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WO 2007/018463 A2
YU-CHING SU ET AL, "Impact of sequence diversity in the Moraxella catarrhalis UspA2/UspA2H head domain on vitronectin binding and antigenic variation", MICROBES AND INFECTION, (2013), vol. 15, no. 5, pages 375 - 387
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(54) Title: USPA2 PROTEIN CONSTRUCTS AND USES THEREOF

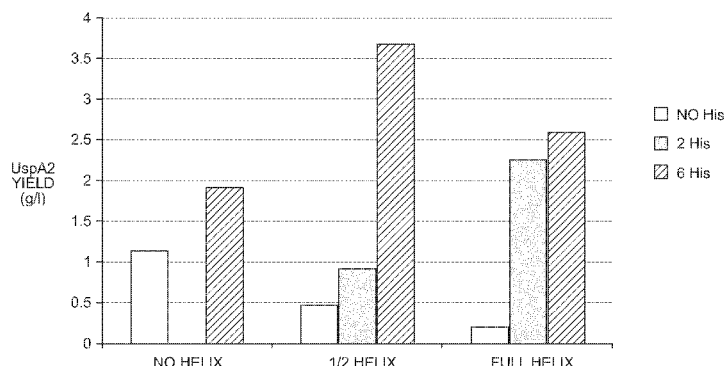
UspA2 YIELD FROM PROTEIN CONSTRUCTS MC-001, MC-002, MC-004,
MC-005, MC-006, MC-007, MC-008 AND MC-010 EVALUATED
IN FERMENTER; DATA FROM TABLE 4. His = HISTIDINE.

FIG. 3

(57) Abstract: The present invention relates to compositions comprising *Moraxella catarrhalis* (*M. catarrhalis*) Ubiquitous surface protein A2 (UspA2). More particularly, the present application relates to UspA2 protein constructs and immunogenic compositions, comprising the constructs, vaccines comprising such immunogenic compositions and therapeutic uses of the same. The invention further relates to compositions comprising UspA2 in combination with at least one antigen from *Haemophilus influenzae*, immunogenic compositions comprising the antigens, vaccines comprising such immunogenic compositions and therapeutic uses of the same.

USPA2 PROTEIN CONSTRUCTS AND USES THEREOF

FIELD OF THE INVENTION

[01] The present invention relates to compositions comprising *Moraxella catarrhalis* (*M. catarrhalis*, *M. cat.*) Ubiquitous surface protein A2 (UspA2). More particularly, the present application relates to UspA2 protein constructs and immunogenic compositions comprising the constructs, vaccines comprising such immunogenic compositions and therapeutic uses of the same.

BACKGROUND OF THE INVENTION

[02] Ubiquitous surface protein A2 (UspA2) is a trimeric autotransporter that appears as a lollipop-shared structure in electron micrographs (Hoiczky et al. EMBO J. 19: 5989-5999 (2000)). It is composed of a N-terminal head, followed by a stalk which ends by an amphipathic helix and a C-terminal membrane domain. (Hoiczky et al. EMBO J. 19: 5989-5999 (2000)). UspA2 contains a very well conserved domain (Aebi et al., Infection & Immunity 65(11) 4367-4377 (1997)), which is recognized by a monoclonal antibody that was shown protective upon passive transfer in a mouse *Moraxella catarrhalis* challenge model (Helminen et al. J Infect Dis. 170(4): 867-72 (1994)).

[03] UspA2 has been shown to interact with host structures and extracellular matrix proteins like fibronectin (Tan et al., J Infect Dis. 192(6): 1029-38 (2005)) and laminin (Tan et al., J Infect Dis. 194(4): 493-7 (2006)), suggesting it can play a role at an early stage of *Moraxella catarrhalis* infection.

[04] UspA2 also seems to be involved in the ability of *Moraxella catarrhalis* to resist the bactericidal activity of normal human serum. (Attia AS et al. Infect Immun 73(4): 2400-2410 (2005)). It (i) binds the complement inhibitor C4bp, enabling *Moraxella catarrhalis* to inhibit the classical complement system, (ii) prevents activation of the alternative complement pathway by absorbing C3 from serum and (iii) interferes with the terminal stages of the complement system, the Membrane Attack Complex (MAC), by binding the complement regulator protein vitronectin. (de Vries et al., Microbiol Mol Biol Rev. 73(3): 389-406 (2009)).

[05] *Moraxella catarrhalis* is an important and common respiratory pathogen that has been associated with increased risk of exacerbations in chronic obstructive pulmonary disease (COPD) in adults. (Sateesh et al., Journal of Chronic Obstructive Pulmonary Disease 3:109-115 (2006)).

[06] A need for vaccines for *Moraxella catarrhalis* exists.

BRIEF SUMMARY OF THE INVENTION

[07] As a first aspect, the present invention provides the proteins of formula (I).

[08] $A - (R_1)_m - (B)_n$ (formula I)

[09] wherein:

A is UspA2 from *Moraxella catarrhalis* or an immunogenic fragment thereof;

R_1 is an amino acid;

m is 0, 1 or 2;

B is histidine; and

n is 0, 1, 2, 3, 4, 5 or 6.

[9a] In a particular aspect, the present invention provides an isolated protein comprising formula I:

$A - (R_1)_m - (B)_n$ (formula I)

wherein:

A is an immunogenic fragment of UspA2 from *Moraxella catarrhalis* having at least 90% identity to any one of SEQ ID NOs:39 to 43;

R_1 is an amino acid;

m is 0 or 2;

B is histidine; and

n is 1, 2, 3, 4, 5 or 6.

[10] As a second aspect, the present invention provides immunogenic compositions comprising proteins of formula (I) and proteins of the invention. The composition may further

comprise a pharmaceutically acceptable adjuvant. The composition may comprise an excipient.

[11] In a third aspect, the present invention provides a method for the treatment or prevention of a condition or disease caused wholly or in part by *Moraxella catarrhalis*. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention.

[12] In a fourth aspect, the present invention provides a method for the treatment or prevention of otitis media. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention.

[13] In a fifth aspect, the present invention provides a method for the treatment or prevention of exacerbations in chronic obstructive pulmonary disease. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention.

[14] In a sixth aspect, the present invention provides a method for the treatment or prevention of pneumonia. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention.

[15] In a seventh aspect, the present invention provides a pharmaceutical composition comprising a protein of formula (I) or a protein of the invention for use in the treatment or prevention of a condition or disease caused wholly or in part by *Moraxella catarrhalis*. Pharmaceutical compositions may further comprise a pharmaceutically acceptable adjuvant.

[16] In an eighth aspect, the present invention provides nucleic acids encoding the proteins of the invention.

[17] In a ninth aspect, the present invention provides a process of producing nucleic acids of the invention.

[18] In a tenth aspect, the present invention provides a composition comprising at least one antigen from *Moraxella catarrhalis* and at least one antigen from *Haemophilus influenzae*. The composition may further comprise a pharmaceutically acceptable adjuvant. The composition may comprise an excipient.

[19] In an additional aspect, the present invention provides a method for the treatment or prevention of a condition or disease caused wholly or in part by *Moraxella catarrhalis* and/or *Haemophilus influenzae*. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention.

[20] In a further aspect, the present invention provides a method for the treatment or prevention of exacerbations in chronic obstructive pulmonary disease. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention and a therapeutically effective amount of at least one antigen from *Haemophilus influenzae*.

[21] The present invention also provides a pharmaceutical composition comprising a protein of formula (I) or a protein of the invention for use in the treatment or prevention of a condition or disease caused wholly or in part by *Moraxella catarrhalis* in combination with at least one antigen from *Haemophilus influenzae*. Pharmaceutical compositions may further comprise a pharmaceutically acceptable adjuvant.

[22] Further aspects of the present invention are described in the detailed description of particular embodiments, examples and claims which follow.

[22a] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

[22b] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: A typical fermentation profile with the High Cell Density Induction (HCDI) processes and the parameters monitored during 20L-scale fed-batch fermentation.

Figure 2: A typical fermentation profile with the Low Cell Density Induction (LCDI) processes and the parameters monitored during 20L-scale fed-batch fermentation.

Figure 3: UspA2 yield from protein constructs MC-001, MC-002, MC-004, MC-005, MC-006, MC-007, MC-008 and MC-010 evaluated in fermenter; data from Table 4.

Figure 4: Molecular weight distribution of purified MC-005 determined by sedimentation velocity analytical ultracentrifugation. The majority of protein is found as a trimer, with a small proportion of a higher molecular weight oligomer that may correspond to dimer of trimer. MW

= molecular weight. kDa =kilodalton.

Figure 5: Molecular weight distribution of purified MC-001 determined by sedimentation velocity analytical ultracentrifugation. Majority of protein is found as a trimer.

Figure 6: Molecular weight distribution of purified MC-001 determined by sedimentation velocity analytical ultracentrifugation. The sample presents multiple species and is highly polydisperse. The sedimentation coefficient of the major species detected doesn't correspond to the one of the trimers normally detected in the other lots.

Figure 7: Molecular weight distribution of purified MC-001 determined by sedimentation velocity analytical ultracentrifugation. Majority of protein is found as a trimer.

Figure 8: Molecular weight distribution of purified MC-007 determined by sedimentation velocity analytical ultracentrifugation. Majority of protein is found as a trimer.

Figure 9: Far-UV circular dichroism (CD) spectra of UspA2 constructs giving an indication of protein secondary structures.

Figure 10: Secondary structures monitoring by circular dichroism (CD) during thermal unfolding of MC-005 (UspA2 Δ helix + 6His). Visual analysis of the spectra clearly shows that protein loses most of its secondary structures at 33°C.

Figure 11: Secondary structures monitoring by circular dichroism (CD) during thermal unfolding of MC-007 (UspA2 full helix + 6His). Visual analysis of the spectra shows that loss of secondary structure is slower compared to the construct without helix. Structural changes are detectable upon heating to 33°C, but complete unfolding seems to occur between 35°C and 37°C.

Figure 12: MALDI spectrum of MC-001 lot opt-01. The mass observed at 57427Da may be coherent with the demethionylated protein, while the peak at 57620Da could correspond to the complete protein.

Figure 13: MALDI spectrum of MC-011 lot BMP37. The mass observed may be coherent with the demethionylated protein. The two other peaks at +186Da and +366Da are unidentified.

Figure 14: Protective efficacy of MC-001 and MC-007 in a mouse model of lung colonization.

Figure 15: Antibody response directed against UspA2 induced after intramuscular administration in mice, where PII and PIII indicate, respectively, anti-IgG levels in sera collected at day 28 (post II) and day 42 (post III).

Figure 16: Bactericidal titers induced by UspA2 against a homologous strain formulated with different adjuvants (AS01_E, AS04_C and AIPO₄).

Figure 17: Antibody response directed against UspA2 induced after intramuscular administration in mice, using different formulations of antigens and adjuvants.

Figure 18: Bactericidal titers induced by UspA2 against a homologous strain, using different formulations of antigens and adjuvants.

Figure 19: IgG response induced against PD in mice by PD-PEPiiA-UspA2 vaccine (a trivalent NTHi-M.cat. vaccine), formulated with different adjuvants.

Figure 20: IgG response induced against PE in mice by PD-PEPiiA-UspA2 vaccine (a trivalent NTHi-M. cat. vaccine), formulated with different adjuvants.

Figure 21: IgG response induced against PiiA in mice by PD-PEPiiA-UspA2 vaccine (a trivalent NTHi-M. cat. vaccine), formulated with different adjuvants.

Figure 22: Immunogenicity of PE in the bivalent PD-PEPiiA and trivalent PD-PEPiiA-UspA2 formulations with AS01E.

Figure 23: Immunogenicity of PiiA in the bivalent PD-PEPiiA and trivalent PE-PiiA-UspA2 formulations with AS01E.

Figure 24: Immunogenicity of PD in the bivalent PD-PEPiiA and trivalent PE-PiiA-UspA2 formulations with AS01E.

Figure 25: Effect of the tetravalent PD/ PEPiiA/ UspA2/ AS01_E vaccine formulation on mouse lungs pre-sensitized with heat inactivated *M. cat.* - Perivascularitis and peribronchiolitis in PBS immunized mice.

Figure 26: Effect of the tetravalent PD/ PEPiiA/ UspA2/ AS01_E vaccine formulation on mouse lungs pre-sensitized with heat inactivated *M. cat.* - Day 2 post-immunization.

Figure 27: Effect of the tetravalent PD/ PEPiiA/ UspA2/ AS01_E vaccine formulation on mouse lungs pre-sensitized with heat inactivated *M. cat.* - Day 7 post-immunization.

Figure 28: Effect of the tetravalent PD/ PEPiIA/ UspA2/ AS01_E vaccine formulation on mouse lungs pre-sensitized with heat inactivated *M. cat.* - Day 14 post-immunization.

Figure 29: Effect of the tetravalent PD/ PEPiIA/ UspA2/ AS01_E vaccine formulation on mouse lungs pre-sensitized with heat inactivated *M. cat.* – Detailed results

Figure 30: Post-vaccination lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing IL17. Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 31: Post-vaccination lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing TNF α . Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 32: Post-vaccination lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing IFN γ . Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 33: Post-vaccination lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing IL13. Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 34: Post-challenge lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing IL17. Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 35: Post-challenge lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing TNF α . Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 36: Post-challenge lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing IFN γ . Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

Figure 37: Post-challenge lung CD4 T cell responses upon *M. cat.* WC re-stimulation. Lung CD4 cells expressing IL13. Restimulated with heat-inactivated *M. cat* whole cells (WC) or medium.

DETAILED DESCRIPTION OF THE INVENTION

[23] Unless otherwise explained or defined herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. For example, definitions of common terms in molecular biology can be found in Benjamin Lewin, *Genes V*, published by Oxford University Press, 1994 (ISBN 0-19-854287-9); Kendrew et al. (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0-632-02182-9); and Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 1-56081-569-8).

[24] The singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. Additionally, numerical limitations given with respect to concentrations or levels of a substance, such as an antigen may be approximate. Thus, where a concentration is indicated to be (for example) approximately 200 pg, it is intended that the concentration includes values slightly more or slightly less than ("about" or "~") 200 pg.

[25] Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of this disclosure, suitable methods and materials are described below.

[26] The term "comprises" means "includes". Thus, unless the context requires otherwise, the word "comprises," and variations such as "comprise" and "comprising" will be understood to imply the inclusion of a stated compound or composition (e.g., nucleic acid, polypeptide,

antigen) or step, or group of compounds or steps, but not to the exclusion of any other compounds, composition, steps, or groups thereof. The abbreviation, "e.g." is derived from the Latin *exempli gratia*, and is used herein to indicate a non-limiting example. Thus, the abbreviation "e.g." is synonymous with the term "for example."

[27] In order to facilitate review of the various embodiments of this disclosure, the following explanations of terms are provided. Additional terms and explanations are provided in the context of this disclosure.

[28] A "subject" as used herein is a mammal, including humans, non-human primates, and non-primate mammals such as members of the rodent genus (including but not limited to mice and rats) and members of the order Lagomorpha (including but not limited to rabbits).

[29] As used herein "UspA2" means Ubiquitous surface protein A2 from *Moraxella catarrhalis*. UspA2 may consist of or comprise the amino acid sequence of SEQ ID NO: 1 from ATCC 25238.

MKTMKLLPLKIAVTSAMI IGLGAASTANAQAKNDITLEDLPYLIKKIDQNELEADIGDIT
ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
AIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDIAKNNESIEDLYD
FGHEVAESIGEIIHAHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
NIQDLATYNELQDQYAKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDA
LNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINN
IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDSDRVTAIDTK
VNAFDGRITALDSKVENGMAAQAALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRV
NPNLAFKAGAAINTSGNKKGSYNIGVNYEF (SEQ ID NO: 1)

as well as sequences with at least or exactly 63%, 66%, 70%, 72%, 74%, 75%, 77%, 80%, 84%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identity, over the entire length, to SEQ ID NO: 1. Comparison of 38 sequences of UspA2 from *Moraxella catarrhalis* (Table 1, SEQ ID NO: 1 – SEQ ID NO: 38) demonstrated approximately 63% to approximately 100% identity to UspA2 as set forth in SEQ ID NO. 1.

[30] UspA2 as described in SEQ ID NO: 1 contains a signal peptide (for example, amino acids 1 to 29 of SEQ ID NO: 1), a laminin binding domain (for example, amino acids 30 to 177 of SEQ ID NO: 1), a fibronectin binding domain (for example, amino acids 165 to 318 of SEQ ID NO: 1) (Tan et al. JID 192: 1029-38 (2005)), a C3 binding domain (for example, amino acids 30 to 539 of SEQ ID NO: 1 (WO2007/018463), or a fragment of amino acids 30 to 539 of SEQ ID NO: 1, for example, amino acids 165 to 318 of SEQ ID NO: 1 (Hallström T et al. J. Immunol. 186: 3120-3129 (2011)), an amphipathic helix (for example, amino acids 519 to 564 of SEQ ID NO: 1 or amino acids 520-559 of SEQ ID NO: 1, identified using different prediction methods) and a C terminal anchor domain (for example, amino acids 576 to 630 amino acids of SEQ ID NO: 1 (Brooks et al., Infection & Immunity, 76(11), 5330-5340 (2008)).

[31] UspA2 amino acid differences have been described for various *Moraxella catarrhalis* species. See for example, J Bacteriology 181(13):4026-34 (1999), Infection and Immunity 76(11):5330-40 (2008) and PLoS One 7(9):e45452 (2012).

[32] UspA2 may consist of or comprise an amino acid sequence that differs from SEQ ID NO: 1 at any one or more amino acid selected from the group consisting of: AA (amino acid) 30 to 298, AA 299 to 302, AA 303 to 333, AA 334 to 339, AA 349, AA 352 to 354, AA 368 to 403, AA 441, AA 451 to 471, AA 472, AA 474 to 483, AA 487, AA 490, AA 493, AA 529, AA 532 or AA 543. UspA2 may consist of or comprise an amino acid sequence that differs from SEQ ID NO: 1 in that it contains at least one amino acid insertion in comparison to SEQ ID NO: 1. UspA2 may consists of or comprise an amino acid sequence that differs from SEQ ID NO: 1 at any one of the amino acid differences in SEQ ID NO: 2 through SEQ ID NO: 38. For example, SEQ ID NO: 1 may contain K instead of Q at amino acid 70, Q instead of G at amino acid 135 and/or D instead of N at amino acid 216.

[33] Table 1: UspA2 amino acid sequences from 38 strains of *Moraxella catarrhalis* (SEQ ID NO: 1 - SEQ ID NO: 38).

Strain	UspA2 sequences
ATCC 25238 (SEQ ID NO: 1)	MKTMKLLPLKIAVTSAMIIGLGAASTANAQAKNDITLEDLPYLIKKIDQNELEADIGDITALEK YLALSQYGNILALEELNKALEELDEDVGNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQG LADFVEGQREGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGET HAHNEAQNETLKGLITNSLENTNNITKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNI YELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAKQT

	EAIDALNKASSENTQNIEDLAAYNELQDAYAKQOTEADALNKASSENTQNIEDLAAYNELQDA YAKQOTEADALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDR IAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNA ITKNAKSITDLGTVKVDGFSRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSVGK FNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (630 aa)
American 2933 (SEQ ID NO: 2)	MKTMKLLPLKIAVTSAMIIGLGAASTANAQSRDRSLEDIQDSISKLVQDDINTLKQDQQKMNKY LLLNQLANTLITDELNNNVIKNTNSIEALGDEIGWLENDIADLEEGVEELTKNQNTLIEKDEEH DRLIAQNQADIQTLENNVVEELFNLSGRLIDQEADIAKNNASIEELYDFDNEVAERIGEIHAYT EEVNKTLENLITNSVKNTDNIDKNKADIDNNINHIYELAQQQDQHSSDIKTLKNNVEEGLLELS GHLIDQKADLTKDIAKALSNVEEGLLDLSGRLLDQKADLTKDIAKALSNVEEGLLDLSGRLLDQ KADIAQNQTDIQDLAAYNELQDQYAKQOTEADALNKASSENTQNIEDLAAYNELQDAYAKQOT EAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTNRIATAEL GIAENKKDAQIAKAQANANKTAIDENKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDG FDGRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSVGKFNATAALGGYGSKSAVA IGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (613 aa)
American 2912 (SEQ ID NO: 3)	MKTMKLLPLKIAVTSALIIGLGAASTANAQQQLQTETFLPNFLSNDNYDLTDPFYHNMILGDTA LLDKQDGSQPQLKFYSNDKDSVPDSLLFSKLLHEQQQLNGFKKGDITIIPLDKDGKPVYQVDYKLD GKGKKQKRRQVYSVTTKTATDDVDNSAYSRLGKVDLDDEMFLNHDITSLYDVTANQQDAI KDLKKGKGLNKLKELDKVGVLSRDIGSLNDDVAQNNESIEDLYDFSQEVADSIGEIHANHK AQNETLQDLITNSVENTNNITKNKADIQALENNVVEELFNLSGRLIDQKADLTDKIKTLESNVE EGLLELSGHLIDQKADIAKNQADIAQNQANIQDLAAYNELQDAYAKQOTEADALNKASSENTQ NIEDLAAYNELQDAYAKQOTEADALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSD IKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDENKASADTK FAATADAITKNGNAITKNAKSITDLGTVKVDGFSRVTALDTKVNAFDGRITALDSKVENGMAAQ AALSGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGV NYEF (644 aa)
American 2908 (SEQ ID NO: 4)	MKTMKLLPLKIAVTSALIVGLGAASTANAQLVERFFPNIFLDKPLAKQHYHNVVVGDTISIVSDL QSNSDQLKFYSDDDEGLVPDSLLFNKMLHEQLLNGFKREGDTIIPLDENGKPVYKVDYKLDGKEPR KVYSVTTKIATAEDVATSSYANGIQKDIDDLDFDHQVTERLTQHGKTIYRNGERILANEESVQ YLNKEVQNNIEHIYELAQQQDQHSSDIKTLKESNVEKGLLELSGHLIDQKADLTDKIKTLESNVE EGLLDLSGRLLIDQKADLTDKIKTLESNVEEGLLDLSGRLLIDQKADIAQNQANIQDLAAYNELQD QYAKQOTEADALNKASSENTQNIEDLAAYNELQDAYAKQOTEADALNKASSENTQNIAKNQ ADIANNINNIYELAQQQDQHSSDIKTLAKASAANTNRIATAELGIAENKKDAQIAKAQANANKTA IDENKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFSRVTALDTKVNAFDGRITAL DSKVENGMAAQAALSGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTS

