteria used for the purification of the protein were grown in sterile broth containing 10 g casamino acids (Difco, Detroit, Ml) and 15 g yeast extract (BBL, Cockeysville, MD) per liter. The isolates were stored at -70°C in Mueller-Hinton broth containing 40% glycerol.

Purification of UspA2. Bacterial cells (~400 g wet wt. of *M. catarrhalis* O35E) were washed twice with 2 liters of pH 6.0, 0.03 M sodium phosphate ($NaPO_4$) containing 1.0% Triton® X-100 (TX-100) (J.T. Baker Inc., Philipsburg, NJ) (pH 6.0) by stirring at room temperature for 60 min. Cells containing the UspA2 protein were pelleted by centrifugation at 13,700 × g for 30 min at 4°C. Following centrifugation, the pellet was resuspended in 2 liters of pH 8.0, 0.03 M Tris(hydroxymethyl)aminomethane-HCl (Tris-HCl) containing 1.0% TX-100 and stirred overnight at 4°C to extract the UspA2 protein. Cells were pelleted by centrifugation at 13,700 × g for 30 min at 4°C. The supernatant, containing the UspA2 protein, was collected and further clarified by sequential microfiltration through a 0.8 μm membrane (CN.8, Nalge, Rochester, NY) then a 0.45 μm membrane (cellulose acetate, low protein binding, Corning, Corning, NY).

The entire filtered crude extract preparation was loaded onto a 50 × 217 mm (~200 ml) TMAE column [650(S), 0.025-0.4 mm, EM Separations, Gibbstown, NJ] equilibrated with pH 8.0, 0.03 M Tris-HCl buffer containing 0.1% TX-100 (THT). The column was washed with 400 ml of equilibration buffer followed by 600 ml of 0.25 M NaCl in 0.03 M THT. UspA2 was subsequently eluted with 800 ml of 1.0 M NaCl in 0.03 M THT. Fractions were screened for UspA2 by SDS-PAGE and pooled. Pooled fractions (~750 ml), containing UspA2, were concentrated approximately two-fold by ultrafiltration using an Amicon stirred cell (Amicon Corp., Beverly, MA) with a YM-100 membrane under nitrogen pressure. The TMAE concentrate was split into two 175 ml aliquots and each aliquot buffer exchanged by passage over a 50 × 280 mm (~550 ml) Sephadex G-25 (Coarse) column (Pharmacia Biotech, Piscataway, NJ) equilibrated with pH 7.0, 10 mM $NaPO_4$ containing 0.1% TX-100 (10 mM PT). The buffer exchanged material was subsequently loaded onto a 50 × 217 mm (~425 ml) ceramic hydroxyapatite column (Type I, 40 μm, Bio-Rad) equilibrated with 10 mM PT. The column was washed with 450 ml of the equilibration buffer followed by 900 ml of pH 7.0, 0.1M $NaPO_4$ containing 0.1% TX-100. UspA2 was then eluted with a linear pH 7.0 $NaPO_4$ concentration gradient between 0.1 and 0.2 M $NaPO_4$ containing 0.1% TX-100. An additional volume of pH 7.0, 0.2 M $NaPO_4$ containing 0.1% TX-100 was applied to the column and collected to maximize the recovery of UspA2. Fractions were screened for UspA2 by SDS-PAGE and pooled. The column was then washed with 900 ml of pH 7.0, 0.5 M $NaPO_4$

containing 0.1% TX-100. The fractions from this wash were screened for UspA1 by SDS-PAGE, pooled, and stored at 4°C. This pool was used for the purification of UspA1.

Purification of UspA1. The UspA1 enriched fractions collected during four separate purifications of UspA2 were pooled. The combined UspA1 pools were concentrated approximately threefold by ultrafiltration using an Amicon stirred cell with a YM-100 membrane under nitrogen pressure. The UspA1 concentrate was split into two 175 ml aliquots and the buffer exchanged by passage over a 50 × 280 mm (~550 ml) Sephadex G-25 column equilibrated with 10 mM PT. The buffer exchanged material was subsequently loaded onto a 50 × 217 mm (~425 ml) ceramic hydroxyapatite column (Bio-Rad) equilibrated with 10 mM PT. The column was washed with 450 ml of the equilibration buffer followed by 900 ml of pH 7.0, 0.25 M $NaPO_4$ containing 0.1% TX-100. UspA1 was subsequently eluted with a linear $NaPO_4$ gradient of pH 7.0, 0.25-0.5 M $NaPO_4$ containing 0.1% TX-100. The fractions containing UspA1 were identified by SDS-PAGE and pooled.

SDS-PAGE and Western blot Analysis. SDS-PAGE was carried out as described by Laemmli (1970) using 4 to 20% (w/v) gradient acrylamide gels (Integrated Separation Systems (ISS), Natick, MA). Proteins were visualized by staining the gels with Coomassie Brilliant Blue R250. Gels were scanned using a Personal Densitometer SI (Molecular Dynamics Inc., Sunnyvale, CA) and molecular weights were estimated with the Fragment Analysis software (version 1.1) using the prestained molecular weight markers from ISS as standards. Transfer of proteins to polyvinylidene difluoride (PVDF) membranes was accomplished with a semi-dry electroblotter and electroblot buffers (ISS). The membranes were probed with protein specific antisera or MAb's followed by goat anti-mouse alkaline phosphatase conjugate as the secondary antibody (BioSource International, Camarillo, CA). Western blots were developed with the BCIP/NBT Phosphatase Substrate System (Kirkegaard and Perry Laboratories, Gaithersburg, MD).

Protein Estimation. Protein concentrations were estimated by the BCA assay (Pierce, Rockford, IL), using bovine serum albumin as the standard.

Enzymatic and Chemical Cleavages of UspA2 and UspA1.

(i) CNBr Cleavage. Approximately 0.3 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in 100 µl of 88% (v/v) formic acid containing 12 M urea. Following resuspension, 100 µl of 88% (v/v) formic acid containing 2 M CNBr (Sigma, St. Louis, MO) was added and the mixture incubated overnight at room temperature in the dark.

(ii) Trypsin and Chymotrypsin Cleavage. Approximately 2 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in a total volume of 1 ml of phosphate-buffered saline (PBS) containing 0.1% TX-100. This preparation was added directly to a vial containing 25 µg of either trypsin or chymotrypsin (Boehringer Mannheim, Indianapolis, IN). The reaction mixture was incubated for 48 h at 37°C.

(iii) Endoproteinase Lys-C Cleavage. Approximately 2 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in a total volume of 1.0 ml of PBS containing 0.1% TX-100. This preparation was added directly to a vial containing 15 µg of endoproteinase Lys-C (Boehringer Mannheim). The reaction mixture was incubated for 48 h at 37°C.

(iv) Separation of Peptides. The above cleavage reaction mixtures were centrifuged in an Eppendorf centrifuge at 12,000 rpm for 5 min and the supernatant loaded directly onto a Vydac Protein C4 HPLC column (The Separations Group, Hesperia, CA). The solvents used were 0.1% (v/v) aqueous trifluoroacetic acid (TFA) [Solvent A] and acetonitrile:H_20:TFA, 80:20:0.1 (v/v/v) [Solvent B] at a flow rate of 1.0 ml/min. Following the initial wash with Solvent A, the peptides were eluted with a linear gradient between 0 and 100% of Solvent B and detected by absorbance at 220 nm. Suitable fractions were collected, dried in a Speed-Vac concentrator (Jouan Inc., Winchester, VA) and resuspended in distilled water. The fractions were separated by SDS-PAGE in 10 to 18% (w/v, acrylamide) gradient gels (ISS) in a Tris-Tricine buffer system (Schägger and von Jagow, 1987). The fractions containing a single peptide band were submitted directly for N-terminal sequence analysis. Fractions displaying multiple peptide bands in SDS-PAGE were electrophoretically transferred onto a PVDF membrane as described above. The membrane was stained with Coomassie Brilliant Blue R-

250 and the individual bands excised before submitting them for N-terminal sequence analysis (Matsudaira, 1987).

Determination of subunit size. Determination of molecular weight by Matrix Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF) mass spectrometry (Hillenkamp and Karas, 1990) was done on a Lasermat 2000 Mass Analyzer (Finnigan Mat, Hemel Hempstead, UK) with 3,5-dimethoxy-4-hydroxy-cinnamic acid as the matrix. Cold ethanol precipitation was done on samples containing ≥0.1% (v/v) TX-100 to remove the detergent. The final ethanol concentration was 90% (v/v). The precipitated protein was resuspended in water.

Determination of aggregate sizes by gel filtration chromatography. Approximately 1 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in a total volume of 1.0 ml of PBS containing 0.1% TX-100. Two hundred microliters of the preparation were applied to a Superose-6 HR 10/30 gel filtration column (10 × 30 mm, Pharmacia) equilibrated in PBS /0.1% TX-100 at a flow rate of 0.5 ml/min. The column was calibrated using the HMW Calibration Kit (Pharmacia) which contains aldolase with a size of 158,000, catalase with a size of 232,000; ferritin with a size of 440,000; thyroglobulin with a size of 669,000; and blue dextran with sizes between 2000 and 2,000,000.

Amino Acid Sequence Analysis. N-terminal sequence analysis was carried out using an Applied Biosystems Model 477A Protein/Peptide Sequencer equipped with an on-line Model 120A PTH Analyzer (Applied Biosystems, Foster City, CA). The phenylthiohydantoin (PTH) derivatives were identified by reversed-phase HPLC using a Brownlee PTH C-18 column (particle size 5 μm, 2.1 mm i.d. × 22 cm 1.; Applied Biosystems).

Immunizations. Female BALB/c mice (Taconic Farms, Germantown, NY), age 6-8 weeks, were immunized subcutaneously with two doses of UspA1 or UspA2 four weeks apart. To prepare the vaccine, purified UspA1 or UspA2 was added to aluminum phosphate, and the mixture rotated overnight at 4°C. 3-O-deacylated monophosphoryl lipid A (MPL) (Ribi ImmunoChem Research, Inc.) was added just prior to administration. Each dose of vaccine contained 5 μg of purified protein, 100 μg of aluminum phosphate and 50 μg of MPL resuspended in a 200 μl volume. Control mice were injected with 5 μg of CRM_{197} with the same adjuvants. Serum samples were collected before the first vaccination and two weeks after the second immunization. Mice were housed in a specific-pathogen free facility and provided water and food *ad libitum*.

Monoclonal antibodies. The 17C7 MAb was secreted by a hybridoma (ATCC HB11093). MAbs 13-1, 29-31, 45-2, and 6-3 were prepared as previously described (Chen *et al.*, 1995).

Murine model of *M. catarrhalis* pulmonary clearance. This model was performed as described previously (Chen *et al.*, 1995).

Enzyme linked immunosorbent assay (ELISA) procedures. Two different ELISA procedures were used. One was used to examine the reactivity of sera to whole bacterial cells and the other the reactivity to the purified proteins.

For the whole cell ELISA, the bacteria were grown overnight on Mueller-Hinton agar and swabbed off the plate into PBS. The turbidity of the cells was adjusted to 0.10 at 600 nm and 100 μl added to the wells of a 96 well Nunc F Immunoplate (Nunc, Roskilde, Denmark). The cells were dried overnight at 37°C, sealed with a mylar plate sealer and stored at 4°C until needed. On the day of the assay, the residual protein binding sites were blocked by adding 5% non-fat dry milk in PBS with 0.1% Tween 20 (Bovine Lacto Transfer Technique Optimizer [BLOTTO]) and incubating 37°C for one hour. The blocking solution was then removed and 100 μl of sera serially diluted in the wells with blotto. The sera were allowed to incubate for 1 h at 37°C. The plate wells were soaked with 300 ml PBS containing 0.1% Tween 20 for 30 seconds and washed 3 times for 5 seconds with a Skatron plate washer and then incubated 1 hr at 37°C with goat anti-mouse IgG conjugated to alkaline phosphatase (BioSource) diluted 1:1000 in blotto. After washing, the plates were developed at room temperature with 100 μl per well of 1 mg/ml p-nitrophenyl phosphate dissolved in diethanolamine buffer. Development was stopped by adding 50 μl of 3N NaOH to each well. The absorbance of each well was read at 405 nm and titers calculated by linear regression. The titer was reported as the inverse of the dilution extrapolated to an absorption value of 0.10 units.

For the ELISA against the purified proteins, the proteins were diluted to a concentration of 5 μg/ml in a 50 mM sodium carbonate buffer (pH 9.8) containing 0.02% sodium azide (Sigma Chemical Co.). One hundred microliters were added to each well of a 96 well

E.I.A./R.I.A medium binding ELISA plate (Costar Corp., Cambridge, MA) and incubated for 16 hours at 4°C. The plates were washed and subsequently treated the same as described for whole cell ELISA procedure.

Complement-dependent bactericidal assay. For this assay, 20 μl of the bacterial suspension containing approximately 1200 cfu bacteria in PBS supplemented with 0.1 mM $CaCl_2$:, $MgCl_2$ and 0.1% gelatin (PCMG) were mixed with 20 μl of serum diluted in PCMG and incubated for 30 min at 4°C. Complement, prepared as previously described (Chen *et al.*, 1996), was added to a concentration of 20%, mixed, and incubated 30 min at 35°C. The assay was stopped by diluting with 200 μl of cold, 4°C, PCMG. 50 μl of this suspension was spread onto Mueller-Hinton plates. Relative killing was calculated as the percent reduction in cfu in the sample relative to that in a sample in which heat inactivated complement replaced active complement.

Inhibition of bacterial adherence to HEp-2 cells. The effect of specific antibodies on bacterial adherence to HEp-2 cells was examined. A total of 5×10^4 HEp-2 cells in 300 μl of RPMI-10 were added to a sterile 8-well Lab-Tek chamber slide (Nunc, Inc., Naperville, Ill) and incubated overnight in a 5% CO_2 incubator to obtain a monolayer of cells on the slide. The slide was washed with PBS and incubated with 300 μl of bacterial suspension (A_{550}=0.5) or with a bacterial suspension that had been incubated with antisera (1:100) at 37°C for 1 h. The slides were then washed with PBS and stained with the Difco quick stain following the manufacturer's instructions. The slide was viewed and photographed using a light microscope equipped with a camera (Nikon Microphot-SA, Nikon, Tokyo, Japan).

Protein interaction with fibronectin and vitronectin. The interactions of purified UspA1 and UspA2 with fibronectin were examined by dot blot. Human plasma fibronectin (Sigma Chemical Co., St. Louis, MO) was applied to a nitrocellulose membrane, and the membrane blocked with blotto for 1 h at room temperature. The blot was then washed with PBS and incubated with purified UspA1 or UspA2 (2 μg/ml in blotto) overnight at 4°C. After three washes with PBS, the membrane was incubated with the MAb 17C7 diluted in blotto for 2 h at room temperature and then with goat anti-mouse immunoglobulin conjugated to alkaline phosphatase (BIO-RAD Lab. Hercules, Calif.) (1:2,000 in PBS with 5% dry milk, 2 h, room temperature). The membrane was finally developed with a substrate solution containing nitroblue tetrazolium and 5-bromo-chloro-3-indolyl phosphate in 0.1 M tris-HCl buffer (pH 9.8).

Interaction with vitronectin was examined by a similar procedure. The purified UspA1 and UspA2 were spotted onto the nitrocellulose membrane and the membrane blocked with blotto. The membrane was then incubated sequentially with human plasma vitronectin (GIBCO BRL, Grand Island, N.Y., 1 μg/ml in blotto), rabbit anti-human vitronectin serum (GIBCO BRL), goat anti-rabbit IgG-alkaline phosphatase conjugate and substrate.

Interaction with HEp-2 cells by the purified protein. Each well of a 96 well cell culture plate (Costar Corp., Cambridge, Mass.) was seeded with 5×10^4 HEp-2 cells in 0.2 ml RPMI containing 10% fetal calf serum and the plate incubated overnight in a 37°C incubator containing 5% CO_2. Purified UspA1 or UspA2 (1 to 1,000 ng) in blotto was added and incubated at 37°C for 2 h. The plate was washed with PBS, and incubated with the 1:1 mixed mouse antisera to either UspA1 or UspA2 (1:1000 dilution in PBS containing 5% dry milk), the plate was washed and incubated with rabbit anti-mouse IgG conjugated to horseradish peroxidase (1:5,000 in PBS containing 5% dry milk) (Brookwood Biomedical, Birmingham, AL) at room temperature for 1 h. Finally, the plate was washed and developed with a substrate solution containing 2,2'-azino-bis-(3-ethyl-benzthiazoline-6-sulfonic acid) at 0.3 mg/ml in pH 4.0 citrate buffer containing 0.03% hydrogen peroxide (KPL, Gaithersburg, MD). Whole bacteria of strain O35E were included as a positive control. The highest concentration of the bacteria tested had an optical density of A_{550}=1.0. The abscissa for the bacterial data shown in FIG. 7 plots the values for three fold dilutions of the bacterial suspension.

Results

Purification of UspA1 and UspA2. The inventors developed a large-scale, high yield process for extracting and purifying UspA2 from a pellet of *M. catarrhalis* cells. The method consisted of three critical steps. First the UspA2 protein was extracted from the bacteria with pH 8.0, 0.03 M THT. Second, the cell extract was applied to a TMAE column and the UspA2 protein eluted with NaCl. Finally, the enriched fractions from the TMAE chromatography were applied to a ceramic hydroxyapatite column and the UspA2 eluted with a linear $NaPO_4$ gradient. A yield of 250 mg of purified UspA2 was typically obtained from ~400 g wet weight of *M. catarrhalis* O35E strain cells. A single band was seen for the UspA2 in SDS-PAGE gels by Coomassie blue staining. It corresponded to a molecular size of ~240,000 and contained greater than 95% of the protein based on scanning densitometry (FIG. 6A). A second band reacting with the 17C7 MAb at approximately 125,000 could be detected in the UspA2 preparation by western but not by Coomassie blue staining (FIG. 6C). The cells need not be lysed to achieve this high yield, which suggested this protein is present in large amounts on the surface of the bacterium.

A method for the purification of the UspA1 protein was also developed. This protein co-purified with UspA2 through the initial extraction and TMAE chromatography steps. Following hydroxyapatite chromatography, however, UspA1 remained bound to the column and had to be eluted at the higher salt concentration of 500 mM $NaPO_4$. The crude UspA1 preparation obtained in this step was reapplied and eluted from the hydroxyapatite column using a linear sodium phosphate gradient. A total of 80 mg of purified UspA1 was isolated from ~1.6 kg wet wt. of *M. catarrhalis* O35E strain cells. UspA1 purified using this method migrated at three different apparent sizes on SDS-PAGE depending on the method of sample preparation. Unheated samples exhibited a single band at ~280,000, whereas samples heated at 100°C for 3 min resulted in an apparent molecular weight shift to ~350,000. Prolonged heating at 100°C resulted in a shift of the 350,000 band to one at 100,000 (FIG. 6B). Following heating of the sample for 7 min at 100°C, the band at 100,000 contained greater than 95% of the protein based on scanning densitometry of the Coomassie stained gel. In contrast, UspA2 migrated at 240,000 regardless of the duration of the heating when examined by SDS-PAGE. The different migration behaviors indicated the preparations contained two distinctly different proteins

Molecular Weight Determinations. MALDI-TOF mass spectrometric analysis for determination of molecular weight of UspA2 using 3,5-dimethoxy-4-hydroxy-cinnamic acid matrix in presence of 70% (v/v) aqueous acetonitrile and 0.1% TFA resulted in the identification of a predominant species with average molecular mass of 59,518 Da. In addition to the expected $[M+H]^+$ and $[M+2H]^{2+}$ molecular ions, the $[2M+H]^+$ and $[3M+H]^+$ ions were also observed. The latter two ions were consistent with the dimer and the trimer species. Using similar conditions, the inventors were unable to determine the mass of UspA1.

To determine the molecular sizes of the purified proteins in solution, UspA1 and UspA2 were independently run on a Superose-6 HR 10/30 gel filtration column (optimal separation range: 5,000-5,000,000) calibrated with molecular weight standards. Purified UspA1 exhibited a native molecular size of 1,150,000 and UspA2 a molecular size of 830,000. These sizes, however, may be affected by the presence of TX-100.

N-terminal Sequence Analysis of Internal UspA1 and UspA2 Peptides. All attempts to determine the N-terminal sequences of both UspA and UspA1 proved unsuccessful. No sequence could be determined. This suggested two things. First, the N-terminus of both proteins were blocked, and, second, neither protein preparation contained contaminating proteins that were not N-terminally blocked.

Thus, to confirm that the primary sequence of purified UspA1 and UspA2 corresponded to that deduced from their respective gene sequences, internal peptide fragments were generated and subjected to N-terminal sequence analysis. Tables X and XI show the N-terminal sequences obtained for fragments generated from the digestion of the UspA2 and UspA1 proteins, respectively. The sequences matching the primary amino acid sequence deduced from the respective gene sequences are indicated for each fragment. The UspA2 fragments #3 and #4 exhibited sequence similarity with residues 505-515 and 605-614 respectively of the amino acid sequence deduced from the UspA1 gene. In Table XII, UspA1 fragment #3 exhibited sequence similarity with residues #278-294 of the UspA2 primary sequence. These sequences corresponded with the domains within UspA1 and UspA2 that share 93% sequence identity. The remainder of the sequences, however, were unique to the respective proteins.

TABLE X

N-terminal sequences of internal UspA2 peptide cleavage fragments

UspA2 Fragment Sequence[a]	Match[b]	Cleavage
1) LLAEQQLNG SEQ ID NO:73	92-100	Trypsin
2) ALESNVEEGL SEQ ID NO:74	216-225	Lys-C
	245-254	
	274-283	
3) ALESNVEEGLLDLS SEQ ID NO:75	274-288	Trypsin
	*505-515	

TABLE X cont'd

UspA2 Fragment Sequence[a]	Match[b]	Cleavage
4) AKASAANTDR SEQ ID NO:76	378-387 * 605-614	Chymotrypsin
5) AATAADAITKNGN SEQ ID NO:77	439-450	Chymotrypsin
6) SITDLGTKVDGFDGR SEQ ID NO:78	458-472	Lys-C
7) VDALXTKVNALDXKVN SEQ ID NO:79	473-488	Trypsin
8) AAQAALSGLFVPYSVGKFNATAALGGYGSK SEQ ID NO:80	506-535	CNBr

[a] Underlined residues denote mismatch with the nucleotide derived amino acid sequence. Ambiguous residues whose identity could not be verified are denoted by the letter X.

[b] Asterisk (*) indicates match with UspA1. Without asterisk indicates matches with nucleotide derived amino acid sequence of UspA2.

TABLE XI

N-terminal sequences of internal UspA1 peptide cleavage fragments

UspA1 Fragment Sequence[a]	Match[b]	Cleavage
1) LENNVEEPXLNLS	456-468	Lys-C
2) DQKADI	473-478	Trypsin
3) NNVEEGLLDLSGRLIDQK	504-521 * 278-294	Lys-C
4) VAEGFEIF	690-697	Trypsin
5) AGIATNKQELILQNDRLNRI	701-720	Lys-C

[a] As per Table X. X denotes an unidentified amino acid residue.

[b] Asterisk (*) indicates match with UspA2. Without asterisk indicates matches with nucleotide derived amino acid sequence of UspA1.

Reactivity of MAbs with UspA1 and UspA2. The western blot analysis of purified UspA1 and UspA2 revealed that both proteins reacted strongly with the MAb 17C7 described by Helminen *et al.* (1994) (FIG. 7). The reactivity of the proteins with other MAbs was also investigated. The data in Table XII show that, whether assayed by ELISA or western, the

MAbs 13-1, 29-31 and 45-2 only reacted with UspA2, the MAbs 7D7, 29C6, 11A6 and 12D5 only reacted with UspA1, while 17C7 and 6-3 reacted with both UspA1 and UspA2. All the MAbs shown in Table XIII bind to whole bacteria when examined by ELISA. These results indicated that UspA2 was exposed on the surface of the bacterium.

TABLE XII

Summary of reactivity of monoclonal antibodies with purified UspA1, UspA2 and whole bacteria of strain O35E

mAb	Isotype	Reactivity		
		Whole bacterium[a]	Purified UspA1[b]	Purified UspA2[b]
13-1	IgGlκ	+	-	+
29-31	IgGlλ	+	-	+
45-2	IgG2a	+	-	+
17C7	IgG2a	+	+	+
6-3	IgM	+	+	+
7D7	IgG2b	+	+	-
29C6	IgG1	+	+	-
11A6	IgA	+	+	-
12D5	IgG1	+	+	-

[a] Determined by whole cell ELISA.

[b] Determined by ELISA and western blot.

TABLE XIII

Cross-reactivity of antibodies to UspA1 and UspA2 proteins

Antiserum to	**Geometric mean ELISA titer[b] to**	
	UspA1	**UspA2**
UspA1[a]	740,642[c]	10,748[c]
UspA2[a]	19,120[d]	37,615[d]

[a] The preparation of the sera are described in the text.

[b] ELISA titers are for total IgG and IgM antibodies for sera pooled from ten mice.

[c] The difference in titer of the anti-UspA1 with the two purified proteins was statistically different by the Wilcoxon signed rank test (p=0.0002).

[d] The difference in titer of the anti-UspA2 with the two purified proteins was statistically different by the Wilcoxon signed rank test (p=0.01).

Immunogenicity and antibody cross-reactivity. Antisera to the purified UspA1 and UspA2 proteins were generated in mice. The titers of antigen specific antibodies (IgG and IgM) as well as the cross-reactive antibodies in these sera were determined by an ELISA assay using each of the purified proteins (Table XIII). Both proteins elicited antibody titers that were greater against themselves than against the heterologous protein. Thus, the reactivities of both the MAbs (Table XII) as well as the polyclonal antibodies indicate that the proteins possessed both shared and non-shared B-cell epitopes.

Antibody reactivity to whole bacterial cells and bactericidal activity. Antisera to the UspA1 and UspA2 were assayed by whole cell ELISA against the homologous O35E strain and several heterologous isolates (Table XIV). The antibodies to UspA1 and to UspA2 reacted strongest with the O35E strain. The reactivity of the sera toward the heterologous isolates indicated they bound antibodies elicited by both UspA1 and UspA2.

TABLE XIV

ELISA and complement mediated bactericidal titers toward whole bacterial cells of multiple isolates of *M. catarrhalis* elicited by purified UspA1 and purified UspA2

	Whole cell ELISA[a]		Bactericidal titer[b]	
Isolate	**anti-UspA1[a]**	**anti-UspA2[a]**	**anti-UspA1**	**anti-UspA2**
O35E	195,261	133,492	400	800
430-345	12,693	18,217	400	400
1230-359	7,873	13,772	400	400
TTA24	14,341	7,770	800	800

[a] Titer determined for pool of sera from ten mice. The titer of the sera drawn before the first immunization was less than 50 for all isolates.

[b] Bactericidal titers were determined as the inverse of the highest serum dilution killing greater than 50% of the bacteria. The titers for the sera from mice immunized contemporaneously with CRM_{197} were less than 100.

The bactericidal activities of the antisera to UspA1 and UspA2 were determined against O35E and other isolates as well (Table XIV). Both sera had bactericidal titers ranging from 400-800 against O35E and the disease isolates. Anti-CRM_{197} serum, the negative control, as well as sera drawn before immunization, had a titers of <100 against all the strains. These results were consistent with the previous observation that the epitopes shared by the two proteins are highly conserved among isolates and the antibodies toward those isolates are bactericidal.

Pulmonary challenge. Immunized mice were given a pulmonary challenge with the homologous O35E strain or the heterologous TTA24 strain. Relative to the control mice immunized with CRM_{197}, enhanced clearance of both strains was observed regardless of whether the mice were immunized with UspA1 or UspA2 (Table XV). No statistical difference ($p > 0.05$) was seen between the groups of mice immunized with UspA1 and with UspA2.

TABLE XV

Pulmonary clearance of *M. catarrhalis* by mice immunized with purified UspA1 and UspA2

Study	Immunogen	Challenge strain	% clearance[a]	p[a]
1	UspA1	O35E	49.0	0.013
	UspA2		31.8	0.05
	CRM_{197}		0	-
2	UspA1	TTA24	54.6	0.02
	UspA2		66.6	0.0003
	CRM_{197}		0	-

[a]Challenge method described in text. Numbers are the percentage of bacteria cleared from the immunized mice compared to control mice which were immunized with CRM_{197}.

Interaction of purified proteins with HEp-2 cells. The purified UspA1 and UspA2 were tested for their ability to interact with HEp-2 cell monolayer in a 96-well plate using an ELISA. Protein binding to the HEp-2 cells was detected with a 1:1 mix of the mouse antisera to UspA1 and UspA2. Purified UspA1 bound to HEp-2 cells at concentrations above 10 ng. A weak binding by the UspA2 was detected at concentrations above 100 ng (FIG. 7). The attachment of O35E bacteria to HEp-2 cells was used as a positive control. This result, plus the data showing that the anti-UspA1 antibodies inhibited attachment of the bacteria to HEp2 cells, suggests UspA1 plays an important role in bacterial attachment which also suggested that UspA1 was exposed on the bacterial surface.

Interaction of purified proteins with fibronectin and vitronectin. The purified proteins were assayed for their ability to interact with fibronectin and vitronectin by dot blot assays. Human plasma fibronectin immobilized on a nitrocellulose membrane bound purified UspA1 but not UspA2 (FIG. 8), while UspA2 immobilized on the nitrocellulose membrane was capable of binding vitronectin (FIG. 8). Vitronectin binding by the UspA1 was also detected, but the reactivity was weaker. Collagen (type IV), porcine mucin (type III), fetuin and heparin were also tested for interaction with purified UspA1 and purified UspA2, but these did not exhibit detectable binding.

Discussion

Previous UspA purification attempts yielded preparations containing multiple high molecular weight protein bands by SDS-PAGE and western blot. Because each of the bands reacted with the "UspA specific" MAb 17C7, it was thought they represented multiple forms of the UspA protein (Chen *et al.*, 1996). However, the inventors have discovered that there are two distinct proteins, UspA1 and UspA2, that share an epitope recognized by the 17C7 MAb. These two proteins are encoded by different genes. This study shows that UspA1 and UspA2 can be separated from one another. The isolated proteins had different SDS-PAGE mobility characteristics, different reactivity with a set of monoclonal antibodies, and different internal peptide sequences. The results, however, were consistent with the proteins sharing a portion of their peptide sequences, including the MAb 17C7 epitope. The separation of the proteins from one another has allowed the inventors to further demonstrate how the proteins were different as well as examine their biochemical, functional, and immunological characteristics.

In solution, the purified proteins appear to be homopolymers of their respective subunits held together by strong non-covalent forces. This is indicated by the fact that UspA2 lacks any cysteines and treatment of both proteins with reducing agents did not alter their mobilities in SDS-PAGE. Both gene sequences possess leucine zipper motifs that might mediate coil-coil interactions (O'Shea *et al.*, 1991). Even so, it was surprising that the non-covalent bonds of both proteins were not only strong enough to resist dissociation by the conditions normally used to prepare samples for SDS-PAGE, but also high concentrations of chaotropic agents such as urea (Klingman and Murphy, 1994) and guanidine HCl. Of the two proteins, UspA2 appeared to be less tightly aggregated, this was indicated by the fact that its subunit size of 59,500 Da could be determined by mass spectrometry. UspA1, however, was recalcitrant to dissociation by all the methods tried, and this may be the reason its size could not be determined by mass spectrometry. In SDS-PAGE, the dominant UspA2 migrated with an apparent size of 240,000 while a far smaller portion migrated at about 125,000 and could only be detected by western analysis. The mobility of UspA1, however, varied depending on how long the sample was heated. The smallest form was about 100,000. This was consistent with the size of the gene product missing from the *uspA1* mutant but not with the size predicted from the gene sequence of 88,000 Da. In solution, both proteins formed larger aggregates than those seen by SDS-PAGE. Their sizes, as measured by gel filtration chromatography, were 1,150,000 and 830,000 for UspA1 and UspA2 respectively. If the proteins behave this way *in vivo*, UspA1 and UspA2 likely occur as large molecular complexes on the bacterial surface of the bacterium.

The results of the N-terminal amino acid sequence analyses of the UspA2 and UspA1 derived peptides (Tables X and XI) were in agreement with the protein sequences derived from the respective gene sequences. This confirmed that the purified UspA1 and UspA2 proteins were the products of the respective *uspA1* and *uspA2* genes. Further, the experimental and theoretical amino acid compositions of UspA1 and UspA2 were consistent, given the size of the proteins and the accuracy of the amino acid determination. There was, however, a discrepancy between the size determined by mass spectrometry of 59,518 and the size indicated from the gene sequence for UspA2 of 62,483. This discrepancy suggested that this protein either undergoes post-translational processing or proteolytic degradation.