	GNKKGSYNIGVNYEF (591 aa)
Finnish 307 (SEQ ID NO: 5)	MKTMKLLPLKIAVTSAMIIGLGAASTANAQQQQQQQQQQSRTEIFFFNIFFNENHDELDDAYH NIILGDPALLQKQDGSQFQLKFYSNDKDSVPDSILFSKLLHEQQINGFKKGDIIIFLDKDGKFPV YQVDYKLDGKGGKQKRRQVYSVTTTKTATDDDVNSAYS SRGILGKVDDLDDEMNFNLNHDITSLYDV TANQQDAIKGLKKGVKGLNKKELKELDKVGVLSRDIGSLNDDVAQNNESEDLYDFSQEVADSI GEIHAHNKAQNETLQDLITNSVENTNITNKNKADIQALENNVVEELFNLSGRLLDQKADLTKDI KTLESNVEEGLLELSGRLIDQKADIAKNQADIAQNQANIQDLAAYNELQDAYAKQQTEAIDALN KASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTE AIDALNKASSENTQNIKNQADIANNINNIYELAQQQQQHQSSDIKTLAKASAANTDRIAKNKAD ADASFETLTKNQNTLIEKDKERDKLITANKTAIDENKASADTKFAATADAITKNGNAITKNAKS ITDLGTKVDAFDGRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQFPYSVGKFNATAAL GGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (687 aa)
Finnish 353 (SEQ ID NO: 6)	MKTMKLLPLKIAVTSAMIVGLGMASTANAQQQKSPKTETFLPNIFFNEYADDLDTLYHNMIIGD TAITHDDQYKFYADDATEVPDSLFFNKILHUQLLYGFKEGDKIIFLDENGKFPVYKLDKRLENG QKTVYSVTTTKTATADDVNSAYS SRGIQGGIDDLYEANKENVNRLLIEHGDKIFANEESVQYLNREV QNNIENIHELAAQQQQHQSSDIKTLKKNVEKDLLDLSGRLIAQKEDIAQNQTDIQDLATYNELQD QYAAQKQTEAIDALNKASSENTQNIKNNSNHITLLENNIEEGLLELSGRLIDQKADLTKDIAKALE SNVEEGLLDLSGRLLDQKADIAQNQANIQDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI DLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSE NTONIAKNQADIANNINNIYELAQQQQQHQSSDIKTLAKASAANTDRIAKNKADADASFETLTKN QNTLIEKDKERDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGF DGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQFPYSVGKFNATAALGGYG SKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (683 amino acids)
Finnish 358 (SEQ ID NO: 7)	MKTMKLLPLKIAVTSAMMVGLGMASTANAQQQKSPKTEIFLPNLFNDNDNTELTDPHYHNMIIGN TALLTQENQYKFYADDGNGVPSLFFNKILHUQLLHGFKEGGTIIIFLDENGKFPVYKLDSDIVEQG KTKTVYSVTTTKTATADDVNSAYS SRGIQGGIDDLYEANKENVNRLLIEHGDKIFANEESVQYLNRE VQNNIENIHELAAQQQQHQSSDIKTLKKNVEKDLLDLSGRLIAQKEDIAQNQTDIQDLATYNELQ DQYAAQKQTEAIDALNKASSENTQNIKNNSNHITLLENNIEEGLLELSGRLIDQKADLTKDIAKAL ESNVEEGLLDLSGRLLDQKADIAQNQANIQDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI EDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASS ENTQNIKNQADIANNINNIYELAQQQQQHQSSDIKTLAKASAANTDRIAKNKADADASFETLT KNQNTLIEKDKERDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSTDLGTVKVDG FDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQFPYSVGKFNATAALGCGY GSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (684 amino acids)

Finnish 216 (SEQ ID NO: 8)	MKTMKLLPLKIAVTSAMIITGLGAASTANAQQQQKTKTEVFLPNLFDNDYYDLTDPLYHSMILGD TATLFDQQDNSKSQLKFYSNDKDSVPDSLLFSKLLHEQQQLNGFKAGDTIIPLDKDGKPVYTTQDT RTKDGKGVETVYSVTTKIATQDDVEQSAYSRSIQGDIDDLTYDINREVNEYLKATHIDYNERQTEAI DALNKASSANTDRIDTAERIDKNEYDIKALESNVGKDLLDLSGRLIAQKEDIDNNINHIYELA QQQDQHSSDIKTLKNNVEEGLLELSGHLIDQKADLTCKDIKTLENNIEEGLLELSGHLIDQKADL TKDIKTLENNIEEGLLELSGHLIDQKADIAQNQANIQDLAAYNELQDQYAKQTEAIDALNKAS SENTQNIEDLAAYNELQDAYAKQOTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQOTEAID ALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKVSAANTDRIAKNKADADA SFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITD LGTRKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQFPYSVGKFNATAALGGY GSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (684 amino acids)
Dutch H2 (SEQ ID NO: 9)	MKTMKLLPLKIAVTSAMMVGLGMASTANAQQQKSPKTEIFLPNLFDNDNTELTDPHYHNMILGN TALLTQENQYKFYADDGNGVDPDSLLFNKILHDQLLHGFKKGDTIIPLDENGKPVYKLDSDIVEQG KTKTVYSVTTKTATADDVNSAYSRSIQGDIDDLTYEANKENVNRLIEHGDKIFANEESVQYLNRE VQNNIENIYELVQQQDQHSSDIKTLKNNVEKDLLDLSGRLIAQKEDIAQNQNTDIQDLATYNELQ DQYAKQOTEAIDALNKASSENTQNIAKNSNHIXTLENNIEEGLLELSGHLIDQKADLTCKDIKAL ESNVEEGLLDLSGRLIDQKADIAQNQANIQDLAAYNELQDAYAKQOTEAIDALNKASSENTQNI EDLAAYNELQDAYAKQOTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQOTEAIDALNKASS ENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLT KNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTRKVDG FDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQFPYSVGKFNATAALGGY GSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (684 amino acids)
Dutch F10 (SEQ ID NO: 10)	MKTMKLLPLKIAVTSAMIITGLGAASTANAQLAEQFFPNIFSNHAPVKQBYHNVVVGDTSTIVENL QDSDDTQLKFYSNDEYSVPDSLLFNKMLHEQQQLNGFKKGDITIPLDENGKPVYKVDYKLDGQEP RRVYSVTTKIATQDDVDNSPYSRSIQGDIDDLTYEANKENVNRLIEHGDKIFANEESVQYLNKEV QNNIENIYELAQQQDQHSSDIKTLKNNVEEGLLELSGHLIDQKADLTCKDIKTLESNVEEGLLEL SGHLIDQKADIAKNQADIQNQANIQDLAAYNELQDAYAKQOTEAIDALNKASSENTQNIEDLA AYNELQDAYAKQOTEAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAK ASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATAD AITKNGNAITKNAKSITDLGTRKVDADFGRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGL FQFPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (574 amino acids)
Norwegian 1	MKTMKLLPLKIAVTSALIVGLGAASTANAQQQPQTETFFPNIFFNENHDALDDVYHNMILGDTA ITQDNQYKFYADAISEVPDSLLFNKILHDQQLNGFKEGDTIIPLDENGKPVYKLDEKVENGVKK

(SEQ ID NO: 11)	SVYSVTTKTATRADVEQSAYSRGIQGGIDDDLYEANKENVNRLIEHGDKIFANEESVQYLNKEVQ NNIENIHELAAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKADLT KDIKTLESNVEEGLLDLS GRLLDQKADIAQNQANIQDLAAYNELODAYAKQQTEAIDALNKASSENTQNI EDLAAYNELODA YAKQQTEAIDALNKASSENTQNI EDLAAYNELODAYAKQQTEAIDALNKASSENTQNI EDLAAY NELODAYAKQQTEAIDALNKASSENTQNI EDLAAYNELODAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAAQQQDQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQNTLI EKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVDAFDGRVT ALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSGVKFNATAALGGYGSKSAV AIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (678 amino acids)
Norwegian 13 (SEQ ID NO: 12)	MKTMKLLPLKIAVTSAMIVGLGAASTANAQQQQQPRTEFFFPNIEFNENHDALDDVYHNMI LGD TAITQDNQYKFYADAI SEVPDSLLFNKILHDQQLNGFKEGDTIIPLDENGKPVYKLDEKVENG KKS SVYSVTTKTATRADVEQSAYSRGIQGGIDDDLYEANKENVNRLIEHGDKIFANEESVQYLNRE VQNNIENIHELAAQQQDQHSSDIKTLKKNVEKDLLDL SGRLIAQKEDIAQNQTDIQLATYNELO DQYAKQKTEAIDALNKASSENTQNI AKNSNHIKTL ENNIEEGLLELSGHLIDQKADLT KDIKTL ENNIEEGLLELSGHLIDQKADLT KDIKALESNVEEGLLDLS GRLLDQKADIAQNQANIQDLAAY NELODQYAKQKTEAIDALNKASSENTQNI EDLAAYNELODAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAAQQQDQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQNTLI EKDKEHDKLITANKTAIDTNKASADTKFAATADAITKNGNAITKNAKSITDLGTVDGFDGRVT ALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSGVKFNATAALGGYGSKSAV AIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (678 amino acids)
Norwegian 20 (SEQ ID NO: 13)	MKTMKLLPLKIAVTSALIVGLGAASTANAQLVERFFFPNIEFLDKPLAKQHYBNVVVGDT SIVSDL QSNSDQLKFYSDDEGLVPDSLLFNKMLHEQLLNGFKEGDTIIPLDENGKPVYKVDYKLDGKEPR KVYSVTTKIAATAEDVATSSYANGIQKDI DDLYDFDHQVTERLTQH GKTIYRNGERILANEESVQ YLNKEVQNNIEHIYELAAQQQDQHSSDIKTL SNVEKGLLELSGHLIDQKADLT KDIKTL ENNVE EGLLDLSGRLLIDQKADIAQNQANIQDLAAYNELODQYAKQKTEAIDALNKASSENTQNI EDLAA YNELODAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAAQQQDQHSSDIKTLAKA SAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDTNKASADTKFAATADA ITKNGNAITKNAKSITDLGTVDGFDGRVTALEDTKVNALEDTKVNALEDTKVNAFDGRITALDSKV ENGMAAQAALSGLFQPYSGVKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKK GSYNIGVNYEF (587 amino acids)
Norwegian 25 (SEQ ID NO: 14)	MKTMKLLPLKIAVTSAMIVGLGAASTANAQQQQQPRTEFFFPNIEFNENHDALDDVYHNMI LGD TAITQDNQYKFYADAI SEVPDSLLFNKILHDQQLNGFKEGDTIIPLDENGKPVYKLDEKVENG KKS SVYSVTTKTATRADVEQSAYSRGIQGGIDDDLYEANKENVNRLIEHGDKIFANEESVQYLNRE VQNNIENIHELAAQQQDQHSSDIKTLKKNVEKDLLDL SGRLIAQKEDIAQNQTDIQLATYNELO DQYAKQKTEAIDALNKASSENTQNI AKNSNHIKTL ENNIEEGLLELSGHLIDQKADLT KDIKTL

	ENNIEEGLLELSGHLIDQKADLTROTKALESNVEEGLLDLSGRLLDQKADIAQNQANIQDLAAY NELQDQYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLI EKDKEHDKLITANKTAIDTNKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGDFGRVT ALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSGKFNATAALGGYGSKSAV AIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (678 amino acids)
Norwegian 27 (SEQ ID NO: 15)	MKTMKLLPLKIAVTSALIVGLGAASTANAQVRDKSLEDIEALLGKIDISKLEKEKKQKQTELQKY LLLSQYANVLTMEELNKNVEKNTNSIEALGYEIGWLENDIADLEEGVEELTKNQNTLIEKDEEH DRLIAQNQADIKTLENNVVEELFNLSDRLIDQEAADIAKNNASIEELYDFDNEVAERIGETIHAYT EEVNKTLEKLITNSVKNTDNIDKNKADIQALENNVEEGLLELSGHLIDQKADLTROTKALESNV EEGLLDLSGRLLDQKADIAKNQADIAQNQTDIQLAAYNELQDQYAKQKQTEAIDALNKASSENT QNIEDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQKQTEAIDALNK ASSENTQNIKNQADIANNINNIYELAQQQDQHSSDIKTLAKVSAANTDRIAKNKADADASFET LTKNQNTLIEKDKHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVK VDGDFSRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSGKFNATAALGGYGSKS AVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (616 amino acids)
Norwegian 36 (SEQ ID NO: 16)	MKTMKLLPLKIAVTSALIVGLGAASTANAQATETTFPLPNLFDNDYTETTDPLYHGMILGNTAITQ DTQYKFYAENGNEVPDSLFFNKLHDDQQLNGFKEGDTIIPLDENGKPVYKLDEITENGVRKRVY SVTTKTATREDVEQSAYSRSIGQDIDDLYEANKENVNRLIEHGDKIFANEESVQYLNKEVQNNI ENIHELAAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKADLTROTKALESNVEEGLLDLSGHL IDQKADLTROTKALESNVEEGLLDLSGRLLDQKADIAKNQADIAQNQTDIQLAAYNELQDQYAK QKQTEAIDALNKASSENTQNIEDLAAYNELQDQYAKQKQTEAIDALNKASSENTQNIEDLAAYNE LQDQYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDQYAKQKQTEAIDALNKASSENTQNIKN NQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEK DKHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGDFGRVTAL DTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSGKFNATAALGGYGSKSAVAI GAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (676 amino acids)
BC5SV (SEQ ID NO: 17)	MKTMKLLPLKIAVTSALIVGLGAASTANAQNGTSTKLKLNKEYAQYLDNYAQYLDLDDIDDL DKEVGELSQNIKNQANIKDLNKKLSRDIDSLREDVYDNQYEIVNNQADIEKNQDDIKELE NNVGKELLNLSGRLLDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLI DQKSDIAQNQTDIQLATYNELQDQYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDAY AKQKQTEAIDALNKASSENTQNIQLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLA AYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQKQTEAIDALNKASSE NTQNIEDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIKNQADIANNINNIYELAQQQ

	DQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAID ANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITA LDSKVENGMAAQAALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAA INTSGNKKGSSYNIGVNYEF (629 amino acids)
Norwegian 14 (SEQ ID NO: 18)	MKTMKLLPLKIAVTSAMIVGLGMASTANAQQQSRPKTETFLPNIFFNEYADDLDTLYHNMI LGDTAITHDDQYKFYADDATEVPDLSLFFNKILHDQQLLYGFKEGDKIIPLDENGKPVYKLDK RLDNGVQKTVYSVTTKTATADDVNSAYSRGIQGDIDDLYEANKENVNRLEHGDKIFANEE SVQYLNKEVQNNIENIHELAAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQTD IQDLATYNELQDQYAKQTEAIDALNKASSENTQNIAKNSNRIKALENNIEEGLLELSGHL IDQKADLTRDKIKALESNVEEGLLDLSGRLLDQKADIAQNQANIQDLAAYNELQDAYAKQQT EAIDALNKASSENTQNIEDLAAYNELQDAYAKQTEAIDALNKASSENTQNIEDLAAYNEL QDAYAKQQTTEAIDALNKASSENTQNIAKNQADIANNINNIYELAAQQQDQHSSDIKTLAKAS AANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATA DAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVEN GMAAQAALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNK KSSYNIGVNYEF (683 amino acids)
Norwegian 3 (SEQ ID NO: 19)	MKTMKLLPLKIAVTSAMIVGLGAASTANAQAQSNRSLDQVQALLRGIDETRIKKEIQQSQQ PELNKYLTENQLANALNIEELNNNVQKNTQRLDSAATLYGDLSTVPKSIKENKESIKENK ESIKENKESIKENKESIKENKESIKENKESITTLTRKSFQNOVDIVRNNASIEDLYAYGQE VAKSIGEIHAYTEEVNKTLENLITNSVENTNNTKNKADIQALENNVVEELFNLSGRLLDQ KADIDNNINNIYELAAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKADLTRDKIKTLESNV EEGLLDLSGRLLDQKADIAQNQANIQDLAAYNELQDAYAKQQTTEAIDALNKASSENTQNI DLAAYNELQDAYAKQQTTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTTEAIDALNKA SSENTQNIEDLAAYNELQDAYAKQQTTEAIDALNKASSENTQNIAKNQADIANNINNIYELA QQQDQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKT VIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTK VNAFDGRITALDSKVENGMAAQAALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVN PNLAFKAGAAINTSGNKKGSSYNIGVNYEF (700 amino acids)
Finnish 414 (SEQ ID NO: 20)	MKTMKLLPLKIAVTSALIVGLGAASTANAQATETFLPNLFDNDYIETTDPLYHGMI LGNTA ITQDTQYKFYAENGNEVPDLSLFFNKILHDQQLNGFREGDTIIPLDENGKPVYKLDEITENG VKRKVYSVTTKTATREDVEQSAYSRGIQGDIDDLYEANKENVNRLEHGDKIFANEE SVQY LNKEVQNNIENIHELAAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKADLTRDKIKTLENN VEEGLLELSGHLIDQKADLTRDKIKALESNVEEGLLDLSGRLLDQKADIAKNQADIAQNQTD

	IQDLAAYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNELQDQYAQKQTEAIDALN KASSENTQNIEDLAAYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNELQDQYAQK QTEAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHQSSDIKTLAKASAANTDRI AKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNG NAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAA LSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIG VNYEF (676 amino acids)
Japanese Z7476 (SEQ ID NO: 21)	MKTMKLLPLKIAVTSAMTIGLGAASTANAQLAEQFFPNIFSHPVKQHYHNVVVGDTISIV ENLQDSDDTQLKFYSNDEYSVPDLSLLENKMLHEQQQLNGFKKGDPTIIPLDENGKPVYKVDYK LDGQEPRRVYSVTTKIATQDDVDNSPYSRGIQGDIDDLYEANKENVNRLLIEHGDKRIFANEE SVQYILNKEVQNNIENIYELAQQQDQHQSSDIKTLKKNVEEGLLELSGRLIDQKADIAQNQAN IQDLAAYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALN KASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQ QTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYN ELQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHQSSDIKTLAK VSAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAA TADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMAAQ AALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYN IGVNYEF (678 amino acids)
Belgian Z7530 (SEQ ID NO: 22)	MKTMKLLPLKIAVTSAMIIGLGAASTANAQSRDRSLEDIQDSISKLVQDDINTLKDQDQKM NKYLLLNQLANTLITDELNNNVIKNTNSIEALGDEIGWLENDIADLEEGVEELTKNQNTLI EKDEEHDRLIAQNQADIQTLENNVVEELFNLSGRLIDQEADIAKNNASIEELYDFDNEVAE RIGEIHAYTEEVNKTLENLITNSVKNTDNIDKNKADIDNNINHIYELAQQQDQHQSSDIKTL KNNVEEGLLELSGHLIDQKADLTDKIKALESNVEEGLLDLSGRLLDQKADLTDKIKALESN VEEGLLDLSGRLLDQKADIAQNQTDIQDLAAYNELQDQYAQKQTEAIDALNKASSENTQNI EDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHQSS DIKTLAKASAANTNRIATAELGIAENKKDAQIAKAQANANKTAIDENKASADTKFAATADA ITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMAAQAALS GLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVN YEF (613 amino acids)
German Z8063	MKTMKLLPLKIAVTSALIVGLGAASTANAQATNKDITLEDVLKSIEEIDPYELRDYIEYPT AIERFLLLSQYGNLTLEEFNDNIELLDQDVEDLEESVTELAQNQNSLIEQGEAIREDLQG LADFVERQEDKILQNETSIRKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAKSI

(SEQ ID NO: 23)	GEIHAHNEAQNETLKDITNSVKNTDNITKNKADIQALESNVEKGLLELSGHLIDQKADID NNINNIHELAAQQQDQHSSDIKTLKKNVEEGLELSGHLIDQKSDIAQNQANIQDLATYNEL QDQYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAAQQQDQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQN TLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDG FDSRVTAALDTKVNAFDGRITALDSKVENGMAAQAALSGLEFPYSGVKFNATAALGGYGSKS AVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (589 amino acids)
American Q12E (SEQ ID NO: 24)	MKTMKLLPLKIAVTSAMMVGLGMASTANAQQQKSPKTEIFLPNLFNDNTELTDFLYHNMI LGNTALLTQENQYKFYADDGNGVPDSLLFNKILHDQLLHGFKEGDTIIFLDENGKFVYKLD SIVEQGGKTKTVYSVTTKTATADDVNSAYSSEGIQGDIDDLYEANKENVNRLEHGDKIFANE ESVQYLNRVQNNIENIHELAAQQQDQHSSDIKTLKKNVEKDLDDLGRGLIAQKEDIAQNQT DIQDLATYNELQDQYAKQKQTEAIDALNKASSENTQNIAKNSNHIKTLNENIEGGLLELSGH LIDQKADLTRDIKALESNVEEGLLDLGRGLIDQKADIAQNQANIQDLAAYNELQDAYAKQQ TEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNE LQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINNIYELAAQQQDQHSSDIKTLAKA SAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAAT ADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVE NGMAAQAALSGLEFPYSGVKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGN KKGSYNIGVNYEF (684 amino acids)
Greek MC317 (SEQ ID NO: 25)	MKTMKLLPLKIAVTSALIVGLGAASTANAQQQKTKTEVFLPNLFYNDYIIBETDLLYHNMI LGDTAALVDRQNYNSQLKFYSNDEESVPDSLLFSKMLNNQQLNGFKAGDIIIPVDANGQV IYQKDTRVEGGKTRTVLSVTTKIATQQDVDSAYSSEGIQGVNDLDEMNFLNHDITSLYDV TANQQDDIKGLKKGVKDLKKGVEGLNKELEKELDKVEGVLSRDLGSLNDDVAQNNESTEDLY DFSQEVADSIGEIHANKEAQNETLQDLITNSVENTNNTKNKADIQALESNNVVEELFNLSG RLIDQKADLTCKDIKTLKESNVEEGLELSGHLIDQKADIAKNQADIAQNQANIQDLAAYNEL QDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAAQQQDQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQN TLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDG FDGRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLEFPYSGVKFNATAALGGYGSKS AVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (650 amino acids)
American V1122	MKTMKLLPLKIAVTSALIVGLGAVSTTNAQAQSRSLDQIQTKLADLAGKIAAGKNGGCGQNN QNNQNDINKYLFSLQYANILTMEELNNNVVKNSSSIETLETDFGWLENDVADLEDGVEELT KNQNTLIEKDEEHDRLIAQNQADIQTLENNVVEELFNLSDRLLIDQKADIAKNQADIAQNE

(SEQ ID NO: 26)	SIEELYDFDNEVAEKIGEIHAYTEEVNKTLDLITNSVRKNTDNIDKNKADIDNNINHIYEL AQQQDQHSSDIKTLKNNVEEGLLELSGHLIDQKADLT KDIKTLENNVEEGLLDLSGRLIDQ KADIAKNQADIAQNQTDIQDLAAYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNE LQDAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINNIYELAQQQDQHSSDIKTLAKA SAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDENKASADTKFAAT ADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMAAQA ALSGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNI GVNYEF (616 amino acids)
American P44 (SEQ ID NO: 27)	MKTMKLLPLKIAVTSALIVGLGTASTANAQVASPANQKIQQKIKKVRKELRQDIKSLRNDI DSNTADIGSLNDDVADNQDDILDNQADIAKNQDDIEKNQADIKELDKEVGVLSREIGSLND DIADNYTDIIDNYTDIIDNQANI AKNQDDIEKNQADIKELDKEVGVLSREIGSLNDDVADN QDDIAKNQADIQTLENNVEEGLLELSGHLIDQKADIDNNINNIYELAQQQDQHSSDIKTLK KNVEEGLLELSGHLIDQKTDIAQNQANIQDLATYNELODQYAQEQT E AIDALNKASSENTQ NIAKNSNRIKALESNVEEGLLELSGHLIDQKADLT KDIKALESNVEEGLLELSGHLIDQKA DIAQNQANIQDLAAYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQ TEAIDALNKASSENTQNI AKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIA KNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKVSADTKFAATADAITKNGN AITKNAKSITDLGTVKVD AFDSRV TALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPY SVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (668 amino acids)
American V1171 (SEQ ID NO: 28)	MKTMKLLPLKIAVTSAMIVGLGATSTVNAQVVEQFFPNIFFNENHDELD DAYHNMILGDTA IVSNSQDNSTQLKFYSNDEDSVPDSLLFSKLLHEQQQLNGFKAGDTIIPLDKDGKPVYTKDT RTRKDGKVVETVYSVTTKIATQDDVEQSAYS RGIQGDIDDL YDINREVNEYLKATHDYNERQT EAIDALNKASSANTDRIDTAEERIDKNEYDIKALESNVEEGLLELSGHLIDQKADLT KDIK ALESNVEEGLLELSGHLIDQKADLT KDIKALESNVEEGLLDLSGRLIDQKADIAQNQANIQ DLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKA SSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQT EAIDALNKASSENTQNI AKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAK NKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNA ITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAALS GLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVN YEF (674 amino acids)
American	MKTMKLLPLKIAVTSAMIIGLGAASTANAQSRDRSLEDIQDSISKLVQDDIDTLKQDQQKM

TTA24 (SEQ ID NO: 29)	NKYLLLNQLANTLITDELNNNVIKNTNSIEALGDEIGWLENDIADLEEGVEELTKNQNTLI EKDEEHDRLIAQNQADIQTLENNVVEELFNLSGRLLDQEAADIKNNASIEELYDFDNEVAE RIGEIHAYTEEVNKTLENLITNSVKNTDNIDKNKADIDNNINHIYELAQQQDQHSSDIKTL KNNVEEGLLELSGHLIDQKADLTCDIKALESNVEEGLLDLSGRLLDQKADLTCDIKALESN VEEGLLDLSGRLLDQKADIAQNQTDIQLAAYNELQDQYAKQKQTEAIDALNKASSENTQNI EDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIKNQADIANNINNIYELAQQQDQHSS DIKTLAKASAAANTNRIATAELGIAENKKDAQIAKAQANANKTAIDENKASADTKFAATADA ITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMQAQAALS GLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVN YEF (613 amino acids)
American O35E (SEQ ID NO: 30)	MKTMKLLPLKIAVTSAMIVGLGATSTVNAQVVEQFFFNIFENENHDELDDAYHNMI LGDTA IVSNSQDNSTQLKFYSNDEDSVPDSLLFSKLLHEQQQLNGFKAGDTIIFLDKDGKPVYTKDT RTKDGKVVETVYSVTTKIATQDDVEQSAYSIRGIQGDIDDLIDINREVNEYLKATHDYNERQT EAIDALNKASSANTDRIDTAERIDKNEYDIKALESNVEEGLLELSGHLIDQKADLTCDIK ALESNVEEGLLELSGHLIDQKADLTCDIKALESNVEEGLLDLSGRLLDQKADIAKNQADIA QNQTDIQLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIKNQADIANNINNIYELAQQ QDQHSSDIKTLAKASAAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAI DANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVN AFDGRITALDSKVENGMQAQAALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPN LAFKAGAAINTSGNKKGSYNIGVNYEF (576 amino acids)
American SP12-6 (SEQ ID NO: 31)	MKTMKLLPLKIAVTSAMMVGLGMASTANAQQQKSPKTEIFELFNLFNDNTELTDPYHNMI LGNTALLTQENQYKFYADGNGVFPDSLLFNKILHDQLLHGFKEGDTIIFLDENGKPVYKLD SIVEQGGTKTVYSVTTKTATADDVNSAYSIRGIQGDIDDLIEANKENVNRLIEHGDKIFANE ESVQYLNREVQNNIENIHELAAQQQDQHSSDIKTLKKNVEKDLLDLSGRLLAQKEDIAQNQT DIQDLATYNELQDQYAKQKQTEAIDALNKASSENTQNIKNNSNHIKTLENNIEEGLLELSGH LIDQKADLTCDIKALESNVEEGLLDLSGRLLDQKADIAQNQANIQLAAYNELQDAYAKQQ TEAIDALNKASSENTQNIEDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLAAYNE LQDAYAKQKQTEAIDALNKASSENTQNIKNQADIANNINNIYELAQQQDQHSSDIKTLAKA SAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAAT ADAITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVE NGMAQAQAALSGLFQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGN KKGSYNIGVNYEF (684 amino acids)
American	MKTMKLLPLKIAVTSAMIIGLGAASTANAQATETFLPNLFNDNYTETTDPLYHGMILCNTA

SP12-5 (SEQ ID NO: 32)	ITQDTQYKFYAENGNEVPDSLFFNKLHDDQQLNGFKEGDTIIPLDENGKFPVYKLDEITENG VKKRVYSVPTTKTATREDVEQSAYSRSIGQGDIDDLYEANKENVNRLIEHGDKIFANEESVQY LNKEVQNNIENIHELAAQQDDQHSSDIKTLKKNVEEGLLELSGRLLIAQKEDIAQNQTDIQL ATYNELQDQYAKQKQTEAIDALNKASSENTQNIARNSNHIKTLENNIEEGLLELSGHLIDQK ADLTFRDIKALESNVEEGLLDLSGRLLDQKADIAKNQADIAQNQTDIQLAAYNELQDQYAK KQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLAAY NELQDAYAKQKQTEAIDALNKASSENTQNIARNSNHIKTLENNIEEGLLELSGHLIDQK KASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFA ATADAITKNGNAITRNAKSITDLGTVKVDGDFGRVTALDTKVNAFDGRITALDSK VENGMAAQAALSGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTS GNKKGSYNIGVNYEF (686 amino acids)
Swedish BC5 (SEQ ID NO: 33)	MKTMKLLPLKIAVTSAMIIGLGAASTANAQAKNDITLEDLPYLIKKIDQNELEADIGDITALEK YLALSOYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQG LADPVEGQEGKILQNETSIKKNTQRLVNGFEIEKNKDAIARNNESIEDLYDFGHEVAESIGE HAHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSGRLLIDQKADIDNNINNI YELAAQQDDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQANIQLATYNELQDQYAKQK EADALNKASSENTQNIEDLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQDA YAKQKQTEAIDALNKASSENTQNIARNSNHIKTLENNIEEGLLELSGHLIDQKADIDNNINNI IAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNA ITRNAKSITDLGTVKVDGDFSRVTALDTKVNAFDGRITALDSKVENGMAAQAALSGLFQPYSVGK FNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (630 amino acids)
American 7169 (SEQ ID NO: 34)	MKTMKLLPLKIAVTSALIVGLGAASTANAQAQDRSLEQIQDKLANIVEKIEQAKSQNGQSQ KDINQYLLLSQYANVLTMEELNNNVKNSSSIETLDNDIAWLNDLIDLDKEVGVLSDIG SLHDDVAQNQADIKTLKKNVVEELFNLSDRLLDQEAQNNESIEDLYDFGREVAESIGE IHANEAQNETLKDLITNSVKNNTDNITKNKADIQALENDVGKELLNLSGRLLIDQKADIDNN INHIYELAAQQDDQHSSDIKTLKKNVEEGLLELSGHLIDQKADLTFRDIKALESNVEEGLLDL SGRLLDQKADIAQNQANIQLAAYNELQDAYAKQKQTEAIDALNKASSENTQNIEDLAAYNE LQDAYAKQKQTEAIDALNKASSENTQNIARNSNHIKTLENNIEEGLLELSGHLIDQKADIDNN SAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAAT ADAITKNGNAITRNAKSITDLGTVKVDGDFSRVTALDTKVNAFDGRITALDSKVENGMAAQA ALSGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNI GVNYEF (616 amino acids)
Finnish	MKTMKLLPLKIAVTSAMIIGLGATSTVNAQVVEQFFENIFFNENHDELDDAYHNMILGDTA

FIN2344 (SEQ ID NO: 35)	IVSNSQDNSTQLKFYSNDEDSVPDSLLFSKLLHEQQNLNGFKAGDTIIPLDKDGKPVYTKDT RTKDGKVEFVYSVTTKIATQDDVEQSAYSIRGIQGGIDDDLYDINREVNEYLKATHDYNERQT EALDALNKASSANTDRIDTAERIDKNEYDIKALESNVGKDLLDLSGRLIAQKEDIDNNIN HIYELAQQQDQHSSDIKTLKNNVEEGLLELSGHLIDQKADLTCDIKTLESNVEEGLLDLSG RLIDQKADIAQNQANIQDLAAYNELQDQYAKQKQTEAIDALNKASSENTQNIEDLAAYNELQ DAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKVSA ANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATAD AITKNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMMAQAAL SGLFQFPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGV NYEF (614 amino acids)
American V1116 (SEQ ID NO: 36)	MKTMKLLPPLKIAVTSAMIIGLGAASTANAQTTETFLPNLFDNDYTETTDPLYHGMILGDTA ITQDTQYKFAENGNEVPDSLFFNKILHDQLLNGFKAGDTIIPLDENGKPVYKLDERTENG VKRKVYSVTTKTATQADVEQSAYSIRGIQGGIDDDLYEANKENVNRLIEHGDKIFANEESVQY LNREVQNNIENIHELAAQQDQHSSDIKTLKNNVEKDLLDLSGRLIAQKEDIAQNQTDIQL ATYNELQDQYAKQKQTEAIDALNKASSENTQNIAKNSNHIKTLENNIEECLELSGHLIDQK ADLTCDIKALESNVEEGLLDLSGRLIDQKADIAQNQANIQDLAAYNELQDAYAKQQTEAID ALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAY AKQQTEAIDALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANT DRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAIT KNGNAITKNAKSITDLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMMA QAALSGLFQFPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSY NIGVNYEF (679 amino acids)
American V1145 (SEQ ID NO: 37)	MKTMKLLPPLKIAVTSALIVGLGAASTANAQETLEEVLESIKQINEQDLQDDIGYNSAJDRY LVLSQYGNLITAKELNENVEKNSNSIAKNSNSIADLEADVGYLAENQNTLIEQNETINQEL EGITHELESFIAYAHAAQDQKNLVNEFEIEKNEDAIKNNESIEDLYDFGHEVAESIGETHA YTREVNKTLENLITNSVKNTDNITKNKADIQALESNVEKELLNLSGRLIDQKADIDNNINH IYELAQQQDQHSSDIKTLKNNVEEGLLELSGHLIDQKSDIAQNQTDIQLATYNELQDQYA KQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAA YNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSEN TQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAID ALNKASSENTQNIAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKAD ADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKN AKSITDLGTVKVDGFDGRVTALDTKVNAFDGRITALDSKVENGMMAQAALSGLFQFPYSVGKF NATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYEF (724

	amino acids)
American V1156 (SEQ ID NO: 38)	MKTMKLLPLKIAVTSALIVGLGAASTANAQAQARDSLEDIQALIGNIDVDKIRSQKQKNP EIFQYLLLNQLSNTLITDELNNNVIKNTNSIETLDNDIAWLNDLIDLDKEVGVLSRDIGS LHDDVAQNQADIKTLENNVVEELFNLSDRLLIDQEAETIAQNNESIEDLYDFGREVAESIGEI HAHNEAQNETLKDILITNSVKNTDNIDKNKADIQALENNVEEGLLELSGHLIDQKADLTKDI KALESNVEEGLLDLSGRLLDQKADIKNQADIAQNQTDIQDLAAYNELQDQYAKQTEAID ALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAY AKQQTEAIDALNKASSENTQNIKNQADIANNINNIYELAQQQDQHSSDIKTLAKVSAANT DRIAKNKADADASFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAIT KNGNAITKNAKSITDLGTVKVDGFSRVTAIDTKVNAFDGRITALDSKVENGMAAQAALSGL FQPYSGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYNIGVNYE F (611 amino acids)

[34] UspA2 may be UspA2 from *M. catarrhalis* strain ATCC(a US registered trademark) 25238™, American 2933, American 2912, American 2908, Finnish 307, Finnish 353, Finnish 358, Finnish 216, Dutch H2, Dutch F10, Norwegian 1, Norwegian 13, Norwegian 20, Norwegian 25, Norwegian 27, Norwegian 36, BC5SV, Norwegian 14, Norwegian 3, Finish 414, Japanese Z7476, Belgium Z7530, German Z8063, American O12E, Greek MC317, American V1122, American P44, American V1171, American TTA24, American O35E, American SP12-6, American SP12-5, Swedish BC5, American 7169, Finnish FIN2344, American V1118, American V1145 or American V1156. UspA2 may be UspA2 as set forth in any of SEQ ID NO: 1 – SEQ ID NO: 38. UspA2 may be UspA2 from another source which corresponds to the sequence of UspA2 in any one of SEQ ID NO: 1 – SEQ ID NO: 38. Corresponding UspA2 sequences may be determined by one skilled in the art using various algorithms. For example, the Gap program or the Needle program may be used to determine UspA2 sequences corresponding to any one of SEQ ID NO: 1 – SEQ ID NO: 38.

[35] UspA2 may be a sequence with at least 95% identity, over the entire length, to any of SEQ ID NO: 1 – SEQ ID NO: 38.

[36] Immunogenic fragments of UspA2 comprise immunogenic fragments of at least 450 contiguous amino acids of SEQ ID NO: 1, 490 contiguous amino acids of SEQ ID NO: 1 (for example, the UspA2 fragment of MC-004 or MC-005), 511 contiguous amino acids of

SEQ ID NO: 1 (for example, the UspA2 fragment of construct MC-001, MC-002, MC-003 or MC-004), 534 contiguous amino acids of SEQ ID NO: 1 (for example, the UspA2 fragment of MC-009 or MC-011) or 535 contiguous amino acids of SEQ ID NO: 1 (for example, the UspA2 fragment of MC-007, MC-008 or MC-010). The immunogenic fragments may elicit antibodies which can bind SEQ ID NO: 1.

[37] Immunogenic fragments of UspA2 may comprise immunogenic fragments of at least 450, 490, 511, 534 or 535 contiguous amino acids of any of SEQ ID NO: 1 – SEQ ID NO: 38. Immunogenic fragments of UspA2 may comprise immunogenic fragments of UspA2 from any of SEQ ID NO: 2 – SEQ ID NO: 38 which correspond to the UspA2 fragment of SEQ ID NO: 1 in any of the UspA2 constructs MC-001, MC-002, MC-003, MC-004, MC-005, MC-006, MC-007, MC-008, MC-009, MC-010 or MC-011. The immunogenic fragments may elicit antibodies which can bind the full length sequence from which the fragment is derived.

[38] Alignments between polypeptides pairs may be calculated by various programs. For example, the Needle program from the EMBOSS package (Free software; EMBOSS: The European Molecular Biology Open Software Suite (2000). Trends in Genetics 16(6): 276—277) and the Gap program from the GCG(a US registered trademark) package (Accelrys Inc.) may be used.

[39] The Gap and Needle programs are an implementation of the Needleman-Wunsch algorithm described in: Needleman, S. B. and Wunsch, C. D. (1970) J. Mol. Biol. 48, 443-453. These programs are using frequently the BLOSUM62 scoring matrix (Steven Henikoff and Jorja G. Henikoff (1992), "Amino acid substitution matrices from protein blocks", Proc. Natl. Acad. Sci. USA 89 (Biochemistry): 10915-10919) with gap open and extension penalties of, respectively, 8 and 2. Sometimes, the PAM250 scoring matrix (Dayhoff et al., (1978), "A model of evolutionary changes in proteins", In "Atlas of Protein sequence and structure" 5(3) M.O. Dayhoff (ed.), 345-352, National Biomedical Research Foundation, Washington) is also used.

[40] Scoring matrices are describing by numbers the tendency of each amino acid to mutate in another, or to be conserved. These numbers are generally computed from statistics of mutations observed in faithful pairwise or multiple alignments, or even in fragments of multiple alignments. Generally, in these tables, if a high positive number is associated with a pair of identical amino acids, it is indicating that this residue has a low tendency for mutation. At the

opposite, a high positive number associated with a pair of different amino acids is indicating a high tendency of mutation between these two. And this is called a "conservative substitution".

[41] Looking at a pairwise alignment, aligned identical residues ("identities") between the two sequences can be observed. A percentage of identity can be computed by multiplying by 100 (1) the quotient between the number of identities and the length of the alignment (for example, in the Needle program output), or (2) the quotient between the number of identities and the length of the longest sequence, or (3) the quotient between the number of identities and the length of the shortest sequence, or (4) the quotient between the number of identities and the number of aligned residues (for example, in the Gap program output).

[42] The percentage of identities of Table 8 have been calculated according the definition (3) of the previous paragraph, using the pairwise alignments computed by the Gap software.

[43] As used herein, "adjuvant" means a compound or substance that, when administered to a subject in conjunction with a vaccine, immunotherapeutic, or other antigen- or immunogen-containing composition, increases or enhances the subject's immune response to the administered antigen or immunogen (as compared to the immune response that would be obtained in the absence of adjuvant). This is to be distinguished from "adjuvant therapy", defined by the National Cancer Institute of the United States Institutes of Health in the context of cancer treatment as additional treatment given after the primary treatment, to lower the risk that the cancer will recur.

[44] The invention further provides proteins of formula (I) containing conservative amino acid substitutions. For example, the proteins of formula (I) may contain a conservative substitution of any amino acid from UspA2 of *Moraxella catarrhalis* as described in any of the sequences set forth herein (for example, any UspA2 sequence set forth in SEQ ID NO. 1 – SEQ ID NO. 38).

[45] As used herein "signal peptide" refers to a short (less than 60 amino acids, for example, 3 to 60 amino acids) polypeptide present on precursor proteins (typically at the N terminus), and which is typically absent from the mature protein. The signal peptide (sp) is typically rich in hydrophobic amino acids. The signal peptide directs the transport and/or secretion of the translated protein through the membrane. Signal peptides may also be called targeting signals, transit peptides, localization signals, or signal sequences. For example, the signal sequence may be a co-translational or post-translational signal peptide.

[46] A heterologous signal peptide may be cleaved from a protein construct by signal peptide peptidases during or after protein transportation or secretion. For example, the signal peptide peptidase is signal peptide peptidase I. A "heterologous" signal peptide is one which is not associated with the protein as it exists in nature.

[47] As used herein "treatment" means the prevention of occurrence of symptoms of the condition or disease in a subject, the prevention of recurrence of symptoms of the condition or disease in a subject, the delay of recurrence of symptoms of the condition or disease in a subject, the decrease in severity or frequency of symptoms of the condition or disease in a subject, slowing or eliminating the progression of the condition and the partial or total elimination of symptoms of the disease or condition in a subject.

[48] As used herein, "optionally" means that the subsequently described event(s) may or may not occur, and includes both event(s) that occur and events that do not occur.

[49] Otitis media is a major cause of morbidity in 80% of all children less than 3 years of age. (Expert Rev. Vaccines 5:517-534 (2006)). More than 90% of children develop otitis media before age 7 (Current Opinion in Investigational Drugs 4:953-958 (2003)). In 2000, there were 16 million visits made to office-based physicians for otitis media in the United States and approximately 13 million antibacterial prescriptions dispensed. (Pediatrics 113:1451-1465 (2004)). In European countries, the reported acute otitis media rates range between 0.125 to 1.24 per child-year. (Expert Review of Vaccines 8:1479-1500 (2009)). Otitis media is a costly infection and the most common reason children receive antibiotics. (Current Infectious Disease Reports 11:177-182 (2009)). Bacteria are responsible for approximately 70% of cases of acute otitis media, with *Streptococcus pneumoniae*, non-typeable *Haemophilus influenzae* (NTHi), and *Moraxella catarrhalis* predominating as the causative agents (Expert Review of Vaccines 5:517-534 (2006)). A subset of children experience recurrent and chronic otitis media and these otitis prone children have protracted middle-ear effusions that are associated with hearing loss and delays in speech and language development. (Current Infectious Disease Reports 11:177-182 (2009)). Recent antibiotic pressure and vaccination with the pneumococcal conjugate vaccine have resulted in the emergence of β -lactamase-producing *Haemophilus influenzae* and *Moraxella catarrhalis* as the leading organisms causing acute otitis media in North America, followed by *Streptococcus pneumoniae* (Pediatr Clin N Am 60 (2013) 391-407).

[50] Since otitis media is a multifactorial disease, the feasibility of preventing otitis media using a vaccination strategy has been questioned. (Current Infectious Disease Reports 11:177-182 (2009)).

[51] The chinchilla model is a robust and validated animal model of otitis media and its prevention (Expert Review of Vaccines 8:1063-1082 (2009)). While the chinchilla model may mimic the natural course of human infection, others have suggested that results in the chinchilla model may vary from one laboratory to the next. (Current Opinion in Investigational Drugs 4:953-958 (2003)).

[52] Various other rodents have also been used for the induction of otitis media and are summarized in Vaccine 26:1501-1524 (2008). The murine animal model is often studied in otitis media research.

[53] The presence of bactericidal antibody is associated with protection from otitis media due to non-typeable *H. influenzae*. (Current Opinion in Infectious Disease 16:129-134 (2003)). However, an immune response need not be bactericidal to be effective against NTHi. Antibodies that merely react with NTHi surface adhesins can reduce or eliminate otitis media in the chinchilla. (Current Opinion in Investigational Drugs 4:953-958 (2003)).

[54] Chronic obstructive pulmonary disease is a chronic inflammatory disease of the lungs and a major cause of morbidity and mortality worldwide. Approximately one in 20 deaths in 2005 in the US had COPD as the underlying cause. (Drugs and Aging 26:985-999 (2009)). It is projected that in 2020 COPD will rise to the fifth leading cause of disability adjusted life years, chronic invalidating diseases, and to the third most important cause of mortality (Lancet 349:1498-1504 (1997)).

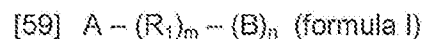
[55] The course of COPD is characterized by progressive worsening of airflow limitation and a decline in pulmonary function. COPD may be complicated by frequent and recurrent acute exacerbations (AE), which are associated with enormous health care expenditure and high morbidity. (Proceedings of the American Thoracic Society 4:554-564 (2007)). One study suggests that approximately 50% of acute exacerbations of symptoms in COPD are caused by non-typeable *Haemophilus influenzae*, *Moraxella catarrhalis*, *Streptococcus pneumoniae*, and *Pseudomonas aeruginosa*. (Drugs and Aging 26:985-999 (2009)). *Haemophilus influenzae* (*H. influenzae*) is found in 20-30% of exacerbations of COPD; *Streptococcus pneumoniae*, in 10-15% of exacerbations of COPD; and *Moraxella catarrhalis*, in 10-15% of

exacerbations of COPD. (New England Journal of Medicine 359:2355-2365 (2008)). *Haemophilus influenzae*, *Streptococcus pneumoniae*, and *Moraxella catarrhalis* have been shown to be the primary pathogens in acute exacerbations of bronchitis in Hong Kong, South Korea, and the Phillipines, while *Klebsiella spp.*, *Pseudomonas aeruginosa* and *Acinetobacter spp.* constitute a large proportion of pathogens in other Asian countries/regions including Indonesia, Thailand, Malaysia and Taiwan (Respirology, (2011) 16, 532-539; doi:10.1111/j.1440.1843.2011.01943.x). In Bangladesh, 20% of patients with COPD showed positive sputum culture for *Pseudomonas*, *Klebsiella*, *Streptococcus pneumoniae* and *Haemophilus influenzae*, while 65% of patients with AECOPD (acute exacerbation of COPD) showed positive cultures for *Pseudomonas*, *Klebsiella*, *Acinetobacter*, *Enterobacter*, *Moraxella catarrhalis* and combinations thereof. (Mymensingh Medical Journal 19:576-585 (2010)). However, it has been suggested that the two most important measures to prevent COPD exacerbation are active immunizations and chronic maintenance of pharmacotherapy. (Proceedings of the American Thoracic Society 4:554-564 (2007)).

[56] Community-acquired pneumonia (CAP) has been described as the leading cause of death from infectious disease and the six-ranked cause of death overall in the United States. *Moraxella catarrhalis* is one of the pathogens associated with CAP in North America (Clin Chest Med 26 (2005) 37 -55) and is one of the pathogens associated with moderate to severe community acquired pneumonia in Japan (J Infect Chemother. 2014 Nov 20. pii: S1341-321X(14)00396-1. doi: 10.1016/j.jiac.2014.11.006. [Epub ahead of print]).

[57] There is a need for effective vaccines against *M. catarrhalis*.

[58] The present invention relates to proteins of formula (I).



[60] wherein:

A is UspA2 from *Moraxella catarrhalis* or an immunogenic fragment thereof;

R₁ is an amino acid;

m is 0 or 2;

B is histidine; and

n is 0, 1, 2, 3, 4, 5 or 6.

[61] In one particular embodiment, R_1 and m are defined wherein $(R_1)_m$ is AS (alanine serine). In another embodiment, R_1 is non-native amino acids.

[62] In one embodiment, the proteins of formula (I) and proteins of the invention are defined wherein m is 0. In one embodiment, when m is 0, n is 2. In another embodiment of the invention, when m is 0, n is not 0.

[63] In one embodiment, m is 2.

[64] In one particular embodiment, n is selected from the group consisting of 1, 2 and 6. In another embodiment, n is selected from the group consisting of 2 and 6. In one particular embodiment, n is 2. In another embodiment, n is 6.

[65] In one embodiment, n is selected from the group consisting of 0, 1, 2, and 6, or any subset thereof.

[66] In one embodiment n is 0. In another embodiment, when n is 0, m is 2.

[67] In one embodiment, n is 1. In one embodiment, n is 3. In one embodiment, n is 4. In one embodiment, n is 5.

[68] In one embodiment, the proteins of formula (I) further contain a methionine (M) at the amino terminus; a protein with the following formula: methionine- A - $(R_1)_m$ - $(B)_n$. These are included within proteins of the invention. In one particular embodiment, when m is 0 and n is 0, the proteins of formula (I) and proteins of the invention are non-native proteins.

[69] In one embodiment, the proteins of formula (I) and proteins of the invention are non-native proteins.