The data also suggest that both proteins are exposed on the bacterial surface. That at least one of the proteins is exposed is evident from the finding that the MAb 17C7 and polyclonal sera react with whole cells. The reactivities of the UspA2 specific monoclonal antibodies 13-1, 29-31 and 45-2 with the bacterial cells in the whole cell ELISA provided evidence that the UspA2 is a surface protein (Table XII). The reactivities of the UspA1 specific MAbs 7D7, 29C6, 11A6 and 12D5 with the bacterial cells in the whole cell ELISA provided evidence that the UspA1 is a surface protein (Table XII). Further evidence for surface exposure of UspA1 was indicated by the inhibitory effect of the antiserum on bacterial attachment to HEp-2 cells. The sera to the UspA2 lacked this activity. Thus, both UspA1 and UspA2 appeared to be surface exposed on the bacterium.

Surface exposure of the proteins is probably important for the two proteins' functions. One function for UspA1 appears to be meditation of adherence to host tissues. The evidence for this was that UspA1 antibodies inhibited bacterial binding to HEp-2 cells and the purified protein itself bound to the cells. The relevance of binding to HEp-2 cells is that they are epithelial cells derived from the larynx, a common site of *M. catarrhalis* colonization (Schalen *et al.*, 1992). This confirms the inventors findings that mutants that do not express UspA1 fail to bind epithelial cells. The inventors' also showed that UspA1 binds fibronectin. Fibronectin has been reported to be a host receptor for other pathogens (Ljungh and Wadström, 1995; Westerlund and Korhonen, 1993). Examination of the gene sequence, however, failed to reveal any similarity with the fibronectin binding motifs reported for Gram positive organisms (Westerlund and Korhonen, 1993). Thus, it is fairly clear that UspA1 plays a role in host adherence, possibly *via* cell associated fibronectin.

The function of UspA2 is less certain. Antibodies toward it did not block adherence to the HEp-2 or Chang cell lines, nor did the purified protein bind to those cells. Yet, UspA2 bound vitronectin strongly. Pathogen binding of vitronectin has been linked to host cell adherence (Gomez-Duarte *et al.*, 1997; Limper *et al.*, 1993); however, van Dijk and his co-workers have reported that vitronectin binding by *M. catarrhalis* may be used by the bacteria to subvert host defenses (Verdiun *et al.*, 1994). The soluble form of vitronectin, known as complement factor S, regulates formation of the membrane attack complex (Su, 1996). They suggest that the binding of vitronectin to the *M. catarrhalis* surface inhibits the formation of the membrane attack complex, rendering the bacteria resistant to the complement dependent killing activity of the sera. They have also described two types of human isolates: one that binds vitronectin and is resistant to the lytic activity of the serum and the other that does not bind vitronectin and is serum sensitive (Hol *et al.*, 1993). It must be noted, however, that vitronectin, like all the extracellular matrix proteins, has many forms and serves multiple functions in the host (Preissner, 1991; Seiffert, 1997). Thus, the interaction of both UspA1 and UspA2 with the extracellular matrix proteins fibronectin and vitronectin may serve the bacterium in ways beyond subverting host defenses or as receptors for bacterial adhesion.

Even though the two proteins share epitopes and sequences, they have different biochemical activities and likely serve different biological functions. If an immune response to the respective protein interferes with its function, it ought to be considered as a vaccine candidate. The results of the immunological studies in mice indicated that both proteins would be good vaccine candidates. Mice immunized with either UspA1 or UspA2 developed high antibody titers toward the homologous and heterologous bacterial isolates. Further, the sera from these mice had complement dependent bactericidal activity toward all the isolates tested. In addition, immunized mice exhibited enhanced pulmonary clearance of the homologous isolate and heterologous isolates. It is important to note that antibodies elicited by the proteins were partially cross-reactive. This was expected since both react with the 17C7 MAb and share amino acid sequence.

EXAMPLE V: The Level and Bactericidal Capacity of Child and Adult Human Antibodies Directed against the Proteins UspA1 and UspA2

To determine if humans have naturally acquired antibodies to the UspA1 and UspA2 of the *M. catarrhalis* and the biological activity of these antibodies if present, sera from healthy humans of various ages was examined using both ELISA and a bactericidal assay. It was found that healthy people have naturally acquired antibodies to both UspA1 and UspA2 in their sera, and the level of these antibodies and their bactericidal capacity were age-dependent. These results also indicate that naturally acquired antibodies to UspA1 and UspA2 are biologically functional, and thus support their use as vaccine candidates to prevent *M. catarrhalis* disease.

Material and methods

Bacteria. The *M. catarrhalis* strains O35E and TTA24 were as described in Example I. An ATCC strain (ATCC 25238) and three other clinical isolates from the inventors' collection were also used.

Human sera. Fifty-eight serum samples were collected from a group of ten children at 2, 4, 6, 7, 15 and 18 months of age who had received routine childhood immunizations. Individual sera from twenty-six adults and fifteen additional children 18-36 months of age were also assayed. All sera were obtained from clinically healthy individuals. Information on *M. catarrhalis* colonization and infection of these subjects was not collected. The sera were stored at -70°C.

Purification of UspA1 and UspA2. Purified UspA1 and UspA2 were made from the O35E strain of *M. catarrhalis* as described in Example IV herein. Each protein preparation contained greater than 95% of the specific protein based on densitometric scanning of Coomassie brilliant blue stained SDS-PAGE. Based on western blot analysis using monoclonal antibodies, each purified protein contained no detectable contamination of the other.

Purification of UspA1 and UspA2 specific antibodies from human plasma. Human plasmas from two healthy adults were obtained from the American Red Cross (Rochester, N.Y.) and pooled. The antibodies were precipitated by adding ammonium sulfate to 50% saturation. The precipitate was collected by centrifugation and dialyzed against PBS. A nitrocellulose membrane (2 × 3 inches) was incubated with UspA1 or UspA2 at 0.5 mg/ml in PBS containing 0.1% (vol/vol) Triton X-100 for 1 h at room temperature, washed twice with PBS and residual binding sites on the membrane blocked with 5% (wt/vol) dry milk in PBS for 2 h at room temperature. The membrane was then sequentially washed twice with PBS, 100 mM glycine (pH 2.5) and finally with PBS before incubation with the dialyzed antibody preparation. After incubating for 4 h at 4°C, the membrane was washed again with PBS, and then 10 mM Tris buffer (pH 8.0) containing 1 M sodium chloride to remove non-specific proteins. The bound antibodies were eluted by incubation in 5 ml of 100 mM glycine (pH 2.5) for 2 min with shaking. One ml of Tris-HCl (1M, pH 8.0) was immediately added to the eluate to neutralize the pH. The eluted antibodies were dialyzed against PBS and stored at -20°C.

Enzyme-linked immunosorbent assay (ELISA). Antibody titers to the O35E and other *M. catarrhalis* strains were determined by a whole-cell ELISA as previously described using biotin-labeled rabbit anti-human IgG or IgA antibodies (Brookwood Biomedical, Birmingham, Alabama) (Chen *et al.*, 1996). Antibody titers to UspA1 and UspA2 were determined by a similar method except that the plates were coated with 0.1 μg of purified protein in 100 μg of PBS per well overnight at room temperature. The IgG subclass antibodies to UspA1 or UspA2 were determined using sheep anti-human IgG subclass antibodies conjugated to alkaline phosphatase (The Binding Site Ltd., San Diego, Calif.). The antibody end point titer was defined as the highest serum dilution giving an A_{415} greater than three times that of the control. The control wells received all treatments except human sera and usually had absorbance values ranging from 0.03 to 0.06.

The specificity of biotin-labeled rabbit anti-human IgG and IgA antibodies was determined against purified human IgG, IgM and IgA (Pierce, Rockford, IL) by ELISA. No cross-reactivity was found. The assay sensitivity determined by testing against purified human antibodies of appropriate isotype in an ELISA was 15 and 60 ng/ml in the IgG and IgA assays, respectively. Likewise, the specificity of the human IgG subclass antibody assays was confirmed in ELISA against purified human myeloma IgG subclass proteins (ICN Biomedicals, Inc., Irvine, CA), and the assay sensitivity was 15 ng/ml in the IgG1, IgG3 and IgG4 assays, and 120 ng/ml in the IgG2 assay. Two control sera were included to control for assay to assay variation.

Complement dependent bactericidal assay. The bactericidal activity of the human sera was determined as described previously (Chen *et al.*, 1996). In some studies, the sera were absorbed with purified UspA1 or UspA2 prior to the assay. The absorption of specific antibodies from these sera was accomplished by adding the purified proteins to 20 or 50 μg/ml final concentration. The final serum dilution was 1:10. The mixtures were incubated for 2 h at 4°C and the precipitate removed by micro-centrifugation. The purified human antibodies specific for UspA1 and UspA2 were assayed against five *M. catarrhalis* strains in a similar manner.

Statistics. Statistical analysis was performed on logarithmic transformed titers using JMP software (SAS institute, Cary, N.C.). To allow transformation, a value of one half the lowest serum dilution was assigned to sera which contained no detectable titers. Comparison of IgG levels among the age groups was done by analysis of variance, and the relationship of antibody titer and the bactericidal titer was determined by logistic regression. A p value less than 0.05 was considered significant.

Results

Comparison of serum IgG and IgA titers to UspA1 and UspA2 in children and adults. The IgG and IgA antibody titers in the sera from ten children collected longitudinally between 2-18 months of age, as well as the random samples from fifteen 18-36 month old children and twenty-six adults were determined against the whole bacterial cells of the O35E strain, the purified UspA1 and the purified UspA2 by ELISA. IgG titers to all three antigens were detected in almost all the sera (FIG. 9). The IgG titers to UspA1 and UspA2 exhibited strong age-dependent variation when compared to IgG titers to the O35E bacterium (FIG. 9). The adult sera had significantly higher IgG titers to the purified proteins than sera from children of various age groups($p<0.01$). Sera from children at 6-7 months of age had the lowest IgG titers to UspA proteins and the mean titer at this age was significantly lower than that at 2 months .of age ($p<0.05$).

The level of IgA antibodies to UspA1, UspA2 and O35E bacterial cells were age dependent (FIG. 9). A serum IgA titer against the UspA1 and UspA2 was detected in all twenty-six adults and children of 18-36 months of age. For children less than 18 months of age, the proportion exhibiting antigen specific IgA titers increased with age. The mean IgA titers to

UspA1, UspA2 or O35E bacterium in these sera were low for the first 7 months of age but gradually increased thereafter (FIG. 9).

Age-dependent subclass distribution of IgG antibodies to UspA1 and UspA2. The IgG subclass titers to the UspA1 and UspA2 antigens were determined on sera from ten adult sera and thirty-five children's sera. The subclass distribution was found to be age-dependent. The most prominent antibodies to the UspA1 and UspA2 antigens were of the IgG1 and IgG3 subclasses, which were detected in almost all sera. The IgG2 and IgG4 titers were either undetectable or extremely low. Therefore, only data on IgG1 and IgG3 subclasses are reported (FIG. 10). The IgG3 titers against UspA1 or UspA2 in the adult sera were significantly higher than the IgG1 titers ($p<0.05$). The same subclass profile was seen in the sera from the 2 month old children, although the difference between IgG1 and IgG3 titers did not reach statistical significance, probably because of the smaller sample size. Sera from children between 4 and 36 months of age all had a similar subclass profile which was different from that of the adults and 2 month old children. The IgG1 titers in children's sera were either higher than or equivalent to the IgG3 titers. The mean IgG1 titer to either UspA1 or UspA2 was significantly higher than IgG3 titer to the same antigens in these children's sera ($p<0.05$).

Bactericidal activity. The bactericidal titers of seventeen sera representing different age groups were determined (Table XVI). All the adult sera and three out of five sera from the two month old children which had high IgG titers to the UspA proteins had strong bactericidal activity. Sera from 6 month old children had the least bactericidal activity. All five sera from this age group had a marginal bactericidal titer of 50, the lowest dilution assayed. The bactericidal activity of the sera from 18 to 36 month old children was highly variable with titers ranging from less than 50 to 500. There was a significant linear relationship between the bactericidal titers and the IgG antibody titers against both UspA1 and UspA2 by logistic regression analysis ($p<0.01$) (FIG. 11).

TABLE XVI

The level of IgG antibodies to UspA1 and UspA2 from normal human serum and the serum bactericidal activity

Subject[a]	Age	ELISA IgG titer[b]		BC titer[c]
		UspA1	UspA2	
1	2 month	17,127	6,268	500
	6 month	4,273	1,363	50
	15 month	798	250	<50
2	2 month	12,078	12,244	500
	6 month	1,357	878	50
	18 month	14,041	14,488	200
3	2 month	30,283	20,362	500
	6 month	1,077	1,947	50
	18 month	2,478	1,475	<50
4	2 month	2,086	869	<50
	6 month	530	802	50
	18 month	9,767	8,591	200
5	2 month	3,233	2,655	<50
	6 month	2,246	360	50
	18 month	26,693	43,703	500
6	1.5-3 year	4,036	2,686	50
7	1.5-3 year	2,037	1,251	50
8	1.5-3 year	341	251	<50
9	1.5-3 year	2,538	1,200	500
10	1.5-3 year	1078	1,370	500
11	1.5-3 year	1,265	953	50

TABLE XVI (Continued)

Subject[a]	Age	ELISA IgG titer[b]		BC titer[c]
		UspA1	UspA2	
12	adult	161,750	87,180	450
13	adult	873,680	248,290	>1350
14	adult	154,650	146,900	450
15	adult	10,330	7,860	50
16	adult	35,780	31,230	150
17	adult	19,130	132,200	450

[a] Three consecutive samples from subjects 1 through 5 were collected at the stated ages.

[b] ELISA end point titers to purified UspA1 or UspA2 from the O35E strain were determined as the highest serum dilution giving an A_{415} greater than three times the background.

[c] BC titers: bactericidal titer assayed against the O35E strain. Sera were assayed at 1:50, 100, 200, and 500. Bactericidal titer was determined as the highest serum dilution resulting in killing of 50% or more of the bacteria relative to the control. Control bacteria were incubated with test serum and heat inactivated complement serum.

Bactericidal activity of sera absorbed with purified UspA1 or UspA2. Because normal human sera contain antibodies to numerous antigens of *M. catarrhalis* as indicated by western blot, an absorption method was used to determine the contribution of UspA1 and UspA2 specific antibodies towards the bactericidal activity. Six adult sera were absorbed with purified UspA1 or UspA2, and the change in ELISA reactivity to UspA proteins determined. A reduction in ELISA reactivity was seen for all the sera after absorption (Table XVII). Further, absorption with one protein resulted in a reduction of IgG titers to the other protein. Reduction of UspA2 reactivity was of the same degree regardless of whether the absorbent was UspA1 or UspA2. In contrast, there was less reduction in UspA1 reactivity after absorption with UspA2 than with UspA1 (Table XVII). This indicated that antibodies to UspA1 and UspA2 were partially cross-reactive.

TABLE XVII

ELISA titer of adult sera before and after absorption[a]

Absorbent	IgG titers to UspA1 in sample[b]					
	#1	#2	#3	#4	#5	#6
saline	161,750	873,680	154,650	10,330	35,780	19,130
UspA1	2,450	2,210	3,160	1,650	<500	3,010
UspA2	42,620	90,150	33,570	6,420	3,490	4, 130
	IgG titers to UspA2[b]					
saline	87,180	248,290	146,900	7,860	31,230	13,200
UspA1	2,800	2,120	2,700	2,220	<500	<500
UspA2	<500	1,820	3,010	2,960	<500	<500

[a] Absorption: An aliquot of adult serum was diluted and added with purified UspA1 or UspA2 from O35E strain to a final 50 µg/ml protein concentration and final 1:10 serum dilution. The mixtures were incubated at 4°C for 2 h, and precipitates removed by microcentrifugation.

[b] IgG titers against the UspA1 and UspA2 proteins were end point titers determined with a starting serum dilution of 1:500.

The bactericidal titers of the absorbed sera were determined and compared with those seen before absorption (Table XVIII). Absorption with either UspA1 or UspA2 resulted in complete loss of bactericidal activity (<50) for all six sera when assayed against the O35E strain, the strain from which the purified proteins were made (Table XVIII). The bactericidal activity of the absorbed sera was also reduced by at least three fold when assayed against the a heterologous strain 1230-359. Absorption using UspA1 resulted in greater reduction of the bactericidal titer against the heterologous strain in 3 out of 6 samples compared to absorptions using UspA2 (Table XVIII). This result was consistent with the difference in the reductions of ELISA titers to the UspA1 after absorption with the two proteins. Absorption using the combined proteins UspA1 and UspA2 did not result in further reduction of the bactericidal activity compared to UspA1 alone. All six human sera contained antibodies to a 74 kDa OMP from *M. catarrhalis* as determined by western blot analysis, and absorption using the purified 74 kDa protein did not affect the bactericidal activity of either the O35E strain or the 1230-357 strain. This indicated that antibodies to the UspA proteins were the major source of the bactericidal activity against *M. catarrhalis* in adult sera.

TABLE XVIII

Bactericidal titer of the adult human sera before and after absorption[a]

Adsorbent	**Bactericidal titer to O35E strain in sample**[b]					
	#1	**#2**	**#3**	**#4**	**#5**	**#6**
saline	450	>1350	450	50	150	450
UspA1	<50	<50	<50	<50	<50	<50
UspA2	<50	150	<50	<50	<50	<50
	Bactericidal titer to 1230-359 strain[b]					
saline	450	4050	>1350	150	150	450
UspA1	50	150	<50	<50	50	150
UspA2	150	1350	450	<50	50	50

[a] Sera were the same as those described in Table XVII.

[b] Bactericidal titer: The bactericidal activity was measured against the O35E or 1230-359 strains with 3-fold diluted sera starting at 1:50. The highest serum dilution resulting in 50% or greater killing was determined as the bactericidal titer. The purified UspA1 and UspA2 proteins used for absorption were made from the O35E strain.

Because only small volumes of the children sera were available, absorption of these sera was done using a mixture of UspA1 and UspA2 proteins. Absorption resulted in the complete loss or a significant reduction of bactericidal activity in four out of seven sera (Table XIX). The four sera including three from two month old children all had an initial bactericidal titer of 200 or greater prior to absorption. The other three sera, which did not show a change in bactericidal titer upon absorption, all had a marginal titer of 50 before absorption. The reduction in ELISA reactivity to the UspA proteins after absorption confirmed that the antibody concentration had been reduced. This suggested that antibodies specific for the UspA1 and UspA2 proteins in children's sera were also a major source of the bactericidal activity towards *M. catarrhalis*.

TABLE XIX

Bactericidal activity of children's sera before and after absorption with pooled purified UspA1 and UspA2[a]

Sample	Age (months)	Unabsorbed serum		Absorbed serum	
		A_{415}[b]	BC titer[c]	A_{415}[b]	BC titer[c]
1	2	0.84	200	0.29	<50
2	2	0.93	200	0.19	<50
3	2	0.98	500	0.38	50
4	18	0.88	200	0.43	50
5	15	0.66	50	0.25	50
6	18	0.62	50	0.32	50
7	15	0.68	50	0.35	50

[a] Absorption: Each serum was absorbed with a mixture of UspA1 and UspA2 proteins from O35E strain at final protein concentrations of 200, 50 or 20 μg/ml. The same result was seen for all three absorptions of each sample. Only the data from the assay using 20 μg/ml of protein are shown.

[b] A_{415}: The absorbance at 415 nm in ELISA using the mixture of UspA1 and UspA2 as detection antigen. Sera were tested at a 1:300 dilution.

[c] BC titer: Highest serum dilution resulting in 50% or greater killing of the O35E strain in the assay. Sera were assayed at dilutions 1:50, 200, and 500.

Affinity purified antibodies to UspA1 and UspA2: To confirm their cross-reactivity and bactericidal activity, antibodies to UspA1 or UspA2 from adult plasma were isolated by an affinity purification procedure. The purified antibodies reacted specifically with the UspA1 and the UspA2 proteins but not with non-UspA proteins in the O35E lysates in a western blot assay. The purified antibodies to one protein also reacted to the other with almost equivalent titer in ELISA (Table XX). Both antibody preparations exhibited reactivity with five *M. catarrhalis* strains in the whole-cell ELISA and bactericidal assay (Table XXI). The bactericidal titers against all five *M. catarrhalis* strains ranged between 400 and 800, which was equivalent to 0.25-0.50 μg/ml of the protein in the purified antibody preparations (Table XXI).

TABLE XX

Cross-reactivity of affinity purified human antibodies to UspA1 and UspA2 in ELISA

Antibodies purified to[a]	IgG titers against[b]	
	UspA1	UspA2
UspA1	50,468	20,088
UspA2	53,106	52,834

[a] The antibodies were purified from plasma pooled from two healthy adults by immune elution using purified UspA1 or UspA2 from the O35E strain immobilized on nitrocellulose membrane.

[b] ELISA end point titers are the highest antibody dilutions giving an A_{415} greater than three times the background.

TABLE XXI

Whole cell ELISA titer and bactericidal titer of affinity purified human antibodies to UspA1 and UspA2[a]

Assay	Whole cell ELISA titer[b]		BC titer[c]	
strain	Ab to UspA1	Ab to UspA2	Ab to UspA1	Ab to UspA2
O35E	12,553	9,939	400	800
ATCC25238	30,843	29,512	400	400
TTA24	51,511	57,045	800	800
216:96	31,140	23,109	400	400
1230-359	8,495	16,458	800	800

[a] The purified antibody preparations were the same as described in Table XX. The specific reactivities of the purified antibodies to UspA proteins, but not other outer membrane proteins, were confirmed by western blots.

[b] ELISA end point titers are the highest antibody dilutions giving an A_{415} greater than three times the background when assayed against whole bacterial cells.

[c] BC titer: Highest antibody dilution resulting in 50% or greater killing of the bacterial inoculum in the assay. Antibodies (120 μg/ml) were assayed at dilutions 1:100, 200, 400, and 800.

Discussion

Previous studies examining human antibodies to *M. catarrhalis* whole cells or outer membrane proteins usually focused on a single age group. Further, the biological function of the antibodies was left largely undetermined (Chapman *et al.*, 1985), and the antigens eliciting the functional antibodies were not identified. Thus, these previous studies did not provide information as to the role of naturally acquired antibodies in protection against *M. catarrhalis* diseases, nor did they provide clear information as to what antigens are suitable for vaccine development. The data from this study indicate that the IgG antibodies to UspA1 and UspA2 are present in normal human sera and their levels are age-dependent. These antibodies are an important source of serum bactericidal activity in both children and adults.

These data indicated that most children had serum IgG antibodies to both UspA1 and UspA2 at two months of age although the level varied from individual to individual, and the IgG subclass profile in these infant sera was similar to that in adult sera. The infant sera had bactericidal activity. The absorption studies suggested that the bulk of the bactericidal antibodies in these sera were directed against the UspA1 and the UspA2 proteins. These results suggest that the IgG antibodies detected in the two month old children are of maternal origin. This is consistent with the report that umbilical cord serum contains high titers of antibodies to an extract of *M. catarrhalis* whole cells (Ejlertsen *et al.*, 1994b).

Due to the lack of clinical information on the study subjects and small number of subjects examined in this study, it could not be determined whether maternal antibodies against UspA, although bactericidal *in vitro,* were protective in young children. However, at two months of age the children had significantly higher serum IgG titers against the UspA proteins and only a few of these children had a low level of IgA antibodies to *M. catarrhalis* as compared to children at 15-18 months of age. If serum IgA reflects prior mucosal exposure to the bacterium, then most of the children are not infected by *M. catarrhalis* in the first few months of age. One of the reasons may be that the maternal antibodies present in the young children protect them from infection at this age. This is consistent with the finding that young children seldom carry this bacterium and do not develop *M. catarrhalis* disease during the first months of life (Ejlertsen *et al.*, 1994a).

Children may become susceptible to *M. catarrhalis* infection as maternal antibodies wane. In this study, the sera from 6 to 7 month old children had the lowest level of IgG antibodies to the UspA proteins and barely detectable bactericidal titers against whole cells of *M. catarrhalis*. By 15 months of age, nearly all children had serum IgA antibodies to the UspA proteins, and the level of IgA antibodies had significantly increased along with the level of IgG antibodies and bactericidal activity when compared with children of 6 to 7 months of age. This suggested that these children had been exposed to the bacterium and mounted an antibody response. The fifteen sera from the group of 18-36 month old children all had IgG and IgA titers to the UspA proteins and the bactericidal titers varied greatly. The UspA specific IgG antibodies in the older children's sera had different characteristics than the antibodies from the two month old children. First, the IgG1 antibody titer was significantly higher than the IgG3 titer in children's sera, while the opposite was true for the 2 month old children (FIG. 10). Second, most sera from 2 month old children had bactericidal activity, while bactericidal activity was barely detectable in the sera from children of 6 months or older. The low antibody level and the low serum bactericidal activity seen in children between 6-36 months of age is consistent with the epidemiological findings that children of this age group have the highest colonization rate and highest incidence of *M. catarrhalis* disease (Bluestone, 1986; Ejlertsen *et al.*, 1994b; Leinonen *et al.*, 1981; Roitt *et al.*, 1985; Ruuskanen and Heikkinen, 1994; Sethi *et al.*, 1995; Teele *et al.*, 1989).

Adults, a population usually resistant to *M. catarrhalis* infections (Catlin, 1990; Ejlertsen *et al.*, 1994a), were found to have consistently higher levels of IgG antibodies to the UspA proteins as well as higher serum bactericidal activity than children. The bactericidal activity of the adult sera was clearly antibody-mediated since immunoglobulin depleted sera had no activity (Chen *et al.*, 1996), and the antibodies purified from adult plasma exhibited complement dependent bactericidal activity. The antibodies purified from human sera using UspA1 or UspA2 from a single isolate exhibited killing against multiple strains. This result indicates that humans developed bactericidal antibodies toward the conserved epitopes of UspA proteins in response to natural infections.

In all adult samples, the IgG antibodies were primarily of the IgG1 and IgG3 subclasses with IgG3 being higher. This is consistent with previous reports that the IgG3 subclass is a major constituent of the immune response to *M. catarrhalis* in adults and children greater than 4 years of age, but not in younger children (Carson *et al.*, 1994; Goldblatt *et al.*, 1990). Of the four IgG subclasses in humans, IgG3 constitutes only a minor component of the total immunoglobulin in serum. However, IgG3 antibody has the highest affinity to interact with C1q, the initial step in the classic complement pathway leading to elimination of the bacterium by both complement-dependent killing and opsono-phagocytosis (Roitt *et al.*, 1985). Since IgG3 antibody is efficiently transferred across the placenta, it may also confer protective immunity to infants. The data from this study indicate that IgG3 antibody to the UspA proteins is an important component of the immune response to natural infection and has *in vitro* biological activity.

As clinical information related to *M. catarrhalis* infection was not collected for the study subjects, it is unknown how the antibodies to UspA1 or UspA2 were induced. When antibodies made against the UspA proteins in guinea pigs were tested for reactivity with other bacterial species, including *Pseudomonas aeruginosa, Neisseria meningitidis, Neisseria gonorrhoeae, Bordetella pertussis, Escherichia coli,* and nontypable *Haemophilus influenzae* by western blot, no reactivity was detected. This suggests that the antibodies were elicited as a specific response to the UspA antigens of *M. catarrhalis.* This is consistent with the high colonization rate and the endemic nature of this organism in human populations. Since the affinity purified antibodies to the two UspA proteins were cross-reactive, it could not be determined whether the human antibodies were elicited by one or both proteins. It seemed clear that the shared sequence between these two proteins was the main target of the bactericidal antibodies.

In summary, this study demonstrated that antibodies to the two UspA proteins are present in nearly all humans regardless of age. The overall level and subclass distribution of these antibodies, however, were age-dependent. IgG antibodies against UspA1 and UspA2 were cross-reactive, and are a major source of serum bactericidal activity in adults. The level of these antibodies and serum bactericidal activity appears to correlate with age-dependent resistance to *M. catarrhalis* infection. Since humans make an antibody response to many other *M. catarrhalis* antigens in addition to UspA1 and UspA2 after natural infection, it remains to be determined if immunization with one or both UspA proteins will confer adequate protection in susceptible populations.

EXAMPLE VI: UspA2 as a Carrier for Oligosaccharides

UspA2 as a pneumococcal saccharide carrier.

This study demonstrates that UspA2 can serve as a carrier for a pneumococcal saccharide. A seven valent pneumococcal polysaccharide was conjugated to UspA2 by reductive amination. Swiss Webster mice were immunized on wk 0 and wk 4 and a final bleed taken on wk 6. Each mouse was immunized subcutaneously (s.c.) in the abdomen with 1 μg carbohydrate per dose with aluminum phosphate as the adjuvant. A group of mice was immunized with the PP7F- CRM conjugate as a control. The data for the sera from the 6 wk bleed are shown in Table XXII, Table XXIII, and Table XXIV. The conjugate elicited antibodies against both the polysaccharide as well as bactericidal antibodies to *M. catarrhalis*. These results demonstrate that UspA2 can serve a carrier for eliciting antibodies to this pneumococcal saccharide and retain its immunogenicity to UspA2.

TABLE XXII

Titers elicited by 7F conjugates to the pneumococcal polysaccharide 7F

Antigen	IgG ELISA titer to Pn Ps 7F*
PP7F-UspA2 mix	<100
PP7F-UspA2 conjugate	9,514
PP7F-CRM conjugate	61,333

*Pool of sera from five mice.

TABLE XXIII

ELISA titers of sera against whole cells of three *M. catarrhalis* isolates

Immunogen	Strain Tested		
Group[1]	035E	430-345	1230-359
PP7F-UspA2[2] mix	51,409	4,407	9,124
PP7F CRM conjugate	56	49	47
PP7F UspA2 conjugate	31,111	3,529	8,310

[1] Vaccine group consists of 5 Swiss-Webster mice. Each group immunized at wk 0 and wk 3 and serum collected at wk 6.

[2]Vaccine composed of 1 μg Pneumo Type 7F and 1 μg UspA2 adjuvanted with aluminum phosphate.

TABLE XXIV

Complement dependent bactericidal antibodies against three *M. catarrhalis* isolates

Immunogen Group[1]	Strain Tested		
	035E	430- 345	1230- 359
PP7F- UspA2 mix	400	400	400
PP7F CRM conjugate	<100	<100	<100
PP7F UspA2 conjugate	400	400	200

[1]BC_{50} titer is highest serum dilution at which >50% of bacteria were killed as compared to serum from wk 0 mice. The most concentrated serum tested was a 1:100 dilution.

UspA2 as an *Haemophilus* b Oligosaccharide Carrier.

This study demonstrates that UspA2 can serve as a carrier for an *Haemophilus influenzae* type b oligosaccharide (HbO). An HbO sample (average DP=24) was conjugated to UspA2 by aqueous reductive amination in the presence of 0.1% Triton X-100. The ratio of the HbO to UspA2 was 2:1 by weight. Conjugation was allowed to proceed for 3 days at 35°C and the conjugate diafiltered using an Amicon 100K cutoff membrane. The conjugate ratio (mg carbohydrate/mg UspA2) was 0.43:1. The carbohydrate was determined by orcinal assay and the protein by Lowry. The number of hydroxy-ethyl lysines was determined by amino acid analysis and found to be 12.6.

The immunogenicity of the conjugate was examined by immunizing Swiss-Webster mice. The mice were immunized twice on wk 0 and wk 4 with 1 μg of carbohydrate. No adjuvant was used with the conjugate, but was used with UspA2. The sera were pooled and titered. The reactivity toward HbPS by the radioantigen binding assay (RABA) was similar to that seen when HbO is conjugated to CRM_{197} (Table XXV). The whole cell titer toward the homologous *M. catarrhalis* isolate (O35E) was similar to that seen for non-conjugated USpA2 (Table XXVI), as were the bactericidal titers (Table XXVII). Thus, when a carbohydrate antigen that typically elicits a RABA titer less than 0.10 is conjugated to UspA2, it becomes immunogenic.

TABLE XXV

Comparison of immunogenicity of HbO conjugated to UspA2 to HbO conjugated to CRM_{197} to *Haemophilus* b polysaccharide by Radioantigen Binding Assay (RABA)

Week	HbO-CRM_{197}	Hbo-UspA2
0	<0.10	<0.10
3	2.51	2.87
4	4.46	3.56
6	58.66	18.92

TABLE XXVI

Comparison of immunogenicity of HbO-UspA2 conjugate with non-conjugated UspA2 by ELISA against whole cell of the O35E isolate to *M. catarrhalis*

Week	UspA2[a]	Hbo-UspA2
0	<50	<50
4	54,284	17,424
6	345,057	561,513

[a] 5 μg UspA2 adjuvanted with 500 μg aluminum phosphate.