[70] In one embodiment, the proteins of formula (I) are defined wherein A is UspA2 from *M. catarrhalis*. In another embodiment, the proteins of formula (I) are defined wherein A is UspA2 as set forth in an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29,

SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38 or any subset of SEQ ID NO: 1 through SEQ ID NO: 38. In another embodiment, the proteins of formula (I) are defined wherein A is UspA2, wherein UspA2 is at least 63%, 66%, 70%, 72%, 74%, 75%, 77%, 80%, 84%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical, over the entire length, to SEQ ID NO: 1. In another embodiment, the proteins of formula (I) are defined wherein A is UspA2, wherein UspA2 is approximately 75% to 100% identical to the UspA2 amino acid sequence set forth in SEQ ID NO: 1. In another embodiment, A is UspA2 wherein UspA2 is approximately 90% to 100% identical to the UspA2 amino acid sequence set forth in SEQ ID NO: 1. In another embodiment, A is UspA2 wherein UspA2 is at least 95% identical to the UspA2 amino acid sequence set forth in SEQ ID NO: 1. In another embodiment, the proteins of formula (I) are defined wherein A is UspA2, wherein UspA2 is approximately 75% to 100% identical to the UspA2 amino acid sequence set forth in any one of SEQ ID NO: 1 – SEQ ID NO: 38. In another embodiment, A is UspA2 wherein UspA2 is approximately 90% to 100% identical to the UspA2 amino acid sequence set forth in any one of SEQ ID NO: 1 – SEQ ID NO: 38. In additional embodiment, A is UspA2 wherein UspA2 is at least 95% identical to UspA2 as set forth in any of SEQ ID NO: 1 – SEQ ID NO: 38. In a particular embodiment, A is UspA2 having the amino acid sequence set forth in SEQ ID NO: 1.

[71] In another embodiment, the proteins of formula (I) are defined wherein A is an immunogenic fragment of UspA2 from *M. catarrhalis*. In another embodiment, A is an immunogenic fragment of UspA2 wherein UspA2 has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38 or any subset of SEQ ID NO: 1 through SEQ ID NO: 38. In another embodiment, A is an immunogenic fragment of UspA2, wherein UspA2 is approximately 75% to 100% identical to the amino acid sequence set forth in SEQ ID NO: 1. In another embodiment, A is an immunogenic fragment of UspA2, wherein UspA2 is approximately 90% to 100% identical to SEQ ID NO: 1. In an another embodiment, A is an immunogenic fragment of UspA2, wherein

UspA2 is at least 95% identical to SEQ ID NO: 1. In another embodiment, A is an immunogenic fragment of UspA2, wherein UspA2 is approximately 75% to 100% identical to the amino acid sequence set forth in any one of SEQ ID NO: 1 – SEQ ID NO: 38. In another embodiment, A is an immunogenic fragment of UspA2, wherein UspA2 is approximately 90% to 100% identical to any one of SEQ ID NO: 1 – SEQ ID NO: 38. In an additional embodiment, A is an immunogenic fragment of UspA2, wherein UspA2 is at least 95% identical to any of SEQ ID NO: 1 – SEQ ID NO: 38. In a particular embodiment, A is an immunogenic fragment of UspA2 wherein UspA2 has the amino acid sequence set forth in SEQ ID NO: 1.

[72] In another embodiment, A is an immunogenic fragment of UspA2 from *M. catarrhalis* selected from the group consisting of amino acids 30-540 of SEQ ID NO: 1 (SEQ ID NO: 39), amino acids 31-540 of SEQ ID NO: 1 (SEQ ID NO: 40), amino acids 30-519 of SEQ ID NO: 1 (SEQ ID NO: 41), amino acids 30-564 of SEQ ID NO: 1 (SEQ ID NO: 42) and amino acids 31-564 of SEQ ID NO: 1 (SEQ ID NO: 43). More specifically, in one embodiment, A is SEQ ID NO: 43, amino acids 31-564 of SEQ ID NO: 1. In an additional embodiment, A is SEQ ID NO: 42, amino acids 30-564 of SEQ ID NO: 1. In another embodiment, A is an immunogenic fragment of UspA2 from *M. catarrhalis* selected from the group consisting of amino acids 30-540 of SEQ ID NO: 1 (SEQ ID NO: 39), amino acids 31-540 of SEQ ID NO: 1 (SEQ ID NO: 40) and amino acids 30-519 of SEQ ID NO: 1 (SEQ ID NO: 41). In another embodiment, A is an immunogenic fragment of UspA2 with at least 52% (American 2908), 55% (Norwegian 25), 57% (Japanese Z7476), 62% (Finnish FIN2344), 64% (American 2912), 69% (American P44), 73% (American 7169), 76% (Norwegian 27), 81% (American V1145), 88% (German Z8063) or 100% (Swedish BC5) identity to SEQ ID NO: 39. In another embodiment, A is an immunogenic fragment of UspA2 with at least 52 % (American 2908), 57% (Dutch F10), 62% (American 2933), 65% (Greek MC317), 67% (American V1122), 70% (American P44), 73% (American 7169), 76% (Norwegian 3), 81% (German Z8063), 100% (Swedish BC5) identical to SEQ ID NO: 43.

[73] In another embodiment, A is an immunogenic fragment of UspA2 from *M. catarrhalis* from SEQ ID NO: 2 through SEQ ID NO: 38 where the fragment comprises the amino acids that align with amino acids 30-540 of SEQ ID NO: 1 (SEQ ID NO: 39), amino acids 31-540 of SEQ ID NO: 1 (SEQ ID NO: 40), amino acids 30-519 of SEQ ID NO: 1 (SEQ ID NO: 41), amino acids 30-564 of SEQ ID NO: 1 (SEQ ID NO: 42) or amino acids 31-564 of SEQ ID NO:

1 (SEQ ID NO: 43). In one embodiment, the Gap program (from the GCG package), or the Needle program (from the EMBOSS package), implementing the Needleman-Wunsch algorithm, may be used to align the sequences.

[74] UspA2 - SEQ ID NO: 1

MKTMKLLPLKIAVTSAMIIGLGAASTANAQAKNDITLEDLPYLIKKIDQNELEADIGDIT
ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
AIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYD
FGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
NIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDA
LNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINN
IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDSDRVTAIDTK
VNAFDGRITALDSKVENGMAAQAALSGLFPYSVCKFNATAALGGYGSKSAVAIGAGYRV
NPNLAFKAGAAINTSGNKKGSYNIGVNYEF

[75] Amino acids 30-540 of UspA2 from SEQ ID NO: 1, SEQ ID NO:39

QAKNDITLEDLPYLIKKIDQNELEADIGDIT
ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
AIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYD
FGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
NIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDA
LNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINN
IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDSDRVTAIDTK

[76] Amino acids 31-540 of UspA2 from SEQ ID NO: 1, SEQ ID NO: 40

AKNDITLEDLPYLIKKIDQNELEADIGDIT
ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
AIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYD

FGHEVAESIGEIH AHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
 RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
 NIQDLATYNELODQYAQKQTEAIDALNKASSENTQNIEDLAAYNELODAYAKQQTEAIDA
 LNKASSENTQNIEDLAAYNELODAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINN
 IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
 ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDSRV TALDTK

[77] Amino acids 30-519 of UspA2 from SEQ ID NO: 1, SEQ ID NO: 41

QAKNDITLEDLPYLIKKIDQNELEADIGDIT
 ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
 AIKEDLOGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYD
 FGHEVAESIGEIH AHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
 RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
 NIQDLATYNELODQYAQKQTEAIDALNKASSENTQNIEDLAAYNELODAYAKQQTEAIDA
 LNKASSENTQNIEDLAAYNELODAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINN
 IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
 ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKS

[78] Amino acids 30-564 of UspA2 from SEQ ID NO: 1, SEQ ID NO: 42

QAKNDITLEDLPYLIKKIDQNELEADIGDIT
 ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
 AIKEDLOGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYD
 FGHEVAESIGEIH AHNEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
 RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
 NIQDLATYNELODQYAQKQTEAIDALNKASSENTQNIEDLAAYNELODAYAKQQTEAIDA
 LNKASSENTQNIEDLAAYNELODAYAKQQTEAIDALNKASSENTQNI AKNQADIANNINN
 IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
 ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDSRV TALDTK
 VNAFDGRITALDSKVENGM AAQAA

[79] Amino acids 31-564 of UspA2 from SEQ ID NO: 1, SEQ ID NO: 43

AKNDITLEDLPYLIKKIDQNELEADIGDIT
 ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE
 AIKEDLQGLADDFVEGQEGKILQNETSIKKNTQRLVNGFEIEKNKDAIAKNNESIEDLYD
 FGHEVAESIGEIHANEAQNETLKGLITNSIENTNNITKNKADIQALENNVVEELFNLSG
 RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
 NIQDLATYNELQDQYAKQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQOTEAIDA
 LNKASSENTQNIEDLAAYNELQDAYAKQOTEAIDALNKASSENTQNIAKNQADIANNINN
 IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
 ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDSRVTALDTK
 VNAFDGRITALDSKVENGMAAQAA

[80] In another embodiment, A is an immunogenic fragment of UspA2 from *M. catarrhalis* that differs from SEQ ID NO: 1 in one or more of the following amino acids: AA (amino acid) 30 to 298, AA 299 to 302, AA 303 to 333, AA 334 to 339, AA 349, AA 352 to 354, AA 368 to 403, AA 441, AA 451 to 471, AA 472, AA 474 to 483, AA 487, AA 490, AA 493, AA 529, AA 532 or AA 543. In another embodiment, A is an immunogenic fragment of UspA2 from *M. catarrhalis* that differs from SEQ ID NO: 1 in that it contains at least one amino acid insertion in comparison to SEQ ID NO: 1.

[81] In another embodiment, A is an immunogenic fragment of UspA2 that contains a laminin binding domain and a fibronectin binding domain.

[82] In an additional embodiment, A is an immunogenic fragment of UspA2 that contains a laminin binding domain, a fibronectin binding domain and a C3 binding domain.

[83] In a further embodiment, A is an immunogenic fragment of UspA2 that contains a laminin binding domain, a fibronectin binding domain, a C3 binding domain and an amphipathic helix.

[84] The laminin binding domain, fibronectin binding domain, C3 binding domain or amphipathic helix may be as defined for SEQ ID NO: 1 or may be the corresponding sequence in any one of SEQ ID NO: 2 through SEQ ID NO: 38.

[85] Proteins of formula (I) and proteins of the invention are useful as immunogens in subjects such as mammals, particularly humans. In particular, the proteins of formula (I) and proteins of the invention are useful in inducing an immune response against *M. catarrhalis* in subjects, particularly humans. The proteins of formula (I) and proteins of the invention are useful in the treatment or prevention of *M. catarrhalis* infection or disease. More specifically, the proteins of formula (I) and proteins of the invention are useful in the treatment or prevention of otitis media and/or COPD and/or AECOPD and/or pneumonia.

[86] The present invention relates to immunogenic compositions comprising UspA2 from *M. catarrhalis* or an immunogenic fragment thereof. The present invention also relates to vaccines comprising such immunogenic compositions and therapeutic uses of the same. Immunogenic compositions and vaccines of the present invention are useful in the treatment or prevention of *M. catarrhalis* infection or disease. More specifically, immunogenic compositions and vaccines described herein are useful in the treatment or prevention of otitis media and/or COPD and/or AECOPD and/or pneumonia.

[87] In one embodiment, the immunogenic composition comprises UspA2 from *M. catarrhalis*. UspA2 may be any one of SEQ ID NO: 1 through SEQ ID NO: 38 or a UspA2 sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 1 through SEQ ID NO: 38. UspA2 may also be a UspA2 sequence at least 63% (American 2908), 66% (Japanese Z7476), 70% (Dutch F10), 72% (Finnish 358), 74% (American P44), 77% (Finnish 307), 80% (Norwegian 3), 84% (American V1145), 90% (German Z8063) or 100% (Swedish BC5) identical to that of SEQ ID NO. 1.

[88] In another embodiment, the immunogenic composition comprises an immunogenic fragment of UspA2. The immunogenic fragment of UspA2 may be SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42 or SEQ ID NO.43, or a sequence having at least 90%, 95%, 96%, 97%, 98%, 99% sequence identity to any one of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42 or SEQ ID NO.43. The immunogenic fragment of UspA2 may be a UspA2 sequence at least 52% (American 2908), 55% (Norwegian 25), 57% (Japanese Z7476), 62% (Finnish FIN2344), 64% (American 2912), 69% (American P44), 73% (American 7169), 76% (Norwegian 27), 81% (American V1145), 88% (German Z8063) or 100% (Swedish BC5) identical to SEQ ID NO. 39. The immunogenic fragment of UspA2 may also be a UspA2 sequence at least 52 % (American 2908), 57% (Dutch F10), 62% (American 2933), 65% (Greek MC317), 67% (American V1122), 70% (American P44), 73% (American

7169), 76% (Norwegian 3), 81% (German Z8063), 100% (Swedish BC5) identical to SEQ ID NO. 43. Amino acid differences have been described in UspA2 from various *Moraxella catarrhalis* species.

[89] UspA2 contains a laminin binding domain (for example, amino acids 30-177 of SEQ ID NO: 1, SEQ ID NO: 44). In one embodiment, the fragment of UspA2 comprises the laminin binding region of SEQ ID NO: 1. In an additional embodiment, the fragment of UspA2 comprises the laminin binding region of any one of SEQ ID NO: 2 – SEQ ID NO: 38.

[90] Amino acids 30-177 of SEQ ID NO: 1, SEQ ID NO: 44:
QAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDVG
WNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNL
VNGFETIEKNKDAIAKNNESIED.

[91] UspA2 contains a fibronectin binding domain (for example, amino acids 165-318 of SEQ ID NO: 1, SEQ ID NO: 45). In one embodiment, the fragment of UspA2 comprises the fibronectin binding region of SEQ ID NO: 1. In an additional embodiment, the fragment of UspA2 comprises the fibronectin binding region of any one of SEQ ID NO: 2 – SEQ ID NO: 38. The fibronectin binding domain of SEQ ID NO: 45 also has C3 binding properties.

[92] Amino acids 165-318 of SEQ ID NO: 1, SEQ ID NO: 45:

KDAIAKNNESIEDLYD
FGHEVAESIGEIIHAHNEAQNETLKGITNSIENTNNITKNKADIQALENNVVEELFNLSG
RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
NIQDLATYNELQDQYAQK.

[93] UspA2 contains a complement component 3 (C3) binding domain (for example, amino acids 30-539 of SEQ ID NO: 1, SEQ ID NO: 46, or amino acids 165-318 of SEQ ID NO: 1, SEQ ID NO: 45). In one embodiment, the fragment of UspA2 comprises the C3 binding region of SEQ ID NO: 1. In an additional embodiment, the fragment of UspA2 comprises a C3 binding domain of any one of SEQ ID NO: 2 – SEQ ID NO: 38.

[94] Amino acids 30-539 of SEQ ID NO: 1, SEQ ID NO: 46:

QAKNDITLEDLPYLIKKIDQNELEADIGDIT
ALEKYLALSQYGNILALEELNKALEELDEDVGWNQNDIANLEDDVETLTKNQNALAEQGE

AIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNLVNGFEIEKNKDAIAKNNESIEDLYD
 FGHEVAESIGETIAHNEAQNETLKGITNSIENTNNITKNKADIQALENNVVEELFNLSG
 RLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGLLELSGHLIDQKTDIAQNQA
 NIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNTIEDLAAYNELQDAYAKQQTEAIDA
 LNKASSENTQNTIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIAKNQADIANNINN
 IYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKDKEHDKL
 ITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDSDRVTAIDT

[95] UspA2 contains an amphipathic helix (for example, amino acids 519-564 of SEQ ID NO: 1 or or amino acids 520-559 of SEQ ID NO:1). In one embodiment, the fragment of UspA2 comprises amino acids 519-564 of SEQ ID NO: 1. In another embodiment, the fragment of UspA2 comprises amino acids 520-559 of SEQ ID NO:1. In an additional embodiment, the fragment of UspA2 comprises an amphipathic helix of any one of SEQ ID NO: 2 – SEQ ID NO:38.

[96] In one embodiment, the immunogenic composition comprises a protein of formula (I) wherein A is an immunogenic fragment of UspA2 that comprises a laminin binding domain and a fibronectin binding domain.

[97] In an additional embodiment, the immunogenic composition comprises a protein of formula (I) wherein A is an immunogenic fragment of UspA2 that comprises a laminin binding domain, a fibronectin binding domain and a C3 binding domain.

[98] In a further embodiment, the immunogenic composition comprises a protein of formula (I) wherein A is an immunogenic fragment of UspA2 that comprises a laminin binding domain, a fibronectin binding domain, a C3 binding domain and an amphipathic helix.

[99] In another embodiment, the immunogenic composition comprises a protein as defined by formula (I). The immunogenic composition may contain, for example, a protein of formula (I) with an additional methionine at the amino terminus.

[100] In one embodiment, the present immunogenic compositions may be administered with other antigens. For example, the present immunogenic composition may be administered with antigens from *H. influenzae*. For example, the protein of formula (I) may be administered with Protein D (PD) from *H. influenzae*. Protein D may be as described in WO91/18926. The present immunogenic composition may be administered with Protein E (PE) and Pilin A (PilA)

from *H. Influenzae*. Protein E and Pilin A may be as described in WO2012/139225; the contents of which are incorporated herein by reference. Protein E and Pilin A may be presented as a fusion protein.

[101] In another embodiment, the immunogenic compositions of the invention may be administered with additional antigens from other bacterial species also known to cause otitis media, COPD, AECOPD or pneumonia.

[102] The amount of the immunogenic composition which is required to achieve the desired therapeutic or biological effect will depend on a number of factors such as the use for which it is intended, the means of administration, the recipient and the type and severity of the condition being treated, and will be ultimately at the discretion of the attendant physician or veterinarian. In general, a typical dose for the treatment of a condition caused in whole or in part by *M. catarrhalis* in a human, for instance, may be expected to lie in the range of from about 0.001 mg - 0.120 mg. More specifically, a typical dose for the treatment of a condition caused wholly or in part by *M. catarrhalis* in a human may lie in the range of from about 0.003 mg to about 0.03 mg of protein. The present invention provides an immunogenic composition comprising a protein of formula (I) or a protein of the invention for use in the treatment or prevention of a condition or disease caused wholly or in part by *M. catarrhalis*. The immunogenic composition may contain additional antigens; a typical dose for the treatment of a condition caused wholly or in part by *H. influenzae* in a human may lie in the range of from about 0.005 mg to about 0.05 mg for each additional antigen. This dose may be administered as a single unit dose. Several separate unit doses may also be administered. For example, separate unit doses may be administered as separate priming doses within the first year of life or as separate booster doses given at regular intervals (for example, every 1, 5 or 10 years). The present invention also provides an immunogenic composition comprising a protein of formula (I) or a protein of the invention for use in the treatment or prevention of a condition or disease caused wholly or in part by *Moraxella catarrhalis* in combination with at least one antigen from *Haemophilus influenzae*.

[103] Formulations comprising the immunogenic compositions of the invention may be adapted for administration by an appropriate route, for example, by the intramuscular, sublingual, transcutaneous, intradermal or intranasal route. Such formulations may be prepared by any method known in the art.

[104] The immunogenic compositions of the present invention may additionally comprise an adjuvant. When the term "adjuvant" is used in this specification, it refers to a substance that is administered in conjunction with the immunogenic composition to boost the patient's immune response to the immunogenic component of the composition.

[105] Suitable adjuvants include an aluminum salt such as aluminum hydroxide gel or aluminum phosphate or alum, but may also be a salt of calcium, magnesium, iron or zinc, or may be an insoluble suspension of acylated tyrosine, or acylated sugars, cationically or anionically derivatized saccharides, or polyphosphazenes. In one embodiment, the protein may be adsorbed onto aluminium phosphate. In another embodiment, the protein may be adsorbed onto aluminium hydroxide. In a third embodiment, alum may be used as an adjuvant.

[106] Suitable adjuvant systems which promote a predominantly Th1 response include: non-toxic derivatives of lipid A, Monophosphoryl lipid A (MPL) or a derivative thereof, particularly 3-de-O-acylated monophosphoryl lipid A (3D-MPL) (for its preparation see GB 2220211 A); and a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with either an aluminum salt (for instance aluminum phosphate or aluminum hydroxide) or an oil-in-water emulsion. In such combinations, antigen and 3D-MPL are contained in the same particulate structures, allowing for more efficient delivery of antigenic and immunostimulatory signals. Studies have shown that 3D-MPL is able to further enhance the immunogenicity of an alum-adsorbed antigen (Thoenen et al. Vaccine (1998) 16:708-14; EP 689454-B1).

[107] AS01 is an Adjuvant System containing MPL (3-O-desacyl-4'- monophosphoryl lipid A), QS21 ((*Quillaja saponaria* Molina, fraction 21) Antigenics, New York, NY, USA) and liposomes. AS01B is an Adjuvant System containing MPL, QS21 and liposomes (50 µg MPL and 50 µg QS21). AS01E is an Adjuvant System containing MPL, QS21 and liposomes (25 µg MPL and 25 µg QS21). In one embodiment, the immunogenic composition or vaccine comprises AS01. In another embodiment, the immunogenic composition or vaccine comprises AS01B or AS01E. In a particular embodiment, the immunogenic composition or vaccine comprises AS01E.

[108] AS02 is an Adjuvant System containing MPL and QS21 in an oil/water emulsion. AS02V is an Adjuvant System containing MPL and QS21 in an oil/water emulsion (50 µg MPL and 50 µg QS21).

[109] AS03 is an Adjuvant System containing α-Tocopherol and squalene in an oil/water (o/w) emulsion. AS03_A is an Adjuvant System containing α-Tocopherol and squalene in an o/w emulsion (11.86 mg tocopherol). AS03_B is an Adjuvant System containing α-Tocopherol and squalene in an o/w emulsion (5.93 mg tocopherol). AS03_C is an Adjuvant System containing α-Tocopherol and squalene in an o/w emulsion (2.97 mg tocopherol). In one embodiment, the immunogenic composition or vaccine comprises AS03.

[110] AS04 is an Adjuvant System containing MPL (50 µg MPL) adsorbed on an aluminum salt (500 µg Al³⁺). In one embodiment, the immunogenic composition or vaccine comprises AS04.

[111] A system involving the use of QS21 and 3D-MPL is disclosed in WO 94/00153. A composition wherein the QS21 is quenched with cholesterol is disclosed in WO 96/33739. An additional adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil in water emulsion is described in WO 95/17210. In one embodiment the immunogenic composition additionally comprises a saponin, which may be QS21. The formulation may also comprise an oil in water emulsion and tocopherol (WO 95/17210). Unmethylated CpG containing oligonucleotides (WO 96/02555) and other immunomodulatory oligonucleotides (WO 0226757 and WO 03507822) are also preferential inducers of a TH1 response and are suitable for use in the present invention.

[112] Additional adjuvants are those selected from the group of metal salts, oil in water emulsions, Toll like receptor agonists, (in particular Toll like receptor 2 agonist, Toll like receptor 3 agonist, Toll like receptor 4 agonist, Toll like receptor 7 agonist, Toll like receptor 8 agonist and Toll like receptor 9 agonist), saponins or combinations thereof.

[113] The present invention provides a process for preparing an immunogenic composition comprising combining a protein of formula (I) or a protein of the invention with an adjuvant.

[114] The present invention further provides a vaccine containing an immunogenic composition of the invention and a pharmaceutically acceptable adjuvant.

[115] Possible excipients include arginine, pluronic acid and/or polysorbate. In a preferred embodiment, polysorbate 80 (for example, TWEEN(a US registered trademark) 80) is used. In a further embodiment, a final concentration of about 0.03% to about 0.06% is used. Specifically, a final concentration of about 0.03%, 0.04%, 0.05% or 0.06% polysorbate 80 (w/v) may be used.

[116] The present invention provides a process for preparing an immunogenic composition or vaccine comprising combining a protein of formula (I) or protein of the invention with a pharmaceutically acceptable excipient.

[117] The present invention also provides nucleic acids encoding the proteins of the invention. The term "nucleic acid" refers to a polymeric form of nucleotides. Nucleotides can be ribonucleotides, deoxyribonucleotides, or modified forms of either ribonucleotides or deoxyribonucleotides. The term includes single and double forms of DNA. The nucleic acids are preferably substantially free from other nucleic acids.

[118] The present invention provides a process of producing nucleic acids of the invention. Nucleic acids of the invention may be prepared by methods known by those skilled in the art. For example, the nucleic acids of the invention may be synthesized in part or in whole. The nucleic acids may be prepared by digesting longer amino acids or joining shorter amino acids.