TABLE XXVII

Bactericidal of sera toward two *M. catarrhalis* isolates.

Isolate	UspA2[a]	Hbo-UspA2
O35E	4,500	>4,500
345	n.d.	450

[a] 5 μg UspA2 adjuvanted with 500 μg aluminum phosphate.

n.d. = not determined

EXAMPLE VII: Association of mouse serum sensitivity with expression of mutant forms of UspA2

When bacteria are killed in the presence of serum that lack specific antibodies toward them, it is called "serum sensitivity." In the case of *M. catarrhalis,* the mutants lacking an intact UspA2 protein have been found to be serum sensitive. These mutants were constructed so that one (O35E.1; refer to Example IX for a description of isolates O35E.1, O35E.2 and O35E.12) did not express UspA1, one (O35E.2) did not express UspA2, and one (O35E.12) did not express either protein based on a lack of reactivity with the 17C7 monoclonal antibody. The O35E.2 and O35E.12, however, expressed a smaller truncated form UspA2 (tUspA2) that reacts with antibodies prepared by immunizing mice with purified UspA2. The tUspA2 could be detected in a western blot of bacterial lysates using either polyclonal anti-UspA2 sera or the MAb 13-1. The size of the smaller form was consistent with the gene truncation used for the construction of the two mutants.

This bactericidal capacity was tested by mixing the non-immune mouse sera, a 1:5 dilution of human complement and a suspension of bacteria (Approx. 1000 cfu) in the wells of a microtiter plate. The mouse sera were tested at both a 1:50 and 1:100 dilution. The number of surviving bacteria was then determined by spreading a dilution of this bacterial suspension on agar growth medium. The killing was considered significant when fewer than 50% viable bacteria as cfu's were recovered relative to the samples without mouse sera. Killing by the non-immune sera was seen only for the mutants lacking a "complete" UspA2 (Table XXVIII).

TABLE XXVIII

Bactericidal activity of the pre- immune sera from Balb/c mice

Mutant	Proteins Expressed	Bactericidal Activity of Normal Mouse Sera
035E	UspA1 & UspA2	-
035E.1	UspA2	-
O35E.2	UspA1 & tUspA2	+
035E.12	tUspA2	+

EXAMPLE VIII: Identification of a Decapeptide Epitope in UspA1 that Binds MAb 17C7

It was clear from the work with different strains of *M. catarrhalis* and analyses of their protein sequences of UspA1 that certain epitopic regions must exist which are similar,if not identical, in all of the strains and provide the basis of the immunogenic response in humans. In order to identify such immunogenic epitope(s), peptides spanning the UspA1 region known to contain the binding site for MAb 17C7 were prepared and examined for their ability to bind to MAb 17C7.

Specifically, overlapping synthetic decapeptides, as shown in Table XXIX and FIG. 12, that were N-terminally bound to a membrane composed of derivatized cellulose were obtained from Research Genetics Inc. (Huntsville, AL). After five washes with PBS-Tween containing 5% (w/v) non-fat dry milk, the membrane was subsequently incubated with MAb 17C7 (in the form of hybridoma culture supernatant) overnight at 4°C. Following three washes with PBS-Tween, the membrane was incubated overnight at 4°C with gentle rocking with 10^6 cpm of radioiodinated (specific activity 2×10^7 cpm/μg protein), affinity-purified goat anti-mouse immunoglobulin. The membrane was then washed as before and exposed to X-ray film (Fuji RX safety film, Fuji Industries, Tokyo, Japan).

TABLE XXIX

Decapeptides Used to Identify Binding Site for MAb 17C7

PEPTIDE #	PEPTIDE SEQUENCE	
9	SGRLLDQKAD	SEQ ID NO:81
10	QKADIDNNIN	SEQ ID NO:82
11	NNINNIYELA	SEQ ID NO:83
12	NNIYELAQQQ	SEQ ID NO:84
13	YELAQQQDQH	SEQ ID NO:18
14	AQQQDQHSSD	SEQ ID NO:85
15	QDQHSSDIKT	SEQ ID NO:86
16	HSSDIKTLKN	SEQ ID NO:87
17	DIKTLKNNVE	SEQ ID NO:88
18	TLKNNVEEGL	SEQ ID NO:89
19	EEGLLDLSGR	SEQ ID NO:90
20	LSGRLIDQKA	SEQ ID NO:91
21	DQKADIAKNQ	SEQ ID NO:92
22	AKNQADIAQN	SEQ ID NO:93
23	IAQNQTDIQD	SEQ ID NO:94
24	DIQDLAAYNE	SEQ ID NO:95

It is clear from the dot blot results shown in the autoradiograph (FIG. 13) that peptide 13, YELAQQQDQH (SEQ ID NO:18) exhibited optimal binding of MAb 17C7 with peptide 14 (SEQ ID NO:85) exhibiting less than optimal binding. This same peptide (SEQ ID NO:18) is present in UspA2 which explains why both proteins bind to MAb 17C7.

Interestingly, peptide 12 shows no binding and binding by peptides 15, 16, 19, 22, 23 is probably non-specific. Thus, a comparison of peptides 12, 13, and 14 yields the conclusion that the 7-mer AQQQDQH (SEQ ID NO:17) is an essential epitope for MAb 17C7 to bind to UspA1 and UspA2. This conclusion is in agreement with the current understanding that an immunogenic epitope may comprise as few as five, six or seven amino acid residues.

Example IX: Phenotypic Effect of Isogenic *uspA1* and *uspA2* Mutations on *M. catarrhalis* Strain O35E

Materials and Methods

Bacterial strains, plasmids and growth conditions. The bacterial strains and plasmids used in this study are listed in Table XXX. *M. catarrhalis* strains were routinely grown at 37°C on Brain-Heart Infusion (BHI) agar plates (Difco Laboratories, Detroit, MI) in an atmosphere of 95% air-5% CO_2 supplemented, when necessary, with kanamycin (20 μg/ml) (Sigma Chemicals Co., St. Louis, MO) or chloramphenicol (0.5 μg/ml) (Sigma), or in BHI broth. The BHI broth used to grow *M. catarrhalis* cells for attachment assays was sterilized by filtration. *Escherichia coli* strains were cultured on Luria-Bertani (LB) agar plates (Maniatis *et al.*, 1982) supplemented, when necessary, with ampicillin (100 μg/ml), kanamycin (30 μg/ml), or chloramphenicol (30 μg/ml).

TABLE XXX

Bacterial Strains and Plasmids Used in this Study

Strain or plasmid	Description	Source or reference
M. catarrhalis		
035E	Wild-type isolate from middle ear fluid	Helminen *et al.*, 1994
O35E.1	Isogenic mutant of O35E with a kan cartridge in the *uspA1* structural gene	Aebi *et al.*, 1997
O35E.2	Isogenic mutant of O35E with a kan cartridge in the *uspA2* structural gene	Aebi *et al.*, 1997

TABLE XXX (Continued)

Strain or plasmid	Description	Source or reference
O35E.12	Isogenic mutant of O35E with a kan cartridge in the *uspA2* structural gene and a cat cartridge in the *uspA1* structural gene	This study
P-44	Wild-type isolate that exhibits rapid hemagglutination	Soto-Hernandez *et al.*, 1989
P-48	Wild-type isolate that exhibits slow hemagglutination	Soto-Hernandez *et al.*, 1989
Escherichia coli		
DH5α	Host for cloning studies	Stratagene
Plasmids		
pBluescript II	Cloning vector; Amp^r	Stratagene
p*USPA1*	pBluescript II SK+ with a 2.7 kb insert containing most of the *uspA1* gene of *M. catarrhalis* strain O35E	Aebi *et al.*, 1997
p*USPA1*CAT	p*USPA1* with a cat cartridge replacing the 0.6 kb *Bgl*II fragment of the *uspA1* gene	This study

Characterization of outer membrane proteins. Whole cell lysates and outer membrane vesicles of *M. catarrhalis* strains were prepared as described (Murphy and Loeb, 1989; Patrick *et al.*, 1987). Proteins present in these preparations were resolved by SDS-PAGE and detected by staining with Coomassie blue or by western blot analysis as described (Helminen *et al.*, 1993a).

Monoclonal antibodies (MAbs). MAb 17C7, a murine IgG antibody that reacts with a conserved epitope of both UspA1 and UspA2 from *M. catarrhalis* strain O35E, as described in earlier examples herein, was used for immunologic detection of these proteins. MAb 17C7 was used in the form of hybridoma culture supernatant fluid in western blot analysis and in the indirect antibody-accessibility assay. MAb 3F12, an IgG MAb specific for the major outer membrane protein of *Haemophilus ducreyi* (Klesney-Tait *et al.*, 1997), was used as a negative control in the indirect antibody-accessibility assay.

Molecular cloning methods. Chromosomal DNA of *M. catarrhalis* strain O35E was used as the template in a polymerase chain reaction (PCR™) system together with oligonucleotide primers derived from either just after the start of the strain O35E *uspA1* open reading frame (*i.e.*, P1 in FIG. 14) or just after the end of this open reading frame (*i.e.*, P2 in FIG. 14). These primers were designed to contain a *Bam*HI restriction site at their 5′-end. The sequence of these primers was:

P1 - 5′-CGGGATCCGTGAAGAAAAATGCCGCAGGT-3′ (SEQ ID NO:96);

P2 - 5′-CGGGATCCCGTCGCAAGCCGATTG-3′ (SEQ ID NO:97).

DNA fragments were amplified using a PTC 100 Programmable Thermal Controller (MJ Research, Inc., Cambridge, MA) and the GeneAmp PCR™ kit (Roche Molecular Systems, Inc., Branchburg, NJ). PCR™ products were extracted from 0.7% agarose gel slices using the Qiaex Gel Extraction Kit (Qiagen, Inc., Chadsworth, CA) and digested with *Bam*HI (New England Biolabs, Inc., Beverly, MA) for subsequent ligation into the *Bam*HI site of pBluescript II SK+ (Stratagene, La Jolla, CA). Ligation reactions were performed with overnight incubation at 16°C using T4 DNA ligase (Gibco BRL, Inc., Gaithersburg, MD). Competent *E. coli* DH5α cells were transformed with the ligation reaction mixture according to a standard heat-shock procedure (Sambrook *et al.*, 1989) and the desired recombinants were selected by culturing in the presence of an appropriate antimicrobial compound. The 1.3 kb chloramphenicol (*cat*) resistance cartridge was prepared by excision (using *Bam*HI) from pUCΔECAT (Wyeth-Lederle, Rochester, NY). The *cat* cartridge was subsequently ligated into *Bgl*II restriction sites located in the mid-portion of cloned segment from the *uspA1* gene and, after transformation of competent *E. coli* DH5 cells, recombinant clones were identified by selection on solidified media containing chloramphenicol.

Transformation of *M. catarrhalis*. The electroporation method used for transformation of *M. catarrhalis* strain O35E has been described in detail (Helminen *et al.*, 1993b). Briefly, a 30-ml portion of a logarithmic-phase broth culture (10^9 colony forming units [cfu]/ml) was harvested by centrifugation, washed three times with 10% (v/v) glycerol in distilled water, and resuspended in 100 μl of the same solution. A 20-μl portion of these cells was electroporated with 5 μg of linear DNA (*i.e.*, the truncated *uspA1* gene containing the *cat* cartridge) in 5 μl of water in a microelectroporation chamber (Cel-Porator Electroporation system; Bethesda Research Laboratories, Gaithersburg, MD) by applying a field strength of 16.2 kV over a distance of 0.15 cm. Following electroporation, the cell suspension was transferred to 1 ml of BHI broth and incubated with shaking at 37°C for 90 min. Ten 100-μl portions were then spread on BHI agar plates containing the appropriate antimicrobial compound.

Southern blot analysis. Chromosomal DNA purified from wild-type and mutant *M. catarrhalis* strains strains was digested with either *Pvu*II or *Hind*III (New England Biolabs) and Southern blot analysis was performed as described (Sambrook *et al.*, 1989). Double-stranded DNA probes were labeled with ^{32}P by using the Random Primed DNA Labeling Kit (Boehringer-Mannheim, Indianapolis, IN).

Indirect antibody-accessibility assay. Overnight BHI broth cultures of *M. catarrhalis* strain O35E and its isogenic mutants were diluted in PBS buffer containing 10% (v/v) fetal bovine serum and 0.025% (w/v) sodium azide (PBS-FBS-A) to density of 110 Klett units (ca. 10^9 cfu/ml) as measured with a Klett-Summerson colorimeter (Klett Manufacturing Co., New York, NY). Portions (100 μl) of this suspension were added to 1 ml of MAb 17C7 or MAb 3F12 culture supernatant. After incubation at 4°C for one hour with gentle agitation, the bacterial cells were washed once and suspended in 1 ml of PBS-FBS-A. Affinity-purified goat anti-mouse immunoglobulin, radiolabeled with ^{125}I to a specific activity of 10^8 cpm per μg, was added and the mixture was incubated for one hour at 4°C with gentle agitation. The cells were then washed four times with 1 ml of PBS-FBS-A, suspended in 500 μl of triple detergent

(Helminen *et al.*, 1993a) and transferred to glass tubes. The radioactivity present in each sample was measured by using a gamma counter.

Autoagglutination and hemagglutination assays. The ability of *M. catarrhalis* strains to autoagglutinate was assessed using bacterial cells grown overnight on a BHI agar plate. These cells were resuspended in PBS to a turbidity of 400 Klett units in a glass tube and subsequently allowed to stand at room temperature for ten minutes at which time the turbidity of this suspension was again determined. Rapid and slow autoagglutination were defined as turbidities of less that and greater than 200 Klett units, respectively, after 10 minutes. The hemagglutination slide assay using heparinized human group O Rh^+ erythrocytes was performed as previously described (Soto-Hernandez *et al.*, 1989).

Serum bactericidal assay. Complement-sufficient normal adult human serum was prepared by standard methods. Complement inactivation was achieved by heating the serum for 30 min at 56°C. A *M. catarrhalis* broth culture in early logarithmic phase was diluted in Veronal-buffered saline containing 0.10% (w/v) gelatin (GVBS) to a concentration of $1\text{-}2 \times 10^5$ cfu/ml, and 20 μl portions were added to 20 μl of native or heat-inactivated normal human serum together with 160 μl of Veronal-buffered saline containing 5 mM $MgCl_2$ and 1.5 mM $CaCl_2$. This mixture was incubated at 37°C in a stationary water bath. At time 0 and at 15 and 30 min, 10 μl aliquots were removed, suspended in 75 μl of BHI broth and spread onto prewarmed BHI agar plates.

Adherence assay. A method used to measure adherence of *Haemophilus influenzae* to Chang conjunctival cells *in vitro* (St. Geme III and Falkow, 1990) was adapted for use with *M. catarrhalis*. Briefly, $2\text{-}3 \times 10^5$ HEp-2 cells (ATCC CCL 23) or Chang conjunctival cells (ATCC CCL 20.2) were seeded into each well in a 24-well tissue culture plate (Corning-Costar) and incubated for 24 h before use. A 0.3 ml volume from an antibiotic-free overnight culture of *M. catarrhalis* was inoculated into 10 ml of fresh BHI medium lacking antibiotics and this culture was subsequently allowed to grow to a concentration of approximately 5×10^8 cfu/ml (120 Klett units) with shaking in a gyrotory water bath. The culture was harvested by centrifugation at 6,000 × g at 4-8°C for 10 min. The supernatant was discarded and a Pasteur pipet was used to gently resuspend the bacterial cells in 5 ml of pH 7.4 phosphate-buffered saline (PBS) or PBS containing 0.15% (w/v) gelatin (PBS-G). The bacterial cells were centrifuged again and this final pellet was gently resuspended in 6-8 ml of PBS or PBS-G.

Portions (25 μl) of this suspension (10^7 CFU) were inoculated into the wells of a 24-well tissue culture plate containing monolayers of HEp-2 or Chang cells. These tissue culture plates were centrifuged for 5 min at 165 × g and then incubated for 30 min at 37°C. Non-adherent bacteria were removed by rinsing the wells gently five times with PBS or PBS-G, and the epithelial cells were then released from the plastic support by adding 200 μl of PBS containing 0.05% trypsin and 0.02% EDTA. This cell suspension was serially diluted in PBS or PBS-G and spread onto BHI plates to determine the number of viable *M. catarrhalis* present. Adherence was expressed as the percentage of bacteria attached to the human cells relative to the original inoculum added to the well.

Results

Construction of an isogenic *M. catarrhalis* mutant lacking expression of both UspA1 and UspA2. Construction of *M. catarrhalis* mutants lacking the ability to express either UspA1 (mutant strain O35E.1) or UspA2 (mutant strain O35E.2) has been described in previous examples (Aebi *et al.*, 1997). For constructing a double mutant that lacked expression of both UspA1 and UspA2, the 0.6 kb *Bgl*II fragment of pUSPA1 (FIG. 14A) was replaced by a *cat* cassette, yielding the recombinant plasmid p*USPA1*CAT. Using the primers P1 and P2, the 3.2 kb insert of p*USPA1*CAT was amplified by PCR™. This PCR™ product was used to electroporate the kanamycin-resistant *uspA2* strain O35E.2 and yielded the chloramphenicol- and kanamycin-resistant transformant O35E.12, a putative *uspA1 uspA2* double mutant.

Southern blot analysis was used to confirm that strains O35E.1, O35E.2, and O35E.12 were isogenic mutants and that allelic exchange had occurred properly, resulting in replacement of the wild-type *uspA1* or *uspA2* gene, or both, with the mutated allele. Chromosomal DNA preparations from the wild-type parent strain O35E, the *uspA1* mutant O35E.1, the *uspA2* mutant O35E.2, and the putative *uspA1 uspA2* mutant strain O35E.12 were digested to completion with *Pvu*II and probed in Southern blot analysis with DNA fragments derived from these two *M. catarrhalis* genes or with the *kan* cartridge. For probing with the *cat* cartridge, chromosomal DNA from strain O35E.12 was digested with *Hind*III.

The *uspA1*-specific DNA probe was obtained by PCR™-based amplification of *M. catarrhalis* strain O35E chromosomal DNA using the primers P3 and P4 (FIG. 14A). A 500-bp *uspA2*-specific DNA fragment was amplified from O35E chromosomal DNA by PCR™ with the primers P5 and P6 (FIG. 14B). Use of these two gene-specific probes together with the *kan* and *cat* cartridges in Southern blot analysis confirmed that strain O35E.12 was a *uspA1 uspA2* double mutant.

Characterization of selected proteins expressed by the wild-type and mutant *M. catarrhalis* strains. Proteins present in outer membrane vesicles extracted from the the wild-type and these three mutant strains were resolved by SDS-PAGE and either stained with Coomassie blue (FIG. 15A) or probed with MAb 17C7 in western blot analysis (FIG. 15B). The wild-type parent strain O35E possessed a very high molecular weight band detectable by Coomassie blue staining (FIG. 15A, lane 1, closed arrow) that was also similarly abundant in the *uspA1* mutant O35E.1 (FIG. 15A, lane 2). The *uspA2* mutant O35E.2 (FIG. 15A, lane 3) had a much reduced level of expression of a band in this same region of the gel; this band was not visible at all in the *uspA1 uspA2* double mutant O35E.12 (FIG. 2, panel A, lane 4).

Western blot analysis revealed that the wild-type strain (FIG. 15B, lane 1) expressed abundant amounts of MAb 17C7-reactive antigen, most of which had a very high molecular weight, in excess of 220,000. The wild-type strain also exhibited discrete antigens with apparent molecular weights of approximately 120,000 and 85,000 which bound this MAb (FIG. 15B, lane 1, open and closed arrows, respectively). The *uspA1* mutant O35E.1 (FIG. 15B, lane 2) lacked expression of the 120 kDa antigen, which was proposed to be the monomeric form of UspA1, but still expressed the 85 kDa antigen. The amount of very high molecular weight MAb 17C7-reactive antigen expressed by this *uspA1* mutant appeared to be equivalent to that expressed by the wild-type strain. The *uspA2* mutant O35E.2 (FIG. 15B, lane 3) expressed the 120 kDa antigen but lacked expression of the 85 kDa antigen which was proposed to be the monomeric form of the UspA2 protein. In contrast to the *uspA1* mutant, the *uspA2* mutant had relatively little very high molecular weight antigen reactive with MAb 17C7. Finally, the *uspA1 uspA2* double mutant O35E.12 (FIG. 15B, lane 4) expressed no detectable MAb 17C7-reactive antigens.

Binding of MAb 17C7 to whole cells of the wild-type and mutant strains. The indirect antibody-accessibility assay was used to determine whether both UspA1 and UspA2 are exposed on the surface of *M. catarrhalis* and accessible to antibody. Whole cells of both the wild-type strain O35E and the *uspA1* mutant O35E.1 bound similar amounts of MAb 17C7 (Table XXXI). This result suggested that *UspA2* is expressed on the surface of *M. catarrhalis*, or at least on the surface of the *uspA1* mutant. The *uspA2* mutant O35E.2 bound substantially less MAb 17C7 than did the wild-type strain, but the level of binding was still at least an order of magnitude greater than that obtained with an irrelevant IgG Mab directed against a *H. ducreyi* outer membrane protein (Table XXXI). As expected from the western blot analysis, the *uspA1 uspA2* double mutant O35E.12 did not bind MAb 17C7 at a level greater than obtained with the negative controls involving the *H. ducreyi*-specific MAb (Table XXXI).

TABLE XXXI

Binding of MAb 17C7 to the Surface of Wild-Type and Mutant Strains of *M. catarrhalis*

	Binding[a] of	
Strain	**MAb 17C7**	**MAb 3F12b**
O35E (wild-type)	145,583[c]	4,924
O35E.1 (*uspA1* mutant)	154,119	4,208
O35E.2 (*uspA2* mutant)	96,721	4,455
O35E.12 (*uspA1 uspA2* double mutant)	6,081	3,997

[a] Counts per min of ^{125}I-labeled goat anti-mouse immunoglobulin bound to MAbs attached to the bacterial cell surface, as determined in the indirect antibody-accessibility assay.

[b] MAb 3F12, a murine IgG antibody specific for a H. ducreyi outer membrane protein (Klesney-Tait *et al.*, 1997), was included as a negative control.

[c] The values represent the mean of two independent studies.

Characterization of the growth, autoagglutination, and hemagglutination properties of the wild-type and mutant strains. The colony morphology of these three mutant strains grown on BHI agar plates did not differ from that of the wild-type strain parent strain. Similarly, the rate and extent of growth of all four of these strains in BHI broth were very similar if not identical (FIG. 16). In an autoagglutination assay performed as described in above in the Materials and Methods section of this example, all four strains exhibited the same rate of autoagglutination. Finally, there was no detectable difference between the wild-type parent and the three mutants in a hemagglutination assay using human group O erythrocytes (Soto-Hernandez *et al.*, 1989). Control hemagglutination studies were performed using a pair of *M. catarrhalis* isolates (*i.e.*, strains P-44 and P48) previously characterized as having rapid or slow rates, respectively, of hemagglutination (Soto-Hernandez *et al.*, 1989).

Effect of the *uspA1* and *uspA2* mutations on the ability of *M. catarrhalis* to adhere to human cells. Preliminary studies revealed that the wild-type *M. catarrhalis* strain O35E adhered readily to HeLa cells, HEp-2 cells, and Chang conjunctival cells *in vitro*. To determine whether lack of expression of UspA1 or UspA2 affected this adherence ability, the wild-type and the three mutant strains were first used in an attachment assay with Hep-2 cells. In this set of studies, PBS was used as the diluent for washing the HEp-2 cell monolayers and for serial dilution of the trysinized HEp-2 cell monolayer at the completion of the assay. Both the wild-type strain and the *uspA2* mutant O35E.2 exhibited similar levels of attachment to HEp-2 monolayers (Table XXXI). The *uspA1* mutant O35E.1, however, was less able to adhere to these HEp-2 cells; lack of expression of UspA1 reduced the level of attachment by approximately six-fold (Table XXXII). The *uspA1 uspA2* double mutant O35E.12 exhibited a similarly reduced level of attachment (Table XXXII).

TABLE XXXII

Adherence of Wild-Type and Mutant Strains of *M. catarrhalis* to HEp-2 and Chang Conjunctival Cells *in vitro*

Strain	Adherence[a] to			
	HEp-2 cells[b]		Chang cells[c]	
O35E (wild-type)	14.7 ± 4.9		51.4 ± 30.8	
O35E.1 (*uspA1* mutant)	2.4 ± 0.9	(0.006[d])	0.8 ± 0.5	(0.002[d])
O35E.2 (*uspA2* mutant)	19.1 ± 7.0	(0.213[d])	55.9 ± 16.7	(0.728[d])
O35E.12 (*uspA1 uspA2* double mutant)	2.3 ± 1.8	(0.011[d])	0.6 ± 0.2	(0.002[d])

[a] Adherence is expressed as the percentage of the original inoculum that was adherent to the human epithelial cells at the end of the 30 min incubation period. Each number represents the mean (± S.D.) of two independent studies.

[b] PBS was used for washing of the monolayers and for serial dilutions of adherent *M. catarrhalis.*

[c] PBS-G was used for washing of the monolayers and for serial dilutions of adherent *M. catarrhalis.*

[d] P value when compared to the wild-type strain O35E using the two-tailed Student t-test.

Control studies revealed, however, that *M. catarrhalis* cells did not survive well in the PBS used for washing of the HEp-2 monolayer and serial dilution of the attached *M. catarrhalis* organisms. When 10^8 CFU of the wild-type and mutant *M. catarrhalis* strains were suspended in PBS, serially diluted, and allowed to stand for 30 min on ice, the viable number of bacteria decreased to 10^7 CFU. In contrast, when PBS containing 0.15% (w/v) gelatin (PBS-G) was used for this same type of experiment, there was no reduction in the viability of these *M. catarrhalis* strains over the duration of the experiment. When the HEp-2 cell-based attachment studies were repeated using PBS-G for washing the HEp-2 cell monolayer and as the diluent, there was only a three-fold reduction in adherence of the *uspA1* mutant relative to that obtained with the wild-type parent strain. This finding suggested that the original six-fold difference in attachment ability observed between the wild-type and *uspA1* mutant strain may have been attributable in part to viability problems caused by the use of the PBS wash and diluent.

Subsequent studies using Chang conjunctival cells as the target for bacterial attachment together with a PBS-G wash and diluent revealed a substantial difference in the attachment abilities of the wild-type strain and the *uspA1* mutant (Table XXXII). Whereas the wild-type and *uspA2* mutant exhibited similar levels of attachment to the Chang cells, the extent of attachment of the *uspA1* mutant was nearly two orders of magnitude less than that of the wild-type parent strain. The *uspA1 uspA2* double mutant also exhibited a much reduced level of attachment similar to obtained with the *uspA1* mutant (Table XXXII).

Effect of the *uspA1* and *uspA2* mutations on serum resistance of *M. catarrhalis*. Similar to the majority of disease isolates of *M. catarrhalis* (Hol *et al.*, 1993; 1995; Verduin *et al.*, 1994), the wild-type strain O35E was resistant to killing by normal human serum *in vitro* (Helminen *et al.*, 1993b). To examine the effect of the lack of expression of UspA1 or UspA2 on serum resistance, the wild-type strain and the three mutant strains were tested in a serum bactericidal assay. Both the wild-type strain (FIG. 17, closed diamonds) and the *uspA1* mutant O35E.1 (FIG. 17, closed triangles) were able to grow in the presence of normal human serum, indicating that lack of expression of UspA1 did not adversely affect the ability of strain O35E.1 to resist killing by normal human serum. However, both the *uspA2* mutant O35E.2 (FIG. 17, closed circles) and the *uspA1 uspA2* double mutant O35E.12 (FIG. 17, closed squares), having in common the lack of expression of UspA2, were readily killed by normal human serum. Heat-based inactivation of the complement system present in this normal human serum eliminated the ability of this serum to kill these latter two mutants (FIG. 17, open circles and squares).