[119] The present invention provides a method for the treatment or prevention of otitis media. The method comprises administering to a subject in need thereof a therapeutically effective amount of a protein of formula (I) or a protein of the invention.

[120] The present invention provides a method for the treatment or prevention of exacerbations in chronic obstructive pulmonary disease. The exacerbation of COPD may be an acute exacerbation. The method comprises administering to a subject in need thereof a therapeutically effective amount of the protein of formula (I) or a protein of the invention.

[121] The present invention provides a method for the treatment or prevention of pneumonia. The method comprises administering to a subject in need thereof a therapeutically effective amount of the protein of formula (I) or a protein of the invention.

[122] The present invention provides a pharmaceutical composition comprising a protein of formula (I) or a protein of the invention for use in the treatment or prevention of a condition or

disease caused wholly or in part by *Moraxella catarrhalis*. Pharmaceutical compositions may further comprise a pharmaceutically acceptable adjuvant.

[123] The present invention provides use of (a) proteins of formula (I) and proteins of the invention, (b) an immunogenic composition comprising a protein of formula (I) or protein of the invention or (c) a vaccine comprising (c1) a protein of formula (I) or protein of the invention or (c2) immunogenic composition comprising a protein of formula (I) or protein of the invention for the manufacture of a medicament for treating or preventing *M. catarrhalis* infection or disease.

[124] The present invention provides use of (a) proteins of formula (I) and proteins of the invention, (b) an immunogenic composition comprising a protein of formula (I) or protein of the invention or (c) a vaccine comprising (c1) a protein of formula (I) or protein of the invention or (c2) immunogenic composition comprising a protein of formula (I) or protein of the invention for the manufacture of a medicament for treating or preventing otitis media.

[125] The present invention provides use of (a) proteins of formula (I) and proteins of the invention, (b) an immunogenic composition comprising a protein of formula (I) or protein of the invention or (c) a vaccine comprising (c1) a protein of formula (I) or protein of the invention or (c2) immunogenic composition comprising a protein of formula (I) or protein of the invention for the manufacture of a medicament for treating or preventing acute exacerbations of chronic obstructive pulmonary disease (AECOPD).

[126] The present invention provides a use of (a) proteins of formula (I) and proteins of the invention, (b) an immunogenic composition comprising a protein of formula (I) or protein of the invention or (c) a vaccine comprising (c1) a protein of formula (I) or protein of the invention or (c2) immunogenic composition comprising a protein of formula (I) or protein of the invention for the manufacture of a medicament for treating or preventing pneumonia.

[127] The following examples are intended for illustration only and are not intended to limit the scope of the invention in any way.

[128] In the examples, the following terms have the designated meaning:

6xhis = six histidines;

xg = centrifugal force (number gravities)

AS = alanine serine

BSA = bovine serum albumin;
°C = degrees Celsius;
CaCl₂ = calcium chloride;
CD = circular dichroism;
CHCl₃ = chloroform;
CH₃CN = acetonitrile;
CO₂ = carbon dioxide;
Da = dalton;
DNA = deoxyribonucleic acid;
DO = dissolved oxygen;
DSC = differential scanning calorimetry;
EDTA = ethylenediaminetetraacetic acid;
h = hour;
H₂O = water;
H₂O₂ = hydrogen peroxide;
HCDI = high cell density induction;
HCl = hydrogen chloride;
His = his = histidine;
IMAC = immobilized metal affinity chromatography;
IPTG = isopropyl β-D-1-thiogalactopyranoside;
kVolts = kilovolts
L = liter;
LB = Luria-Bertani;
LCDI = low cell density induction;
MeOH = methanol;
ml = milliliter;
NaCl = sodium chloride;
RPM = rpm = revolutions per minute;
min = minute;
mM = millimolar;
μg = microgram;
μL = microliter;
MW = molecular weight;
m/z = mass/charge;

NaCl = sodium chloride;

NaPO₄ = sodium phosphate;

ng = nanogram;

NH₄OH = ammonium hydroxide;

nm = nanometer;

O.D. = optical density;

PBS = phosphate buffered saline;

PCR = polymerase chain reaction;

psi = pounds per square inch;

PVDF = polyvinylidene difluoride;

SDS-PAGE = sodium dodecyl sulphate polyacrylamide gel electrophoresis;

TFA = trifluoroacetic acid

T_m = melting point;

T_{m1} = first melting point;

T_{m2} = second melting point;

w/v = weight/volume.

[129] EXAMPLES

Example 1: Protein Constructs

Protein constructs were produced with different fragments of UspA2 with and without additional amino acids. The following table describes protein constructs made.

Table 2: Protein constructs containing UspA2 protein.

Construct ID	Description	N-terminal	C-Terminal
MC-001	UspA2 + 1/2 helix + 6His	UspA2 fragment (A.A.: 30-540 of SEQ ID NO: 1, SEQ ID NO: 47)	ASHHHHHH
	A.A.	30	540 541 548
MC-002	UspA2 + 1/2 helix	UspA2 fragment (A.A.: 30-540 of SEQ ID NO: 1, SEQ ID NO: 47)	
	A.A.	30	540
MC-003	UspA2 + 1/2 helix +1His	UspA2 fragment (A.A.: 30-540 of SEQ ID NO: 1, SEQ ID NO: 47)	H
	A.A.	30	540 541
MC-004	UspA2 + 1/2 helix + 2His	UspA2 fragment (A.A.: 30-540 of SEQ ID NO: 1, SEQ ID NO: 47)	HH
	A.A.	30	540 541 542
MC-005	UspA2 Δ helix + 6His	UspA2 fragment (A.A.: 30-519 of SEQ ID NO: 1, SEQ ID NO: 48)	ASHHHHHH
	A.A.	30	519 520 527
MC-006	UspA2 Δ helix	UspA2 fragment (A.A.: 30-519 of SEQ ID NO: 1, SEQ ID NO: 48)	
	A.A.	30	519
MC-007	UspA2 + helix + 6His	UspA2 fragment (A.A.: 30-564 of SEQ ID NO: 1, SEQ ID NO: 49)	ASHHHHHH
	A.A.	30	564 565 572
MC-008	UspA2 + helix + 2His	UspA2 fragment (A.A.: 30-564 of SEQ ID NO: 1, SEQ ID NO: 49)	HH
	A.A.	30	564 565 566
MC-009	UspA2 + helix + 2His Δ Q	UspA2 fragment (A.A.: 31-564 of SEQ ID NO: 1, SEQ ID NO: 50)	HH
	A.A.	31	564 565 566
MC-010	UspA2 + helix	UspA2 fragment (A.A.: 30-564 of SEQ ID NO: 1, SEQ ID NO: 49)	
	A.A.	30	564
MC-011	UspA2 + 1/2helix + 6His Δ Q	UspA2 fragment (A.A.: 31-540 of SEQ ID NO: 1, SEQ ID NO: 51)	ASHHHHHH
	A.A.	31	540 541 548

A.A. = amino acid

The DNA and amino acid sequences for each protein constructs listed in Table 2 are set forth below.

PROTEIN CONSTRUCT SEQUENCES:

MC-001 (DNA) - SEQ ID NO: 52

ATGCAGGCCAAAAATGATATTACCCTGGAAGATCTGCCGTATCTGATCAAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGCCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCTGACCAAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAAGCAGATATTCAGGCGCTGGAAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCTGAAAAAAAACGTTGAAGAAGGT
CTGCTGGAACGTCTGGTCACCTGATCGATCAGAAAACCTGATATTGCCCAGAATCAGGCAAAT
ATTGAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCGAAGACCC
CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAAATGGCAAT
GCCATCACCAAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAGTTGATGGTTTTTGATAGC
CGTGTGACCGCACTGGATACCAAAGCAAGCCATCATCATCACCACCACTAA.

MC-001 (protein) – (M)(UspA2 amino acids 30 - 540)(ASHHHHHH) SEQ ID NO: 53

MQAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFEVGEQEGKILQNETSIKKNTQRN
LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
TKNKADIQALENNVVEELFNLSGRLLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAY

NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI
IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDS
RVTALDTKASHHHHHH

MC-002 (DNA) - SEQ ID NO: 54

ATGCAGGCCAAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCCTGACCAAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTCAGGAAGGCCAAAATTCTGCAGAACGAAACAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCCTGAAAGGTCTGATTACCAACAGCATCGAAAAATACCAATAACATT
ACCAAAAAACAAAGCAGATATTCAGGCGCTGGAAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCCTGAAAAAAAACGTTGAAGAAGGT
CTGCTGGAACCTGTCTGGTCACCTGATCGATCAGAAACTGATATTGCCCAGAATCAGGCAAAT
ATTGAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACAGAACACC
CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAAATGGCAAT
GCCATCACCAAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAGTTGATGGTTTTGATAGC
CGTGTGACCGCACTGGATACCAAATAA

MC-002 (Protein) – (M)(UspA2 amino acids 30-540) SEQ ID NO: 55

MQAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQRN
LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHANNEAQNETLKGILITNSIENTNNI
TKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAKQTEAIDALNKASSENTQNIEDLAAY
NELQD

AYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNIKNO
ADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTLIEKD
KEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFSRVTA
DTK

SEQ ID NO: 56

ATGCAGGCCAAAAATGATATTACCCTGGAAGATCTGCCGTATCTGATCAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCCTGACCAAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTGAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCCTGAAAAAAAACGTTGAAGAAGGT
CTGCTGGAACCTGTCTGGTCACCTGATCGATCAGAAAACCTGATATTGCCCAGAATCAGGCAAAAT
ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAAACACCCAGAATATCGAAGATCTGGCAGCATAC
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCAGAACACC
CTGATTGAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAATGGCAAT
GCCATCACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAAGTTGATGGTTTTGATAGC
CGTGTGACCGCACTGGATACCAAAGTTAATGCATTTGATGGTCGTATTACCGCTCTGGATAGT
AAAGTTGAAAATGGAATGGCAGCACAAAGCAGCACACTAA

SEQ ID NO: 57

MQAKNDITLEDLPYLIKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFEVGEQEGKILQNETSIKKNQ
LVNGFEIEKNKDAIAKNNESIEDLYDFEGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
TKNKADIQALENNVVEELENLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAKQTEAIDALNKASSENTQNIEDLAAY

NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQN
IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDG
RVTALDTKVNAFDGRITALDSKVENGMAAQAAH

MC-003 (DNA) – SEQ ID NO: 87

ATGCAGGCCAAAAATGATATTACCCTGGAAGATCTGCCGTATCTGATCAAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCCTGACCAAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAAGCAGATATTCAGGCGCTGGAAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAACCCCTGAAAAAAAACGTTGAAGAAGGT
CTGCTGGAAGTGTCTGGTCACCTGATCGATCAGAAACTGATATTGCCCAGAATCAGGCAAAT
ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCAGAACACC
CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAAT
GCCATCACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAGTTGATGGTTTTGATAGC
CGTGTGACCGCACTGGATACCAAACACTAA

MC-003 (Protein) – (M)(UspA2 amino acids 30-540)(H) – SEQ ID NO: 88

MQAKNDITLEDLPYLIKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQRN
LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
TKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAY

NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQN
IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFD
RVTALDTKH

MC-004 (DNA) - SEQ ID NO: 58

ATGCAGGCCAAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCCTGACCAAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTGAGGAAGGCAAAATTTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCCTGAAAAAACGTTGAAGAAGGT
CTGCTGGAAGTGTCTGGTCACCTGATCGATCAGAAACTGATATTGCCCAGAATCAGGCAAAT
ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAAACACCCAGAATATCGAAGATCTGGCAGCATA
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCAGAACACC
CTGATTGAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAAATGGCAAT
GCCATCACCAAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAGTTGATGTTTTGATAGC
CGTGTGACCGCACTGGATACCAAACATCATTA

MC-004 (Protein) – (M)(UspA2 amino acids 30-540)(HH) SEQ ID NO: 59

MQAKNDITLEDLPYLIKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNQORN
LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHANNEAQNETLKGLITNSIENTNNI
TKNRADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNOANIQDLATYNELQDQYAKQTEAIDALNKASSENTQNIEDLAAY
NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQN

IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDS
RVTALDTKHH

MC-005 (DNA) - SEQ ID NO: 60

ATGCAGGCCAAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATFACCGCACTGGAAAAATATCTGGCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCCTGACCAAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTCAGGAAGGCCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCCTGAAAAAAAACGTTGAAGAAGGT
CTGCTGGAACCTGCTGGTCACCTGATCGATCAGAAAACCTGATATTGCCCCAGAATCAGGCCAAAT
ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
AACGAACTGCAGGATGCCATATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCAGAACATPGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAAATATCAATAATATCTATGAACTGGCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACAGAACACC
CTGATTGAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAAATTTGCAGCAACCGCAGATGCAATTACCAAAAAATGGCAAT
GCCATCACCAAAAAATGCCAAAAGCGCAAGCCATCATCATCACCACCACTAA

MC-005 (Protein) – (M)(UspA2 amino acids 30-519)(ASHHHHHH) SEQ ID NO: 61

MQAKNDITLEDLPYLIKIBQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQRN
LVNGFEEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHANNEAQNETLKLGLITNSIENTNNI
TKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAKQTEAIDALNKASSENTQNIEDLAAY
NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQN
IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSASHHHHHH

MC-006 (DNA) - SEQ ID NO: 62

ATGCAGGCCAAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG
TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCTGACCAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCTGAAAAAAAACGTTGAAGAAGGT
CTGCTGGAACGTCTGGTCACCTGATCGATCAGAAACTGATATTGCCCAGAATCAGGCAAAT
ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCGAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAAATATCAATAATATCTATGAACTGGCCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
ATTGCCGAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCAGAACACC
CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAAT
GCCATCACCAAAAATGCCAAAAGCTAA

MC-006 (Protein) – (M)(UspA2 amino acids 30-519) SEQ ID NO: 63

MQAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQRN
LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
TKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELODQYAKQTEAIDALNKASSENTQNIEDLAAY
NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQN
IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKS

MC-007 (DNA) - SEQ ID NO: 64

ATGCAGGCCAAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAAATCGATCAG
AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG

TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
 GGTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCTGACCAAAAATCAG
 AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
 GAAGGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
 CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
 GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
 GAAGCACAGAATGAAACCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
 ACCAAAAACAAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
 AGCGGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
 GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCTGAAAAAACGTTGAAGAAGGT
 CTGCTGGAACGTCTGGTCACCTGATCGATCAGAAAACCTGATATTGCCCAGAATCAGGCAAAT
 ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
 ATTGATGCCCTGAATAAAGCGAGCAGCGAAACACCCAGAATATCGAAGATCTGGCAGCATAC
 AACGAACTGCAGGATGCCATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
 AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
 GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
 ATCGCCAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCCAGCAG
 CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGT
 ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCAGAACACC
 CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
 AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAAT
 GCCATCACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAGTTGATGGTTTTGATAGC
 CGTGTGACCGCACTGGATACCAAAGTTAATGCATTTGATGGTCGTATTACCGCTCTGGATAGT
 AAAGTTGAAAATGGTATGGCAGCACAGGCAGCAGCAAGCCATCATCATCACCACCACCTAA

MC-007 (Protein) – (M)(UspA2 amino acids 30-564)(ASHHHHHH) SEQ ID NO: 65

MQAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
 GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTRQ
 LVNGFEEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
 TRKNADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
 LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYQKQTEAIDALNKASSENTQNIEDLAAY
 NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQ
 IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
 LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFD
 RVTAIDTKVNAFDGRITALDSKVENGMAAQAAASHHHHHH

MC-008 (DNA) - SEQ ID NO: 66

ATGCAGGCCAAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAATCGATCAG
 AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG

TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCTGACCAAAAATCAG
AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
GAAGGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
GAAGCACAGAATGAAACCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
ACCAAAAAACAAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
AGCGGTCTGCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCTGAAAAAACGTTGAAGAAGGT
CTGCTGGAACCTGTCTGGTCACCTGATCGATCAGAAAACCTGATATTGCCCAGAATCAGGCAAT
ATTGAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
ATTGATGCCCTGAATAAAGCGAGCAGCGAAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
AACGAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAAT
ATCGCCAAAAATCAGGCCGATATTGCCAACAAATATCAATAATATCTATGAACTGGCCCAGCAG
CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAAATACCGATCGT
ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACAGAACACC
CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAAT
GCCATCACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAGTTGATGGTTTTGATAGC
CGTGTGACCGCACTGGATACCAAAGTTAATGCATTTGATGGTTCGTATTACCGCTCTGGATAGT
AAAGTTGAAAATGGTATGGCAGCACAGGCAGCACACCACTAA

MC-008 (Protein) -- (M)(UspA2 30-564)(HH) SEQ ID NO: 67

MQAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFEVGEQEGKILQNETSIKKNTQRN
LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
TKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
LLELSGHLIDQKTDIAQNQANIQDLATYNELODQYAQKQTEAIDALNKASSENTQNIEDLAAY
NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELODAYAKQQTEAIDALNKASSENTQNI
IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDS
RVTALDTKVNAFDGRITALDSKVENGMAAQAHH

MC-009 (DNA) - SEQ ID NO: 68

ATGGCGAAAAATGATATTACCCTGGAAGATCTGCCGTATCTGATCAAAAAATCGATCAGAAC
GAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAGTAT

GGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTGGGT
 TGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCCTGACCAAAAATCAGAAT
 GCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGTGAA
 GGTGAGGAAGGCCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAATCTG
 GTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATTGAA
 GATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAACGAA
 GCACAGAATGAAACCCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATTACC
 AAAAACAAAGCAGATATTCAGGCGCTGGAATAATGTTGTGGAAGAACTGTTAATCTGAGC
 GGTGCTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAACAACATTTATGAACTGGCA
 CAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCCTGAAAAAACGTTGAAGAAGGTCTG
 CTGGAACCTGTCTGGTCACCTGATCGATCAGAAACTGATATTGCCCAGAATCAGGCAAATATT
 CAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCAATT
 GATGCCCTGAATAAAGCGAGCAGCGAAACACCCAGAATATCGAAGATCTGGCAGCATACAAC
 GAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCAAGC
 TCTGAAACACGCAGAACATTGAAGATCTGGCTGCCATATAATGAATTACAGGATGCGTATGCC
 AAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAATATC
 GCCAAAAATCAGGCCGATATTGCCAACAATATCAATAATATCTATGAACTGGCCAGCAGCAG
 GATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGTATT
 GCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACAGAACACCCCTG
 ATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCAAAAT
 AAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAATGCC
 ATCACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAGTTGATGGTTTTGATAGCCGT
 GTGACCGCACTGGATACCAAAGTTAATGCATTTGATGGTTCGTATTACCGCTCTGGATAGTAAA
 GTTGAAAATGGTATGGCAGCACAGGCAGCACACCACTAA

MC-009 (Protein) – (M)(UspA2 31-564)(HH) SEQ ID NO: 69

MAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDVG
 WNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQORN
 VNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHANEAQNETLKGLITNSIENTNNIT
 KNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGL
 LELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYN
 ELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI
 AKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
 IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFSR
 VTALDTKVNAFDGRITALDSKVENGMAAQAHH

MC-010 (DNA) - SEQ ID NO: 70

ATGCAGGCCAAAATGATATTACCCCTGGAAGATCTGCCGTATCTGATCAAAAAATCGATCAG
 AACGAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAG

TATGGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTG
 GGTTGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCTGACCAAAAATCAG
 AATGCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGT
 GAAGGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAAT
 CTGGTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATT
 GAAGATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAAC
 GAAGCACAGAATGAAACCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATT
 ACCAAAAACAAAGCAGATATTCAGGCGCTGGAAAATAATGTTGTGGAAGAACTGTTTAATCTG
 AGCGGTCTGCTGATTGATCAGAAAGCCGATATCGATAATAACATTAAACAACATTTATGAACTG
 GCACAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCCTGAAAAAACCGTTGAAGAAGGT
 CTGCTGGAACCTGTCTGGTCACCTGATCGATCAGAAAACCTGATATTGCCCAGAATCAGGCAAAT
 ATTCAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCA
 ATTGATGCCCTGAATAAAGCGAGCAGCGAAACACCCAGAATATCGAAGATCTGGCAGCATAAC
 AACGAACTGCAGGATGCCATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCA
 AGCTCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTAT
 GCCAAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCCTCTTCTGAAAATACACAGAAT
 ATCGCCAAAAATCAGGCCGATATTGCCAACAAATATCAATAATATCTATGAACTGGCCAGCAG
 CAGGATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAAATACCGATCGT
 ATTGCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACAGAACACC
 CTGATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCA
 AATAAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAAT
 GCCATACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAGTTGATGGTTTTTGATAGC
 CGTGTGACCGCACTGGATACCAAAGTTAATGCATTTGATGGTTCGTATTACCGCTCTGGATAGT
 AAAGTTGAAAATGGTATGGCAGCACAGGCAGCATAA

MC-010 (Protein) – (M)(UspA2 amino acids 30-564) SEQ ID NO: 71

MQAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEDV
 GWNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFEVGEQEGKILQNETSIKKNTQRN
 LVNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNI
 TKNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEG
 LLELSGHLIDQKTDIAQNQANIQDLATYNELQDQYQKQTEAIDALNKASSENTQNIEDLAAY
 NELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQN
 IAKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNT
 LIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTKVDGFDS
 RVTALDTKVNAFDGRITALDSKVENGMAAQAA

MC-011 (DNA) - SEQ ID NO: 72

ATGGCGAAAAATGATATTACCCTGGAAGATCTGCCGTATCTGATCAAAAAAATCGATCAGAAC
 GAACTGGAAGCCGATATTGGTGATATTACCGCACTGGAAAAATATCTGGCACTGAGCCAGTAT

GGAAATATTCTGGCCCTGGAAGAACTGAATAAAGCTCTGGAAGAGCTGGATGAAGATGTGGGT
TGGAATCAGAATGATATCGCCAATCTGGAAGATGATGTTGAAACCCTGACCAAAAATCAGAAT
GCACTGGCAGAACAGGGTGAAGCAATTAAAGAAGATCTGCAGGGTCTGGCAGATTTTGTGAA
GGTCAGGAAGGCAAAATTCTGCAGAACGAAACCAGCATCAAAAAAACACCCAGCGTAATCTG
GTGAATGGCTTTGAAATTGAAAAAACAAAGATGCCATTGCCAAAAACAACGAAAGCATTGAA
GATCTGTATGATTTTGGTCATGAAGTTGCCGAAAGCATTGGTGAAATTCATGCACATAACGAA
GCACAGAATGAAACCCTGAAAGGTCTGATTACCAACAGCATCGAAAATACCAATAACATTACC
AAAAACAAAGCAGATATTCAGGCGCTGGAATAATGTTGTGGAAGAACTGTTTAATCTGAGC
GGTCGTCTGATTGATCAGAAAGCCGATATCGATAATAACATTAACAACATTTATGAACTGGCA
CAGCAGCAGGATCAGCATAGCAGCGATATCAAAACCCTGAAAAAACGTTGAAGAAGGTCTG
CTGGAAGTGTCTGGTCACCTGATCGATCAGAAACTGATATTGCCCAGAATCAGGCAATATTT
CAGGATCTGGCCACCTATAATGAACTGCAGGATCAGTATGCACAGAAACAGACCGAAGCAATT
GATGCCCTGAATAAAGCGAGCAGCGAAAACACCCAGAATATCGAAGATCTGGCAGCATACAAC
GAACTGCAGGATGCCTATGCAAAACAGCAGACTGAAGCCATCGACGCACTGAACAAGGCAAGC
TCTGAAAACACGCAGAACATTGAAGATCTGGCTGCCTATAATGAATTACAGGATGCGTATGCC
AAACAGCAGACCGAAGCGATTGATGCGCTGAACAAAGCCTCTTCTGAAAATACACAGAATATC
GCCAAAAATCAGGCCGATATTGCCAACAAATATCAATAATATCTATGAACTGGCCAGCAGCAG
GATCAGCACTCTTCTGATATCAAAACACTGGCAAAAGCAAGCGCAGCAAATACCGATCGTATT
GCGAAAAACAAAGCCGATGCAGATGCAAGCTTTGAAACACTGACGAAAAACCAGAACACCCTG
ATTGAAAAAGATAAAGAACATGATAAACTGATCACCGCCAATAAAACCGCAATTGATGCAAAT
AAAGCCAGCGCAGATACCAAATTTGCAGCAACCGCAGATGCAATTACCAAAAATGGCAATGCC
ATCACCAAAAATGCCAAAAGCATTACCGATCTGGGCACCAAAGTTGATGGTTTTGATAGCCGT
GTGACCGCACTGGATACCAAAGCAAGCCATCATCATCACCACCCTAA

MC-011 (Protein) -- (M)(UspA2 amino acids 31-540)(ASHHHHHH) SEQ ID NO: 73

MAKNDITLEDLPYLIKKIDQNELEADIGDITALEKYLALSQYGNILALEELNKALEELDEBVG
WNQNDIANLEDDVETLTKNQNALAEQGEAIKEDLQGLADFVEGQEGKILQNETSIKKNTQRNL
VNGFEIEKNKDAIAKNNESIEDLYDFGHEVAESIGEIHAHNEAQNETLKGLITNSIENTNNIT
KNKADIQALENNVVEELFNLSGRLIDQKADIDNNINNIYELAQQQDQHSSDIKTLKKNVEEGL
LELSGHLIDQKTDIAQNQANIQDLATYNELQDQYAQKQTEAIDALNKASSENTQNIEDLAAYN
ELQDAYAKQQTEAIDALNKASSENTQNIEDLAAYNELQDAYAKQQTEAIDALNKASSENTQNI
AKNQADIANNINNIYELAQQQDQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSITDLGTVKVDGFDNR
VTALDTKASHHHHHH

Vector Construction and Transformation

DNA Sequence for UspA2 from strain ATCC 25238 – SEQ ID NO: 74.