All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Board of Regents, The University of Texas System
(B) STREET: 201 W. 7th Street
(C) CITY: Austin
(D) STATE: Texas
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 78701

(ii) TITLE OF INVENTION: UspA1 AND UspA2 ANTIGENS OF MORAXELLA CATARRHALIS

(iii) NUMBER OF SEQUENCES: 98

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/033,598
(B) FILING DATE: 20-DEC-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
1               5                   10                  15

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

Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
        35                  40                  45

Gln Ala Thr Asn Ser Lys Gly Thr Gly Ala His Ile Gly Val Asn Asn
    50                  55                  60

Asn Asn Glu Ala Pro Gly Ser Tyr Ser Phe Ile Gly Ser Gly Gly Tyr
65                  70                  75                  80

Asn Lys Ala Asp Arg Tyr Ser Ala Ile Gly Gly Gly Leu Phe Asn Lys
                85                  90                  95
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Ala Thr Asn Glu Tyr Ser Thr Ile Val Gly Gly Gly Tyr Asn Lys Ala
            100                 105                 110

Glu Gly Arg Tyr Ser Thr Ile Gly Gly Gly Ser Asn Asn Glu Ala Thr
        115                 120                 125

Asn Glu Tyr Ser Thr Ile Val Gly Gly Asp Asp Asn Lys Ala Thr Gly
    130                 135                 140

Arg Tyr Ser Thr Ile Gly Gly Gly Asp Asn Asn Thr Arg Glu Gly Glu
145                 150                 155                 160

Tyr Ser Thr Val Ala Gly Gly Lys Asn Asn Gln Ala Thr Gly Thr Gly
                165                 170                 175

Ser Phe Ala Ala Gly Val Glu Asn Gln Ala Asn Ala Glu Asn Ala Val
            180                 185                 190

Ala Val Gly Lys Lys Asn Ile Ile Glu Gly Glu Asn Ser Val Ala Ile
        195                 200                 205

Gly Ser Glu Asn Thr Val Lys Thr Glu His Lys Asn Val Phe Ile Leu
    210                 215                 220

Gly Ser Gly Thr Thr Gly Val Thr Ser Asn Ser Val Leu Leu Gly Asn
225                 230                 235                 240

Glu Thr Ala Gly Lys Gln Ala Thr Thr Val Lys Asn Ala Glu Val Gly
                245                 250                 255

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

Val Val Ser Val Gly Ser Glu Gly Gly Glu Arg Gln Ile Val Asn Val
        275                 280                 285

Gly Ala Gly Gln Ile Ser Asp Thr Ser Thr Asp Ala Val Asn Gly Ser
    290                 295                 300

Gln Leu His Ala Leu Ala Thr Val Val Asp Asp Asn Gln Tyr Asp Ile
305                 310                 315                 320

Val Asn Asn Arg Ala Asp Ile Leu Asn Asn Gln Asp Asp Ile Lys Asp
                325                 330                 335

Leu Gln Lys Glu Val Lys Gly Leu Asp Asn Glu Val Gly Glu Leu Ser
            340                 345                 350

Arg Asp Ile Asn Ser Leu His Asp Val Thr Asp Asn Gln Gln Asp Asp
        355                 360                 365

Ile Lys Glu Leu Lys Arg Gly Val Lys Glu Leu Asp Asn Glu Val Gly
    370                 375                 380

Val Leu Ser Arg Asp Ile Asn Ser Leu His Asp Asp Val Ala Asp Asn
385                 390                 395                 400
```

```
Gln Asp Asp Ile Ala Lys Asn Lys Ala Asp Ile Lys Gly Leu Asn Lys
                405                 410                 415

Glu Val Lys Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg Asp Ile
            420                 425                 430

Gly Ser Leu His Asp Asp Val Ala Thr Asn Gln Ala Asp Ile Ala Lys
        435                 440                 445

Asn Gln Ala Asp Ile Lys Thr Leu Glu Asn Asn Val Glu Glu Glu Leu
    450                 455                 460

Leu Asn Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn
465                 470                 475                 480

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
                485                 490                 495

Ser Asp Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Asp
            500                 505                 510

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
        515                 520                 525

Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr
    530                 535                 540

Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp
545                 550                 555                 560

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
                565                 570                 575

Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
            580                 585                 590

Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser
        595                 600                 605

Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala
    610                 615                 620

Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly
625                 630                 635                 640

Glu Ala Leu Val Glu Gln Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly
                645                 650                 655

Phe Ala Ala His Ala Asp Ile Gln Asp Lys Gln Ile Leu Gln Asn Gln
            660                 665                 670

Ala Asp Ile Thr Thr Asn Lys Thr Ala Ile Glu Gln Asn Ile Asn Arg
        675                 680                 685

Thr Val Ala Asn Gly Phe Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala
    690                 695                 700
```

```
Thr Asn Lys Gln Glu Leu Ile Leu Gln Asn Asp Arg Leu Asn Arg Ile
705                 710                 715                 720

Asn Glu Thr Asn Asn Arg Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr
                725                 730                 735

Ala Leu Lys Glu Gln Gly Gln His Phe Asn Asn Arg Ile Ser Ala Val
            740                 745                 750

Glu Arg Gln Thr Ala Gly Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr
        755                 760                 765

Leu Pro Ser Pro Ser Arg Ala Gly Glu His His Val Leu Phe Gly Ser
    770                 775                 780

Gly Tyr His Asn Gly Gln Ala Ala Val Ser Leu Gly Ala Ala Gly Leu
785                 790                 795                 800

Ser Asp Thr Gly Lys Ser Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp
                805                 810                 815

Ala Gly Gly Leu Ser Gly Gly Val Gly Gly Ser Tyr Arg Trp Lys
            820                 825                 830
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
ATCAGCATGT GAGCAAATGA CTGGCGTAAA TGACTGATGA GTGTCTATTT AATGAAAGAT    60

ATCAATATAT AAAAGTTGAC TATAGCGATG CAATACAGTA AAATTTGTTA CGGCTAAACA   120

TAACGACGGT CCAAGATGGC GGATATCGCC ATTTACCAAC CTGATAATCA GTTTGATAGC   180

CATTAGCGAT GGCATCAAGT TGTGTTGTTG TATTGTCATA TAAACGGTAA ATTTGGTTTG   240

GTGGATGCCC CATCTGATTT ACCGTCCCCC TAATAAGTGA GGGGGGGGGG GAGACCCCAG   300

TCATTTATTA GGAGACTAAG ATGAATAAAA TTTATAAAGT GAAGAAAAAT GCCGCAGGTC   360

ACTTGGTGGC ATGTTCTGAA TTTGCCAAAG GTCATACCAA AAAGGCAGTT TTGGGCAGTT   420

TATTGATTGT TGGGGCGTTG GGCATGGCAA CGACGGCGTC TGCACAAGCA ACCAACAGCA   480

AAGGCACAGG CGCGCACATC GGTGTTAACA ATAACAACGA AGCCCCAGGC AGTTACTCTT   540

TCATCGGTAG TGGCGGTTAT AACAAAGCCG ACAGATACTC TGCCATCGGT GGTGGCCTTT   600

TTAACAAAGC CACAAACGAG TACTCTACCA TCGTTGGTGG CGGTTATAAC AAAGCCGAAG   660
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GCAGATACTC TACCATCGGT GGTGGCAGTA ACAACGAAGC CACAAACGAG TACTCTACCA 720

TCGTTGGTGG CGATGACAAC AAAGCCACAG GCAGATACTC TACCATCGGT GGTGGCGATA 780

ACAACACACG CGAAGGCGAA TACTCAACCG TCGCAGGGGG CAAGAATAAC CAAGCCACAG 840

GTACAGGTTC ATTTGCCGCA GGTGTAGAGA ACCAAGCCAA TGCCGAAAAC GCCGTCGCCG 900

TGGGTAAAAA GAACATTATC GAAGGTGAAA ACTCAGTAGC CATCGGCTCT GAGAATACCG 960

TTAAAACAGA ACACAAAAAT GTCTTTATTC TTGGCTCTGG CACAACAGGT GTAACGAGTA 1020

ACTCAGTGCT ACTGGGTAAT GAGACCGCTG GCAAACAGGC GACCACTGTT AAGAATGCCG 1080

AAGTGGGTGG TCTAAGCCTA ACAGGATTTG CAGGGGAGTC AAAAGCTGAA AACGGCGTAG 1140

TTTCTGTGGG TAGTGAAGGC GGTGAGCGTC AAATCGTTAA TGTTGGTGCA GGTCAGATCA 1200

GTGACACCTC AACAGATGCT GTTAATGGCT CACAGCTACA TGCTTTGGCC ACAGTTGTTG 1260

ATGACAACCA ATATGACATT GTTAACAACC GAGCTGACAT TCTTAACAAC CAAGATGATA 1320

TCAAAGATCT TCAGAAGGAG GTGAAAGGTC TTGATAATGA GGTGGGTGAA TTAAGCCGAG 1380

ACATTAATTC ACTTCATGAT GTTACTGACA ACCAACAAGA TGACATCAAA GAGCTTAAGA 1440

GGGGGGTAAA AGAGCTTGAT AATGAGGTGG GTGTATTAAG CCGAGACATT AATTCACTTC 1500

ATGATGATGT TGCTGACAAC CAAGATGACA TTGCTAAAAA CAAAGCTGAC ATCAAAGGTC 1560

TTAATAAGGA GGTGAAAGAG CTTGATAAGG AGGTGGGTGT ATTAAGCCGA GACATTGGTT 1620

CACTTCATGA TGATGTTGCC ACCAACCAAG CTGACATTGC TAAAAACCAA GCGGATATCA 1680

AAACACTTGA AAACAATGTC GAAGAAGAAT TATTAAATCT AAGCGGTCGC CTGCTTGATC 1740

AGAAAGCGGA TATTGATAAT AACATCAACA ATATCTATGA GCTGGCACAA CAGCAAGATC 1800

AGCATAGCTC TGATATCAAA ACACTTAAAA ACAATGTCGA AGAAGGTTTA TTGGATCTAA 1860

GCGGTCGCCT CATTGATCAA AAAGCAGATA TTGCTAAAAA CCAAGCTGAC ATTGCTCAAA 1920

ACCAAACAGA CATCCAAGAT CTGGCCGCTT ACAATGAGCT ACAAGACCAG TATGCTCAAA 1980

AGCAAACCGA AGCGATTGAC GCTCTAAATA AAGCAAGCTC TGAGAATACA CAAAACATTG 2040

CTAAAAACCA AGCGGATATT GCTAATAACA TCAACAATAT CTATGAGCTG GCACAACAGC 2100

AAGATCAGCA TAGCTCTGAT ATCAAAACCT TGGCAAAAGT AAGTGCTGCC AATACTGATC 2160

GTATTGCTAA AAACAAAGCT GAAGCTGATG CAAGTTTTGA AACGCTCACC AAAAATCAAA 2220

ATACTTTGAT TGAGCAAGGT GAAGCATTGG TTGAGCAAAA TAAAGCCATC AATCAAGAGC 2280

TTGAAGGGTT TGCGGCTCAT GCAGATATTC AAGATAAGCA AATTTTACAA AACCAAGCTG 2340

ATATCACTAC CAATAAGACC GCTATTGAAC AAAATATCAA TAGAACTGTT GCCAATGGGT 2400

TTGAGATTGA GAAAAATAAA GCTGGTATTG CTACCAATAA GCAAGAGCTT ATTCTTCAAA 2460

ATGATCGATT AAATCGAATT AATGAGACAA ATAATCGTCA GGATCAGAAG ATTGATCAAT 2520

TAGGTTATGC ACTAAAAGAG CAGGGTCAGC ATTTTAATAA TCGTATTAGT GCTGTTGAGC 2580

GTCAAACAGC TGGAGGTATT GCAAATGCTA TCGCAATTGC AACTTTACCA TCGCCCAGTA 2640

GAGCAGGTGA GCATCATGTC TTATTTGGTT CAGGTTATCA CAATGGTCAA GCTGCGGTAT 2700

CATTGGGCGC GGCTGGGTTA AGTGATACAG GAAAATCAAC TTATAAGATT GGTCTAAGCT 2760

GGTCAGATGC AGGTGGATTA TCTGGTGGTG TTGGTGGCAG TTACCGCTGG AAATAAAGCC 2820

TAAATTTAAC TGCTGTGTCA AAAAATATGG TCTGTATAAA CAGACCATAT TTTTATCCAA 2880

AAAAATTATC TTAACTTTTA TAAAGTATTA TAAGCCAAAG CTGTAATAAT AAGAGATGTT 2940

GAAATAAGAG ATGTTAAAGC TGCTAGACAA TCGGCTTGCG ACGATAAAAT AAGATACCTG 3000

GAATGGACAG CCCCAAAACC AATGCTGAGA TGATAAAAAT CGCCTCAAAA AAATGACGCA 3060

TCATAACGAT AAATAAATCC ATATCAAATC CAAAATAGCC AATTTGTACC ATGCTAACCA 3120

TGGCTTTATA GGCAGCGATT CCCGGCATCA TACAAATCAA GCTAGGTACA ATCAAGGCTT 3180

TAGGTGGCAG GCCATGACGC TGAGCAAAAT GTACACCCAA AAAGCTACCC GCCATCGCCC 3240

CAAAGAATGT TGCCACAACC AAATGCACAC CAAAAATTAC CATCACTTGT TTTAAACCAA 3300

AACCAAGTGG TGTTACCATC ATGCAATGCA TGATGTATTG CTTTGTCAA 3349

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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

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

Phe Pro Asn Ile Phe Phe Asn Glu Asn His Asp Glu Leu Asp Asp Ala
35 40 45

Tyr His Asn Met Ile Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln
50 55 60

```
Asp Asn Ser Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu Asp Ser Val
65                  70                  75                  80

Pro Asp Ser Leu Leu Phe Ser Lys Leu Leu His Glu Gln Gln Leu Asn
                85                  90                  95

Gly Phe Lys Ala Gly Asp Thr Ile Ile Pro Leu Asp Lys Asp Gly Lys
            100                 105                 110

Pro Val Tyr Thr Lys Asp Thr Arg Thr Lys Asp Gly Lys Val Glu Thr
        115                 120                 125

Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp Val Glu Gln
    130                 135                 140

Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu Tyr Asp
145                 150                 155                 160

Ile Asn Arg Glu Val Asn Glu Tyr Leu Lys Ala Thr His Asp Tyr Asn
                165                 170                 175

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

Asn Thr Asp Arg Ile Asp Thr Ala Glu Glu Arg Ile Asp Lys Asn Glu
        195                 200                 205

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

Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile
225                 230                 235                 240

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

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
            260                 265                 270

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu
        275                 280                 285

Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn
    290                 295                 300

Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
305                 310                 315                 320

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
                325                 330                 335

Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn
            340                 345                 350

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
        355                 360                 365
```

```
Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg
    370                 375                 380

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
385                 390                 395                 400

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
                405                 410                 415

Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
            420                 425                 430

Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
        435                 440                 445

Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp
    450                 455                 460

Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu
465                 470                 475                 480

Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser
                485                 490                 495

Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe
            500                 505                 510

Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly
        515                 520                 525

Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn
    530                 535                 540

Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn
545                 550                 555                 560

Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
                565                 570
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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CTGGTGGTCG CAGGGGGCGT CTCTGCCAAT CAGTACACTA CGCCGCACCC TGACCGAAAC     60

GCTCCGCCAA ATCGATGCGT CGGTGTACCA TGCCCCGACC GAGCTATGCA CGGATAATGG    120

TGCGATGATC GCCTATGCTG GCTTTTGTCG GCTAATCCGT GGACAGTCGG ATGACTTGGT    180

GGTTCGCTGC ATTCCCCGAT GGGATATGAC GACGCTTGGC GTATCTGCTC ATAAATAGCC    240
```

ACATCAATCA TACCAACCAA ATCATACCAA CCAAATCGTA CAAACGGTTG ATACATGCCA 300

AAAATACCAT ATTGAAAGTA GGGTTTGGGT ATTATTTATG TAACTTATAT CTAATTTGGT 360

GTTGATACTT TGATAAAGCC TTGCTATACT GTAACCTAAA TGGATATGAT AGAGATTTTT 420

CCATTTATGC CAGCAAAAGA GATAGATAGA TAGATAGATA GATAGATAGA TAGATAGATA 480

GATAGATAGA TAGATAGATA AAACTCTGTC TTTTATCTGT CCGCTGATGC TTTCTGCCTG 540

CCACCGATGA TATCATTTAT CTGCTTTTTA GGCATCAGTT ATTTCACCGT GATGACTGAT 600

GTGATGACTT AACTACCAAA AGAGAGTGCT AAATGAAAAC CATGAAACTT CTCCCCCTAA 660

AAATCGCTGT AACCAGTGCC ATGATTGTTG GCTTGGGTGC GACATCTACT GTGAATGCAC 720

AAGTAGTGGA ACAGTTTTTT CCGAATATCT TTTTTAATGA AAACCATGAT GAATTAGATG 780

ATGCATACCA TAATATGATC TTAGGGGATA CTGCGATTGT ATCTAATTCA CAAGATAATA 840

GTACTCAATT GAAATTTTAT TCTAATGATG AAGATTCAGT TCCTGACAGC CTACTCTTTA 900

GTAAACTACT TCATGAGCAG CAACTTAATG GTTTTAAAGC AGGTGACACA ATCATTCCTT 960

TGGATAAGGA TGGCAAACCT GTTTATACAA AGGACACGAG AACAAAGGAT GGTAAAGTAG 1020

AAACAGTTTA TTCGGTCACC ACCAAAATCG CTACCCAAGA TGATGTTGAA CAAAGTGCAT 1080

ATTCACGAGG CATTCAAGGT GATATCGATG ATCTGTATGA CATTAACCGT GAAGTCAATG 1140

AATACTTAAA AGCAACACAT GATTATAATG AAAGACAAAC TGAAGCAATT GACGCTCTAA 1200

ACAAAGCAAG CTCTGCGAAT ACTGATCGTA TTGATACTGC TGAAGAGCGT ATCGATAAAA 1260

ACGAATATGA CATTAAAGCA CTTGAAAGCA ATGTCGAAGA AGGTTTGTTG GAGCTAAGCG 1320

GTCACCTCAT TGATCAAAAA GCAGATCTTA CAAAAGACAT CAAAGCACTT GAAAGCAATG 1380

TCGAAGAAGG TTTGTTGGAG CTAAGCGGTC ACCTCATTGA TCAAAAAGCA GATCTTACAA 1440

AAGACATCAA AGCACTTGAA AGCAATGTCG AAGAAGGTTT GTTGGATCTA AGCGGTCGTC 1500

TGCTTGATCA AAAAGCAGAT ATCGCTAAAA ACCAAGCTGA CATTGCTCAA AACCAAACAG 1560

ACATCCAAGA TCTAGCCGCT TACAACGAGC TACAAGATGC CTATGCCAAA CAGCAAACCG 1620

AAGCGATTGA CGCTCTAAAC AAAGCAAGCT CTGAGAATAC ACAAAACATT GCTAAAAACC 1680

AAGCGGATAT TGCTAATAAC ATCAACAATA TCTATGAGCT GGCACAACAG CAAGATCAGC 1740

ATAGCTCTGA TATCAAAACC TTGGCAAAAG CAAGTGCTGC CAATACTGAT CGTATTGCTA 1800

AAAACAAAGC CGATGCTGAT GCAAGTTTTG AAACGCTCAC CAAAAATCAA AATACTTTGA 1860

TTGAAAAAGA TAAAGAGCAT GACAAATTAA TTACTGCAAA CAAAACTGCG ATTGATGCCA 1920

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ATAAAGCATC TGCGGATACC AAGTTTGCAG CGACAGCAGA CGCCATTACC AAAAATGGAA   1980

ATGCTATCAC TAAAAACGCA AAATCTATCA CTGATTTGGG TACTAAAGTG GATGGTTTTG   2040

ACGGTCGTGT AACTGCATTA GACACCAAAG TCAATGCCTT AGACACCAAA GTCAATGCCT   2100

TTGATGGTCG TATCACAGCT TTAGACAGTA AAGTTGAAAA CGGTATGGCT GCCCAAGCTG   2160

CCCTAAGTGG TCTATTCCAG CCTTATAGCG TTGGTAAGTT TAATGCGACC GCTGCACTTG   2220

GTGGCTATGG CTCAAAATCT GCGGTTGCTA TCGGTGCTGG CTATCGTGTG AATCCAAATC   2280

TGGCGTTTAA AGCTGGTGCG GCGATTAATA CCAGTGGTAA TAAAAAAGGC TCTTATAACA   2340

TCGGTGTGAA TTACGAGTTT TAATTGTCTA TCATCACCAA AAAAAAGCAG TCAGTTTACT   2400

GGCTGCTTTT TTATGGGTTT TTGTGGCTTT TGGTTGTGAG TGATGGATAA AAGCTTATCA   2460

AGCGATTGAT GAATATCAAT AAATGATTGG TAAATATCAA TAAAGCGGTT TAGGGTTTTT   2520

GGATATCTTT TAATAAGTTT AAAAACCCCT GCATAAAATA AAGCTGGGCA TCAGAGCTGC   2580

GAGTAGCGGC ATACAG                                                   2596
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 892 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
1               5                   10                  15

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

Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
        35                  40                  45

Gln Ala Thr Lys Gly Thr Gly Lys His Val Val Asp Asn Lys Asp Asn
    50                  55                  60

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

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

Lys Gly Asn Tyr Ser Thr Val Gly Gly Gly Ser Ser Asn Thr Ala Lys
            100                 105                 110
```

```
Gly Glu Lys Ser Thr Ile Gly Gly Gly Asp Thr Asn Asp Ala Asn Gly
        115                 120                 125

Thr Tyr Ser Thr Ile Gly Gly Gly Tyr Tyr Ser Arg Ala Ile Gly Asp
    130                 135                 140

Ser Ser Thr Ile Gly Gly Gly Tyr Tyr Asn Gln Ala Thr Gly Glu Lys
145                 150                 155                 160

Ser Thr Val Ala Gly Gly Arg Asn Asn Gln Ala Thr Gly Asn Asn Ser
                165                 170                 175

Thr Val Ala Gly Gly Ser Tyr Asn Gln Ala Thr Gly Asn Asn Ser Thr
            180                 185                 190

Val Ala Gly Gly Ser His Asn Gln Ala Thr Gly Glu Gly Ser Phe Ala
        195                 200                 205

Ala Gly Val Glu Asn Lys Ala Asn Ala Asn Asn Ala Val Ala Leu Gly
    210                 215                 220

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

Asn Thr Ile Asp Ser Gly Lys Gln Asn Val Phe Ile Leu Gly Ser Ser
                245                 250                 255

Thr Asn Thr Thr Asn Ala Gln Ser Gly Ser Val Leu Leu Gly His Asn
            260                 265                 270

Thr Ala Gly Lys Lys Ala Thr Ala Val Ser Ser Ala Lys Val Asn Gly
        275                 280                 285

Leu Thr Leu Gly Asn Phe Ala Gly Ala Ser Lys Thr Gly Asn Gly Thr
    290                 295                 300

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

Ala Gly Asn Ile Ser Ala Asp Ser Thr Asp Ala Val Asn Gly Ser Gln
                325                 330                 335

Leu Tyr Ala Leu Ala Thr Ala Val Lys Ala Asp Ala Asp Glu Asn Phe
            340                 345                 350

Lys Ala Leu Thr Lys Thr Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala
        355                 360                 365

Gln Asp Ala Leu Ile Ala Gln Asn Gln Thr Asp Ile Thr Ala Asn Lys
    370                 375                 380

Thr Ala Ile Glu Arg Asn Phe Asn Arg Thr Val Val Asn Gly Phe Glu
385                 390                 395                 400

Ile Glu Lys Asn Lys Ala Gly Ile Ala Lys Asn Gln Ala Asp Ile Gln
                405                 410                 415
```

```
Thr Leu Glu Asn Asn Val Gly Glu Glu Leu Leu Asn Leu Ser Gly Arg
            420                 425                 430

Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr
        435                 440                 445

Asp Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
    450                 455                 460

Lys Lys Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
465                 470                 475                 480

Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Asn Asn
                485                 490                 495

Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys
            500                 505                 510

Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp
        515                 520                 525

Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
    530                 535                 540

Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Ala Asn
545                 550                 555                 560

Thr Asp Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala Glu Asn Lys Lys
                565                 570                 575

Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Glu Asn Lys Asp Gly Ile
            580                 585                 590

Ala Lys Asn Gln Ala Asp Ile Gln Leu His Asp Lys Lys Ile Thr Asn
        595                 600                 605

Leu Gly Ile Leu His Ser Met Val Ala Arg Ala Val Gly Asn Asn Thr
    610                 615                 620

Gln Gly Val Ala Thr Asn Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp
625                 630                 635                 640

Ile Ala Asn Asn Ile Lys Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
                645                 650                 655

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn
            660                 665                 670

Thr Asp Arg Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala Ser Phe Glu
        675                 680                 685

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala Leu
    690                 695                 700

Val Glu Gln Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly Phe Ala Ala
705                 710                 715                 720
```

```
His Ala Asp Val Gln Asp Lys Gln Ile Leu Gln Asn Gln Ala Asp Ile
                725                 730                 735

Thr Thr Asn Lys Ala Ala Ile Glu Gln Asn Ile Asn Arg Thr Val Ala
            740                 745                 750

Asn Gly Phe Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala Thr Asn Lys
        755                 760                 765

Gln Glu Leu Ile Leu Gln Asn Asp Arg Leu Asn Gln Ile Asn Glu Thr
    770                 775                 780

Asn Asn Arg Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr Ala Leu Lys
785                 790                 795                 800

Glu Gln Gly Gln His Phe Asn Asn Arg Ile Ser Ala Val Glu Arg Gln
                805                 810                 815

Thr Ala Gly Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr Leu Pro Ser
            820                 825                 830

Pro Ser Arg Ala Gly Glu His His Val Leu Phe Gly Ser Gly Tyr His
        835                 840                 845

Asn Gly Gln Ala Ala Val Ser Leu Gly Ala Ala Gly Leu Ser Asp Thr
    850                 855                 860

Gly Lys Ser Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp Ala Gly Gly
865                 870                 875                 880

Leu Ser Gly Gly Val Gly Gly Ser Tyr Arg Trp Lys
                885                 890
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGTGAGCAAA TGACTGGCGT AAATGACTGA TGAATGTCTA TTTAATGAAA GATATCAATA 60

TATAAAAGTT GACTATAGCG ATGCAATACA GTAAAATTTG TTACGGCTAA ACATAACGAC 120

GGTCCAAGAT GGCGGATATC GCCATTTACC AACCTGATAA TCAGTTTGAT AGCCATTAGC 180

GATGGCATCA AGTTGTGTTG TTGTATTGTC ATATAAACGG TAAATTTGGT TTGGTGGATG 240

CCCCATCTGA TTTACCGTCC CCCTAATAAG TGAGGGGGGG GGAGACCCCA GTCATTTATT 300

AGGAGACTAA GATGAACAAA ATTTATAAAG TGAAAAAAAA TGCCGCAGGT CACTTGGTGG 360

CATGTTCTGA ATTTGCCAAA GGCCATACCA AAAAGGCAGT TTTGGGCAGT TTATTGATTG 420

```
TTGGGGCATT GGGCATGGCA ACGACGGCGT CTGCACAAGC AACCAAAGGC ACAGGCAAGC    480
ACGTTGTTGA CAATAAGGAC AACAAAGCCA AAGGCGATTA CTCTACCGCC AGTGGTGGCA    540
AGGACAACGA AGCCAAAGGC AATTACTCTA CCGTCGGTGG TGGCGATTAT AACGAAGCCA    600
AAGGCAATTA CTCTACCGTC GGTGGTGGCT CTAGTAATAC CGCCAAAGGC GAGAAATCAA    660
CCATCGGTGG TGGCGATACT AACGACGCCA ACGGCACATA CTCTACCATC GGTGGTGGCT    720
ATTATAGCCG AGCCATAGGC GATAGCTCTA CCATCGGTGG TGGTTATTAT AACCAAGCCA    780
CAGGCGAGAA ATCAACGGTT GCAGGGGGCA GGAATAACCA AGCCACAGGC AACAACTCAA    840
CGGTTGCAGG CGGCTCTTAT AACCAAGCCA CAGGCAACAA CTCAACGGTT GCAGGTGGCT    900
CTCATAACCA AGCCACAGGT GAAGGTTCAT TTGCAGCAGG TGTAGAGAAC AAAGCCAATG    960
CCAACAACGC CGTCGCTCTA GGTAAAAATA ACACCATCGA TGGCGATAAC TCAGTAGCCA   1020
TCGGCTCTAA TAATACCATT GACAGTGGCA AACAAAATGT CTTTATTCTT GGCTCTAGCA   1080
CAAACACAAC AAATGCACAA AGCGGCTCCG TGCTGCTGGG TCATAATACC GCTGGCAAAA   1140
AAGCAACCGC TGTTAGCAGT GCCAAAGTGA ACGGCTTAAC CCTAGGAAAT TTTGCAGGTG   1200
CATCAAAAAC TGGTAATGGT ACTGTATCTG TCGGTAGTGA GAATAATGAG CGTCAAATCG   1260
TCAATGTTGG TGCAGGTAAT ATCAGTGCTG ATTCAACAGA TGCTGTTAAT GGCTCACAGC   1320
TATATGCTTT GGCCACAGCT GTCAAAGCCG ATGCCGATGA AAACTTTAAA GCACTCACCA   1380
AAACTCAAAA TACTTTGATT GAGCAAGGTG AAGCACAAGA CGCATTAATC GCTCAAAATC   1440
AAACTGACAT CACTGCCAAT AAAACTGCCA TTGAGCGAAA TTTTAATAGA ACTGTTGTCA   1500
ATGGGTTTGA GATTGAGAAA AATAAAGCTG GTATTGCTAA AAACCAAGCG GATATCCAAA   1560
CGCTTGAAAA CAATGTCGGA GAAGAACTAT TAAATCTAAG CGGTCGCCTG CTTGATCAAA   1620
AAGCGGATAT TGATAATAAC ATCAACAATA TCTATGATCT GGCACAACAG CAAGATCAGC   1680
ATAGCTCTGA TATCAAAACA CTTAAAAAAA ATGTCGAAGA AGGTTTGTTG GATCTAAGTG   1740
GTCGCCTCAT TGATCAAAAA GCAGATCTTA CGAAAGACAT CAAAACACTT GAAAACAATG   1800
TCGAAGAAGG TTTGTTGGAT CTAAGCGGTC GCCTCATTGA TCAAAAAGCA GATATTGCTA   1860
AAAACCAAGC TGACATTGCT CAAAACCAAA CAGACATCCA AGATCTGGCC GCTTACAACG   1920
AGCTACAAGA CCAGTATGCT CAAAAGCAAA CCGAAGCGAT TGACGCTCTA AATAAAGCAA   1980
GCTCTGCCAA TACTGATCGT ATTGCTACTG CTGAATTGGG TATCGCTGAG AACAAAAAAG   2040
ACGCTCAGAT CGCCAAAGCA CAAGCCAATG AAAATAAAGA CGGCATTGCT AAAAACCAAG   2100
```

```
CTGATATCCA GTTGCACGAT AAAAAAATCA CCAATCTAGG TATCCTTCAC AGCATGGTTG    2160

CAAGAGCGGT AGGAAATAAC ACACAAGGTG TTGCTACCAA TAAAGCTGAC ATTGCTAAAA    2220

ACCAAGCAGA TATTGCTAAT AACATCAAAA ATATCTATGA GCTGGCACAA CAGCAAGATC    2280

AGCATAGCTC TGATATCAAA ACCTTGGCAA AAGTAAGTGC TGCCAATACT GATCGTATTG    2340

CTAAAAACAA AGCTGAAGCT GATGCAAGTT TTGAAACGCT CACCAAAAAT CAAAATACTT    2400

TGATTGAGCA AGGTGAAGCA TTGGTTGAGC AAAATAAAGC CATCAATCAA GAGCTTGAAG    2460

GGTTTGCGGC TCATGCAGAT GTTCAAGATA AGCAAATTTT ACAAAACCAA GCTGATATCA    2520

CTACCAATAA GGCCGCTATT GAACAAAATA TCAATAGAAC TGTTGCCAAT GGGTTTGAGA    2580

TTGAGAAAAA TAAAGCTGGT ATTGCTACCA ATAAGCAAGA GCTTATTCTT CAAAATGATC    2640

GATTAAATCA AATTAATGAG ACAAATAATC GTCAGGATCA GAAGATTGAT CAATTAGGTT    2700

ATGCACTAAA AGAGCAGGGT CAGCATTTTA ATAATCGTAT TAGTGCTGTT GAGCGTCAAA    2760

CAGCTGGAGG TATTGCAAAT GCTATCGCAA TTGCAACTTT ACCATCGCCC AGTAGAGCAG    2820

GTGAGCATCA TGTCTTATTT GGTTCAGGTT ATCACAATGG TCAAGCTGCG GTATCATTGG    2880

GTGCGGCTGG GTTAAGTGAT ACAGGAAAAT CAACTTATAA GATTGGTCTA AGCTGGTCAG    2940

ATGCAGGTGG ATTATCTGGT GGTGTTGGTG GCAGTTACCG CTGGAAATAG AGCCTAAATT    3000

TAACTGCTGT ATCAAAAAAT ATGGTCTGTA TAAACAGACC ATATTTTTAT CTAAAAACTT    3060

ATCTTAACTT TTATGAAGCA TCATAAGCCA AAGCTGAGTA ATAATAAGAG ATGTTAAAAT    3120

AAGAGATGTT AAAACTGCTA AACAATCGGC TTACGACGAT AAAATAAAAT ACCTGGAATG    3180

GACAGCCCCA AAACCAATGC TGAGATGATA AAAATCGCCT CAAAAAAATG ACGCATCATA    3240

ACGATAAATA AATCCATATC AAATCCAAAA TAGCCAATTT GTACCATGCT AACCATGGCT    3300

TTATAGGCAG CGATTCCCGG CATCATACAA ATCAAGCTAG GTACAATCAA GGCTTTAGGC    3360

GGCAGGCCAT GACGCTGAGC A                                              3381
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
Val Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Ser Val
1               5                   10                  15
```

```
Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
            20                  25                  30

Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
        35                  40                  45

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

Gly Ala Tyr Val Gly Gly Gly Val Ile Asn Gln Ala Lys Gly Asn Tyr
65                  70                  75                  80

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

Val Ile Ser Gly Gly Phe Asp Asn Gln Ala Lys Gly Glu His Ser Thr
            100                 105                 110

Ile Ala Gly Gly Glu Ser Asn Gln Ala Thr Gly Arg Asn Ser Thr Val
        115                 120                 125

Ala Gly Gly Ser Asn Asn Gln Ala Val Gly Thr Asn Ser Thr Val Ala
    130                 135                 140

Gly Gly Ser Asn Asn Gln Ala Lys Gly Ala Asn Ser Phe Ala Ala Gly
145                 150                 155                 160

Val Gly Asn Gln Ala Asn Thr Asp Asn Ala Val Ala Leu Gly Lys Asn
                165                 170                 175

Asn Thr Ile Asn Gly Asn Asn Ser Ala Ala Ile Gly Ser Glu Asn Thr
            180                 185                 190

Val Asn Glu Asn Gln Lys Asn Val Phe Ile Leu Gly Ser Asn Thr Thr
        195                 200                 205

Asn Ala Gln Ser Gly Ser Val Leu Leu Gly His Glu Thr Ser Gly Lys
    210                 215                 220

Glu Ala Thr Ala Val Ser Arg Ala Arg Val Asn Gly Leu Thr Leu Lys
225                 230                 235                 240

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

Ser Gln Gly Lys Glu Arg Gln Ile Val His Val Gly Ala Gly Gln Ile
            260                 265                 270

Ser Asp Asp Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Tyr Ala Leu
        275                 280                 285

Ala Thr Ala Val Asp Asp Asn Gln Tyr Asp Ile Glu Ile Asn Gln Asp
    290                 295                 300

Asn Ile Lys Asp Leu Gln Lys Glu Val Lys Gly Leu Asp Lys Glu Val
305                 310                 315                 320
```

```
Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp Asp Val Ala Asp
                325                 330                 335

Asn Gln Ala Asp Ile Ala Lys Asn Lys Ala Asp Ile Lys Glu Leu Asp
            340                 345                 350

Lys Glu Met Asn Val Leu Ser Arg Asp Ile Val Ser Leu Asn Asp Asp
        355                 360                 365

Val Ala Asp Asn Gln Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Lys
    370                 375                 380

Thr Leu Glu Asn Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg
385                 390                 395                 400

Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn His Ile Tyr
                405                 410                 415

Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
            420                 425                 430

Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala
        435                 440                 445

Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu
    450                 455                 460

Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr
465                 470                 475                 480

Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr
                485                 490                 495

Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys
            500                 505                 510

Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val
        515                 520                 525

Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala
    530                 535                 540

Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser
545                 550                 555                 560

Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala
                565                 570                 575

Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr
            580                 585                 590

Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr
        595                 600                 605

Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
    610                 615                 620
```

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
GCCGCACCTG ACCGAGACGC TCCGCCAAAT CAATGCGTCG GTGTACTATG CCCCGACCGA     60