ATGAAAACCATGAACTTCTCCCTCTAAAAATCGCTGTAACCAAGTGCCATGATTATTGGCTTGGGTG
 CGGCATCTACTGCGAATGCGCAGGCTAAAAATGATATAACTTTAGAGGATTTACCATATTTAATAAA
 AAAGATTGACCAAAATGAATTGGAAGCAGATATCGGAGATATTACTGCTCTTGAAAAGTATCTAGCA
 CTTAGCCAGTATGGCAATATTTTAGCTCTAGAAGAGCTCAACAAGGCTCTAGAAGAGCTCGACGAG
 GATGTTGGATGGAATCAGAATGATATTGCAAACTTGGAAGATGATGTTGAAACGCTCACCAAAAT
 CAAAATGCTTTGGCTGAACAAGGTGAGGCAATTAAAGAAGATCTTCAAGGGCTTGCGAGATTTTGTA
 GAAGGGCAAGAGGGTAAAATTCTACAAAATGAACTTCAATTAATAAAAAATACTCAGAGAAACCTTG
 TCAATGGGTTTGAGATTGAGAAAAATAAGATGCTATTGCTAAAAACAATGAGTCTATCGAAGATCT
 TTATGATTTTGGTCATGAGGTTGCAGAAAGTATAGGCGAGATACATGCTCATAATGAAGCGCAAAA
 TGAAACTCTTAAAGGCTTGATAACAAACAGTATTGAGAATACTAATAATATTACCAAAAACAAAGCT
 GACATCCAAGCACTTGAAAACAATGTCGTAGAAGAACTATTCAATCTAAGCGGTGCGCTAATTGAT
 CAAAAGCAGATATTGATAATAACATCAACAATATCTATGAGCTGGCACAACAGCAAGATCAGCATA
 GCTCTGATATCAAAACACTTAAAAAAATGTCGAAGAAGGTTTGTGGAGCTAAGCGGTGACCTAAT
 TGATCAAAAACAGATATTGCTCAAAACCAAGCTAACATCCAAGATCTGGCCACTTACAACGAGCTA
 CAAGACCAGTATGCTCAAAAGCAAACCGAAGCGATTGACGCTCTAAATAAAGCAAGCTCTGAGAAT
 ACACAAAACATCGAAGATCTGGCCGCTTACAACGAGCTACAAGATGCCTATGCCAAACAGCAAACC
 GAAGCAATTGACGCTCTAAATAAAGCAAGCTCTGAGAATACACAAAACATCGAAGATCTGGCCGCT
 TACAACGAGCTACAAGATGCCTATGCCAAACAGCAAACCGAAGCCATTGACGCTCTAAATAAAGCA
 AGCTCTGAGAATACACAAAACATTGCTAAAAACCAAGCGGATATTGCTAATAACATCAACAATATCT
 ATGAGCTGGCACAACAGCAAGATCAGCATAGCTCTGATATCAAAACCTTGGCAAAAGCAAGTGCTG
 CCAATACTGATCGTATTGCTAAAAACAAAGCCGATGCTGATGCAAGTTTTGAAACGCTCACCAAAAA
 TCAAATACTTTGATTGAAAAAGATAAAGAGCATGACAAATTAATTACTGCAAAACAAACTGCGATT
 GATGCCAATAAAGCATCTGCGGATACCAAGTTTGCAGCGACAGCAGACGCCATTACCAAAAAATGG
 AATGCTATCACTAAAAACGCAAAATCTATCACTGATTTGGGCACTAAAGTGGATGGTTTTGACAGT
 CGTGTAAGTGCATTAGACACCAAAGTCAATGCCTTTGATGGTCGTATCACAGCTTTAGACAGTAAA
 GTTGAAAACGGTATGGCTGCCCAAGCTGCCCTAAGTGGTCTATTCCAGCCTTATAGCGTTGGTAAG
 TTTAATGCGACCGCTGCACCTTGGTGGCTATGGCTCAAAATCTGCGGTTGCTATCGGTGCTGGCTAT
 CGTGTGAATCCAAATCTGGCGTTTAAAGCTGGTGGCGGATTAATACCAGTGGTAATAAAAAAGGC
 TCTTATAACATCGGTGTGAATTACGAGTTCTAA

Protein Sequence for UspA2 from strain ATCC 25238. - SEQ ID NO. 1 as described above.

Vector Construction

To generate the construct MC-001, DNA fragment coding for an UspA2 gene fragment (amino acids 30 to 540 from strain ATCC 25238) including the *NdeI* / *XhoI* restriction sites to facilitate the cloning (the starting methionine is encoded by *NdeI* site) and the DNA sequence corresponding to the AS (alanine serine) amino acids linker and 6xhis amino acids was codon-optimized (non-native) and synthesized by GENEART(a US registered trademark). Codon-optimized means that the nucleotide sequence was changed from the native sequence without changing the amino acid sequence in order to better fit with the codon usage in *Escherichia coli* for optimal expression. The UspA2 fragment was cloned according to standard methods into the pET-26b expression vector using the *NdeI* / *XhoI* restriction sites.

To generate MC-002, MC-003, and MC-004 constructs, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 30-540 from strain ATCC 25238) using the MC-001 construct as a template, the primer UspA2Nde opt (which contains the methionine start codon), and the primer UspA2opt delta His, A2opt 1His delta AS, and A2opt 2His delta AS, respectively. The UspA2 fragment was cloned according to standard methods into the pET-26b expression vector using the *NdeI* / *XhoI* restriction sites.

To generate the construct MC-005, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 30-519 from strain ATCC 25238) using the MC-001 vector as a template with the primers UspA2Nde opt (which contains the methionine start codon) and R delta hairpin A2opt His. DNA sequence corresponding to *NdeI* restriction site was incorporated into the 5' primer and *XhoI* restriction site was incorporated into the 3' primer. In addition, DNA sequence corresponding to the AS amino acids linker and 6xhis amino acids was incorporated into the 3' primer. The generated PCR product was then inserted into the pET-26b(+) cloning vector (NOVAGEN(a US registered trademark)).

To generate the construct MC-006, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 30-519 from strain ATCC 25238) using the MC-005 construct as a template with the primers UspA2Nde opt (which contains the methionine start codon) and delta His delta hélice. DNA sequence corresponding to *NdeI* restriction site was incorporated into the 5' primer and *XhoI* restriction site was incorporated into the 3' primer.

The generated PCR product was then inserted into the pET-26b(+) cloning vector (NOVAGEN(a US registered trademark)).

To generate the construct MC-007, DNA fragment coding for an UspA2 gene fragment (amino acids 30 to 564 from strain ATCC 25238) including the *NdeI* / *XhoI* restriction sites to facilitate the cloning (starting methionine is encoded by *NdeI* site) and the DNA sequence corresponding to the AS amino acids linker and 6xhis amino acids was codon-optimized and synthesized by GENEART(a US registered trademark) (plasmid: 1026399). The UspA2 fragment was cloned according to standard methods into the pET-26b expression vector using the *NdeI* / *XhoI* restriction sites.

To generate the construct MC-008, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 30-564 from strain ATCC 25238) using the MC-007 construct as a template with the primers UspA2Nde opt (which contains the methionine start codon) and 2His hélice deltaAS. DNA sequence corresponding to *NdeI* restriction site was incorporated into the 5' primer and *XhoI* restriction site was incorporated into the 3' primer. The generated PCR product was then inserted into the pET-26b(+) cloning vector (NOVAGEN(a US registered trademark)).

To generate the construct MC-009, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 31-564 from strain ATCC 25238) using the 1026399 plasmid as the template and the primers N-term cyto Abis (which contains the methionine start codon) and 2His hélice deltaAS. DNA sequence corresponding to *NdeI* restriction site was incorporated into the 5' primer including the glutamine deletion and *XhoI* restriction site was incorporated into the 3' primer including two histidine residues. The generated PCR product was then inserted into the pET-26b(+) cloning vector (NOVAGEN (a US registered trademark)). DNA sequencing of the final construct was performed to confirm the correct sequence.

To generate the construct MC-010, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 30-564 from strain ATCC 25238) using the MC-007 construct as a template with the primers UspA2 Nde opt (which contains the methionine start codon) and cyto hélice dHis dAS. DNA sequence corresponding to *NdeI* restriction site was incorporated into the 5' primer and *XhoI* restriction site was incorporated into the 3' primer.

The generated PCR product was then inserted into the pET-26b(+) cloning vector (NOVAGEN (a US registered trademark)).

To generate the construct MC-011, a polymerase chain reaction was performed to amplify the UspA2 gene fragment (amino acids 31-540 from strain ATCC 25238) using the MC-001 construct as a template with the primers N-term cyto Abis (which contains the methionine start codon) and N-term reverse. DNA sequence corresponding to NdeI restriction site was incorporated into the 5' primer and XhoI restriction site was incorporated into the 3' primer. The generated PCR product was then inserted into the pET-26b(+) cloning vector (NOVAGEN(a US registered trademark)).

A detailed list of PCR primer sequences used for amplifications is illustrated in Table 3. The polymerase chain reaction was performed using Expand High Fidelity PCR System kit (Roche) according to manufacturer's recommendations. Ligation was performed using Rapid DNA Ligation Kit (Roche) according to manufacturer's recommendations.

Table 3: PCR primer sequences used for UspA2 amplifications

Primer ID	DNA Sequence 5' – 3'
UspA2 Nde opt	GAATTCTTAATTAACATATGCAGGCCAAAAATGATATTACCCTG (SEQ ID NO:75)
UspA2opt delta His	GGCGCGCCTCGAGTTATTATTTGGTATCCAGTGCGGTCACACG (SEQ ID NO:76)
UspA2opt 1His delta AS	GGCGCGCCTCGAGTTAGTGTTTGGTATCCAGTGCGGTCACACG (SEQ ID NO:77)
UspA2opt 2His delta AS	GGCGCGCCTCGAGTTAGTGTTTGGTATCCAGTGCGGTCACACG (SEQ ID NO:78)
R delta hairpin A2opt His	GGCGCGCCTCGAGTTAGTGTTGTTGATGATGATGGCTTGCCTTTTGGCATTITG GTGATGGCAT (SEQ ID NO:79)
Delta His delta hélice	CCGCTCGAGCTAGCTTTTGGCATTITTGGTGATGGC (SEQ ID NO:80)
N term cytoAbis	GGAATTCCATATGGCGAAAAATGATATTACCCTGGAAGATCTG (SEQ ID NO:81)
2His hélice delta	GGCGCGCCTCGAGTTAGTGTTGCTGCTGCTGCCATACCATT (SEQ ID

AS	NO:82)
Cyto hélice dHis dAS	GGCGCGCCTCGAGTTATGCTGCCTGTGCTGCCATACCATT (SEQ ID NO:83)
N term reverse	CAGTTCATTATAGGTGGCCAGATCCTG (SEQ ID NO:84)

Transformation

Escherichia coli (*E. coli*) BLR (DE3), modified BLR (DE3) or B834(DE3) cells were transformed with plasmid DNA according to standard methods with CaCl_2 -treated cells (Hanahan D. « Plasmid transformation by Simanis. » In Glover, D. M. (Ed), DNA cloning. IRL Press London. (1985): p. 109-135.). Briefly, BLR (DE3) competent cells were gently thawed on ice. Approximately 4 μl of plasmid (10-100 ng) were mixed using 50-100 μl competent cells. Thereafter, this formulation was incubated on ice for 5 min. To perform the transformation reaction, the formulation was heat pulsed at 42°C for 30 seconds then incubated on ice for 2 minutes. Approximately 0.5 ml of SOC medium (Super Optimal broth with Catabolite repression) was added to the transformed cells and the cell culture was incubated at 37°C for one hour before plating on Luria-Bertani (LB) agar with 50 $\mu\text{g}/\text{ml}$ kanamycin. Around 150 μl of transformed cell culture was plated and incubated overnight at 37°C.

BLR (DE3): BLR is a *recA*⁻ derivative of BL21 (F⁻ *ompT* *hsdSB*(rB⁻ mB⁻) *gal dcm* (DE3). This *E. coli* strain used for expression of recombinant proteins improves plasmid monomer yields and may help stabilize target plasmids containing repetitive sequences or whose products may cause the loss of the DE3 prophage (Studier, F.W. (1991) J. Mol. Biol. 219: 37-44). The detailed genotype of *E. coli* BLR (DE3) has been published by NOVAGEN(a US registered trademark). (F⁻ *ompT* *hsdSB* (rB⁻ mB⁻) *gal dcm* Δ (*srl-recA*)306::Tn10 (TetR) (DE3).

B834 (DE3) is the parental strain for BL21. These hosts are methionine auxotrophs and allow high specific activity labeling of target proteins with 35S-methionine and selenomethionine for crystallography. The detailed genotype of *E. coli* B834 (DE3) has been published by NOVAGEN(a US registered trademark): F⁻ *ompT* *hsdSB*(rB⁻ mB⁻) *gal dcm met* (DE3).

Modified BLR (DE3): In order to prevent (phospho)gluconoylation, *Pgl* gene was inserted in the biotin locus located in the BLR (DE3) genome. In addition, to prevent the Ile-Val substitutions, the C219Y mutation in the threonine deaminase gene was corrected.

Genotype: (F- ompT hsdSB (rB- mB-) gal dcm Δ(srl-recA)306::Tn10 (TetR); Δ(bioA-bioD)::Pgl; TD + (C219Y) (DE3).

Example 2: Protein expression using shake flask

Escherichia coli strains transformed with recombinant plasmid were used to inoculate 100 ml of LB broth (Becton, Dickinson and Company) ± 1% (weight/volume, w/v) glucose (Laboratoire MAT, catalogue number: GR-0101) and 50 µg/ml kanamycin (Sigma). This preculture was generally grown overnight at 37°C. Twelve ml of the preculture is used to inoculate 500 ml LB broth+50 µg/ml kanamycine. Cultures were incubated at 37°C with agitation of 150 RPM to reach an O.D._{600nm} of ~0.6.

At an O.D._{600nm} ~0.6, the BLR (DE3) cultures were induced for the expression of the recombinant protein by addition of 1 mM isopropyl β-D-1-thiogalactopyranoside (IPTG; EMD Chemicals Inc., catalogue number: 5815) and incubated overnight at 23°C with agitation of 150 RPM. After the induction period, the cultures were centrifuged at 6370g for 20 minutes and the pellets from 350 ml culture were frozen at -20°C separately.

Example 3: Protein purification using phosphate buffer (MC-001 construct and MC-011 construct)

Each bacterial pellet obtained after induction in shake flask was resuspended in 30 ml 20 mM potassium phosphate buffer (pH 8.0) containing 10 mM NaCl and Roche COMPLETE(a US registered trademark) Protease Inhibitor Cocktail (1 tablet/50 ml ml buffer). Cell lysis is performed by 3 X French Press extractions (20 000 psi) and clarification is performed by 30 minutes centrifugation at 23700g. Supernatant is harvested and filtrated on 0.22 µm.

6xHis tagged-proteins were purified on immobilized metal affinity chromatography (IMAC) using XK16 column and 20 ml NiNTA resin (Qiagen) previously equilibrated with 20 mM potassium phosphate buffer (pH 8.0) containing 10 mM NaCl or PBS buffer pH 8.0 containing 500 mM arginine. The soluble components were loaded on at up to 4 ml/min (producing a "flow through fraction"). After loading on the column, the column was washed with 60ml of 20 mM potassium phosphate buffer (pH 8.0) containing 10 mM NaCl at a rate of 4 ml/min

producing a "wash fraction #1. A second wash using same buffer + 10 mM imidazole was performed, producing a "wash fraction #2. Elution was performed using same buffer containing 200 or/and 500 mM imidazole.

Samples from elution fractions were analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Samples containing the protein were dialyzed against 5 liters of 20 mM potassium phosphate buffer (pH 8.0) containing 10 mM NaCl. Protein concentration was determined using Lowry method.

Example 4: Protein purification using arginine containing buffer (MC-001, MC-005 and MC-007)

Each bacterial pellet obtained after induction in shake flask (Example 3) or fermenter (Example 5) was resuspended in 30 ml PBS buffer + 500 mM arginine pH8.0 and Roche COMPLETE(a US registered trademark) Protease Inhibitor Cocktail (1 tablet/50 ml buffer). Alternatively, fermentation cell paste ($\approx$ 7g) was resuspended in 90 ml PBS buffer containing 500 mM arginine pH8.0 and Roche COMPLETE(a US registered trademark) Protease Inhibitor Cocktail (1 tablet/50 ml buffer).

Cell lysis was performed by 2 or 3 X French Press extractions (20 000 psi) and clarification was performed by 30 minutes centrifugation at 23 700g 4°C. Supernatant was harvested and filtrated on 0.22 μ m. 6xHis tagged-proteins were purified on immobilized metal affinity chromatography (IMAC) using XK16 column and 80 ml NINTA resin (Qiagen) previously equilibrated with PBS buffer + 500 mM arginine pH 8.0 . The soluble components were loaded on at up to 4 ml/min (producing a "flow through fraction"). After loading on the column, the column was washed with the same buffer, then with 20 mM potassium phosphate buffer (pH 8.0) containing 10 mM NaCl at a rate of 4-6 ml/min producing a "wash fraction #1." A second wash using same buffer + 10 mM imidazole was performed, producing a "wash fraction #2." Elution was performed using same buffer + 200 mM imidazole or 500 mM imidazole. In further elution vials, 5 mM EDTA final concentration was added.

Samples from elution fractions were analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Samples containing the proteins were dialyzed against 5 liters of 20 mM potassium phosphate buffer (pH 8.0) containing 10 mM NaCl and 5 mM EDTA. Protein concentration was determined using Lowry method.

This protocol may be used with other 6xHis tagged-proteins.

Example 5: Fermentation

The following fermentation procedure may be used:

Working seeds are frozen aliquots of flask-grown *Escherichia coli* BLR(DE3) or BLR(DE3)-derived strains transformed with a pET26b derivative containing a sequence coding for a specific antigen candidate recombinant protein construct.

A working seed (WS) is removed from frozen storage, thawed and used to inoculate an Erlenmeyer flask containing pre-culture media. Manipulation of the seed and flask culture are performed aseptically under a Laminar Air Flow (LAF) Hood or Biological Safety Cabinet (BSC). The pre-culture flask is incubated typically between 30°C - 37°C under 200 RPM agitation speed for the time needed to reach an Optical Density at 650 nm (OD_{650nm}) between 1.0 and 3.0, typically between 4 – 6 hrs.

A 20L fermentor is prepared by Clean-In-Place followed by an automated steam sterilisation sequence. Starting medium is transferred aseptically into the fermentor. A bottle filled with NH_4OH 25 % is aseptically connected to the fermentor for automatic pH control. The initial pH of the starting medium is adjusted to target pH by addition of NH_4OH solution. Irradiated antifoam is added using a syringe through a septum in the head-plate. A bottle filled with Feed medium is aseptically connected to the fermentor. Feed addition is controlled by either a pO_2 -cascade (control dissolved oxygen) to or a pre-programmed feed-curve. Agitation is controlled either by a pO_2 -cascade or a pre-programmed agitation-curve.

Initial fermentor parameters are typically as follows:

- Temperature: 28°C - 32°C
- Pressure: 0.5 barg (7 psi)
- Air flow rate: 2 VVM (Vessel Volumes per Minute)
- pH: Regulated at 6.8 by addition of NH_4OH 25%.

An aliquot of this pre-culture (typically between 5ml – 50ml) is used to inoculate the starting fermentor media by syringe addition through a septum on the fermentor head-plate. The phases of Fermentation Culture are:

- Batch Phase: Biomass is accumulated using carbon source in starting media.

- Fed-batch Phase: Feed media is introduced either according to pO₂-cascade control or pre-programmed feed curve. Biomass accumulation continues on carbon source in feed media.
- Induction Phase: Expression of the recombinant protein antigen is induced by addition of IPTG solution to the culture in the fermentor.

At harvest, the culture is collected typically in 1L centrifugation bottles and centrifuged to separate the solid pellet (cell-paste) fraction from the liquid supernatant fraction. The supernatant is discarded, and the wet cell weight (solid pellet) is recorded and the cell-paste bags stored at -20°C.

The following procedure may also be used:

Escherichia coli standard pre-culture

Each standard pre-culture were prepared using a frozen seed culture of *Escherichia coli* strains. These strains are BLR(DE3) strains transformed with a pET26b derivative containing a sequence coding for the specific construct to be evaluated.

The seed culture was thawed to room temperature and 400 µl were used to inoculate a 2 litre Erlenmeyer flask containing 400 ml of preculture medium (adapted from Zabriskie et al. (J. Ind. Microbiol. 2:87-95 (1987))).

The inoculated flask was then incubated at 37 °C (± 1°C) and 200 rpm. The pre-culture was stopped after 6h of incubation. At this step the optical density at 650nm (OD_{650nm}) is about 2. The pre-culture was used to inoculate medium in a fermenter as soon as the culture was stopped.

20L scale fedbatch fermentation

Method

A 20 litre fermenter (Biolafitte) was used. Nine litres of batch phase medium were aseptically transferred into the fermenter. The pH of the medium was readjusted to 6.8 with base addition. 1 ml of undiluted irradiated antifoam (SAG 471) was also added to the fermenter. The temperature (28°C), head pressure (0.5 bar), aeration rate (20 litres sparged air per minute) and initial agitation speed (300 rpm) were then set prior to inoculation. The level of

dissolved oxygen in these conditions was 100%. The head pressure and aeration rate were maintained at a constant level during the fermentation.

Inoculation was achieved by the addition of an equivalent 10 ml OD_{650nm} = 2 of pre-culture (prepared as described above, in Example 2) following the next formula:

$$\text{Preculture Volume (ml)} = \frac{20}{\text{Preculture Final OD}_{650\text{nm}}}$$

During batch phase (0-15h), the temperature was maintained at 28°C. The level of dissolved oxygen was set at 20%. The level of dissolved oxygen (DO) was regulated by increasing stirring when the DO fell below 20%. Glucose exhaustion resulted in an increase in DO and a concomitant decrease in stirring.

When glucose is exhausted, the feeding rate is started based on a pH signal that increases above 7.0. From this point forward, the feeding rate was controlled by oxygen demand, increasing the flow rate when dissolved oxygen tends to drop below the 20% set point. At this step the agitation speed is maintained at 900 rpm.

During the fed-batch phase (before induction), the pH was maintained at 6.8 by addition of base, the temperature was regulated at 30°C.

Two strategies were applied to produce the protein:

The "High Cell Density Induction" (HCDI) is applied when culture is induced with 1 mM IPTG (isopropyl-beta-D-thiogalactopyranoside) at an optical density of 80 ± 5 , typically reached after 40h of culture. The temperature was maintained at 28°C and feeding rate still controlled by oxygen demand with a constant agitation speed at 900 rpm.