GCTATGCACG GATAATGGTG CGATGATCGC CTATGCTGGC TTTTGTCGGC TAAGCCGTGG    120

ACAGTCGGAT GACTTGGCGG TTCGCTGCAT TCCCCGATGG GATATGACAA CGCTTGGTAT    180

CGAATATGAT AATTAGGCTG TGGTATTTGA GTTTTGAGTA ATGTACCTAC TACCACTAAT    240

TTATCATACA ATACATAAAC ATAAAAAACA TCGGTATTGT TAAAAAACAA TACCCAAGTT    300

AAAATAGCTC AATACTTTAC CATAGCACAA AGAAACTTGT GAACGAAACA TTTAATAATT    360

GCCCAAAATG TCACTGCACA CACTTTGTAA AAGCAGGTTT GGGCAATGGC AAACAACGAT    420

ACAAATGCAA AGGTTACCAT CACTATTTTT CTGTGAAGCA ACGAAGCAAC CAAAAAAGTA    480

ATGACATTAA AAAAACAAGC CATTGATACA AACAGTAAAC AAATCTTAGG CTTTGTCTGT    540

GGTAAAACAG ACACTAACAC CTTTAAACGA CTTTATCAGC AGTTAAATAC CCATAACATT    600

CAACTGTTTT TTAGTGACTA CTGGAAATCT TATCGTCAAG TCATTTTAAA GCCAAAACAT    660

ATAACAAGCA AAGCTCAAAC TTTTACCATA GAGGACTATA ATAGTCTCAT TGGGCATTTC    720

ATAGCAAGAT TTACAAGAAA GTCAAAGTAT TATTCTAAAT CCGAAAAAAT GATAGAAAAC    780

ACGTTGAATT TATTATTTGC TAAGTGGAAT GGTAGCTTAA GATATGTATT TTAATTTAAC    840

AATGCCAAAA ACATCAATTA CAGTAAGATT TTAGGCGTTT TGCAGTTGCT ACTTTAGTAA    900

AGCTTTGTTA TACTAGCTGT TAATATACTC AAGCTTGTTT GTGTTTGAGC TATGTTTATT    960

TTATAGCAGT AGTTGGTTAT AAAATATAAA TAAAGCTAAG CTCGAGGGTT TGGTAATGGT   1020

TTTTTATGTT TATAATACCA ACAGAGTATC TATACAGCTA AAATAGCTAA TACCTTAGGT   1080

GTATTACAAG TAAAAATCCT TTGTTAATCA GGGAGTGTAT TATATGTATA TTTCCTTTGT   1140

ATTTGGTTAT AGCAATCCCT TGGTAAGAAA TCATATCTAT TTTTTATTGT TCAATTATTC   1200

AGGAGACTAA GGTGAACAAA ATTTATAAAG TGAAAAAAAA TGCCGCAGGT CATTCGGTGG   1260

CATGTTCTGA ATTTGCCAAA GGCCATACCA AAAAGGCAGT TTTGGGCAGT TTATTGATTG   1320

TTGGGGCATT GGGCATGGCA ACGACAGCGT CTGCACAAAC AGGCAGTACA AATGCAGCCA   1380
```

```
ACGGCAATAT AATCAGCGGC GTAGGCGCGT ACGTCGGTGG TGGCGTTATA AACCAAGCCA   1440
AAGGCAATTA CCCTACCGTC GGTGGTGGCT TTGATAACCG AGCCACAGGC AATTACTCTG   1500
TCATCAGTGG TGGCTTTGAT AACCAAGCCA AAGGCGAGCA CTCTACCATC GCAGGGGGTG   1560
AGAGTAACCA AGCTACAGGT CGTAACTCAA CGGTTGCAGG GGGTTCTAAT AACCAAGCCG   1620
TGGGTACAAA CTCAACGGTT GCAGGGGGTT CTAATAACCA AGCCAAAGGT GCAAATTCAT   1680
TTGCAGCAGG TGTAGGTAAC CAAGCCAATA CCGACAACGC CGTCGCTCTA GGTAAAAATA   1740
ACACCATCAA TGGCAATAAC TCAGCAGCCA TCGGCTCTGA GAATACCGTT AACGAAAATC   1800
AAAAAAATGT CTTTATTCTT GGCTCTAACA CAACAAATGC ACAAAGCGGC TCAGTACTGC   1860
TAGGTCATGA AACCTCTGGT AAAGAAGCGA CCGCTGTTAG CAGAGCCAGA GTGAACGGCT   1920
TAACCCTAAA AAATTTTTCA GGCGTATCAA AAGCTGATAA TGGTACTGTA TCTGTCGGTA   1980
GTCAGGGTAA AGAGCGTCAA ATCGTTCATG TTGGTGCAGG TCAGATCAGT GATGATTCAA   2040
CAGATGCTGT TAATGGCTCA CAGCTATATG CTTTGGCTAC AGCTGTTGAT GACAACCAAT   2100
ATGACATTGA AATAAACCAA GATAATATCA AAGATCTTCA GAAGGAGGTG AAAGGTCTTG   2160
ATAAGGAAGT GGGTGTATTA AGCCGAGACA TTGGTTCACT TCATGATGAT GTTGCTGACA   2220
ACCAAGCTGA TATTGCTAAA AACAAAGCTG ACATCAAAGA GCTTGATAAG GAGATGAATG   2280
TATTAAGCCG AGACATTGTC TCACTTAATG ATGATGTTGC TGATAACCAA GCTGACATTG   2340
CTAAAAACCA AGCGGATATC AAAACACTTG AAAACAATGT CGAAGAAGGT TTATTGGATC   2400
TAAGCGGTCG CCTCATTGAT CAAAAAGCAG ATATTGATAA TAACATCAAC CATATCTATG   2460
AGCTGGCACA ACAGCAAGAT CAGCATAGCT CTGATATCAA AACCTTGGCA AAAGCAAGTG   2520
CTGCCAATAC TGATCGTATT GCTAAAAACA AAGCCGATGC TGATGCAAGT TTTGAAACAC   2580
TCACCAAAAA TCAAAATACT TTGATTGAAA AAGATAAAGA GCATGACAAA TTAATTACTG   2640
CAAACAAAAC TGCGATTGAT GCCAATAAAG CATCTGCGGA TACCAAGTTT GCAGCGACAG   2700
CAGACGCCAT TACCAAAAAT GGAAATGCTA TCACTAAAAA CGCAAAATCT ATCACTGATT   2760
TGGGTACTAA AGTGGATGGT TTTGACGGTC GTGTAACTGC ATTAGACACC AAAGTCAATG   2820
CCTTTGATGG TCGCATCACA GCTTTAGACA GTAAAGTTGA AAACGGTATG GCTGCCCAAG   2880
CTGCCCTAAG TGGTCTATTC CAGCCTTATA GCGTTGGTAA GTTTAATGCG ACCGCTGCAC   2940
TTGGTGGCTA TGGCTCAAAA TCTGCGGTTG CTATCGGTGC TGGCTATCGT GTGAATCCAA   3000
ATCTGGCGTT TAAAGCTGGT GCGGCGATTA ATACCAGTGG CAATAAAAAA GGCTCTTATA   3060
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ACATCGGTGT GAATTACGAG TTCTAATTGT CTATCATCAC CAAAAAAAGC AGTCAGTTTA   3120

CTGGCTGCTT TTTTATGGGT TTTTATGGCT TTTGGTTGTG AGTGATGGAT AAAAGCTTAT   3180

CAAGCGATTG ATGAATATCA ATAAATGATT GGTAAATATC AATAAAGCGG TTTAGGGTTT   3240

TTGGATATCT TTTAATAAGT TTAAAAACCC CTGCATAAAA TAAAGCTGGC ATCAG        3295
```

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 941 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
1               5                   10                  15

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

Ser Leu Leu Ile Val Gly Ile Leu Gly Met Ala Thr Thr Ala Ser Ala
        35                  40                  45

Gln Met Ala Thr Thr Pro Ser Ala Gln Val Val Lys Thr Asn Asn Lys
    50                  55                  60

Lys Asn Gly Thr His Pro Phe Ile Gly Gly Gly Asp Tyr Asn Thr Thr
65                  70                  75                  80

Lys Gly Asn Tyr Pro Thr Ile Gly Gly Gly His Phe Asn Thr Ala Glu
                85                  90                  95

Gly Asn Tyr Ser Thr Val Gly Gly Gly Phe Thr Asn Glu Ala Ile Gly
            100                 105                 110

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

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

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

Thr Val Val Gly Gly Ser Asn Asn Gln Ala Lys Gly Glu His Ser Thr
                165                 170                 175

Ile Ala Gly Gly Lys Asn Asn Gln Ala Thr Gly Asn Gly Ser Phe Ala
            180                 185                 190

Ala Gly Val Glu Asn Lys Ala Asp Ala Asn Asn Ala Val Ala Leu Gly
        195                 200                 205
```

```
Asn Lys Asn Thr Ile Glu Gly Thr Asn Ser Val Ala Ile Gly Ser Asn
    210                 215                 220

Asn Thr Val Lys Thr Gly Lys Glu Asn Val Phe Ile Leu Gly Ser Asn
225                 230                 235                 240

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

Thr Ala Gly Lys Ala Ala Thr Thr Val Asn Asn Ala Glu Val Asn Gly
            260                 265                 270

Leu Thr Leu Glu Asn Phe Ala Gly Ala Ser Lys Ala Asn Ala Asn Asn
        275                 280                 285

Ile Gly Thr Val Ser Val Gly Ser Glu Asn Asn Glu Arg Gln Ile Val
    290                 295                 300

Asn Val Gly Ala Gly Gln Ile Ser Ala Thr Ser Thr Asp Ala Val Asn
305                 310                 315                 320

Gly Ser Gln Leu His Ala Leu Ala Lys Ala Val Ala Lys Asn Lys Ser
                325                 330                 335

Asp Ile Lys Gly Leu Asn Lys Gly Val Lys Glu Leu Asp Lys Glu Val
            340                 345                 350

Gly Val Leu Ser Arg Asp Ile Asn Ser Leu His Asp Asp Val Ala Asp
        355                 360                 365

Asn Gln Asp Ser Ile Ala Lys Asn Lys Ala Asp Ile Lys Gly Leu Asn
    370                 375                 380

Lys Glu Val Lys Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg Asp
385                 390                 395                 400

Ile Gly Ser Leu His Asp Asp Val Ala Asp Asn Gln Asp Ser Ile Ala
                405                 410                 415

Lys Asn Lys Ala Asp Ile Lys Gly Leu Asn Lys Glu Val Lys Glu Leu
            420                 425                 430

Asp Lys Glu Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp
        435                 440                 445

Asp Val Ala Thr Asn Gln Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile
    450                 455                 460

Lys Thr Leu Glu Asn Asn Val Glu Glu Glu Leu Leu Asn Leu Ser Gly
465                 470                 475                 480

Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile
                485                 490                 495

Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr
            500                 505                 510
```

```
Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu
        515                 520                 525

Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Lys Asn
    530                 535                 540

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln
545                 550                 555                 560

Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr
                565                 570                 575

Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
            580                 585                 590

Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Ala
        595                 600                 605

Asn Thr Asp Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala Glu Asn Lys
    610                 615                 620

Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Glu Asn Lys Asp Gly
625                 630                 635                 640

Ile Ala Lys Asn Gln Ala Asp Ile Gln Leu His Asp Lys Lys Ile Thr
                645                 650                 655

Asn Leu Gly Ile Leu His Ser Met Val Ala Arg Ala Val Gly Asn Asn
            660                 665                 670

Thr Gln Gly Val Ala Thr Asn Lys Ala Asp Ile Ala Lys Asn Gln Ala
        675                 680                 685

Asp Ile Ala Asn Asn Ile Lys Asn Ile Tyr Glu Leu Ala Gln Gln Gln
    690                 695                 700

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala
705                 710                 715                 720

Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala Ser Phe
                725                 730                 735

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala
            740                 745                 750

Leu Val Glu Gln Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly Phe Ala
        755                 760                 765

Ala His Ala Asp Val Gln Asp Lys Gln Ile Leu Gln Asn Gln Ala Asp
    770                 775                 780

Ile Thr Thr Asn Lys Thr Ala Ile Glu Gln Asn Ile Asn Arg Thr Val
785                 790                 795                 800

Ala Asn Gly Phe Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala Thr Asn
                805                 810                 815
```

```
Lys Gln Glu Leu Ile Leu Gln Asn Asp Arg Leu Asn Gln Ile Asn Glu
            820                 825                 830

Thr Asn Asn His Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr Ala Leu
        835                 840                 845

Lys Glu Gln Gly Gln His Phe Asn Asn Arg Ile Ser Ala Val Glu Arg
    850                 855                 860

Gln Thr Ala Gly Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr Leu Pro
865                 870                 875                 880

Ser Pro Ser Arg Ala Gly Glu His His Val Leu Phe Gly Ser Gly Tyr
                885                 890                 895

His Asn Gly Gln Ala Ala Val Ser Leu Gly Ala Ala Gly Leu Ser Asp
            900                 905                 910

Thr Gly Lys Ser Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp Ala Gly
        915                 920                 925

Gly Leu Ser Gly Gly Val Gly Gly Ser Tyr Arg Trp Lys
    930                 935                 940
```

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
TTCTGTGAGC AAATGACTGG CGTAAATGAC TGATGAGTGT CTATTTAATG AAAGATATCA      60

ATATATAAAA GTTGACTATA GCGATGCAAT ACAGTAAAAT TTGTTACGGC TAAACATAAC     120

GACGGTCCAA GATGGCGGAT ATCGCCATTT ACCAACCTGA TAATCAGTTT GATAGCCATT     180

AGCGATGGCA TCAAGTTGTG TTGTTGTATT GTCATATAAA CGGTAAATTT GGTTTGGTGG     240

ATGCCCCATC TGATTTACCG TCCCCCTAAT AAGTGAGGGG GGGGGGGAGA CCCCAGTCAT     300

TTATTAGGAG ACTAAGATGA ACAAAATTTA TAAAGTGAAA AAAAATGCCG CAGGTCACTT     360

GGTGGCGTGT TCTGAATTTG CCAAAGGTCA TACCAAAAAG GCAGTTTTGG GCAGTTTATT     420

GATTGTTGGA ATATTGGGTA TGGCAACGAC AGCATCTGCA CAAATGGCAA CGACGCCGTC     480

TGCACAAGTA GTCAAGACAA ACAATAAAAA AAACGGCACG CACCCTTTCA TCGGTGGTGG     540

CGATTATAAT ACCACCAAAG GCAATTACCC TACCATCGGT GGTGGCCATT TTAATACCGC     600

CGAAGGCAAT TACTCTACCG TCGGTGGTGG CTTTACTAAC GAAGCCATAG GCAAGAACTC     660
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TACCGTCGGT GGTGGCTTTA CTAACGAAGC CATGGGCGAA TACTCAACCG TCGCAGGCGG     720

TGCTAACAAC CAAGCCAAAG GCAATTACTC TACCGTCGGT GGTGGCAATG GCAACAAAGC     780

CATAGGCAAC AACTCAACGG TTGTAGGTGG TTCTAACAAC CAAGCCAAAG GCGAGCACTC     840

TACCATCGCA GGGGGCAAGA ATAACCAAGC TACAGGTAAT GGTTCATTTG CAGCAGGTGT     900

AGAGAACAAA GCCGATGCTA ACAACGCCGT CGCTCTAGGT AACAAGAACA CCATCGAAGG     960

TACAAACTCA GTAGCCATCG GCTCTAATAA TACCGTTAAA ACTGGCAAAG AAAATGTCTT    1020

TATTCTTGGC TCTAACACAA ACACAGAAAA TGCACAAAGT GGCTCCGTGC TGCTGGGTAA    1080

TAATACCGCT GGCAAAGCAG CGACCACTGT TAACAATGCC GAAGTGAACG GCTTAACCCT    1140

AGAAAATTTT GCAGGTGCAT CAAAAGCTAA TGCTAATAAT ATTGGTACTG TATCTGTCGG    1200

TAGTGAGAAT AATGAGCGTC AAATCGTTAA TGTTGGTGCA GGTCAGATCA GTGCCACCTC    1260

AACAGATGCT GTTAATGGCT CACAGCTACA TGCTTTAGCC AAAGCTGTTG CTAAAAACAA    1320

ATCTGACATC AAAGGTCTTA ATAAGGGGGT GAAAGAGCTT GATAAGGAGG TGGGTGTATT    1380

AAGCCGAGAC ATTAATTCAC TTCATGATGA TGTTGCTGAC AACCAAGATA GCATTGCTAA    1440

AAACAAAGCT GACATCAAAG GTCTTAATAA GGAGGTGAAA GAGCTTGATA AGGAGGTGGG    1500

TGTATTAAGC CGAGACATTG GTTCACTTCA TGATGATGTT GCTGACAACC AAGATAGCAT    1560

TGCTAAAAAC AAAGCTGACA TCAAAGGTCT TAATAAGGAG GTGAAAGAGC TTGATAAGGA    1620

GGTGGGTGTA TTAAGCCGAG ACATTGGTTC ACTTCATGAT GATGTTGCCA CCAACCAAGC    1680

TGACATTGCT AAAAACCAAG CGGATATCAA AACACTTGAA AACAATGTCG AAGAAGAATT    1740

ATTAAATCTA AGCGGTCGCC TCATTGATCA AAAAGCGGAT ATTGATAATA ACATCAACAA    1800

TATCTATGAG CTGGCACAAC AGCAAGATCA GCATAGCTCT GATATCAAAA CACTTAAAAA    1860

CAATGTCGAA GAAGGTTTGT TGGATCTAAG CGGTCGCCTC ATTGATCAAA AAGCAGATCT    1920

TACGAAAGAC ATCAAAACAC TTAAAAACAA TGTCGAAGAA GGTTTATTGG ATCTAAGCGG    1980

TCGCCTCATT GATCAAAAAG CAGATATTGC TAAAAACCAA GCTGACATTG CTCAAAACCA    2040

AACAGACATC CAAGATCTGG CCGCTTACAA CGAGCTACAA GACCAGTATG CTCAAAAGCA    2100

AACCGAAGCG ATTGACGCTC TAAATAAAGC AAGCTCTGCC AATACTGATC GTATTGCTAC    2160

TGCTGAATTG GGTATCGCTG AGAACAAAAA AGACGCTCAG ATCGCCAAAG CACAAGCCAA    2220

TGAAAATAAA GACGGCATTG CTAAAAACCA AGCTGATATC CAGTTGCACG ATAAAAAAAT    2280

CACCAATCTA GGTATCCTTC ACAGCATGGT TGCAAGAGCG GTAGGAAATA ATACACAAGG    2340
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TGTTGCTACC AACAAAGCTG ATATTGCTAA AAACCAAGCA GATATTGCTA ATAACATCAA    2400

AAATATCTAT GAGCTGGCAC AACAGCAAGA TCAGCATAGC TCTGATATCA AAACCTTGGC    2460

AAAAGTAAGT GCTGCCAATA CTGATCGTAT TGCTAAAAAC AAAGCTGAAG CTGATGCAAG    2520

TTTTGAAACG CTCACCAAAA ATCAAAATAC TTTGATTGAG CAAGGTGAAG CATTGGTTGA    2580

GCAAAATAAA GCCATCAATC AAGAGCTTGA AGGGTTTGCG GCTCATGCAG ATGTTCAAGA    2640

TAAGCAAATT TTACAAAACC AAGCTGATAT CACTACCAAT AAGACCGCTA TTGAACAAAA    2700

TATCAATAGA ACTGTTGCCA ATGGGTTTGA GATTGAGAAA AATAAAGCTG GTATTGCTAC    2760

CAATAAGCAA GAGCTTATTC TTCAAAATGA TCGATTAAAT CAAATTAATG AGACAAATAA    2820

TCATCAGGAT CAGAAGATTG ATCAATTAGG TTATGCACTA AAAGAGCAGG GTCAGCATTT    2880

TAATAATCGT ATTAGTGCTG TTGAGCGTCA AACAGCTGGA GGTATTGCAA ATGCTATCGC    2940

AATTGCAACT TTACCATCGC CCAGTAGAGC AGGTGAGCAT CATGTCTTAT TTGGTTCAGG    3000

TTATCACAAT GGTCAAGCTG CGGTATCATT GGGCGCGGCT GGATTAAGTG ATACAGGAAA    3060

ATCAACTTAT AAGATTGGTC TAAGCTGGTC AGATGCAGGT GGATTATCTG GTGGTGTTGG    3120

TGGCAGTTAC CGCTGGAAAT AGAGCCTAAA TTTAACTGCT GTATCAAAAA ATATGGTCTG    3180

TATAAACAGA CCATATTTTT ATCTAAAAAA CTTATCTTAA CTTTTATGAA GCATCATAAG    3240

CCAAAGCTGA GTAATAATAA GAGATGTTAA AATAAGAGAT GTTAAAACTG CTAAACAATC    3300

GGCTTGCGAC GATAAAATAA AATACCTGGA ATGGACAGCC CCAAAACCAA TGCTGAGATG    3360

ATAAAAATCG CCTCAAAAAA ATGACGCATC ATAACGATAA ATAAATCCAT ATCAAATCCA    3420

AAATAGCCAA TTTGTACCAT GCTAACCATG GCTTTATAGG CAGCGATTCC CGGCATCATA    3480

CAAATCAAGC TAGGTACAAT CAAGGCTTTA GGCGGCAGGC CATGACGCTG AGCAAAAA      3538
```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 610 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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

Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg Asp Arg Ser
            20                  25                  30
```

```
Leu Glu Asp Ile Gln Asp Ser Ile Ser Lys Leu Val Gln Asp Asp Ile
        35                  40                  45

Asp Thr Leu Lys Gln Asp Gln Gln Lys Met Asn Lys Tyr Leu Leu Leu
    50                  55                  60

Asn Gln Leu Ala Asn Thr Leu Ile Thr Asp Glu Leu Asn Asn Asn Val
65                  70                  75                  80

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

Leu Glu Asn Asp Ile Ala Asp Leu Glu Glu Gly Val Glu Glu Leu Thr
            100                 105                 110

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Glu Glu His Asp Arg Leu
        115                 120                 125

Ile Ala Gln Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn Asn Val Val
    130                 135                 140

Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln Glu Ala Asp
145                 150                 155                 160

Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp Phe Asp Asn
                165                 170                 175

Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr Glu Glu Val
            180                 185                 190

Asn Lys Thr Leu Glu Asn Leu Ile Thr Asn Ser Val Lys Asn Thr Asp
        195                 200                 205

Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile Asn His Ile
    210                 215                 220

Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr
225                 230                 235                 240

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

Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser
            260                 265                 270

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
        275                 280                 285

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

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

Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
                325                 330                 335
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Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
            340                 345                 350

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
        355                 360                 365

Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
    370                 375                 380

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
385                 390                 395                 400

Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
                405                 410                 415

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
            420                 425                 430

Ser Ala Ala Asn Thr Asn Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala
        435                 440                 445

Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Ala Asn
    450                 455                 460

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

Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn
                485                 490                 495

Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly
            500                 505                 510

Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile
        515                 520                 525

Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala
    530                 535                 540

Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr
545                 550                 555                 560

Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala
                565                 570                 575

Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile
            580                 585                 590

Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr
        595                 600                 605

Glu Phe
    610
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCATCAGTAC ATACGCCGCA CCTGACCGAG ACGCTCCGCC AAATCAATGC GTCGGTGTAC 60

TACGCCCCGA CCGAGCTATG CACGGATAAT GGTGCGATGA TCGCTTACGC TGGCTTTTGT 120

CGGCTAAGCC GTGGACAGTC GGATGACTTG GCGGTTCGCT GCATTCCCCG ATGGGATATG 180

ACAACGCTTG GCGTATCTGC TCATAGATAG CCACATCAAT CATACCAACG ATATTGGTAT 240

ATACCAAATT GATACCTGCC AAAAATACCA TATTGAAAGT AGGGTTTGGG TATTATTTAT 300

GTAACTTATA TCTAATTTGG TGTTGATACT TTGATAAAGC CTTGCTATAC TGTAACCTAA 360

ATGGATATGA TAGAGATTTT TCCATTTATG CCAGCAAAAG AGATAGATAG ATAGATAGAT 420

AGATAGATAG ATAGATAGAT AGATAGATAG ATAGATAAAA CTCTGTCTTT TATCTGTCCA 480

CTGATGCTTT CTGCCTGCCA CCGATGATAT CGTTTATCTG CTTTTTTAGG CATCAGTTAT 540

TTCACCGTGA TGACTGATGT GATGACTTAA CCACCAAAAG AGAGTGCTAA ATGAAAACCA 600

TGAAACTTCT CCCTCTAAAA ATCGCTGTAA CCAGTGCCAT GATTATTGGT TTGGGTGCGG 660

CATCTACTGC GAATGCACAG TCTCGGGATA GATCTTTAGA AGATATACAA GATTCAATTA 720

GTAAACTTGT TCAAGATGAT ATAGATACAC TAAAACAAGA TCAGCAGAAG ATGAACAAGT 780

ATCTGTTGCT CAACCAGTTA GCTAATACTT TAATTACAGA CGAGCTCAAC AATAATGTTA 840

TAAAAAACAC CAATTCTATT GAAGCTCTTG GTGATGAGAT TGGATGGCTT GAAAATGATA 900

TTGCAGACTT GGAAGAAGGT GTTGAAGAAC TCACCAAAAA CCAAAATACT TTGATTGAAA 960

AAGATGAAGA GCATGACAGA TTAATCGCTC AAAATCAAGC TGATATCCAA ACACTTGAAA 1020

ACAATGTCGT AGAAGAACTA TTCAATCTAA GCGGTCGCCT AATTGATCAA GAAGCGGATA 1080

TTGCTAAAAA TAATGCTTCT ATTGAAGAGC TTTATGATTT TGATAATGAG GTTGCAGAAA 1140

GGATAGGTGA GATACATGCT TATACTGAAG AGGTAAATAA AACTCTTGAA AACTTGATAA 1200

CAAACAGTGT TAAGAATACT GATAATATTG ACAAAAACAA AGCTGATATT GATAATAACA 1260

TCAACCATAT CTATGAGCTG GCACAACAGC AAGATCAGCA TAGCTCTGAT ATCAAAACAC 1320

TTAAAAACAA TGTCGAAGAA GGTTTGTTGG AGCTAAGCGG TCACCTCATT GATCAAAAAG 1380

CGGATCTTAC AAAAGACATC AAAGCACTTG AAAGCAATGT CGAAGAAGGT TTGTTGGATC 1440

TAAGCGGTCG TCTGCTTGAT CAAAAAGCGG ATCTTACAAA AGACATCAAA GCACTTGAAA 1500

GCAATGTCGA AGAAGGTTTG TTGGATCTAA GCGGTCGTCT GCTTGATCAA AAAGCGGATA 1560

TTGCTCAAAA CCAAACAGAC ATCCAAGATC TGGCCGCTTA CAACGAGCTA CAAGACCAGT 1620

ATGCTCAAAA GCAAACCGAA GCGATTGACG CTCTAAATAA AGCAAGCTCT GAGAATACAC 1680

AAAACATCGA AGATCTGGCC GCTTACAATG AGCTACAAGA TGCCTATGCC AAACAGCAAA 1740

CCGAAGCGAT TGACGCTCTA AATAAAGCAA GCTCTGAGAA TACACAAAAC ATTGCTAAAA 1800

ACCAAGCGGA TATTGCTAAT AACATCAACA ATATCTATGA GCTGGCACAA CAGCAAGATC 1860

AGCATAGCTC TGATATCAAA ACCTTGGCAA AAGCAAGTGC TGCCAATACT AATCGTATTG 1920

CTACTGCTGA ATTGGGCATC GCTGAGAACA AAAAAGACGC TCAGATCGCC AAAGCACAAG 1980

CGAATGCCAA CAAAACTGCG ATTGATGAAA ACAAAGCATC TGCGGATACC AAGTTTGCAG 2040

CAACAGCAGA CGCCATTACC AAAAATGGAA ATGCTATCAC TAAAAACGCA AAATCTATCA 2100

CTGATTTGGG CACTAAAGTG GATGGTTTTG ACGGTCGTGT AACTGCATTA GACACCAAAG 2160

TCAATGCCTT TGATGGTCGT ATCACAGCTT TAGACAGTAA AGTTGAAAAC GGTATGGCTG 2220

CCCAAGCTGC CCTAAGTGGT CTATTCCAGC CTTATAGCGT TGGTAAGTTT AATGCGACCG 2280

CTGCACTTGG TGGCTATGGC TCAAAATCTG CGGTTGCTAT CGGTGCTGGC TATCGTGTGA 2340

ATCCAAATCT GGCGTTTAAA GCTGGTGCGG CGATTAATAC CAGTGGCAAT AAAAAAGGCT 2400

CTTATAACAT CGGTGTGAAT TACGAGTTCT AATTGTCTAT CATCACCAAA AAAAGCAGTC 2460

AGTTTACTGG CTGCTTTTTT ATGGGTTTTT GTGGCTTTTG GTTGTGAGTG ATGGATAAAA 2520

GCTTATCAAG CGATTGATGA ATATCAATAA ATGATTGGTA AATATCAATA AAGCGGTTTA 2580

GGGTTTTTGG ATATCTTTTA ATAAGTTTAA AAACCCCTGC ATAAAATAAA GCTGGGCATC 2640

AGAGCTGCGA GTAGCGGCAT ACAGCGGGAG ATC 2673

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
1               5                   10                  15

Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
            20                  25                  30
```

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Ser Leu Leu Ile Val Gly Ile Leu Gly Met Ala Thr Thr Ala Ser Ala
        35                  40                  45

Gln Gln Thr Ile Ala Arg Gln Gly Lys Gly Met His Ser Ile Ile Gly
    50                  55                  60

Gly Gly Asn Asp Asn Glu Ala Asn Gly Asp Tyr Ser Thr Val Ser Gly
65                  70                  75                  80

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

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

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

Asn Ser Ala Thr Gly Met Tyr Ser Thr Ile Gly Gly Gly Asp Asn Asn
    130                 135                 140

Ser Ala Thr Gly Arg Tyr Ser Thr Ile Ala Gly Gly Trp Leu Asn Gln
145                 150                 155                 160

Ala Thr Gly His Ser Ser Thr Val Ala Gly Gly Trp Leu Asn Gln Ala
                165                 170                 175

Thr Asn Glu Asn Ser Thr Val Gly Gly Gly Arg Phe Asn Gln Ala Thr
            180                 185                 190

Gly Arg Asn Ser Thr Val Ala Gly Gly Tyr Lys Asn Lys Ala Thr Gly
        195                 200                 205

Val Asp Ser Thr Ile Ala Gly Gly Arg Asn Asn Gln Ala Asn Gly Ile
    210                 215                 220

Gly Ser Phe Ala Ala Gly Ile Asp Asn Gln Ala Asn Ala Asn Asn Thr
225                 230                 235                 240

Val Ala Leu Gly Asn Lys Asn Ile Ile Lys Gly Lys Asp Ser Val Ala
                245                 250                 255

Ile Gly Ser Asn Asn Thr Val Glu Thr Gly Lys Glu Asn Val Phe Ile
            260                 265                 270

Leu Gly Ser Asn Thr Lys Asp Ala His Ser Asn Ser Val Leu Leu Gly
        275                 280                 285

Asn Glu Thr Thr Gly Lys Ala Ala Thr Thr Val Glu Asn Ala Lys Val
    290                 295                 300

Gly Gly Leu Ser Leu Thr Gly Phe Val Gly Ala Ser Lys Ala Asn Thr
305                 310                 315                 320

Asn Asn Gly Thr Val Ser Val Gly Lys Gln Gly Lys Glu Arg Gln Ile
                325                 330                 335
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Val Asn Val Gly Ala Gly Gln Ile Arg Ala Asp Ser Thr Asp Ala Val
            340                 345                 350

Asn Gly Ser Gln Leu His Ala Leu Ala Thr Ala Val Asp Ala Glu Phe
        355                 360                 365

Arg Thr Leu Thr Gln Thr Gln Asn Ala Leu Ile Glu Gln Gly Glu Ala
    370                 375                 380

Ile Asn Gln Glu Leu Glu Gly Leu Ala Asp Tyr Thr Asn Ala Gln Asp
385                 390                 395                 400

Glu Lys Ile Leu Lys Asn Gln Thr Asp Ile Thr Ala Asn Lys Thr Ala
                405                 410                 415

Ile Glu Gln Asn Phe Asn Arg Thr Val Thr Asn Gly Phe Glu Ile Glu
            420                 425                 430

Lys Asn Lys Ala Gly Ile Ala Lys Asn Gln Ala Asp Ile Gln Thr Leu
        435                 440                 445

Glu Asn Asp Val Gly Lys Glu Leu Leu Asn Leu Ser Gly Arg Leu Leu
    450                 455                 460

Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr Glu Leu
465                 470                 475                 480

Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Asn
                485                 490                 495

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln
            500                 505                 510

Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Asn Asn Val Glu
        515                 520                 525

Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp
    530                 535                 540

Ile Ala Lys Asn Gln Ala Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
545                 550                 555                 560

Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
                565                 570                 575

Asn Lys Ala Ser Ser Ala Asn Thr Asp Arg Ile Ala Thr Ala Glu Leu
            580                 585                 590

Gly Ile Ala Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala
        595                 600                 605

Asn Glu Asn Lys Asp Gly Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn
    610                 615                 620

Asn Ile Lys Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
625                 630                 635                 640
```

```
Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg
                645                 650                 655

Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala Ser Phe Glu Thr Leu Thr
            660                 665                 670

Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala Leu Val Glu Gln
        675                 680                 685

Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly Phe Ala Ala His Ala Asp
    690                 695                 700

Val Gln Asp Lys Gln Ile Leu Gln Asn Gln Ala Asp Ile Thr Ala Asn
705                 710                 715                 720

Lys Thr Ala Ile Glu Gln Asn Ile Asn Arg Thr Val Ala Asn Gly Phe
                725                 730                 735

Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala Thr Asn Lys Gln Glu Leu
            740                 745                 750

Ile Leu Gln His Asp Arg Leu Asn Arg Ile Asn Glu Thr Asn Asn Arg
        755                 760                 765

Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr Ala Leu Lys Glu Gln Gly
    770                 775                 780

Gln His Phe Asn Asn Arg Ile Ser Ala Val Glu Arg Gln Thr Ala Gly
785                 790                 795                 800

Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr Leu Pro Ser Pro Ser Arg
                805                 810                 815

Ala Gly Glu His His Val Leu Phe Gly Ser Gly Tyr His Asn Gly Gln
            820                 825                 830

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

Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp Ala Gly Gly Leu Ser Gly
    850                 855                 860

Gly Val Gly Gly Ser Tyr Arg Trp Lys
865                 870
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
GTAAATGACT GATGAGTGTC TATTTAATGA AAGATACAAT ATATAAAAGT TGACTATAGC     60
GATGCAATAC AGTAAAATTT GTTACGGCTA AACATAACGA CGGTCCAAGA TGGCGGATAT    120
CGCCATTTAC CAACCTGATA ATCAGTTTGA TAGCCATTAG CGATGGCATC AAGTTGTGTT    180
GTTGTATTGT CATATAAACG GTAAATTTGG TTTGGTGGAT GCCCCATCTG ATTTACCGTC    240
CCCCTAATAA GTGAGAGGGG GGGGGAGACC CCAGTCATTT ATTAGGAGAC TAAGATGAAC    300
AAAATTTATA AAGTGAAAAA AAATGCCGCA GGTCACTTGG TGGCATGTTC TGAATTTGCC    360
AAAGGCCATA CCAAGAAGGC AGTTTTGGGC AGTTTATTGA TTGTTGGAAT ATTGGGTATG    420
GCAACGACAG CATCTGCACA ACAAACAATC GCACGCCAAG GCAAAGGCAT GCACTCTATC    480
ATCGGTGGTG GCAATGACAA CGAAGCCAAC GGCGATTACT CTACCGTCAG TGGTGGCGAT    540
TATAACGAAG CCAAAGGCGA TAGCTCTACC ATCGGTGGTG GCTATTATAA CGAAGCCAAC    600
GGCGATAGCT CTACCATCGG TGGTGGCTTT TATAACGAAG CCAAAGGCGA GAGCTCTACC    660
ATCGGTGGTG GCGATAACAA CTCAGCCACA GGCATGTACT CTACCATCGG TGGTGGCGAT    720
AACAACTCAG CCACAGGCAG GTACTCTACC ATCGCAGGGG GTTGGCTTAA CCAAGCTACA    780
GGTCATAGCT CAACGGTTGC AGGGGGTTGG CTTAACCAAG CTACAAACGA GAATTCTACC    840
GTTGGTGGCG GCAGGTTTAA CCAAGCTACA GGTCGTAACT CAACGGTTGC AGGGGGCTAT    900
AAAAACAAAG CCACAGGCGT AGACTCTACC ATCGCAGGGG GCAGGAATAA CCAAGCCAAC    960
GGTATAGGTT CATTTGCAGC AGGTATAGAC AACCAAGCCA ATGCCAACAA CACCGTCGCT   1020
CTAGGTAACA AGAACATCAT CAAAGGTAAA GACTCAGTAG CCATCGGCTC TAATAATACC   1080
GTTGAAACTG GCAAAGAAAA TGTCTTTATT CTTGGCTCTA ACACAAAAGA TGCACATAGT   1140
AACTCAGTGC TACTGGGTAA TGAGACCACT GGCAAAGCAG CGACCACTGT TGAGAATGCC   1200
AAAGTGGGTG GTCTAAGCCT AACAGGATTT GTAGGTGCAT CAAAAGCTAA TACTAATAAT   1260
GGTACTGTAT CTGTCGGTAA GCAGGGTAAA GAGCGTCAAA TCGTTAATGT TGGTGCAGGT   1320
CAGATCCGTG CTGATTCAAC AGATGCTGTT AATGGCTCAC AGCTACATGC TTTGGCCACA   1380
GCTGTCGATG CAGAATTTAG AACACTCACC CAAACTCAAA ATGCTTTGAT TGAGCAAGGT   1440
GAAGCCATCA ATCAAGAGCT TGAAGGTTTG GCAGATTATA CAAATGCTCA AGATGAGAAA   1500
ATTCTAAAAA ACCAAACTGA CATCACTGCC AATAAAACTG CTATTGAGCA AAATTTTAAT   1560
AGAACTGTTA CCAATGGGTT TGAGATTGAG AAAAATAAAG CTGGTATTGC TAAAAACCAA   1620
GCGGATATCC AAACACTTGA AAACGATGTC GGAAAAGAAC TATTAAATCT AAGCGGTCGC   1680
CTGCTTGATC AAAAAGCAGA TATTGATAAT AACATCAACA ATATCTATGA GCTGGCACAA   1740
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CAGCAAGATC AGCATAGCTC TGATATCAAA ACACTTAAAA ACAATGTCGA AGAAGGTTTG    1800
TTGGATCTAA GCGGTCGCCT CATTGATCAA AAAGCAGATC TTACGAAAGA CATCAAAGCA    1860
CTTGAAAACA ATGTCGAAGA AGGTTTATTG GATCTAAGCG GTCGCCTCAT TGATCAAAAA    1920
GCAGATATTG CTAAAAACCA AGCAGACATC CAAGATTTGG CCGCTTACAA CGAGCTACAA    1980
GACCAGTATG CTCAAAAGCA AACCGAAGCG ATTGACGCTC TAAATAAAGC AAGCTCTGCC    2040
AATACTGATC GTATTGCTAC TGCTGAATTG GGTATCGCTG AGAACAAAAA AGACGCTCAG    2100
ATCGCCAAAG CACAAGCCAA TGAAAATAAA GACGGCATTG CTAAAAACCA AGCAGATATT    2160
GCTAATAACA TCAAAAATAT CTATGAGCTG GCACAACAGC AAGATCAGCA TAGCTCTGAT    2220
ATCAAAACCT TGGCAAAAGT AAGTGCTGCC AATACTGATC GTATTGCTAA AAACAAAGCT    2280
GAAGCTGATG CAAGTTTTGA AACGCTCACC AAAAATCAAA ATACTTTGAT TGAGCAAGGT    2340
GAAGCATTGG TTGAGCAAAA TAAAGCCATC AATCAAGAGC TTGAAGGGTT TGCGGCTCAT    2400
GCAGATGTTC AAGATAAGCA AATTTTACAA AACCAAGCTG ATATCACTGC CAATAAGACC    2460
GCTATTGAAC AAAATATCAA TAGAACTGTT GCCAATGGGT TTGAGATTGA GAAAAATAAA    2520
GCTGGTATTG CTACCAATAA GCAAGAGCTT ATTCTTCAAC ATGATCGATT AAATCGAATT    2580
AATGAGACAA ATAATCGTCA GGATCAGAAG ATTGATCAAT TAGGTTATGC ACTAAAAGAG    2640
CAGGGTCAGC ATTTTAATAA TCGTATTAGT GCTGTTGAGC GTCAAACAGC TGGAGGTATT    2700
GCAAATGCTA TCGCAATTGC AACTTTACCA TCGCCCAGTA GAGCAGGTGA GCATCATGTC    2760
TTATTTGGTT CAGGTTATCA CAATGGTCAA GCTGCGGTAT CATTGGGTGC GGCTGGGTTA    2820
AGTGATACAG GAAAATCAAC TTATAAGATT GGTCTAAGCT GGTCAGATGC AGGTGGATTA    2880
TCTGGTGGTG TTGGTGGTAG TTACCGCTGG AAATAGAGCC TAAATTTAAC TGCTGTATCA    2940
AAAAATATGG TCTGTATAAA CAGACCATAT TTTTATCTAA AAACTTATCT TAACTTTTAT    3000
GAAGCATCAT AAGCCAAAGC TGAGTAATAA TAAGAGATGT TAAAATAAGA GATGTTAAAA    3060
CTGCTAAACA ATCGGCTTAC GACGATAAAA TAAAATACCT GGAATGGACA GCCCCAAAAC    3120
CAATGCTGAG ATGATAAAAA TCGCCTCAAA AAAATGACGC ATCATAACGA TAAATAAATC    3180
CATATCAAAT CCAAAATAGC CAATTTGTAC CATGCTAACC ATGGCTTTAT AGGCAGCGAT    3240
TCCCGGCATC ATACAAATCA AGCTAGGTAC AATCAAGGCT TTAGGCGGCA GG            3292
```

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 889 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
Val Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
1               5                   10                  15

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

Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
        35                  40                  45

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

Trp Ser Ile Ile Gly Ala Gly Arg His Asn Asn Val Gly Gly Ser Ala
65                  70                  75                  80

His His Ser Gly Ile Leu Gly Gly Trp Lys Asn Thr Val Asn Gly Tyr
                85                  90                  95

Thr Ser Ala Ile Val Gly Gly Tyr Gly Asn Glu Thr Gln Gly Asp Tyr
            100                 105                 110

Thr Phe Val Gly Gly Gly Tyr Lys Asn Leu Ala Lys Gly Asn Tyr Thr
        115                 120                 125

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

Ile Ala Gly Gly Phe Ala Asn Leu Ala Glu Gly Asp Asn Ala Thr Ile
145                 150                 155                 160

Ala Gly Gly Phe Glu Asn Arg Ala Glu Gly Ile Asp Ser Val Val Ser
                165                 170                 175

Gly Gly Tyr Ala Asn Gln Ala Thr Gly Glu Ser Ser Thr Val Ala Gly
            180                 185                 190

Gly Ser Asn Asn Leu Ala Glu Gly Lys Ser Ser Ala Ile Gly Gly Gly
        195                 200                 205

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

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

Asn Leu Ala Leu Gly Asn Asn Ala Thr Ile Ser Gly Gly Arg Gln Asn
                245                 250                 255

Glu Ala Ser Gly Asp Arg Ser Thr Val Ala Gly Gly Glu Gln Asn Gln
            260                 265                 270
```

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

Ser Gly Asp Arg Ser Thr Val Ala Gly Gly Glu Gln Asn Gln Ala Ile
    290                 295                 300

Gly Lys Tyr Ser Thr Val Ser Gly Gly Tyr Arg Asn Gln Ala Thr Gly
305                 310                 315                 320

Lys Gly Ser Phe Ala Ala Gly Ile Asp Asn Lys Ala Asn Ala Asp Asn
                325                 330                 335

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

Ala Ile Gly Ser Asn Asn Thr Val Lys Lys Asn Gln Lys Asn Val Phe
        355                 360                 365

Ile Leu Gly Ser Asn Thr Asp Thr Lys Asp Ala Gln Ser Gly Ser Val
    370                 375                 380

Leu Leu Gly Asp Asn Thr Ser Gly Lys Ala Ala Thr Ala Val Glu Asp
385                 390                 395                 400

Ala Thr Val Gly Asp Leu Ser Leu Thr Gly Phe Ala Gly Val Ser Lys
                405                 410                 415

Ala Asn Ser Gly Thr Val Ser Val Gly Ser Glu Gly Lys Glu Arg Gln
            420                 425                 430

Ile Val His Val Gly Ala Gly Arg Ile Ser Asn Asp Ser Thr Asp Ala
        435                 440                 445

Val Asn Gly Ser Gln Leu Tyr Ala Leu Ala Ala Ala Val Asp Asp Asn
    450                 455                 460

Gln Tyr Asp Ile Glu Lys Asn Gln Asp Asp Ile Ala Lys Asn Gln Ala
465                 470                 475                 480

Asp Ile Ala Lys Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn Asp Val
                485                 490                 495

Gly Lys Glu Leu Leu Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala
            500                 505                 510

Asp Ile Asp Asn Asn Ile Asn His Ile Tyr Glu Leu Ala Gln Gln Gln
        515                 520                 525

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu
    530                 535                 540

Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu
545                 550                 555                 560

Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu
                565                 570                 575
```

```
Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln Asn
            580                 585                 590

Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln
        595                 600                 605

Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
    610                 615                 620

Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
625                 630                 635                 640

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
                645                 650                 655

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
            660                 665                 670

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
        675                 680                 685

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
    690                 695                 700

Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
705                 710                 715                 720

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
                725                 730                 735

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
            740                 745                 750

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
        755                 760                 765

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
    770                 775                 780

Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val
785                 790                 795                 800

Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn
                805                 810                 815

Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser
            820                 825                 830

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

Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala
    850                 855                 860

Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser
865                 870                 875                 880
```

Tyr Asn Ile Gly Val Asn Tyr Glu Phe
885

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCCGCACCCT GACCGAGACG CTCCGCCAAA TCGATGCGTC GGTGTACTAT GCCCCGACCG 60

AGCTATGCAC GGATAATGGT GCGATGATCG CCTATGCTGG CTTTTGTCGG CTAAGCCGTG 120

GACAGTCGGA TGACTTGGTG GTTCGCTGTA TTCCCCGATG GGATATGACG ACGCTTGGTA 180

TCGAATATGA TAATTAGGCT GTGGTATTTG AGTTTTGAGT AATGTACCTA CTACCACTAA 240

TTTATCATAC AATACATAAA CATAAAAAAC ATCGGTATTG TTAAAAAACA ATACCCAAGT 300

TAAAATAGCT CAATACTTTA CCATAGCACA AAGAAACTTG TGAACGAAAC ATTTAATAAT 360

TGCCCAAAAT GTTACTGCAC ACACTTTGTA AAAGCAGGCT TGGGCAATGG CAAACAACGA 420

TACAAATGCA AAGGTTGCCA TCACTATTTT TCTGTGAAGC AACGAAGCAA CCAAAAAAGT 480

AATGACATTA AAAAAACAAG CCATTGATAC AAACAGTAAA CAAATCTTAG GCTTTGTCTG 540

TGGTAAAACA GACACTAACA CCTTTAAACG ACTTTATCAG CAGTTAAATA CCCATAGCAT 600

TCAACTGTTT TTTAGTGACT ACTGGAAATC TTATCGTCAA GTCATTTTAA AGCCAAAACA 660

TATAACAAGC AAAGCTCAAA CTTTTACCAT AGAGGGCTAT AATAGTCTCA TTAGGCATTT 720

CATAGCAAGA TTTACAAGAA AGTCAAAGTG TTATTCTAAA TCCGAAAAAA TGATAGAAAA 780

CACGTTGAAT TTATTATTTG CTAAGTGGAA TGGTAGCTTA AGATATGTAT TTTAATTTAA 840

CAATGCCAAA AACATCAATT ACAGTAAGAT TTTAGGCGTT TTGCAGTTGC TACTTTAGTA 900

AAGCTTTGTT ATACTAGCTG TTAGTATACT CAAGCTTGTT TGTGTTTGAG CTATATTTAT 960

TTTATAGCAG TAGTTGGTTA TAAAATATAA ATAAAGCTAA GCTCGAGGGT TTGGTAATGG 1020

TTTTTTATGT TTATAATACC AACAGAGTCT ATACAGCTAA AATAGCTAAT ACCTTAGGTG 1080

TATTACAAGT AAAAATCCTT TGGTTAATCA GGGGGTGTAT TATATGTATA TTTCCTTTGT 1140

ATTTGGTTAT AGCAATCCCT TGGTAAGAAA TCATATCTAT TTTTTATTGT TCAATTATTT 1200

AGGAGACTAA GGTGAACAAA ATTTATAAAG TGAAAAAAAA TGCCGCAGGT CACTTGGTGG 1260

CATGTTCTGA ATTTGCCAAA GGCCATACCA AAAAGGCAGT TTTGGGCAGT TTATTGATTG 1320

TTGGGGCGTT GGGCATGGCA ACGACGGCGT CTGCACAGCC ATTAGTAAGT ACAAATAAGC 1380

CTAATCAGCA GGTAAAGGGT TATTGGTCTA TTATTGGTGC AGGTCGTCAT AATAACGTAG 1440

GTGGATCCGC TCATCACTCA GGGATTCTTG GTGGTTGGAA AAATACAGTC AATGGCTATA 1500

CCTCAGCCAT TGTAGGTGGT TATGGTAACG AAACTCAGGG TGATTATACA TTCGTCGGTG 1560

GTGGTTATAA AAACTTGGCA AAGGGTAATT ATACATTCGT CGGTGGTGGT TATAAAAACT 1620

TGGCAGAGGG TGATAATGCA ACCATCGCTG GTGGTTTTGC AAACTTGGCA GAGGGTGATA 1680

ATGCAACCAT CGCTGGTGGT TTTGAAAACC GTGCAGAGGG TATCGACTCA GTAGTTTCTG 1740

GTGGTTATGC CAACCAAGCT ACAGGAGAAA GCTCAACCGT CGCAGGTGGT TCTAATAACC 1800

TAGCAGAGGG CAAAAGCTCA GCCATTGGTG GTGGCCGTCA AAATGAGGCG TCTGGTGACC 1860

GATCTACTGT CTCAGGTGGT TATAATAACC TAGCAGAGGG CAAAAGCTCA GCCATTGGTG 1920

GCGGTGAGTT TAACTTAGCA TTAGGGAATA ACGCTACCAT TAGTGGTGGC CGTCAAAATG 1980

AGGCGTCTGG TGACCGATCT ACTGTCGCAG GTGGTGAACA AAACCAAGCC ATAGGCAAGT 2040

ATTCTACCAT TAGTGGTGGC CGTCAAAATG AGGCGTCTGG TGACCGATCT ACTGTCGCAG 2100

GTGGTGAACA AAACCAAGCC ATAGGCAAGT ATTCTACCGT TAGTGGTGGC TATCGAAACC 2160

AAGCCACAGG TAAAGGTTCA TTTGCAGCAG GTATAGATAA CAAAGCCAAT GCCGACAACG 2220

CCGTCGCTCT AGGTAACAAG AACACCATCG AAGGTGAAAA CTCAGTAGCC ATCGGCTCTA 2280

ATAATACCGT TAAAAAAAAT CAAAAAAATG TCTTTATTCT TGGCTCTAAC ACAGACACAA 2340

AAGATGCACA AAGCGGCTCA GTACTGCTAG GTGATAATAC CTCTGGTAAA GCAGCGACCG 2400

CTGTTGAGGA TGCCACAGTG GGTGATCTAA GCCTAACAGG ATTTGCAGGC GTATCAAAAG 2460

CTAATAGTGG TACTGTATCT GTCGGTAGTG AGGGTAAAGA GCGTCAAATC GTTCATGTTG 2520

GTGCAGGTCG GATCAGTAAT GATTCAACAG ATGCTGTTAA TGGCTCACAG CTATATGCTT 2580

TGGCCGCAGC TGTTGATGAC AACCAATATG ACATTGAAAA AAACCAAGAT GACATTGCTA 2640

AAAACCAAGC TGACATTGCT AAAAACCAAG CTGACATCCA AACACTTGAA AACGATGTCG 2700

GAAAAGAACT ATTAAATCTA AGCGGTCGCC TCATTGATCA AAAAGCAGAT ATTGATAATA 2760

ACATCAACCA TATCTATGAG CTGGCACAAC AGCAAGATCA GCATAGCTCT GATATCAAAA 2820

CACTTAAAAA AAATGTCGAA GAAGGTTTGT TGGAGCTAAG CGGTCACCTC ATTGATCAAA 2880

AAGCAGATCT TACAAAAGAC ATCAAAGCAC TTGAAAGCAA TGTCGAAGAA GGTTTGTTGG 2940

ATCTAAGCGG TCGCCTCATT GATCAAAAAG CAGATATTGC TCAAAACCAA GCTAACATCC 3000

```
AAGATTTGGC TGCTTACAAC GAGCTACAAG ACCAGTATGC TCAAAAGCAA ACCGAAGCGA    3060

TTGACGCTCT AAATAAAGCA AGCTCTGAGA ATACACAAAA CATCGAAGAT CTGGCCGCTT    3120

ACAACGAGCT ACAAGATGCC TATGCCAAAC AGCAAACCGA AGCCATTGAC GCTCTAAATA    3180

AAGCAAGCTC TGAGAATACA CAAAACATTG CTAAAAACCA AGCGGATATT GCTAATAACA    3240

TCAACAATAT CTATGAGCTA GCACAACAGC AAGATCAGCA TAGCTCTGAT ATCAAAACCT    3300

TGGCAAAAGC AAGTGCTGCC AATACTGATC GTATTGCTAA AAACAAAGCC GATGCTGATG    3360

CAAGTTTTGA AACGCTCACC AAAAATCAAA ATACTTTGAT TGAAAAAGAT AAAGAGCATG    3420

ACAAATTAAT TACTGCAAAC AAAACTGCGA TTGATGCCAA TAAAGCATCT GCGGATACCA    3480

AGTTTGCAGC GACAGCAGAC GCCATTACCA AAAATGGAAA TGCTATCACT AAAAACGCAA    3540

AATCTATCAC TGATTTGGGT ACTAAAGTGG ATGGTTTTGA CGGTCGTGTA ACTGCATTAG    3600

ACACCAAAGT CAATGCCTTT GATGGTCGTA TCACAGCTTT AGACAGTAAA GTTGAAAACG    3660

GTATGGCTGC CCAAGCTGCC CTAAGTGGTC TATTCCAGCC TTATAGCGTT GGTAAGTTTA    3720

ATGCGACCGC TGCACTTGGT GGCTATGGCT CAAAATCTGC GGTTGCTATC GGTGCTGGCT    3780

ATCGTGTGAA TCCAAATCTG GCGTTTAAAG CTGGTGCGGC GATTAATACC AGTGGCAATA    3840

AAAAAGGCTC TTATAACATC GGTGTGAATT ACGAGTTCTA ATTGTCTATC ATCACCAAAA    3900

AAAGCAGTCA GTTTACTGGC TGCTTTTTTA TGGGTTTTTG TGGCTTTTGG TTGTGAGTGA    3960

TGGATAAAAG CTTGTCAAGC GATTGATGAA TATCAATAAA TGATTGGTAA ATATCAATAA    4020

AGCGGTTTAG GGTTTTTGGA TATCTTTTAA TAAGTTTAAA AACCCCTGCA TAAAATAAAG    4080

CTGGCATCAG AGCTGCGAAG TAGCGGCATA CAGCTGGCAA TGCACGCCTG TGCCTAGGGG    4140

GCGTGAGACC ACCCAGCCTT TGCGTTCGTA TTCTAAAATT ACCCAATCAG GCAGAGCGGC    4200

AACTCCATGT TCGGAGGCGA CCAGCTGA                                       4228
```

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
Ala Gln Gln Gln Asp Gln His
1               5
```

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```
Tyr Asp Leu Ala Gln Gln Gln Asp Gln His
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GACGCTCAAC AGCACTAATA CG 22

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCAAGCTGAT ATCACTACC 19

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCAATGCCTT TGATGGTC 18

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGTATGCCGC TACTCGCAGC T 21

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:2..13
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Asn Xaa Ala Xaa Xaa Tyr Ser Xaa Ile Gly Gly Gly Xaa Asn
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
Gln Ala Asp Ile
1
```

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```
Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro Tyr Ser Val Gly
1               5                   10                  15

Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys
            20                  25                  30
```

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```
Gly Lys Ile Thr Lys Asn Ala Ala Arg Gln Glu Asn Gly
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```
Val Ile Gly Asp Leu Gly Arg Lys Val
1               5
```

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:4
          (D) OTHER INFORMATION:/note= "X = any"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

     Ala Leu Glu Xaa Asn Val Glu Glu Gly Leu
     1               5                   10


(2) INFORMATION FOR SEQ ID NO: 30:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 14 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:11..12
          (D) OTHER INFORMATION:/note= "X = any"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

     Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Xaa Xaa Leu Ser
     1               5                   10


(2) INFORMATION FOR SEQ ID NO: 31:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 7 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

     Ala Leu Glu Phe Asn Gly Glu
     1               5


(2) INFORMATION FOR SEQ ID NO: 32:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
```

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:7
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
Ser Ile Thr Asp Leu Gly Xaa Lys Val
1               5
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:13..15
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
Ser Ile Thr Asp Leu Gly Thr Ile Val Asp Gly Phe Xaa Xaa Xaa
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
Ser Ile Thr Asp Leu Gly Thr Ile Val Asp
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:5..19
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
Val Asp Ala Leu Xaa Thr Lys Val Asn Ala Leu Asp Xaa Lys Val Asn
1               5                   10                  15

Ser Asp Xaa Thr
            20
```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
Leu Leu Ala Glu Gln Gln Leu Asn Gly Lys Thr Leu Thr Pro Val
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
Ala Lys His Asp Ala Ala Ser Thr Glu Lys Gly Lys Met Asp
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
Asn Gln Asn Thr Leu Ile Glu Lys Thr Ala Asn Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```
Ile Asp Lys Asn Glu Tyr Ser Ile Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
Ser Ile Thr Asp Leu Gly Thr Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
Asn Gln Asn Thr Leu Ile Glu Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```
Ala Leu His Glu Gln Gln Leu Glu Thr Leu Thr Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
Asn Ser Ser Asp
1
```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
Phe Ala Ala Thr Ala Ile Ala Lys Asp Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 12 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 6 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```
Arg Leu Leu Asp Gln Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 12 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION:12
    (D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Xaa
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 10 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:4..8
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
Ala Lys Ala Xaa Ala Ala Asn Xaa Asp Arg
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala
1               5                   10                  15

Ala Tyr Asn Glu Leu Gln
            20
```

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```
Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
1               5                   10                  15

Gln Gln Gln Asp Gln
            20
```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
Tyr Asn Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```
Ile Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```
Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
1               5                   10                  15

Arg
```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```
Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly Arg
1               5                   10                  15

Thr Ile Asp Gln Arg
            20
```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:11
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
Asn Gln Ala His Ile Ala Asn Asn Ile Asn Xaa Ile Tyr Glu Leu Ala
1               5                   10                  15

Gln Gln Gln Asp Gln Lys
            20
```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala
1               5                   10                  15

Ala Tyr Asn Glu Leu Gln
            20
```

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
Ala Thr His Asp Tyr Asn Glu Arg Gln Thr Glu Ala
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```
Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```
Met Ile Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp Asn Lys
1               5                   10                  15

Thr Gln Leu Lys Phe Tyr Lys
            20
```

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:12..13
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```
Ala Gly Asp Thr Ile Ile Pro Leu Asp Asp Asp Xaa Xaa Pro
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:8
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```
Leu Leu His Glu Gln Gln Leu Xaa Gly Lys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:5
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```
Ile Phe Phe Asn Xaa Gly
1               5
```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
1               5                   10                  15

Ser Ser Asp Ile Lys Thr Leu
            20
```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```
GGTGCAGGTC AGATCAGTGA C                                                  21
```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```
GCCACCAACC AAGCTGAC                                                      18
```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```
AGCGGTCGCC TGCTTGATCA G                                                  21
```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```
CTGATCAAGC AGGCGACCGC T                                                  21
```

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```
CAAGATCTGG CCGCTTACAA                                                   20
```