The "Low Cell Density Induction" (LCDI) process means an induction at an optical density of 40 ± 5 usually reached after 24h of culture. The temperature was decreased to 30°C and the constant feeding rate of 0.5 ml/min is applied. Then 1 mM IPTG is added to the culture. At this step, the DO level was maintained at 20% by controlling the stirring rate.

At the end of the induction phase (72h), cell paste was collected by centrifugation (6,500xg, 4°C for 1h), and stored at -20°C.

Figures 1 and 2 illustrate a typical fermentation profile with the HCDI and the LCDI processes and the parameters monitored during 20L-scale fed-batch fermentation.

Table 4 sets forth the constructs evaluated in fermenter and UspA2 yield obtained for each one.

Table 4

Construct ID	Name	Helix	His tag	Process used	UspA2 Yield (g/l)
MC-008	UspA2 + Helix + 2 His	Full	2 res	HCDI	2.21
MC-007	UspA2 + Helix + 6 His	Full	6 res	LCDI	2.60
MC-010	UspA2 + Helix	Full	No	HCDI	0.22
MC-005	UspA2 Δ Helix + 6 His	No	6 res	LCDI	1.92
MC-006	UspA2 Δ Helix	No	No	LCDI	1.14
MC-004	UspA2+ $\frac{1}{2}$ Helix + 2 His	1/2	2 res	LCDI	0.92
MC-001	UspA2+ $\frac{1}{2}$ Helix + 6 His	1/2	6 res	HCDI	3.68
MC-002	UspA2+ $\frac{1}{2}$ Helix	1/2	No	HCDI	0.49

His=histidine

Figure 3 depicts in graphical form the UspA2 yield in Table 4 from the constructs evaluated in fermenter.

In this figure, UspA2 yield is affected by histidine residues present in the construct . ($p < 0.05$, one way, three levels, Type II ANOVA). A positive correlation between the number of histidine residues and UspA2 fermentation yield was observed, with a yield increase higher than 400% between 0 and 6 residues in fed-batch fermentations.

It was also observed that one histidine residue added to half-helix pattern (MC-003 construct) produced a UspA2 yield of about 1 g/l of protein.

Example 6: Protein characterization

Analytical ultracentrifugation

Analytical ultracentrifugation is used to determine the homogeneity and size distribution in solution of the different species within a protein sample by measuring the rate at which molecules move in response to a centrifugal force. This is based on the calculation of the coefficients of sedimentation of the different species that are obtained by sedimentation velocity experiment, which depend on their molecular shape and mass.

The following protein samples were spun in a Beckman-Coulter ProteomeLab XL-1 analytical ultracentrifuge at 28 000RPM after the AN-60Ti rotor had been equilibrated to 15°C.

- a. MC-005 lot BMP53 , 675µg/ml in 20mM NaPO₄, 10mM NaCl, pH8,0
- b. MC-001 lot BMP13 , 545µg/ml in 20mM NaPO₄, 10mM NaCl, pH8,0
- c. MC-001 lot BMP14 , 545µg/ml in 20mM NaPO₄, 10mM NaCl, pH8,0
- d. MC-001 lot BMP54 , 445µg/ml in 20mM NaPO₄, 10mM NaCl, pH8,0
- e. MC-007 lot BMP70 , 510µg/ml in 20mM NaPO₄, 10mM NaCl, pH8,0

For data collection, from 133 to 325 scans were recorded at 280nm every 5 minutes.

Data analysis was performed using the program SEDFIT (available through the National Institutes for Health) for determination of the C(S) distribution. The C(S) distribution is a representation of the relative intensity of the different components in a mixture of macromolecules separated by their coefficient of sedimentation, which is a function of molecule size and conformation. Determination of the partial specific volume of the proteins at 15°C was performed with the SEDNTERP software from their amino acid sequence. SEDNTERP (SEDNTERP is distributed and supported through the Biomolecular Interaction Technologies Center at the University of New Hampshire) was also used to determine the viscosity and the density of the buffer at 15°C.

Determination of the relative abundance of all species has been performed by considering the total area under the curve of the overall distribution as 100% of the sample and by calculating the percentage of this total area represented by the contribution of every species. C(S) distribution plot (concentration vs sedimentation coefficient) has been used for that calculation, considering that it's a better representation of the raw data than the C(M) distribution (concentration vs molecular weight).

Analytical ultracentrifugation of the different purified constructs allowed observation that UspA2 Δ helix, UspA2 ½ helix and UspA2 full helix with C-terminal his tag are present mainly as trimers in solution when 500mM L-arginine is added during cell lysis prior to purification (Figures 4, 5, 7 and 8).

A heterogeneous size distribution has been observed for UspA2 ½ helix when no L-arginine was added during cell lysis. Two major populations are observed. It was not possible to confirm the molecular weight of the species detected by AUC (analytical ultracentrifugation) with this protein preparation, since the frictional ratio which is essential for molecular weight estimation needs to be calculated from an homogeneous sample. However, based on sedimentation coefficients, none of the observed species seem to correspond to the trimer observed in other samples.

Figure 4 illustrates the molecular weight distribution of purified MC-005 determined by sedimentation velocity analytical ultracentrifugation. The majority of protein is found as a trimer, with a small proportion of a higher molecular weight oligomer that may correspond to dimer of trimer.

Figure 5 illustrates the molecular weight distribution of purified MC-001 determined by sedimentation velocity analytical ultracentrifugation. Majority of protein is found as a trimer.

Figure 6 illustrates the molecular weight distribution of purified MC-001 determined by sedimentation velocity analytical ultracentrifugation. The sample presents multiple species and is highly polydisperse. The sedimentation coefficient of the major species detected doesn't correspond to the one of the trimers normally detected in the other lots.

Figure 7 illustrates the molecular weight distribution of purified MC-001 determined by sedimentation velocity analytical ultracentrifugation. The majority of protein is found as a trimer.

Figure 8 illustrates the molecular weight distribution of purified MC-007 determined by sedimentation velocity analytical ultracentrifugation. The majority of protein is found as a trimer.

Circular dichroism/Secondary Structure

Circular dichroism (CD) is used to determine the secondary structure composition of a protein by measuring the difference in the absorption of left-handed polarized light versus right-handed polarized light which is due to structural asymmetry. The shape and the magnitude of the CD spectra in the far-UV region (190-250nm) are different whether a protein exhibits a beta-sheet, alpha-helix or random coil structure. The relative abundance of each secondary structure type in a given protein sample can be calculated by comparison to reference spectra.

Far UV spectra are measured using an optical path of 0.01cm from 178 to 250nm, with a 1nm resolution and bandwidth on a Jasco J-720 spectropolarimeter. Temperature of the cell is maintained at different temperatures by a Peltier thermostated RTE-111 cell block. A nitrogen flow of 10L/min is maintained during the measurements.

Concentration of the following protein constructs was adjusted to 400µg/ml in 20mM NaPO₄, 10 mM NaCl, pH8,0 buffer.

- a. MC-005 lot BMP53 , in 20mM NaPO₄, 10mM NaCl, pH8,0
- b. MC-001 lot BMP13 , in 20mM NaPO₄, 10mM NaCl, pH8,0
- c. MC-001 lot BMP14 , in 20mM NaPO₄, 10mM NaCl, pH8,0
- d. MC-001 lot BMP54 , in 20mM NaPO₄, 10mM NaCl, pH8,0
- e. MC-007 lot BMP70 , in 20mM NaPO₄, 10mM NaCl, pH8,0

Calculations of secondary structures have been done using the following algorithms:

Selcon 3 (Sreerama and Woody, Anal. Biochem. (1993), 209, 32 ; Sreerama and Woody, Biochemistry, 33, 10022-25 (1994) ; Sreerama et al. Protein Science, 8, 370-380 (1999) ; Johnson W.C.Jr., Proteins:Struc.Func.Genet.35,307-312 (1999))
CDSSTR (Johnson W.C. Proteins:Struc.Func.Genet. 35, 307-312 (1999) modified by Sreerama. N.(Anal.Biochem.,287,252 (2000)).

Displayed results are an average of the percentage calculated with both algorithms and are subjected to a 5% error margin.

Results of the secondary structure calculations for fermentor expressed proteins are displayed in Table 5, considering a 5% error margin.

Table 5: Secondary structure calculations at 22°C

Protein	Helix	Beta	random
MC-005 BMP53	40.8	26.4	34.1
MC-007 BMP70	58.2	18.2	24.7
MC-001 BMP54	53.7	14.2	34.4

Calculations are compatible with the shape and visual analysis of the spectra, where helical content increases with the intensity of minima at 208 and 220nm. Proteins are composed of a high proportion of helical structures, with presence of beta structures.

Superposition of the spectra on Figure 9 shows no significant difference in the shape between constructs. Spectra of MC-005 helix shows a lower intensity which could account for a lower alpha structure that is coherent with the absence of C-terminal helix.

Figure 9 illustrates the far-UV circular dichroism spectra of UspA2 constructs MC-001, MC-005 and MC007 giving an indication of protein secondary structures. Superposition of spectra clearly shows that constructs containing half and full C-terminal helix have no detectable difference in their secondary structures, while the construct without helix generates a spectra with a difference in intensity that could account for a different secondary structure content.

Thermal unfolding

Measurement of far-UV CD spectra at different temperatures during thermal unfolding suggested that MC-005 is less thermally stable than MC-007. The spectra observed at 33°C for MC-005 is similar to the typical spectra of an unfolded protein. For the MC-007 construct, even if partial loss of secondary structures is observed at 33°C, the complete unfolding seems to occur between 35°C and 37°C. This may be an indication of higher thermal stability of the full helix containing construct MC-007.

Figure 10 illustrates secondary structures monitoring by circular dichroism during thermal unfolding of MC-005 (UspA2 Δ helix+6His). Visual analysis of the spectra clearly shows that the protein loses most of its secondary structures at 33°C.

Figure 11 illustrates secondary structures monitoring by circular dichroism during thermal unfolding of MC-007 (UspA2 + helix + 6His). Visual analysis of the spectra shows that loss of secondary structure is slower compared to the construct without helix. Structural changes are detectable upon heating to 33°C, but complete unfolding seems to occur between 35°C and 37°C.

Differential Scanning Calorimetry (DSC) thermal unfolding

Thermal transitions of different UspA2 constructs were compared in order to evaluate the effect of C-terminal helix modifications on thermal stability of the proteins.

Analysis was done on VP-DSC from MicroCal (part of GE Healthcare). The buffer 20mM NaPO₄, 10mM NaCl, 5mM EDTA, pH8 was used as reference and subtracted from the scans. Proteins were equilibrated at initial temperature for 15 minutes before temperature ramping. DSC scans were then conducted from 10°C to 60°C at a heating rate 90°C/hr.

Two transitions were detected in MC-001 and MC-007 constructs and only one in MC-005. Values of the transitions (or T_m) of the different constructs can be found on Table 6.

While the lower T_m of all three proteins is around 32°C, the main difference is the value of the second T_m. The construct containing a full helix (MC-007) has a higher T_m at 37.5°C compared to 34.5°C for the half helix (MC-001).

It has been demonstrated that for MC-001 and MC-007, the first T_m around 32°C is reversible, while the higher T_m is irreversible. For MC-005, the only T_m detected is irreversible.

This may be an indication of a higher thermal stability of full helix containing construct MC-007.

Table 6: Melting points of UspA2 constructs measured by DSC

Constructs	[mg/mL]	T _{m1} (°C)	T _{m2} (°C)
------------	---------	----------------------	----------------------

MC-005 lotBMP53	0.400	31.74	-----
MC-001 lotBMP54	0.400	32.02	34.51
MC-007 lotBMP70	0.400	32.19	37.50

Mass spectrometry

UspA2 protein samples were prepared by protein precipitation with CHCl_3 / MeOH / H_2O system. The protein pellet was centrifuged at the bottom of the eppendorf tube before being gently dried under nitrogen. The dried pellet was then dissolved in 2 μl of pure formic acid before being diluted with 3 μl of ultrapure water and 5 μl of sinapinic acid. Sinapinic acid used as matrix for MALDI-TOF (Matrix-Assisted Laser Desorption/Ionisation followed by Time-Of-Flight spectrometry analyser) analysis is prepared in 50% CH_3CN / 50% H_2O supplemented by TFA 0.1% final concentration.

1 μl of the sample + matrix mixture was spotted onto a Bruker 384 ground stainless steel MALDI target and let to dry for crystallization at room temperature and atmospheric pressure (dried droplet method).

UspA2 mass spectrometry analysis was performed on a Bruker Ultraflex 2 MALDI-TOF mass spectrometer (Bruker Daltonics, Bremen, Germany) in positive ionization and linear mode. Protein samples, co-crystallized in sinapinic acid matrix, were irradiated by a smartbeam laser. Mass measurement of intact UspA2 protein were done over 10.000-100.000 Da mass range with an acceleration voltage of 25 kVolts. Laser attenuation was fine-tuned in order to get the best protein signal as possible and to avoid any fragmentation as well as background over-ionization phenomena. Calibration of the mass spectrometer was performed in close external method with homologous matrix and using the commercial Bruker Protein Calibration mixture 2, by accurate measures on the following calibrators: $[\text{M}+2\text{H}]^{2+}$ (mass measured by MS detector following addition of two H^+ ions to the protein during ionisation) species of

protein A at m/z 22307 Da, $[M+H]^+$ species of trypsinogen at m/z 23982 Da, $[M+H]^+$ species of protein A at m/z 44613 Da and $[M+H]^+$ species of bovine albumin at m/z 66431 Da°. Each presented spectrum results from the sum of 500 individual shots.

The following samples were analyzed:

MC-001 construct with MQAK amino acids (SEQ ID NO: 85) in N-terminal produced in shake flask, lot opt-01, MC-011 construct with MAK amino acids in N-terminal produced in shake flask, lot BMP37.

In Table 7 and Figure 12, MC-001 protein with MQAK amino acids (SEQ ID NO: 85) at the N-terminal extremity has been shown to be at least partially demethionylated, as shown by the measured molecular mass of 57427Da, compared to the expected mass of 57565Da. The other peak of 57620Da may represent the complete non-demethionylated protein, N-acetylated protein, or another modified protein population.

Figure 12 illustrates the MALDI spectrum of MC-001 lot opt-01. The mass observed at 57427Da may be coherent with the demethionylated protein, while the peak at 57620Da could correspond to the complete protein.

As shown in Table 7 and figure 13, MC-011 protein with MAK amino acids at the N-terminal extremity gave a major population in MALDI-MS that may correspond to the demethionylated protein, with a mass of 57265Da, compared to 57437Da for the expected mass based on complete amino acid sequence. The two other peaks at +186Da and +366Da are not close to any expected post-translational modifications, so they couldn't be identified by this experiment.

Table 7: Molecular mass of two UspA2 constructs as measured by MALDI-MS. Both constructs have a main measured mass lower than the one expected from amino acid sequence. The mass of the major population obtained with both constructs may be coherent with a demethionylated protein.

Protein	Theoretical mass (Da)	Measured mass (Da)	Comment
---------	-----------------------	--------------------	---------

MC-001 lot opt-01	57565.8	-57427.9 -57620.3	-Coherent with demethionylation (57434.6) - Coherent with protein containing N-terminal methionine
MC-011 lot BMP37	57437.6	57265.2	Coherent with demethionylation (57306.4)

N-terminal sequencing by Edman's degradation

In order to evaluate if the optimisation of the N-terminal region (optimisation of the amino acid sequence next to the N-terminal methionine) leads to demethionylation of the protein, N-terminal sequencing has been done on the MC-011 construct carrying MAK amino acids on his N-terminal extremity.

The proteins were separated by SDS PAGE on a Novex 4%-20% polyacrylamide gel from Invitrogen, before transfer onto Problot PVDF (polyvinylidene difluoride) (Bio-Rad) membrane. The membrane was stained with amidoblack. The band of interest was then cut and analysis was carried out according to the manufacturer's protocol using an Applied Biosystems Procise sequencer system. Twelve cycles of Edman's degradation were performed.

The N-terminal amino acid sequence obtained is AKNDITLEDLP (SEQ ID NO:86), which corresponds to the N-terminal extremity of the protein starting at the amino acid number two after the initial methionine. This indicates that the mature protein is mainly demethionylated.

Example 7: UspA2 construct MC-001: Bactericidal activity.

Bactericidal Assay

Moraxella catarrhalis was cultivated overnight on Petri dish at 37°C + 5% CO₂. Bacteria were transferred in 12 ml HBSS-BSA (Hank's Buffered Salt Solution with Bovine Serum Album) 0.1% buffer in order to get an OD₆₂₀ of 0.650. Serum samples were heated for 45 min at 56°C to inactivate the endogenous complement. Serial two-fold dilutions of sera in SBA buffer (HBSS-BSA 0.1%) were added on a 96-well round bottom microtitre plate (25 µl/well). Subsequently, 50 µl of SBA buffer were added in each well. Then 25 µl of *Moraxella catarrhalis* strains at 4 10⁶ cfu/ml were added to the wells containing sera and incubated for 15 min at room temperature. Finally 25 µl of freshly thawed baby rabbit complement diluted 1/8 in HBSS-BSA 0.1% were

added to reach a final volume of 125 μ l. Plates were incubated for 1 h at 37 °C with orbital shaking (210 rpm). The reaction was stopped by laying the microplate on ice for at least 5 min.

After homogenization, various dilutions of the suspension (a mixture of bacteria, serum, complement and buffer, at a volume of 125 μ l as discussed in the previous paragraph) were added onto chocolate agar plates and incubated for 24 hours at 37°C with 5% CO₂ and *Moraxella catarrhalis* colonies were counted.

Eight wells without serum sample were used as bacterial controls to determine the number of *Moraxella catarrhalis* colonies per well. The mean number of CFU (colony forming unit) of the control wells was determined and used for the calculation of the killing activity for each serum sample. The bactericidal titers were expressed at the reciprocal dilution of serum inducing 50% of killing.

Anti-UspA2 antisera generated in mice, guinea pigs and rabbits against MC-001 were tested in the bactericidal assay described here above against 20 different *Moraxella catarrhalis* strains isolated from various tissues (blood, sputum, nose, middle ear fluids) in various countries (US, Finland, Netherlands, Norway, Sweden).

As shown below anti-UspA2 antibodies were able to induce a cross-bactericidal killing of *Moraxella catarrhalis*, whatever the percentage of homology of the UspA2 expressed by the tested strain. Moreover bactericidal activity was also shown against strains which only express UspA1 or the chimeric protein UspA2H. As expected, no or only weak bactericidal antibody titres were measured against UspA1 and UspA2 double knock-out mutants.

Table 8: Cross-bactericidal activity of anti-UspA2 MC-001 antibodies generated in mouse, guinea pig and rabbit. 1+2 KO is a double knock out, UspA1 & UspA2. 1KO is a UspA1 knockout only. MEF (AOM) = Middle Ear Fluid (Acute Otitis Media). "/" in the Isolate source column = not aware of the isolate source.

Strains		Isolate source	UspA gene present	Identity % * versus the vaccine sequence ATCC25236	Anti-UspA2 antiserum bactericidal activity		
					Mouse	Guinea pig	Rabbit
ATCC	25238	/	UspA1/UspA2	45.2/100	+++	++	+++
	43617	Bronchiitis	UspA1	40.1	+	+	+
American	2926	/	UspA1	36.4	-	+/-	-
	2933	/	UspA1/UspA2	44.6/62.4	-	++	++
	2912	/	UspA1/UspA2	39.3/64.6	++	++	+++
	2908	/	UspA1/UspA2	43.3/52.8	+++	+++	+++
	307	MEF (AOM)	UspA1/UspA2	47.6/70.1	-	++	+++
Finnish	353	MEF (AOM)	UspA1/UspA2	45/61.8	+	++	++
	358	MEF (AOM)	UspA1/UspA2	47/61.5	+++	+++	+++
	216	MEF (AOM)	UspA1/UspA2	46.6/66.9	+++	+++	+++
	N9	nose	UspA1/UspA2H	41.1/70.1	++	+++	+++
Dutch	H2	sputum	UspA1/UspA2	47/61.6	+++	+++	+++
	F10	sputum	UspA1/UspA2	42.9/61.1	++	+++	+++
	1	Tracheotomy (Pneumonia)	UspA1/UspA2	44.6/60.9	+++	+++	+++
Norwegian	13	Tracheotomy (Pneumonia)	UspA1/UspA2	47.8/55	++	+++	+++
	20	Tracheotomy (Pneumonia)	UspA1/UspA2	33.7/50.6	+++	++	+++
	25	Tracheotomy (Pneumonia)	UspA1/UspA2	47.8/55	++	+++	+++
	27	Tracheotomy (Pneumonia)	UspA1/UspA2	46/76.1	++	+++	+++
	36	Tracheotomy (Pneumonia)	UspA1/UspA2	53.6/61.6	+	++	++
Swedish	BBH18 WT	sputum	UspA1/UspA2H	42.9/57.3	+++	+++	+++
	BBH18 (1+2KO)		-	-	+	-	-
	BBH18 (1KO)		UspA2H	57.3	+++	+++	+++
	RH4 WT	blood	UspA1/UspA2H	37.4/59.9	not done	++	++
	RH4 (1+2KO)		-	-	-	-	+

* determined using the software Gaps/ClustalX versus the ATCC25236 UspA2 fragment AA30-540.

+++ >50000
++ >20000
+ >500
- <200

Table 9: UspA Expression in the *M. catarrhalis* strains in Table 8.

Strains		UspA1 expression	UspA2 expression	UspA2H expression
ATCC	25238	Yes	Yes	No
	43617	Yes	stop codon	No
American	2926	Yes	No	stop codon
	2933	Yes	Yes	No
	2912	Yes	Yes	No
	2908	Yes	Yes	No
Finnish	307	Yes	Yes	No
	353	Yes	Yes	No
	358	Yes	Yes	No
	216	Yes	Yes	No
Dutch	N9	Yes	No	Yes
	H2	Yes	Yes	No
	F10	Yes	Yes	No
Norwegian	1	Yes	Yes	No
	13	Yes	Yes	No
	20	Yes	Yes	No
	25	Yes	Yes	No
	27	Yes	Yes	No
Swedish	36	Yes	Yes	No
	BBH18 WT	Yes	No	Yes
	BBH18 (1+2KO)	No	No	No
	BBH18 (1KO)	No	No	Yes
	RH4 WT	Yes	No	Yes
	RH4 (1+2KO)	No	No	No

Example 8: Protection in a mouse model of lung colonization (MC-001)

Five weeks-old female Balb/c mice (n=8/5 groups) were immunized by the intramuscular route at days 0, 14 and 28 with 50 µl of vaccine containing 10 µg of UspA2 construct MC-001 formulated within AS02V. Mice were intranasally challenged at day 42 with $5 \cdot 10^5$ CFU of various *Moraxella catarrhalis* strains. Bacteria were counted in lungs collected 0, 3 and 6 hours post-challenge. Differences between groups were analysed using the Dunnet test.

As summarised in Table 10, UspA2 construct MC-001 induced a significant protection against both homologous and heterologous strains, including the strain 43617 which does express UspA1 but not UspA2 and the BBH18 strain which expresses the chimeric protein UspA2H (constituted of the N-terminal sequence from UspA1 and the C-terminal sequence from UspA2).

Table 10: Protective efficacy of UspA2. MC-001 construct.