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```
TTGTAAGCGG CCAGATCTTG                                                   20
```

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```
TGCATGAGCC GCAAACCC                                                     18
```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```
Leu Leu Ala Glu Gln Gln Leu Asn Gly
1               5
```

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```
Ala Leu Glu Ser Asn Val Glu Glu Gly Leu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```
Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3788 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
Thr His Glu Phe Ile Arg Ser Thr Ser Glu Gln Glu Asn Cys Glu Ser
1               5                   10                  15

Ala Arg Glu Asn Thr His Glu Asp Ile Ser Lys Glu Thr Thr Glu Ser
            20                  25                  30

Ala Asn Asp Ala Thr Leu Glu Ala Ser Thr Ser Met Glu Phe Thr His
        35                  40                  45

Glu Ser Glu Ala Leu Arg Glu Ala Asp Tyr Asn Thr His Glu Thr Asp
    50                  55                  60

Arg Ile Val Glu Cys His Glu Cys Lys Trp Ile Thr His Gly Glu Arg
65                  70                  75                  80

Arg Ile Thr His Glu Ser Glu Ser Glu Gln Glu Asn Cys Glu Ser Ala
                85                  90                  95

Arg Glu Asn Ala Met Glu Asp Asn Thr His Glu Asp Ile Ser Lys Glu
```

```
            100                 105                 110

Thr Thr Glu Ser Ala Asn Asp His Ala Arg Asp Cys Pro Ile Glu Ser
        115                 120                 125

Ala Thr Thr Ala Cys His Glu Asp Ala Ser Phe Leu Leu Trp Ser Ala
    130                 135                 140

Asn Asp Asp Asn Thr His Ala Val Glu Ala Asn Tyr Ser Pro Glu Cys
145                 150                 155                 160

Ile Ala Leu Cys His Ala Arg Ala Cys Thr Glu Arg Ser Asp Asn Thr
                165                 170                 175

Thr Arg Ala Asn Ser Leu Ala Thr Glu Ala Asn Tyr Ser Glu Gln Glu
            180                 185                 190

Asn Cys Glu Ser Thr His Ala Thr Ile Ser Thr His Glu Arg Glu Ile
        195                 200                 205

Ser Asn Ser Thr Ala Arg Thr Cys Asp Asn Ser Glu Gln Ile Asp Asn
    210                 215                 220

Phe Ile Leu Glu Asn Ala Met Glu Thr Tyr Pro Glu Ser Thr Arg Ala
225                 230                 235                 240

Asn Asp Thr Pro Leu Gly Tyr Ser Glu Gln Ile Asp Asn Glu Ser Pro
                245                 250                 255

Ala Ala Ala Pro Arg Thr Glu Ile Asn Asn Ala Leu Ile Asn Glu Ala
            260                 265                 270

Arg Ser Glu Gln Ile Asp Asn Glu Ser Pro Ala Asn Ala Asp Asn Ala
        275                 280                 285

Asp Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn
    290                 295                 300

Glu Ser Pro Ala Ala Ala Pro Arg Thr Glu Ile Asn Asn Ala Leu Ile
305                 310                 315                 320

Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Glu Ser Pro Ala Asn Ala
                325                 330                 335

Asp Asn Ala Asp Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser Glu Gln
            340                 345                 350

Ile Asp Asn Glu Ser Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr Glu
        355                 360                 365

Ile Asn Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn
    370                 375                 380

Glu Ser Pro Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp Asx Leu Glu
385                 390                 395                 400
```

```
Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Glu Ser Pro Ala
                405                 410                 415

Ala Ala Pro Ala Thr Pro Arg Thr Glu Ile Asn Asn Ala Leu Ile Asn
            420                 425                 430

Glu Ala Arg Ser Glu Gln Ile Asp Asn Glu Ser Pro Ala Asn Ala Pro
        435                 440                 445

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

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

Pro Arg Thr Glu Ile Asn Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu
                485                 490                 495

Gln Ile Asp Asn Thr Thr Ala Ser Pro Ala Asn Ala Pro Ala Thr Asp
            500                 505                 510

Asn Ala Asp Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile
        515                 520                 525

Asp Asn Thr Thr Ala Ser Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr
    530                 535                 540

Glu Ile Asn Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp
545                 550                 555                 560

Asn Thr Thr Ala Ser Pro Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp
                565                 570                 575

Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr
            580                 585                 590

Thr Ala Ser Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr Glu Ile Asn
        595                 600                 605

Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr Thr
    610                 615                 620

Ala Ser Pro Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp Asx Leu Glu
625                 630                 635                 640

Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr Thr Ala Ser
                645                 650                 655

Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr Glu Ile Asn Asn Ala Leu
            660                 665                 670

Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr Thr Ala Ser Pro
        675                 680                 685

Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp Asx Leu Glu Leu Ile Asn
    690                 695                 700
```

```
Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr His Arg Gly His Ser Glu
705                 710                 715                 720

Gln Ile Asp Asn Ile Ser Gly Ile Val Glu Asn Asx Glu Leu Trp Ala
                725                 730                 735

Asn Asp Ala Arg Glu Asn Thr Asn Thr His Glu Asp Ile Ser Lys Glu
            740                 745                 750

Thr Thr Glu Ser Ser Glu Gln Glu Asn Cys Glu Ser Glu Gln Ile Asp
        755                 760                 765

Asn Thr Tyr Pro Glu Thr Pro Leu Gly Tyr Ser Thr Arg Ala Asn Asp
    770                 775                 780

Ser Pro Glu Cys Ile Ala Leu Ala Gln Gln Gln Asp Gln His Ser Glu
785                 790                 795                 800

Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
                805                 810                 815

Asn Ala Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Glu Gln Ile
            820                 825                 830

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
        835                 840                 845

Tyr Asp Leu Ala Gln Gln Gln Asp Gln His Ser Glu Gln Ile Asp Asn
    850                 855                 860

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Gly Ala
865                 870                 875                 880

Cys Gly Cys Thr Cys Ala Ala Cys Ala Gly Cys Ala Cys Thr Ala Ala
                885                 890                 895

Thr Ala Cys Gly Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn
            900                 905                 910

Glu Ala Arg Asp Asx Leu Glu Cys Cys Ala Ala Gly Cys Thr Gly Ala
        915                 920                 925

Thr Ala Thr Cys Ala Cys Thr Ala Cys Cys Ser Glu Gln Ile Asp Asn
    930                 935                 940

Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Thr Cys Ala
945                 950                 955                 960

Ala Thr Gly Cys Cys Thr Thr Thr Gly Ala Thr Gly Gly Thr Cys Ser
                965                 970                 975

Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx
            980                 985                 990

Leu Glu Thr Gly Thr Ala Thr Gly Cys Cys Gly Cys Thr Ala Cys Thr
        995                 1000                1005
```

```
Cys Gly Cys Ala Gly Cys Thr Ser Glu Gln Ile Asp Asn Asp Asn Ala
    1010                1015                1020

Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Asn Xaa Ala Xaa Xaa Tyr
1025                1030                1035                1040

Ser Xaa Ile Gly Gly Gly Xaa Asn Ser Glu Gln Ile Asp Asn Pro Arg
                1045                1050                1055

Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr
            1060                1065                1070

Ala Thr Pro Ser Ile Thr Ile Asn Ser Gln Ala Asp Ile Ser Glu Gln
        1075                1080                1085

Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn
    1090                1095                1100

Ala Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro Tyr Ser Val
1105                1110                1115                1120

Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser
                1125                1130                1135

Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala
            1140                1145                1150

Arg Asn Ala Gly Lys Ile Thr Lys Asn Ala Ala Arg Gln Glu Asn Gly
        1155                1160                1165

Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
    1170                1175                1180

Ala Arg Asn Ala Val Ile Gly Asp Leu Gly Arg Lys Val Ser Glu Gln
1185                1190                1195                1200

Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn
                1205                1210                1215

Ala Ala Leu Glu Xaa Asn Val Glu Glu Gly Leu Ser Glu Gln Ile Asp
            1220                1225                1230

Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa
        1235                1240                1245

Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ala Leu Glu Ser Asn
    1250                1255                1260

Val Glu Glu Gly Leu Xaa Xaa Leu Ser Ser Glu Gln Ile Asp Asn Pro
1265                1270                1275                1280

Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn
                1285                1290                1295

Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Ala Leu Glu Phe Asn Gly
            1300                1305                1310
```

```
Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn
        1315                1320                1325

Glu Ala Arg Asn Ala Ser Ile Thr Asp Leu Gly Xaa Lys Val Ser Glu
    1330                1335                1340

Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
1345                1350                1355                1360

Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Ile
                1365                1370                1375

Thr Asp Leu Gly Thr Ile Val Asp Gly Phe Xaa Xaa Xaa Ser Glu Gln
            1380                1385                1390

Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn
        1395                1400                1405

Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Ser Ile
    1410                1415                1420

Thr Asp Leu Gly Thr Ile Val Asp Ser Glu Gln Ile Asp Asn Pro Arg
1425                1430                1435                1440

Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Val Asp Ala Leu
                1445                1450                1455

Xaa Thr Lys Val Asn Ala Leu Asp Xaa Lys Val Asn Ser Asp Xaa Thr
            1460                1465                1470

Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
        1475                1480                1485

Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn
    1490                1495                1500

Ser Leu Leu Ala Glu Gln Gln Leu Asn Gly Lys Thr Leu Thr Pro Val
1505                1510                1515                1520

Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
                1525                1530                1535

Ala Arg Asn Ala Ala Lys His Asp Ala Ala Ser Thr Glu Lys Gly Lys
            1540                1545                1550

Met Asp Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
        1555                1560                1565

Asn Glu Ala Arg Asn Ala Ala Leu Glu Ser Asn Val Glu Glu Gly Leu
    1570                1575                1580

Leu Asp Leu Ser Gly Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile
1585                1590                1595                1600

Asn Leu Ile Asn Glu Ala Arg Asn Ala Asn Gln Asn Thr Leu Ile Glu
                1605                1610                1615
```

```
Lys Thr Ala Asn Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile
            1620                1625                1630

Asn Leu Ile Asn Glu Ala Arg Asn Ala Ile Asp Lys Asn Glu Tyr Ser
        1635                1640                1645

Ile Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
    1650                1655                1660

Asn Glu Ala Arg Asn Ala Ser Ile Thr Asp Leu Gly Thr Lys Ser Glu
1665                1670                1675                1680

Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
                1685                1690                1695

Asn Ala Asn Gln Asn Thr Leu Ile Glu Lys Ser Glu Gln Ile Asp Asn
            1700                1705                1710

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Leu
        1715                1720                1725

His Glu Gln Gln Leu Glu Thr Leu Thr Lys Ser Glu Gln Ile Asp Asn
    1730                1735                1740

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Asn Ser
1745                1750                1755                1760

Ser Asp Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
                1765                1770                1775

Asn Glu Ala Arg Asn Ala Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
            1780                1785                1790

Thr Leu Thr Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
        1795                1800                1805

Leu Ile Asn Glu Ala Arg Asn Ala Phe Ala Ala Thr Ala Ile Ala Lys
    1810                1815                1820

Asp Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
1825                1830                1835                1840

Asn Glu Ala Arg Asn Ala Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
                1845                1850                1855

Ala Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
            1860                1865                1870

Asn Glu Ala Arg Asn Ala Arg Leu Leu Asp Gln Lys Ser Glu Gln Ile
        1875                1880                1885

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
    1890                1895                1900

Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Xaa Ser Glu Gln Ile
1905                1910                1915                1920
```

```
Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
                1925                1930                1935

Ala Lys Ala Xaa Ala Ala Asn Xaa Asp Arg Ser Glu Gln Ile Asp Asn
            1940                1945                1950

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala
        1955                1960                1965

Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Asn Gln Ala Asp Ile
    1970                1975                1980

Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu
1985                1990                1995                2000

Gln Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn
                2005                2010                2015

Glu Ala Arg Asn Ala Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn
            2020                2025                2030

Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln Ser Glu Gln Ile Asp Asn
        2035                2040                2045

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Tyr Asn
    2050                2055                2060

Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn Ser Glu Gln Ile Asp
2065                2070                2075                2080

Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ile
                2085                2090                2095

Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp Ser Glu Gln Ile
            2100                2105                2110

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
        2115                2120                2125

Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
    2130                2135                2140

Arg Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn
2145                2150                2155                2160

Glu Ala Arg Asn Ala Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu
                2165                2170                2175

Glu Leu Ser Gly Arg Thr Ile Asp Gln Arg Ser Glu Gln Ile Asp Asn
            2180                2185                2190

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Asn Gln
        2195                2200                2205

Ala His Ile Ala Asn Asn Ile Asn Xaa Ile Tyr Glu Leu Ala Gln Gln
    2210                2215                2220
```

```
Gln Asp Gln Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
2225                2230                2235                2240

Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser
                2245                2250                2255

Ile Thr Ile Asn Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile
            2260                2265                2270

Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Ser Glu Gln Ile Asp Asn
        2275                2280                2285

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Thr
    2290                2295                2300

His Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ser Glu Gln Ile Asp Asn
2305                2310                2315                2320

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Lys Ala
                2325                2330                2335

Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Ser Glu Gln Ile Asp Asn
            2340                2345                2350

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Met Ile
        2355                2360                2365

Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp Asn Lys Thr Gln
    2370                2375                2380

Leu Lys Phe Tyr Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile
2385                2390                2395                2400

Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Gly Asp Thr Ile Ile Pro
                2405                2410                2415

Leu Asp Asp Asp Xaa Xaa Pro Ser Glu Gln Ile Asp Asn Pro Arg Thr
            2420                2425                2430

Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala
        2435                2440                2445

Thr Pro Ser Ile Thr Ile Asn Ser Leu Leu His Glu Gln Gln Leu Xaa
    2450                2455                2460

Gly Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
2465                2470                2475                2480

Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr
                2485                2490                2495

Ile Asn Ile Phe Phe Asn Xaa Gly Ser Glu Gln Ile Asp Asn Pro Arg
            2500                2505                2510

Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr
        2515                2520                2525
```

```
Ala Thr Pro Ser Ile Thr Ile Asn Asn Asn Ile Asn Asn Ile Tyr Glu
    2530                2535                2540

Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ser
2545                2550                2555                2560

Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala
                2565                2570                2575

Arg Asn Ala Gly Gly Thr Gly Cys Ala Gly Gly Thr Cys Ala Gly Ala
            2580                2585                2590

Thr Cys Ala Gly Thr Gly Ala Cys Ser Glu Gln Ile Asp Asn Asp Asn
        2595                2600                2605

Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Gly Cys Cys Ala Cys
    2610                2615                2620

Cys Ala Ala Cys Cys Ala Ala Gly Cys Thr Gly Ala Cys Ser Glu Gln
2625                2630                2635                2640

Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu
                2645                2650                2655

Ala Gly Cys Gly Gly Thr Cys Gly Cys Cys Thr Gly Cys Thr Thr Gly
            2660                2665                2670

Ala Thr Cys Ala Gly Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile
        2675                2680                2685

Asn Glu Ala Arg Asp Asx Leu Glu Cys Thr Gly Ala Thr Cys Ala Ala
    2690                2695                2700

Gly Cys Ala Gly Gly Cys Gly Ala Cys Cys Gly Cys Thr Ser Glu Gln
2705                2710                2715                2720

Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu
                2725                2730                2735

Cys Ala Ala Gly Ala Thr Cys Thr Gly Gly Cys Cys Gly Cys Thr Thr
            2740                2745                2750

Ala Cys Ala Ala Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn
        2755                2760                2765

Glu Ala Arg Asp Asx Leu Glu Thr Thr Gly Thr Ala Ala Gly Cys Gly
    2770                2775                2780

Gly Cys Cys Ala Gly Ala Thr Cys Thr Thr Gly Ser Glu Gln Ile Asp
2785                2790                2795                2800

Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Thr Gly
                2805                2810                2815

Cys Ala Thr Gly Ala Gly Cys Cys Gly Cys Ala Ala Ala Cys Cys Cys
            2820                2825                2830
```

```
Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp
        2835                2840                2845

Asx Leu Glu Leu Leu Ala Glu Gln Gln Leu Asn Gly Ser Glu Gln Ile
    2850                2855                2860

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
2865                2870                2875                2880

Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Ser Glu Gln Ile Asp Asn
                2885                2890                2895

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Leu
            2900                2905                2910

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Ser Glu Gln Ile
        2915                2920                2925

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
    2930                2935                2940

Asn Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ser Glu Gln Ile Asp
2945                2950                2955                2960

Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala
                2965                2970                2975

Ala Thr Ala Ala Asp Ala Ile Thr Lys Asn Gly Asn Ser Glu Gln Ile
            2980                2985                2990

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
        2995                3000                3005

Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Ser
    3010                3015                3020

Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala
3025                3030                3035                3040

Arg Asn Ala Val Asp Ala Leu Xaa Thr Lys Val Asn Ala Leu Asp Xaa
                3045                3050                3055

Lys Val Asn Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu
            3060                3065                3070

Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile
        3075                3080                3085

Thr Ile Asn Ser Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro
    3090                3095                3100

Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly
3105                3110                3115                3120

Ser Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
                3125                3130                3135
```

Asn Glu Ala Arg Asn Ala Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp
3140 3145 3150

Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
3155 3160 3165

Ala Arg Asn Ala Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Ser Glu
3170 3175 3180

Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
3185 3190 3195 3200

Asn Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Ser Glu Gln Ile
3205 3210 3215

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
3220 3225 3230

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Ser Glu Gln Ile Asp Asn
3235 3240 3245

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Gln
3250 3255 3260

Gln Gln Asp Gln His Ser Ser Asp Ser Glu Gln Ile Asp Asn Pro Arg
3265 3270 3275 3280

Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Gln Asp Gln His
3285 3290 3295

Ser Ser Asp Ile Lys Thr Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu
3300 3305 3310

Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala His Ser Ser Asp Ile Lys
3315 3320 3325

Thr Leu Lys Asn Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
3330 3335 3340

Leu Ile Asn Glu Ala Arg Asn Ala Asp Ile Lys Thr Leu Lys Asn Asn
3345 3350 3355 3360

Val Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
3365 3370 3375

Asn Glu Ala Arg Asn Ala Thr Leu Lys Asn Asn Val Glu Glu Gly Leu
3380 3385 3390

Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
3395 3400 3405

Ala Arg Asn Ala Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Ser Glu
3410 3415 3420

Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
3425 3430 3435 3440

```
Asn Ala Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Ser Glu Gln Ile
                3445                3450                3455

Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
            3460                3465                3470

Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ser Glu Gln Ile Asp Asn
        3475                3480                3485

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Lys
    3490                3495                3500

Asn Gln Ala Asp Ile Ala Gln Asn Ser Glu Gln Ile Asp Asn Pro Arg
3505                3510                3515                3520

Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ile Ala Gln Asn
                3525                3530                3535

Gln Thr Asp Ile Gln Asp Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu
            3540                3545                3550

Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Asp Ile Gln Asp Leu Ala
        3555                3560                3565

Ala Tyr Asn Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
    3570                3575                3580

Leu Ile Asn Glu Ala Arg Asn Ala Cys Gly Gly Gly Ala Thr Cys Cys
3585                3590                3595                3600

Gly Thr Gly Ala Ala Gly Ala Ala Ala Ala Ala Thr Gly Cys Cys Gly
                3605                3610                3615

Cys Ala Gly Gly Thr Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile
            3620                3625                3630

Asn Glu Ala Arg Asp Asx Leu Glu Cys Gly Gly Gly Ala Thr Cys Cys
        3635                3640                3645

Cys Gly Thr Cys Gly Cys Ala Ala Gly Cys Cys Gly Ala Thr Thr Gly
    3650                3655                3660

Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp
3665                3670                3675                3680

Asx Leu Glu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn
                3685                3690                3695

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
            3700                3705                3710

Ser Asp Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Asp
        3715                3720                3725

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
    3730                3735                3740
```

```
Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr
3745                3750                3755                3760

Asn Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
                3765                3770                3775

Asn Glu Ala Arg Asn Ala Ala Trp Glx Xaa Asp Cys
            3780                3785
```

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```
Ala Ala Thr Ala Ala Asp Ala Ile Thr Lys Asn Gly Asn
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```
Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:5..13
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```
Val Asp Ala Leu Xaa Thr Lys Val Asn Ala Leu Asp Xaa Lys Val Asn
1               5                   10                  15
```

```
(2) INFORMATION FOR SEQ ID NO: 80:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 30 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

     Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro Tyr Ser Val Gly
     1               5                   10                  15

     Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys
                 20                  25                  30


(2) INFORMATION FOR SEQ ID NO: 81:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

     Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp
     1               5                   10


(2) INFORMATION FOR SEQ ID NO: 82:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

     Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
     1               5                   10


(2) INFORMATION FOR SEQ ID NO: 83:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

     Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
     1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```
Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```
Ala Gln Gln Gln Asp Gln His Ser Ser Asp
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
Gln Asp Gln His Ser Ser Asp Ile Lys Thr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
His Ser Ser Asp Ile Lys Thr Leu Lys Asn
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
Asp Ile Lys Thr Leu Lys Asn Asn Val Glu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
Thr Leu Lys Asn Asn Val Glu Glu Gly Leu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```
Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 96:

```
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 29 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGGGATCCGT GAAGAAAAAT GCCGCAGGT                                         29


(2) INFORMATION FOR SEQ ID NO: 97:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CGGGATCCCG TCGCAAGCCG ATTG                                              24


(2) INFORMATION FOR SEQ ID NO: 98:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 79 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

     Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
     1               5                   10                  15

     Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
                 20                  25                  30

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

     Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile
         50                  55                  60

     Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
     65                  70                  75
```

CLAIMS

1. An isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17).

2. The isolated peptide of claim 1, wherein said peptide is about 10 amino acids in length.

3. The isolated peptide of claim 1, wherein said peptide is about 20 amino acids in length.

4. The isolated peptide of claim 1, wherein said peptide is about 30 amino acids in length.

5. The isolated peptide of claim 1, wherein said peptide is about 40 amino acids in length.

6. The isolated peptide of claim 1, wherein said peptide is about 50 amino acids in length.

7. The isolated peptide of claim 1, wherein said peptide is about 60 amino acids in length.

8. The isolated peptide of claim 1, wherein said peptide is at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

9. An antigenic composition comprising (a) an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17) and (b) a pharmaceutically acceptable buffer or diluent.

10. The antigenic composition of claim 9, wherein said antigenic composition further comprises a carrier conjugated to said peptide.

11. The antigenic composition of claim 10, wherein said carrier is KLH, diphtheria toxoid, tetanus toxoid or CRM_{197}.

12. The antigenic composition of claim 9, further comprising an adjuvant.

13. The antigenic composition of claim 12, wherein said adjuvant comprises a lipid.

14. The antigenic composition of claim 9 wherein said peptide is covalently linked to a second antigen.

15. The antigenic composition of claim 14, wherein said second antigen is a peptide antigen.

16. The antigenic composition of claim 14, wherein said second antigen is a non-peptide antigen.

17. The antigenic composition of claim 9, wherein said isolated peptide comprises at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

18. A vaccine composition comprising an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17) and a pharmaceutically acceptable buffer or diluent.

19. The vaccine composition of claim 18, wherein said isolated peptide is further defined as comprising at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

20. A method for inducing an immune response in a mammal comprising the step of providing to said mammal an antigenic composition comprising (a) an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17) and (b) a pharmaceutically acceptable buffer or diluent.

21. The method of claim 20, wherein said isolated peptide is further defined as comprising at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

22. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:1) of the *M. catarrhalis* isolate O35E.

23. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:2) of the *M. catarrhalis* isolate O35E.

24. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:3) of the *M. catarrhalis* isolate O35E.

25. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:4) of the *M. catarrhalis* isolate O35E.

26. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:5) of the *M. catarrhalis* isolate O46E.

27. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:6) of the *M. catarrhalis* isolate O46E.

28. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:7) of the *M. catarrhalis* isolate O46E.

29. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:8) of the *M. catarrhalis* isolate O46E.

30. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:9) of the *M. catarrhalis* isolate TTA24.

31. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:10) of the *M. catarrhalis* isolate TTA24.

32. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:11) of the *M. catarrhalis* isolate TTA24.

33. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:12) of the *M. catarrhalis* isolate TTA24.

34. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:13) of the *M. catarrhalis* isolate TTA37.

35. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:14) of the *M. catarrhalis* isolate TTA37.

36. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:15) of the *M. catarrhalis* isolate TTA37.

37. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:16) of the *M. catarrhalis* isolate TTA37.

38. A method for diagnosing *M. catarrhalis* infection comprising the step of determining the presence, in a sample, of an *M. catarrhalis* amino acid sequence corresponding to residues of epitopic core sequences of said UspA1 or UspA2 antigen.

39. The method of claim 38, wherein said determining comprises PCR.

40. The method of claim 38, wherein said determining comprises immunologic reactivity of an antibody to an *M. catarrhalis* antigen.

41. A method for treating an individual having an *M. catarrhalis* infection comprising providing to said individual an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17).

42. The isolated peptide of claim 41, wherein the said peptide comprises at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

43. A method for preventing or limiting an *M. catarrhalis* infection comprising providing to a subject an antibody that reacts immunologically with an epitope formed by the amino acid sequence AQQQDQH (SEQ ID NO:17).

44. The method of claim 42, wherein said epitope is further defined as comprising at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

45. A method for screening a peptide for reactivity with an antibody that bind immunologically to UspA1 or UspA2 comprising the steps of:

a) providing said peptide;

b) contacting said peptide with said antibody; and

c) determining the binding of said antibody to said peptide.

46. The method of claim 45, wherein said antibody is 17C7, 45-2, 13-1, 29-31, 16A7, 17B1 or 5C12.

47. The method of claim 46, wherein said antibody is 17C7.

48. The method of claim 46, wherein said antibody is 45-2.

49. The method of claim 46, wherein said antibody is 13-1.

50. The method of claim 46, wherein said antibody is 29-31.

51. The method of claim 46, wherein said antibody is 16A7.

52. The method of claim 46, wherein said antibody is 5C12.

53. The method of claim 46, wherein said antibody is 17B1.

54. The method of claim 45, wherein said determining comprises an immunoassay selected from the group consisting of a western blot, an ELISA, and RIA and immunoaffinity separation.

55. A method for screening a UspA1 or UspA2 peptide for the ability to induce a protective immune response against *M. catarrhalis* comprising the steps of:

a) providing said peptide;

b) administering a peptide in a suitable form to an experimental animal;

c) challenging said animal with *M. catarrhalis*; and

d) assaying the infection of said animal with *M. catarrhalis.*

56. The method of claim 56, wherein said animal is a mouse, said challenging is a pulmonary challenge, and said assaying comprises assessing the degree of pulmonary clearance by said mouse.

57. The method of claim 56, wherein said UspA1 peptide encompasses about residues 582-604 (SEQ ID NO:1) of *M. catarrhalis* or the analogous position thereof when compared to *M. catarrhalis* strain O35E.

58. The method of claim 56, wherein said UspA2 peptide encompasses about residues 355-377 (SEQ ID NO:3) of *M. catarrhalis* or the analogous position thereof when compared to *M. catarrhalis* strain O35E.

59. The method of claim 57, wherein said UspA1 peptide includes about residues 452-642 (SEQ ID NO:1) of *M. catarrhalis* or the analogous positions thereof when compared to *M. catarrhalis* strain O35E.

60. The method of claim 58, wherein said UspA2 peptide includes about residues 242-415 (SEQ ID NO:3) of *M. catarrhalis*, or the analogous position thereof when compared to *M. catarrhalis* strain O35E.

61. An isolated peptide having at least about 7 consecutive amino acids from the UspA1 or UspA2 protein of *M. catarrhalis,* wherein said peptide includes residues located within the region defined by about residues 582-604 of said UspA1 protein (SEQ ID NO:1), or by about residues 355-377 of said UspA2 protein (SEQ ID NO:3), or the analogous positions thereof when compared to strain O35E.

62. The isolated peptide of claim 61, wherein said peptide is between 7 and 60 amino acids in length.

63. The isolated peptide of claim 61, wherein said peptide comprises non-UspA1 or non-UspA2 sequences.

64. The isolated peptide of claim 61, wherein said peptide comprises non-*M. catarrhalis* sequences.

65. An antigenic composition comprising

a) an isolated peptide having at least about 7 consecutive amino acids from the UspA1 or UspA2 protein of *M. catarrhalis,* wherein said amino acids include residues located within the region defined by about residues 582-604 of said UspA1 protein (SEQ ID NO:1), or by about residues 355-377 of said UspA2 protein (SEQ ID NO:3), or the analogous positions thereof when compared to strain O35E.

b) a pharmaceutically acceptable buffer or diluent.

66. An antigenic composition comprising

a) an isolated peptide of about 7 to about 60 amino acids comprising at least 7 consecutive residues of the amino acid sequence of UspA1 or UspA2 wherein said isolated peptide acts as a carrier covalently linked to a second antigen; and

b) a pharmaceutically acceptable buffer or diluent.

67. The antigenic composition of claim 66, wherein said second antigen is a peptide antigen.

68. The antigenic composition of claim 66, wherein said second antigen is a non-peptide antigen.

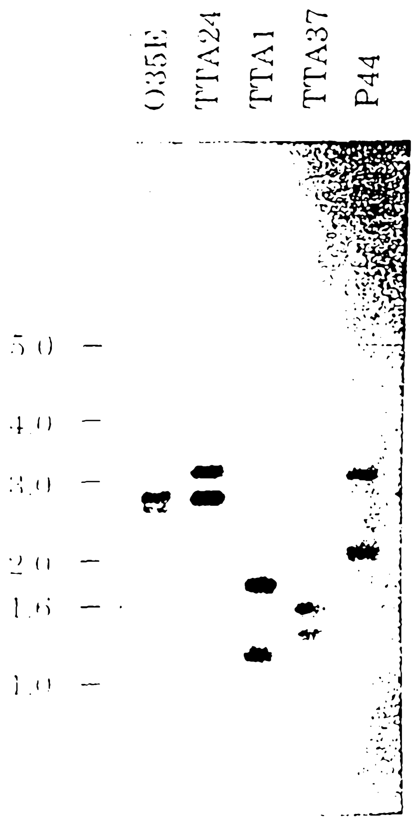


Fig. 1

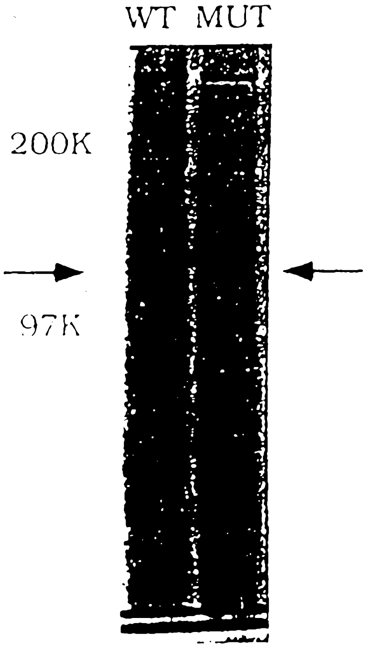


Fig. 2A

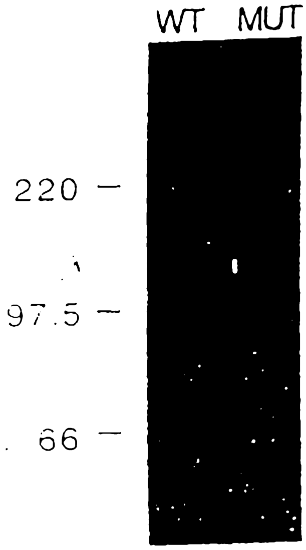


Fig. 2B

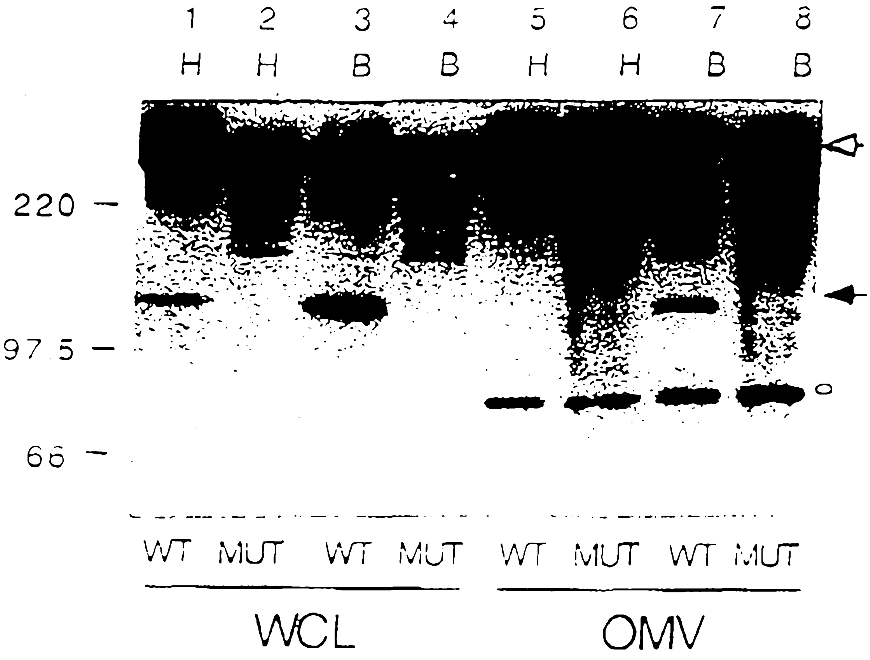

1
2
3
4
5
6
7
8
H
H
B
B
H
H
B
B
220
97.5
66
WT
MUT
WT
MUT
WT
MUT
WT
MUT
WCL
OMV

Fig. 2C

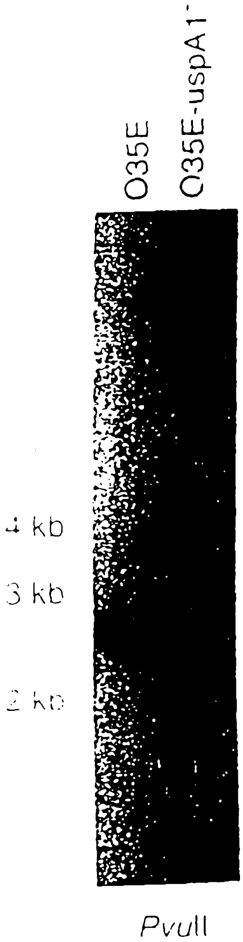
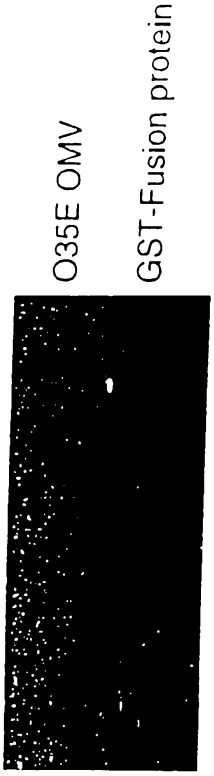


Fig. 3



MAb 17C7

Fig. 4

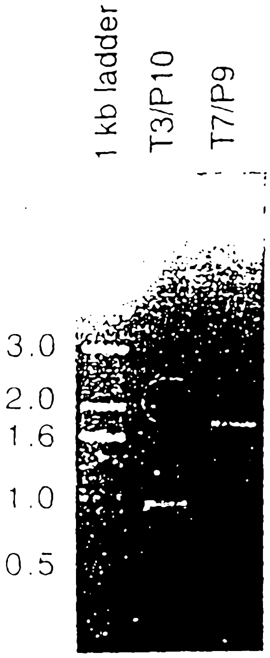


Fig. 5

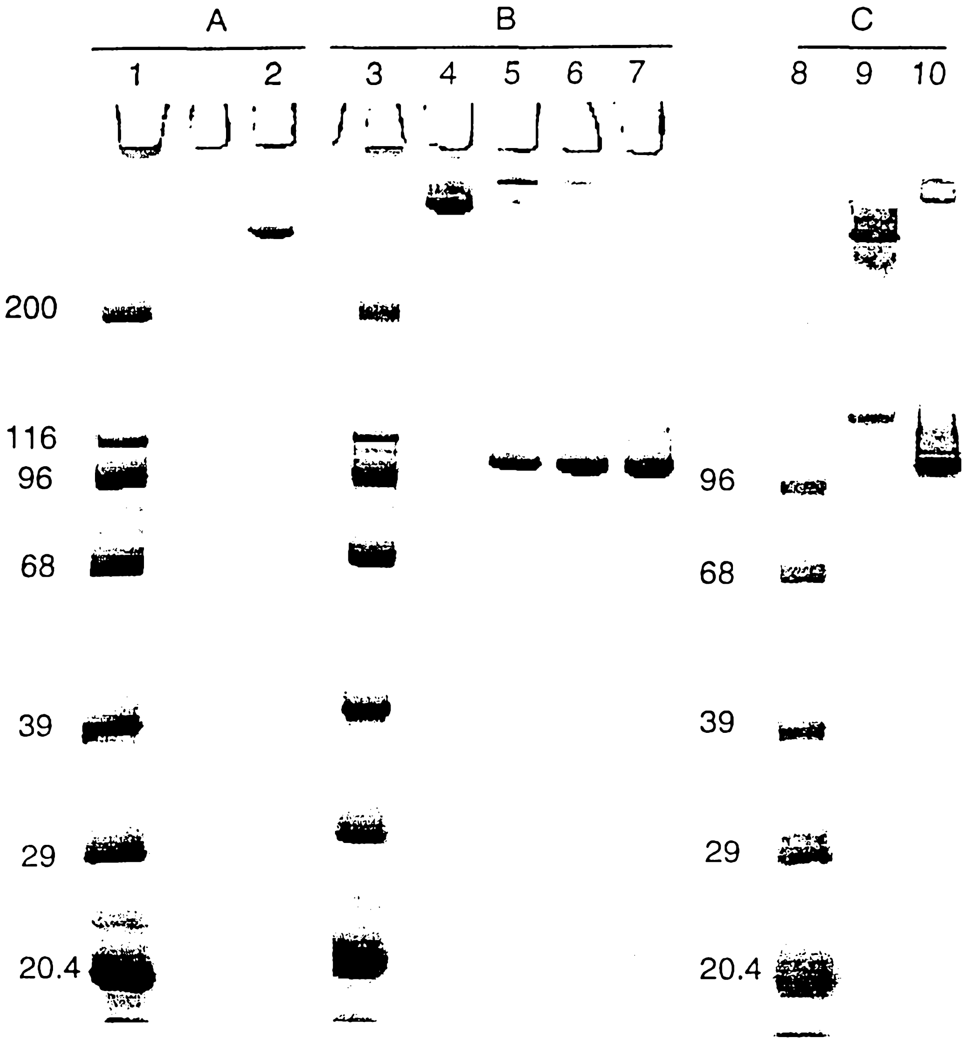


Fig. 6

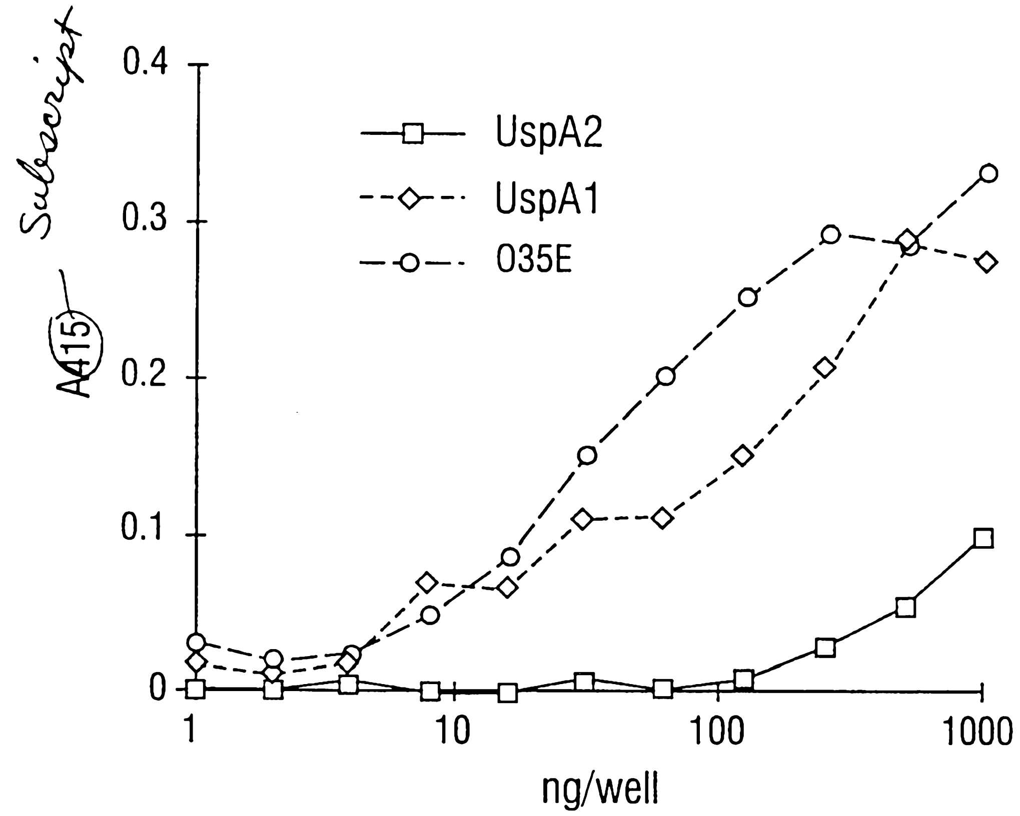

Subscript
A415
0.4
0.3
0.2
0.1
0
1
10
100
1000
ng/well
UspA2
UspA1
O35E

Fig. 7

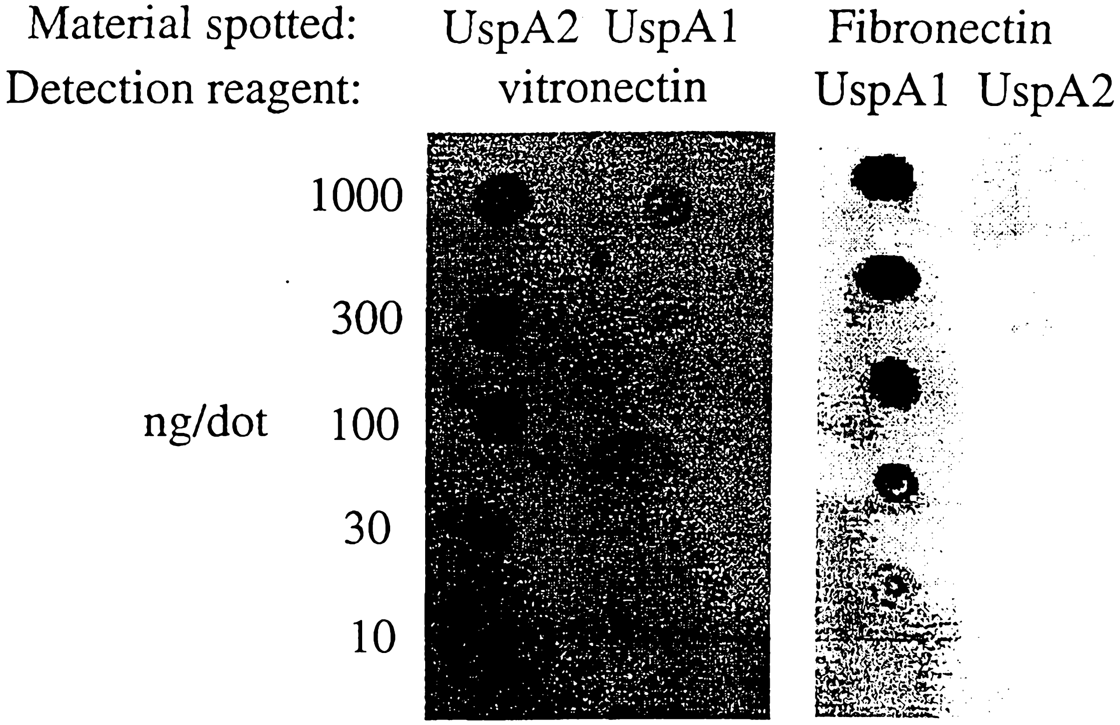

Material spotted:
Detection reagent:
UspA2 UspA1
vitronectin
Fibronectin
UspA1 UspA2
1000
300
ng/dot
100
30
10

Fig. 8

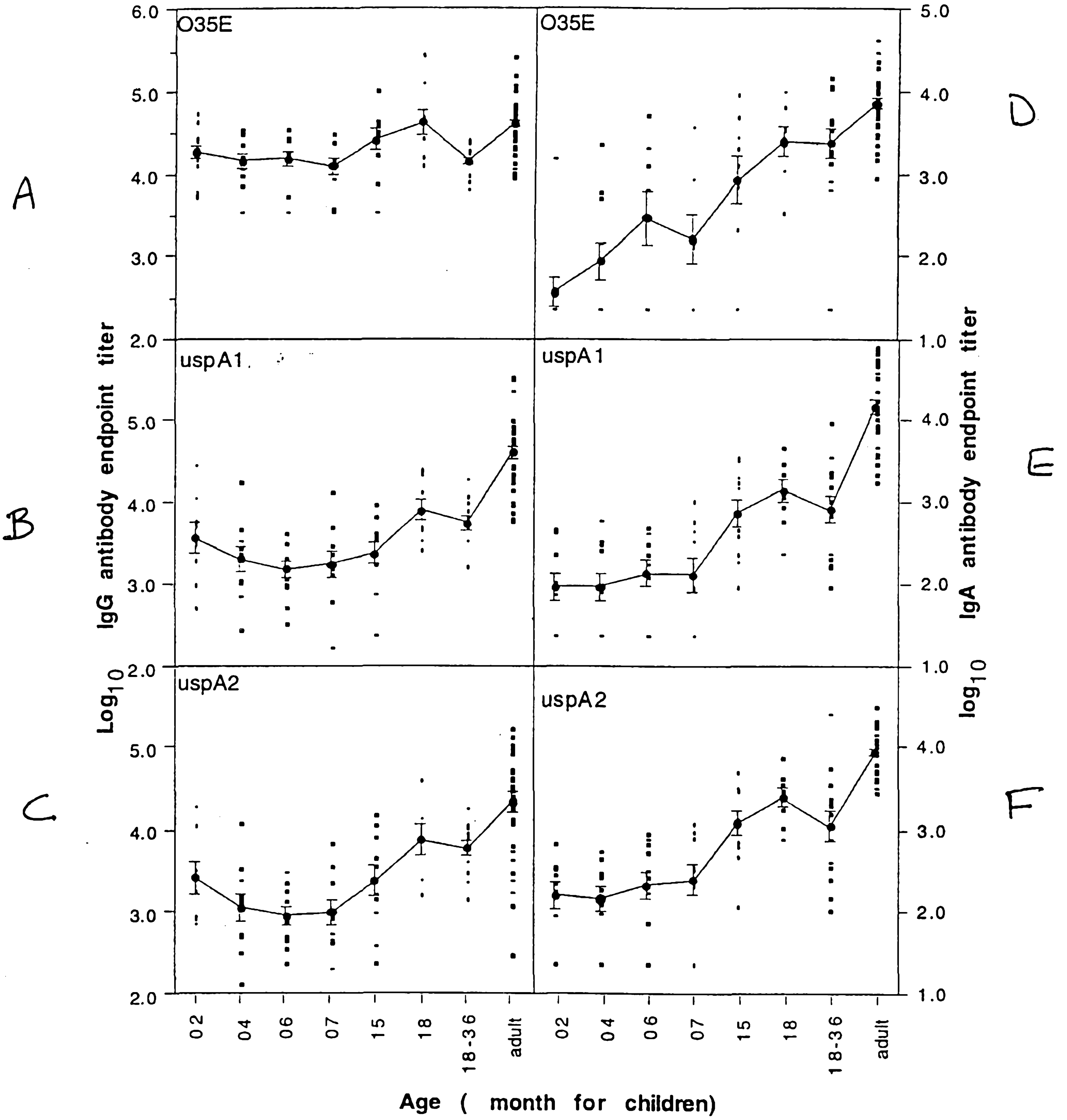
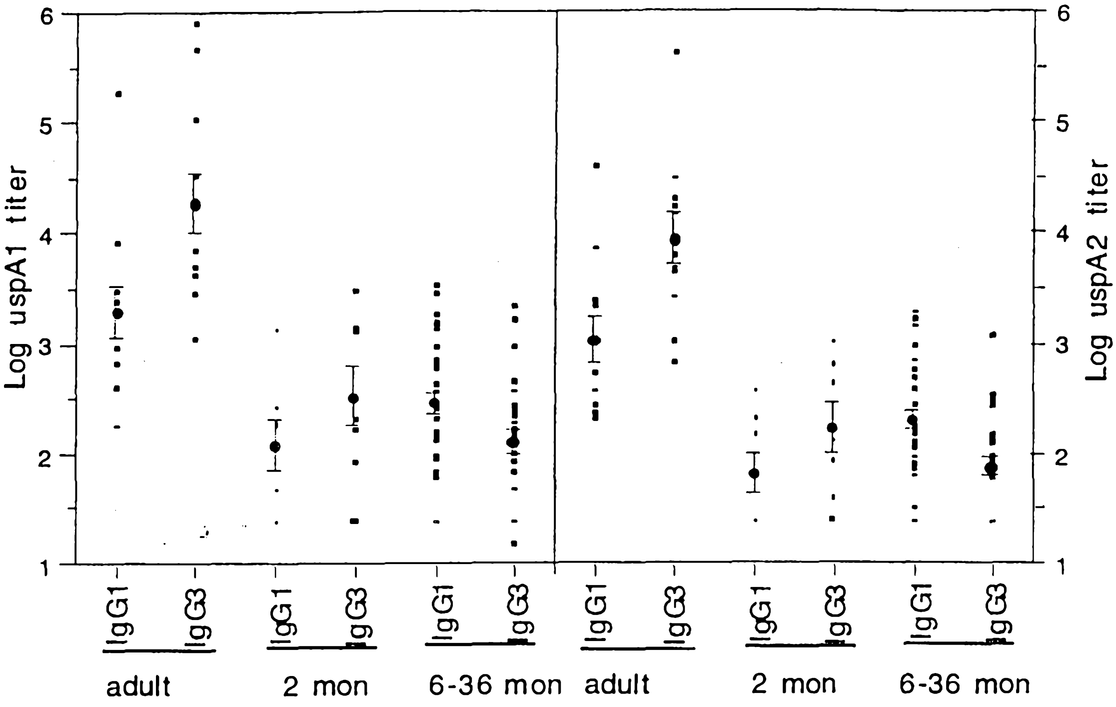

A
B
C
D
E
F
O35E
O35E
uspA1
uspA1
uspA2
uspA2
Log10 IgG antibody endpoint titer
log10 IgA antibody endpoint titer
6.0
5.0
4.0
3.0
2.0
1.0
02
04
06
07
15
18
18-36
adult
Age (month for children)

Fig. 9


Log uspA1 titer
Log uspA2 titer
1
2
3
4
5
6
IgG1
IgG3
adult
2 mon
6-36 mon

A B

Fig. 10

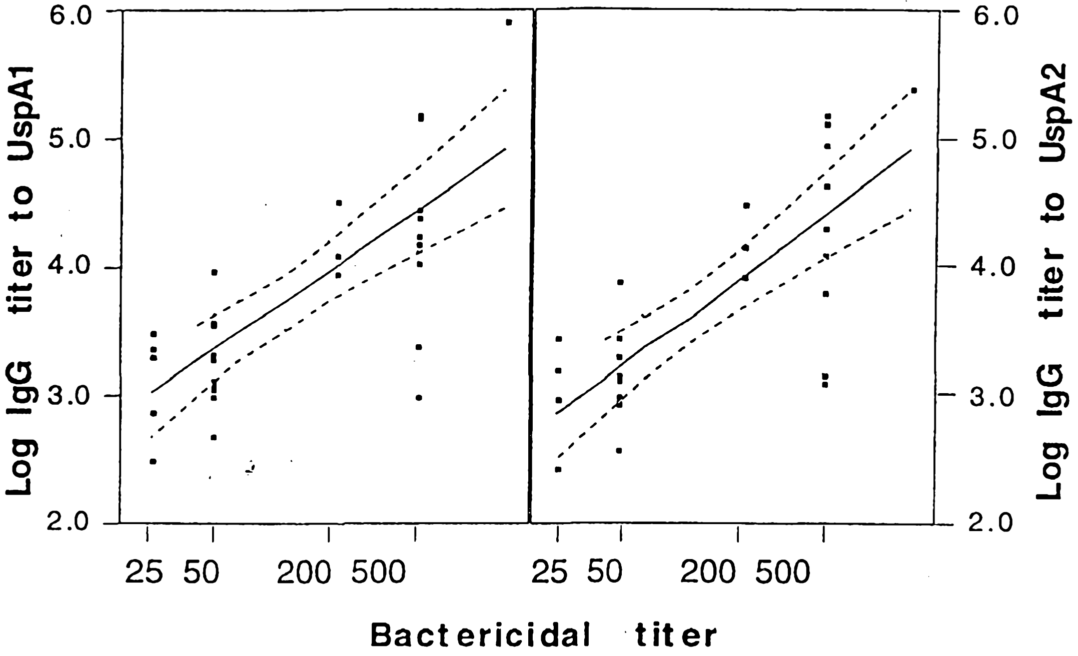

6.0
5.0
4.0
3.0
2.0
Log IgG titer to UspA1
Log IgG titer to UspA2
25 50 200 500
25 50 200 500
Bactericidal titer

Fig. 11

MAb 12C7 EPITOPE MAPPING

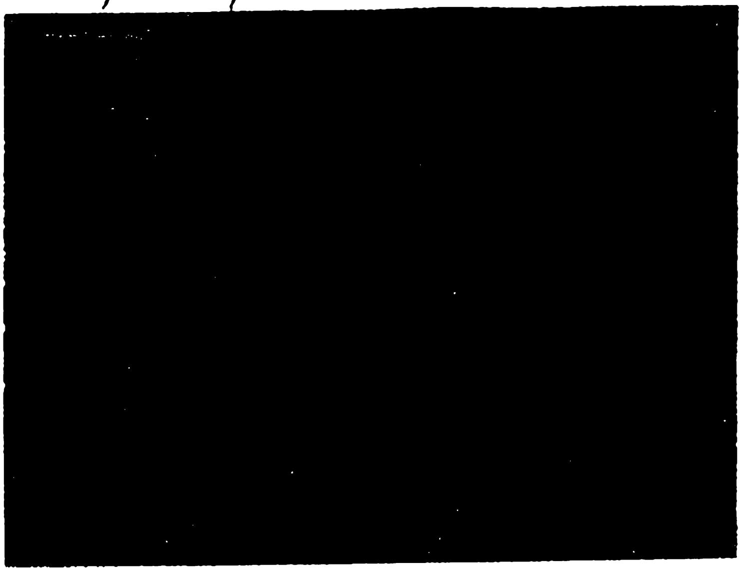


Fig.12

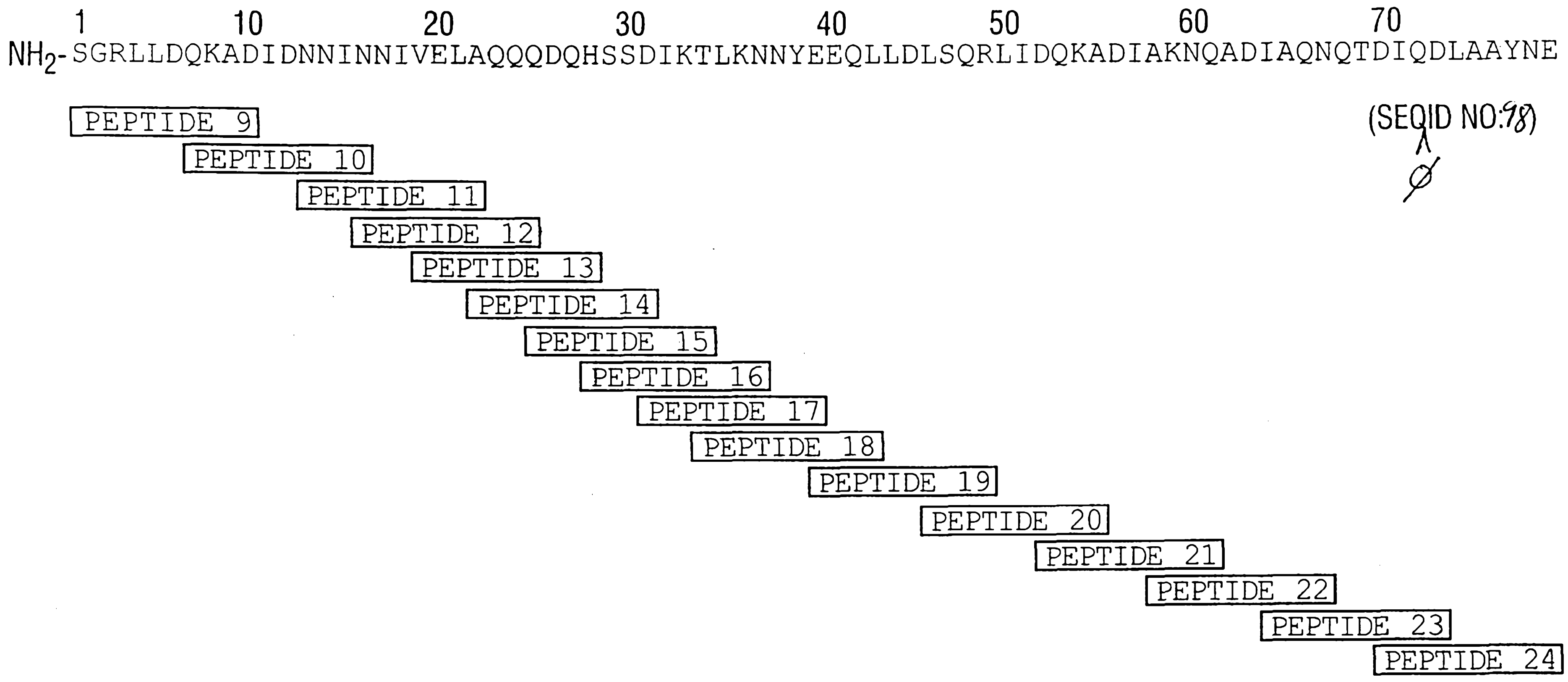

1
10
20
30
40
50
60
70
NH2-SGRLLDQKADIDNNINNIVELAQQQDQHSSDIKTLKNNYEEQLLDLSQRLIDQKADIAKNQADIAQNQTDIQDLAAYNE
(SEQID NO:98)
Ø
PEPTIDE 9
PEPTIDE 10
PEPTIDE 11
PEPTIDE 12
PEPTIDE 13
PEPTIDE 14
PEPTIDE 15
PEPTIDE 16
PEPTIDE 17
PEPTIDE 18
PEPTIDE 19
PEPTIDE 20
PEPTIDE 21
PEPTIDE 22
PEPTIDE 23
PEPTIDE 24

Fig.13

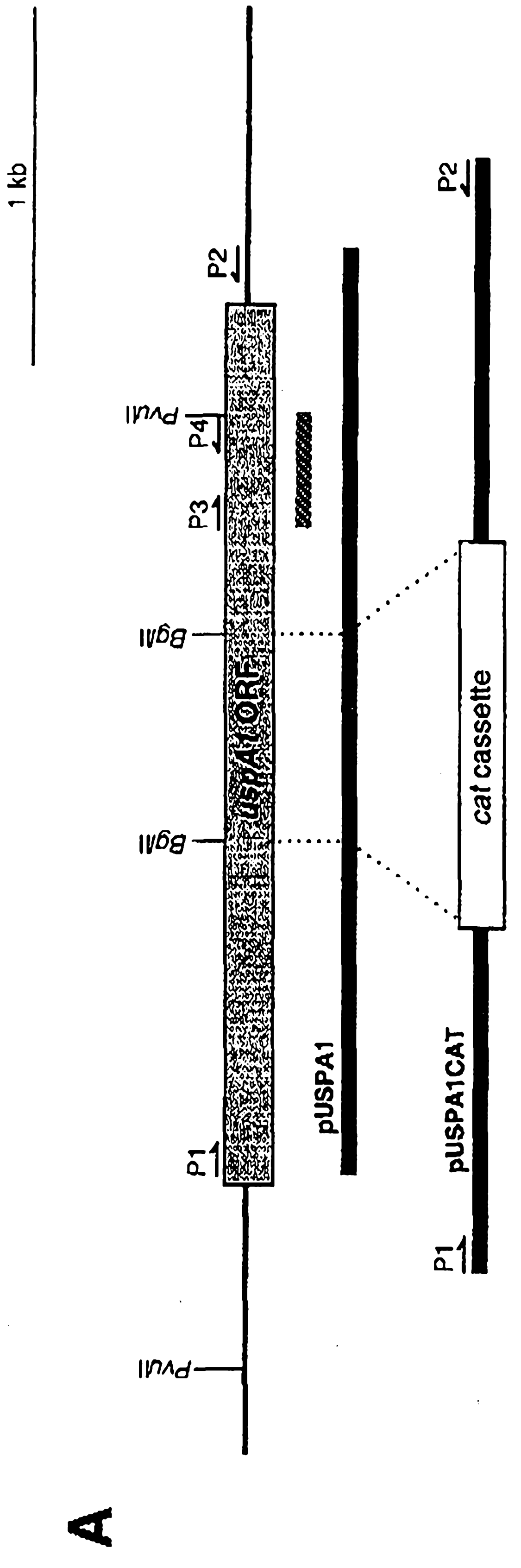


FIG. 14A

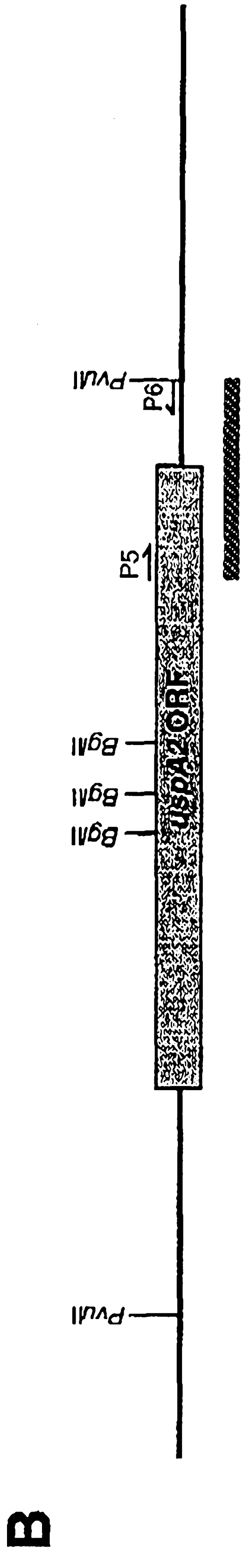


FIG. 14B

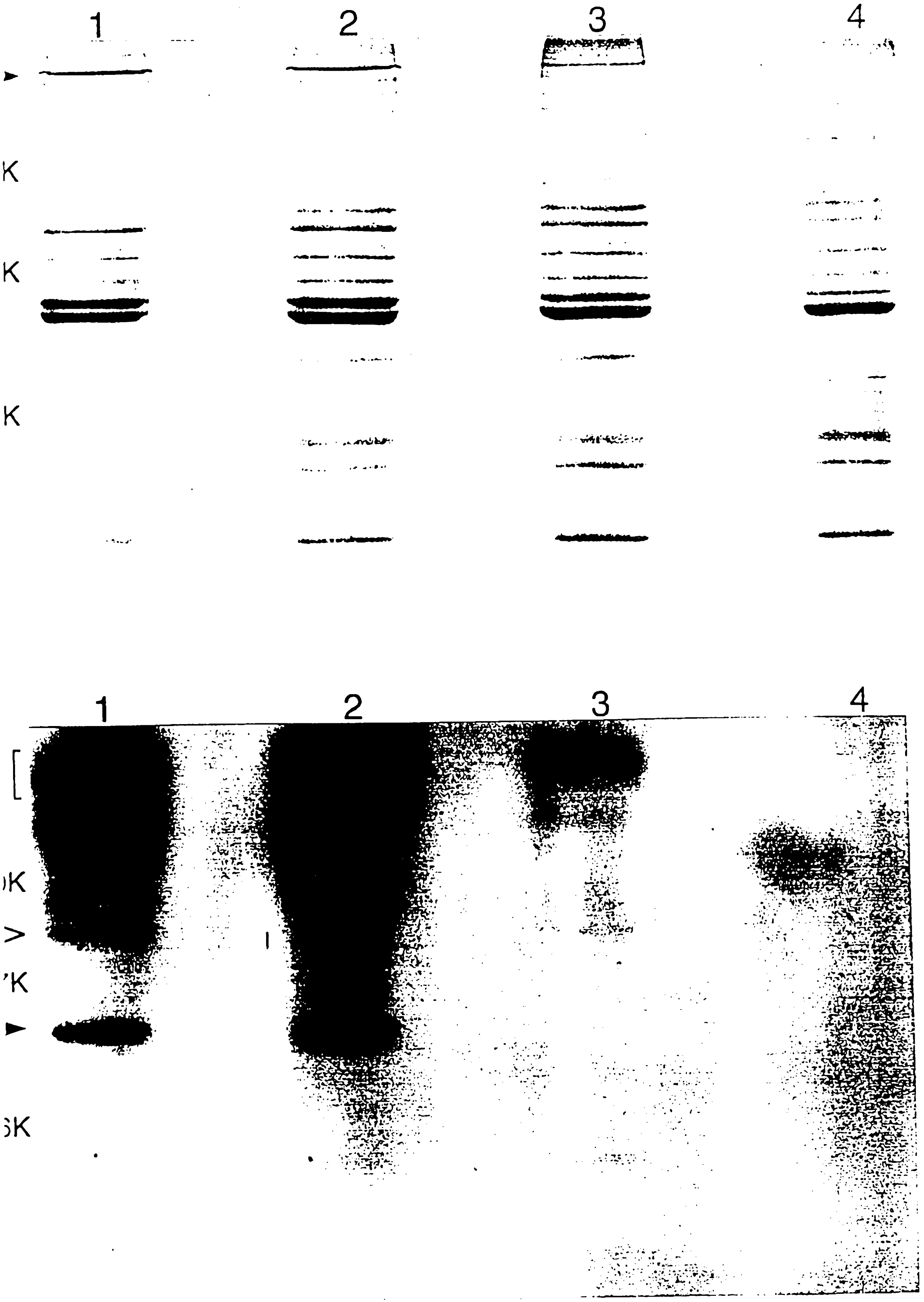


Fig. 15

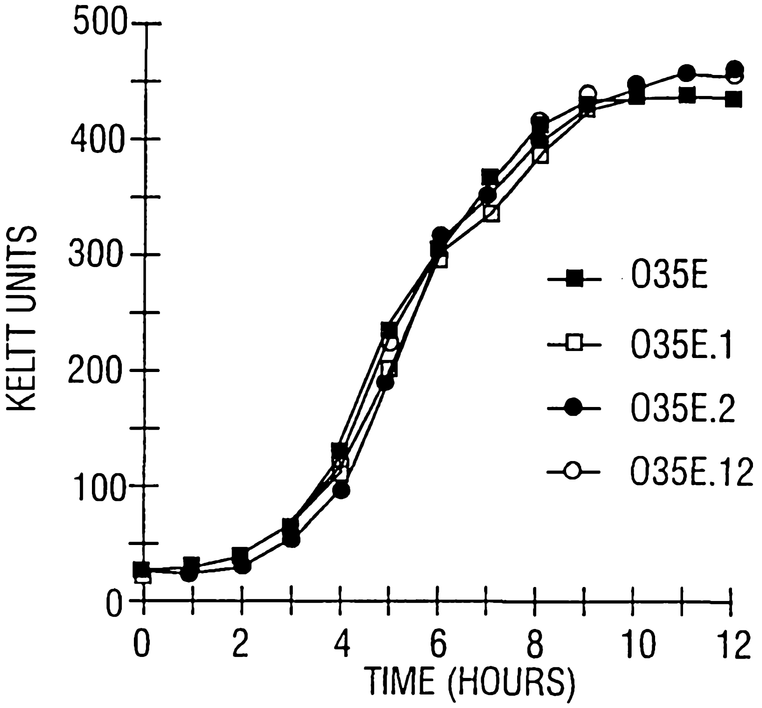


FIG. ~~18~~/16

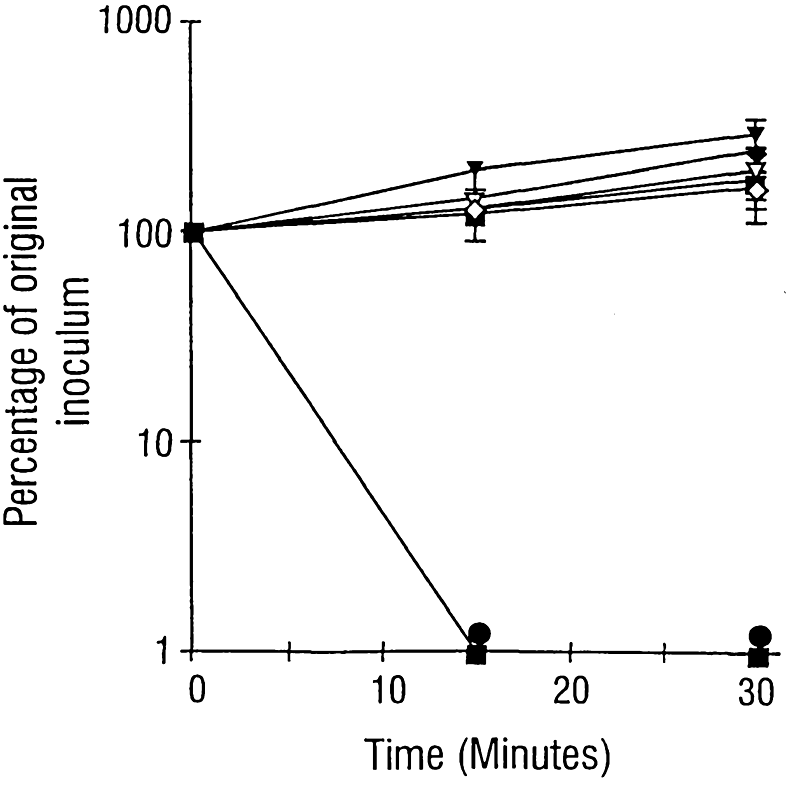


Fig. 16