Strain	UspA expressed	Identity % * versus the vaccinal sequence ATCC25238	Log ₁₀ cfu / ml		p value
			Control group	Vaccine group	
25238	UspA1 & UspA2	45.2/100	5.2	3.1	0.01
43617	UspA1	40.1	4.9	3.6	0.01
F10	UspA1 & UspA2	42.9/61.1	4.3	3.9	0.25
F10	UspA1 & UspA2	42.9/61.1	4.4	3.6	0.01
BBH18	UspA1 & UspA2H	42.9/57.3	4.3	3.5	0.01
20	UspA1 & UspA2	33.7/60.6	4.4	3.9	0.02

* determined using the Gap/ClustalX software versus the ATCC25238 UspA2 fragment AA 30-540

p values in bold are significant (p < 0.05)

Example 9: UspA2 construct MC-007: Antibody bactericidal activity.**Bactericidal Assay**

Moraxella catarrhalis 25238 was cultivated overnight on Petri dish at 37°C + 5% CO₂. Bacteria were transferred in 12 ml HBSS-BSA 0.1% buffer in order to get an OD₆₂₀ of 0.650. Serum samples were heated for 45 min at 56°C to inactivate the endogenous complement. Serial two-fold dilutions of sera in SBA buffer (HBSS-BSA 0.1%) were added on a 96-well round bottom microtitre plate (25 µl/well). Subsequently, 50 µl of SBA buffer were added in each well. Then 25 µl of *Moraxella catarrhalis* 25238 strain at $4 \cdot 10^{11}$ cfu/ml were added to the wells containing sera

and incubated for 15 min at room temperature. Finally 25 μ l of freshly thawed baby rabbit complement diluted 1/8 in HBSS-BSA 0.1% were added to reach a final volume of 125 μ l. Plates were incubated for 1 h at 37 °C with orbital shaking (210 rpm). The reaction was stopped by laying the microplate on ice for at least 5 min. After homogenization, various dilutions of the suspension were added onto chocolate agar plates and incubated for 24 hours at 37°C with 5% CO₂ and *Moraxella* colonies were counted. Eight wells without serum sample were used as bacterial controls to determine the number of *Moraxella catarrhalis* colonies per well. The mean number of CFU of the control wells was determined and used for the calculation of the killing activity for each serum sample. The bactericidal titers were expressed at the reciprocal dilution of serum inducing 50% of killing.

Anti-UspA2 antisera generated in mice with UspA2 construct MC-001 or MC-007 were tested in a bactericidal assay using the protocol described above against the 25238 *Moraxella catarrhalis* homologous strain.

As shown in Table 11, the MC-007 UspA2 construct elicited a high bactericidal response, similar to that induced by the MC-001.

Table 11: Bactericidal activity of anti-UspA2 MC-001 and MC-007 antibodies. Normal mouse sera = sera from mice immunized with AS02V only, not with UspA2.

Samples	Bactericidal titers
Normal mouse sera (AS02V)	-
Mouse Anti-Killed whole cells 25238	++
Mouse anti-UspA2 against UspA2 MC-001	+++
Mouse anti-UspA2 against UspA2 MC-007	+++

Example 10: UspA2 construct MC-007: Protective efficacy in a lung challenge model**Protection in a mouse model of lung colonization**

Five weeks-old female Balb/c mice (8 mice per group, 5 groups max per time point) were immunized by the intramuscular route at days 0, 14 and 28 with 50 µl of vaccine containing 10 µg of UspA2 construct MC-001 formulated with AS02V or MC-007 formulated within AS02V. Mice were intranasally challenged at day 42 with $5 \cdot 10^5$ CFU of *Moraxella catarrhalis* strain ATCC(a US registered trademark) 25238™. Mice were immunized with 10 µg of killed whole cells from *Moraxella catarrhalis* strain ATCC(a US registered trademark) 25238™ (as positive control) (M.cat. WC 25238 in Figure 14) or with AS02V alone (as negative control). Bacteria were counted in lungs collected 0, 3 and 6 hours post-challenge. Differences between groups were analysed using the Dunnet test.

As shown in Figure 14, both UspA2 constructs were similarly protective against ATCC(a US registered trademark) strain 25238™.

Example 11: Immunogenicity of UspA2 MC-009 protein formulations in mice

Groups of 25 female Balb/c mice were immunized by the intramuscular (IM) route at days 0, 14 and 28 with 50 µl of the following formulations:

- MC-009 (1 µg) AIPO4 (1000 µg/ml)
- MC-009 (1 µg) AS04C (AIPO₄/MPL 100/100 per ml)
- MC-009 (1 µg) AS01E (QS21/MPL 50/50 per ml)

Anti-IgG levels were determined in individual sera collected at days 28 (PII) and 42 (PIII) using the following protocol:

ELISA to measure anti-UspA2 antibodies.

Plates were coated overnight at 4°C with 100 µl per well of UspA2 construct MC-009 at 4 µg/ml in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 20 (polysorbate 20) 0.05%. After washing, serial two fold dilutions of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxidase (100 µl per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA Sigma P8787) and 5 µl of H₂O₂ in 10 ml of citrate 0.1M PH (pH) 4.5) was added to each well (100 µl/well) for 15 min in darkness. The reaction was stopped by addition of 50 µl of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter).

The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

As shown in Figure 15, UspA2 induced high antibody levels with each adjuvant formulation.

Bactericidal Assay

The bactericidal assay was performed against *M. catarrhalis* strain (ATCC(a US registered trademark) 25238™) expressing a homologous full length UspA2 using the following protocol: *Moraxella catarrhalis* strain ATCC(a US registered trademark) 25238™ was cultivated overnight on Petri dish at 37°C + 5% CO₂. Bacteria were transferred in 10 ml of BHI (broth heart infusion) in order to get an OD₆₂₀ of 0.650. Serum samples were heated for 45 min at 56°C to inactivate the endogenous complement. Serial two-fold dilutions of sera in SBA buffer (HBSS–BSA 0.1%) were added on a 96-well round bottom microtitre plate (25 µl/well). Subsequently, 50 µl of SBA buffer were added in each well. Then 25 µl of *Moraxella catarrhalis* strain 25238™ at 4 10⁸ cfu/ml were added to the wells containing sera and incubated for 15 min at room temperature. Finally 25 µl of freshly thawed baby rabbit complement diluted 1/8 in HBSS-BSA 0.1% were added to reach a final volume of 125 µl. Plates were incubated for 1 h at 37 °C with orbital shaking (210 rpm). The reaction was stopped by laying the microplate on ice for at least 5 min. A 20 µl aliquot of each well of the

plate was then transferred into the corresponding well of a 96-well flat bottom microplate and 50 μ l of Mueller Hinton Broth–0.9% agar was added to each well. 50 μ l of PBS 0.9% agar was added as a second layer. After 3 hours at 37°C with 5% CO₂ plates were incubated overnight at 25°C, Moraxella colonies were counted using an automated image analysis system (KS 400, Zeiss, Oberkochen, Germany). Eight wells without serum sample were used as bacterial controls to determine the number of Moraxella per well. The mean number of CFU of the control wells was determined and used for the calculation of the killing activity for each serum sample. The bactericidal titers were expressed at the reciprocal dilution of serum inducing 50% of killing.

Figure 16 illustrates the bactericidal titers induced by UspA2 against a homologous strain. In this experiment, UspA2 induced high levels of bactericidal antibodies for each adjuvant formulation. Sera were tested at PIII; five pools of five sera samples were tested.

Example 12: Immunogenicity of UspA2 in combination with PD and PE-PIIA NTHi antigens.

Immunization Protocol

Groups of 25 female Balb/c mice were immunized by the intramuscular (IM) route at days 0, 14 and 28 with 50 μ l of the following formulations:

- UspA2 construct MC-009 (1 μ g) AIPO4
- UspA2 construct MC-009 (1 μ g) AS04C
- UspA2 construct MC-009 (1 μ g) AS01E
- UspA2-PD-PEPIIA (UspA2 construct MC-009, PEPIIA construct LVL-735) AIPO4 (1 μ g of each of UspA2, PD and PEPIIA; 1000 mg/ml AIPO4)
- UspA2-PD-PEPIIA (UspA2 construct MC-009, PEPIIA construct LVL-735) AS04C AIPO4 (1 μ g of each of UspA2, PD and PEPIIA; 100/100 per ml AIPO4/MPL)
- UspA2-PD-PEPIIA (UspA2 construct MC-009, PEPIIA construct LVL-735) AS01E (1 μ g of each of UspA2, PD and PEPIIA; 50/50 per ml QS21/MPL)

ELISA to measure anti-UspA2 antibodies

Anti-UspA2 IgG levels were determined in individual sera collected at days 28 and 42 using the following protocol.

Plates were coated overnight at 4°C with 100 µl per well of UspA2 construct MC-009 at 4 µg/ml in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 20 (polysorbate 20) 0.05%. After washing, serial two fold dilutions of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 µl per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA Sigma P8787) and 5 µl of H₂O₂ in 10 ml of citrate 0.1M PH (pH) 4.5) was added to each well (100 µl/well) for 15 min in darkness. The reaction was stopped by addition of 50 µl of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

ELISA to measure anti-PE antibodies

Plates were coated overnight at 4°C with 100 µl per well of 2 µg/ml of UspA2 in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 0.05%. After washing, serial two fold dilution of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 µl per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA and 5 µl of H₂O₂ in 10 ml of citrate 0.1M PH 4.5) was added to each well (100 µl/well) for 15 min in darkness. The reaction was stopped by addition of 50 µl of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

ELISA to measure anti-PilA antibodies

Plates were coated overnight at 4°C with 100 µl per well of 4 µg/ml of PilA in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 0.05%. After washing, serial two fold dilution of sera were added to microwells in

PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 μ l per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA and 5 μ l of H₂O₂ in 10 ml of citrate 0.1M PH 4.5) was added to each well (100 μ l/well) for 15 min in darkness. The reaction was stopped by addition of 50 μ l of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

ELISA to measure anti-PD antibodies

Plates were coated overnight at 4°C with 100 μ l per well of 8 μ g/ml of PD in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 0.05%. After washing, serial two fold dilution of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 μ l per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA and 5 μ l of H₂O₂ in 10 ml of citrate 0.1M PH 4.5) was added to each well (100 μ l/well) for 15 min in darkness. The reaction was stopped by addition of 50 μ l of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

Bactericidal assay

Bactericidal titres were measured in pooled sera (5 pools/ group) collected at day 42 using the following protocol:

Moraxella catarrhalis was cultivated overnight on Petri dish at 37°C + 5% CO₂. Bacteria were transferred in 10 ml BHi (broth heart infusion) medium in order to get an OD₆₂₀ of 0.650. Serum samples were heated for 45 min at 56 °C to inactivate the endogenous complement. Serial two fold dilutions of sera in SBA buffer (HBSS-BSA 0.1%) were added on a 96-well round bottom microtitre plate (25 μ l/well). Subsequently, 50 μ l of SBA buffer were added in each well. Then 25 μ l of *Moraxella catarrhalis* strain 25238 at 4 10³ cfu/ml were added to the

wells containing sera and incubated for 15 min at room temperature. Finally 25 µl of freshly thawed baby rabbit complement diluted 1/8 in HBSS-BSA 0.1% were added to reach a final volume of 125 µl. Plates were incubated for 1 h at 37 °C with orbital shaking (210 rpm). The reaction was stopped by laying the microplate on ice for at least 5 min. A 20 µl aliquot of each well of the plate was then transferred into the corresponding well of a 96-well flat bottom microplate and 50 µl of Mueller Hinton Broth–0.9% agar was added to each well. 50 µl of PBS 0.9% agar was added as a second layer. After 3 hours at 37°C with 5% CO₂ plates were incubated overnight at 25°C. *Moraxella* colonies were counted using an automated image analysis system (KS 400, Zeiss, Oberkochen, Germany). Eight wells without serum sample were used as bacterial controls to determine the number of *Moraxella* per well. The mean number of CFU of the control wells was determined and used for the calculation of the killing activity for each serum sample. The bactericidal titers were expressed at the reciprocal dilution of serum inducing 50% of killing.

The bactericidal assay was performed against *Moraxella catarrhalis* strain 25238™, expressing a homologous UspA2.

A negative impact of the presence of PD and PE-PilA antigens on UspA2 IgG levels was observed in AS04C (post III) and AS01E (post II) formulations (Figure 17). However the impact remained limited (≤ 2 fold antibody decrease) and was not confirmed in the bactericidal assay (Figure 18). The IgG responses induced against PD, PE and PilA in mice by PE-PEPIL-A-UspA2 vaccine are shown in figure 19, figure 20 and figure 21, respectively.

Therefore, UspA2 was immunogenic when combined with PD and PE-PilA.

Example 13: UspA2 construct MC-009: Immunogenicity of PD and PE-PilA NTHi antigens in combination with UspA2 in mice

Immunization protocol

Groups of 25 female Balb/c mice were immunized by the intramuscular (IM) route at days 0, 14 and 28 with 50 µl of the following formulations:

- PD-PEPIL-A (1 µg of PD and 1 µg of PEPIL-A construct LVL-735) AS01E
- UspA2-PD-PEPIL-A (1 µg of UspA2 construct MC-009, PD and PEPIL-A construct LVL-735) AS01E

The ELISA IgG levels to PD, PE and PIIA were determined in individual sera collected at days 28 (PII) and 42 (PIII).

ELISA to measure anti-PE antibodies

Plates were coated overnight at 4°C with 100 µl per well of 2 µg/ml of UspA2 in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 0.05%. After washing, serial two fold dilution of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 µl per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA and 5 µl of H₂O₂ in 10 ml of citrate 0.1M PH 4.5) was added to each well (100 µl/well) for 15 min in darkness. The reaction was stopped by addition of 50 µl of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

ELISA to measure anti-PIIA antibodies

Plates were coated overnight at 4°C with 100 µl per well of 4 µg/ml of PIIA in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered trademark) 0.05%. After washing, serial two fold dilution of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 µl per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA and 5 µl of H₂O₂ in 10 ml of citrate 0.1M PH 4.5) was added to each well (100 µl/well) for 15 min in darkness. The reaction was stopped by addition of 50 µl of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX (a US registered trademark) Pro software.

ELISA to measure anti-PD antibodies

Plates were coated overnight at 4°C with 100 µl per well of 8 µg/ml of PD in carbonate buffer pH 9.6. The plates were washed three times with NaCl 0.09% TWEEN(a US registered

trademark) 0.05%. After washing, serial two fold dilution of sera were added to microwells in PBS TWEEN(a US registered trademark) 20 0.05%. The plates were placed at room temperature for 30 minutes with shaking. After washing, anti-mouse IgG antibodies (Jackson 115-035-003) conjugated to peroxylase (100 µl per well) were added, and the plates were placed at room temperature for 30 minutes with shaking. Plates were washed as above and the solution of revelation (4 mg of OPDA and 5 µl of H₂O₂ in 10 ml of citrate 0.1M PH 4.5) was added to each well (100 µl/well) for 15 min in darkness. The reaction was stopped by addition of 50 µl of HCl 1N and the absorbance was read at 490 nm (620 nm for the reference filter). The titers were calculated by the 4-parameters method using the SOFTMAX(a US registered trademark) Pro software.

No major impact of the addition of UspA2 on PD and PEPiA immunogenicity in AS01E was observed as shown in figures 22, 23 and 24.

Example 14: Safety of a tetravalent vaccine formulation containing UspA2 in a mouse *Moraxella catarrhalis* lung inflammation model.

To mitigate the risk of inducing undesirable inflammatory responses in the lungs of COPD patients upon immunization with a candidate vaccine aiming at preventing the exacerbations due to Non-typeable *Haemophilus influenzae* (NTHi) and *Moraxella catarrhalis* (*M. cat.*), various animal models were developed and used to assess the safety of this vaccine. The formulation tested contained three NTHi antigens (PD, PE and PiiA, with the two last ones combined as a PEPiA fusion protein), one *M. cat.* antigen (UspA2) and the Adjuvant System 01E (AS01E).

Two models were particularly dedicated to evaluate the safety of the UspA2 component of the vaccine.

Model 1:

- **Objective**

This model aimed at assessing the possible induction of undesirable immune responses in inflamed lungs upon vaccination.

• Study design

C57Bl/6 mice were sensitized by three intranasal administrations of 25 µg of heat-inactivated *M. cat.* strain ATCC(a US registered trademark) 25238™ whole cells (expressing an UspA2 which is 100% homologous to the vaccine UspA2) at days 0, 7 and 14. This treatment induced in the lungs a perivascular and peribronchiolar inflammation (with formation of lymphoid aggregates), alveolitis, pneumonitis, fibrosis and a strong *M.cat.* whole cell-specific IL-17⁺ CD4⁺ T cell response, which altogether mimicked the inflammatory process observed in the lungs of COPD patients (except emphysema).

The mice were then vaccinated at day 42 by the intramuscular route with 1/10th of human dose of the following formulations:

- PD 10 µg/ PEPiIA (LVL735 construct, described in WO2012/139225) 10 µg/ UspA2 (MC009 construct) 10 µg/ AS01_E
- PD 10 µg/ PEPiIA (LVL735 construct) 10 µg/ UspA2 (MC009 construct) 3.3 µg/ AS01_E
- AS01_E (negative control)
- PBS (negative control)

To assess the impact of these formulations on the sensitization-induced lung inflammation:

- Mice were daily monitored from day 43 to day 49 to look at mortality and any clinical signs indicating the induction of adverse events (prostration, piloerection, hunched position).
- A histological analysis of the lungs was performed at days 2, 7 and 14 post-vaccination (with 5 mice per group and time-point) to look at a possible aggravation of the inflammation.
- The induction of potentially undesirable T cell responses was evaluated on pools of lungs collected at days 7 and 14 post-vaccination (with 4 pools/group/time-point and the lungs of 3 mice per pool). The lung T cells were re-stimulated overnight either with UspA2 peptides, heat-inactivated *M. cat.* whole cells (VVC) or medium (as a negative control) and then analyzed by flow cytometry for the expression of CD5, CD4, CD8, IL-17, IL-13, TNF α and IFN γ .

• Results

- No mortality or adverse event was reported.
- Lung histology (Figures 25 to 29):
 - o The alterations observed in the lungs were similar in severity in all groups and characterized by slight to moderate perivascular/bronchiolar mononuclear cell infiltrates.
 - o No alveolitis and/or pneumonitis related to vaccination were observed.
- T cell response:
 - o Strong CD4⁺ T cell responses (mainly IL-17 and TNF α producing cells) were measured in the lungs upon re-stimulation with WC, but regardless of the formulation administered (vaccines or adjuvant alone or PBS) (Figures 30 to 33). Low or no lung CD8⁺ T cell responses were observed (data not shown).
 - o No detectable T cell response was re-stimulated by UspA2 peptides, whatever the group, indicating that no UspA2-specific response was primed or boosted post-vaccination (data not shown).

Model 2:

• Objective

This model aimed at assessing the possible induction of undesirable immune responses in inflamed lungs upon vaccination and *M. cat.* challenge.

• Study design

C57Bl/6 mice were successively:

- Sensitized by three intranasal administrations of 25 μ g of heat-inactivated *M. cat.* strain 25238 WC (expressing an UspA2 which is 100% homologous to the vaccine UspA2) at days 0, 7 and 14 (as in Model 1).
- Vaccinated at day 42 by the intramuscular route with 1/10th of human dose of the following formulations (as in Model 1):
 - PD (10 μ g/ PEPIIA (LVL735 construct) 10 μ g/ UspA2 (MC009 construct) 10 μ g/ AS01_E

- PD 10 µg/ PEPiA (LVL735 construct) 10 µg/ UspA2 (MC009 construct) 3.3 µg/ AS01_E
- AS01_E (negative control)
- PBS (negative control)
- Challenged by one intranasal administration of 25 µg of heat-inactivated *M. cat.* strain F10 WC (expressing an UspA2 which shares 53% homology with the vaccine UspA2) or by one intranasal administration of PBS as a control, both at day 56. The challenge strain was different from the sensitization strain to mimic the situation observed in COPD patients who experience new exacerbations due to newly acquired *M. cat.* strains.

To assess the impact of vaccination and challenge on the sensitization-induced lung inflammation:

- Mice were daily monitored from day 43 to day 63 to look at mortality and any clinical signs indicating the induction of adverse events (prostration, piloerection, hunched position).
- The induction of potentially undesirable T cell responses was evaluated on pools of lungs collected at days 7 and 14 post-challenge (with 4 pools/group/time-point and the lungs of 3 mice per pool). The lung T cells were re-stimulated overnight either with UspA2 peptides, heat-inactivated *M. cat.* F10 WC or medium (as a negative control) and then analyzed by flow cytometry for the expression of CD5, CD4, CD8, IL-17, IL-13, TNF α and IFN γ .

• Results

- No mortality or adverse event was reported.
- T cell response:
 - o Strong post-challenge CD4⁺ T cell responses (mainly IL-17 and TNF α producing cells) were measured in the lungs upon re-stimulation with F10 WC, regardless of the formulation administered (vaccines or adjuvant alone or PBS) (Figures 34 to 37). Not surprisingly, these responses were higher in mice challenged with inactivated bacteria than in mice challenged with PBS. Whatever the challenge, low or no lung CD8⁺ T cell responses were observed (data not shown).
 - o No detectable T cell response was re-stimulated by UspA2 peptides, whatever the group, indicating that no UspA2-specific response was primed or boosted post-challenge (data not shown).

Conclusion

The PD/ PEPIIA/ UspA2/ AS01_E formulations tested and more specifically the UspA2 component of these vaccines were shown safe in a mouse *M. cat.* lung inflammation model.

CLAIMS

1. An isolated protein comprising formula I:
$$A - (R_1)_m - (B)_n \text{ (formula I)}$$

wherein:

A is an immunogenic fragment of UspA2 from *Moraxella catarrhalis* having at least 90% identity to any one of SEQ ID NOs:39 to 43;
 R_1 is an amino acid;
m is 0 or 2;
B is histidine; and
n is 1, 2, 3, 4, 5 or 6.
2. The protein according claim 1 wherein $(R_1)_m$ is AS (alanine serine).
3. The protein according to claim 1 or claim 2 further comprising a methionine at the amino terminal.
4. The protein according to any one of claims 1-3 wherein A is an immunogenic fragment of UspA2 selected from the group consisting of amino acids 30-540 of SEQ ID NO. 1 (SEQ ID NO: 39), amino acids 31-540 of SEQ ID NO: 1 (SEQ ID NO: 40), amino acids 30-519 of SEQ ID NO: 1 (SEQ ID NO: 41), amino acids 30-564 of SEQ ID NO: 1 (SEQ ID NO: 42) and amino acids 31-564 of SEQ ID NO: 1 (SEQ ID NO: 43).
5. The protein according to any one of claims 1-4 wherein A is an immunogenic fragment of SEQ ID NO:43 or a sequence having at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO. 43.
6. The protein according to any one of claims 1-5 wherein the protein is selected from the group consisting of SEQ ID NO: 53, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 73 and SEQ ID NO: 88.

7. The protein according to any one of claims 1-5 wherein A is an immunogenic fragment of UspA2 comprising a laminin binding domain and a fibronectin binding domain or an immunogenic fragment of UspA2 comprising a laminin binding domain, a fibronectin binding domain and a C3 binding domain.
8. The protein according to any one of claims 1-7 wherein the protein is SEQ ID NO: 69.
9. An immunogenic composition comprising a protein of formula (I) as defined in any one of claims 1-8.
10. The immunogenic composition of claim 9 further comprising at least one antigen from *Haemophilus influenzae*.
11. The immunogenic composition of claim 10 wherein the at least one antigen is Protein D.
12. The immunogenic composition of any one of claims 9-11 further comprising Protein E, PilA or PE and PilA as a fusion protein.
13. A vaccine comprising the protein of any one of claims 1-8 or the immunogenic composition of any one of claims 9-12.
14. The vaccine of claim 13, further comprising an adjuvant, e.g. AS01E.
15. The vaccine of claim 13 or 14 wherein the immunogenic composition contains a protein of SEQ ID NO: 69, Protein D and a PE-PilA fusion protein (optionally LVL-735).
16. The vaccine of claim 15 comprising:
 - (i) 10µg of protein D, 10µg of the PEPilA fusion protein LVL735, 10µg of the UspA2 construct MC009 and the adjuvant AS01E, or
 - (ii) 10µg of protein D, 10µg of the PEPilA fusion protein LVL735, 3.3µg of the UspA2 construct MC009 and the adjuvant AS01E.
17. A method for the treatment or prevention of otitis media, pneumonia or *M. catarrhalis*

infection in a subject in need thereof comprising administering to said subject a therapeutically effective amount of the immunogenic composition according to any one of claims 9-12 or the vaccine of any of claims 13-16.

18. A method for the treatment or prevention of acute exacerbations of chronic obstructive pulmonary disease (AECOPD) in a subject in need thereof comprising administering to said subject a therapeutically effective amount of the immunogenic composition according to any one of claims 9-12 or the vaccine of any one of claims 13-16.

19. Use of the protein of any one of claims 1-8, or the immunogenic composition of any one of claims 9-12, or the vaccine of any one of claims 13-16, for the preparation of a medicament for the treatment or prevention of otitis media, pneumonia or *M. catarrhalis* infection.

20. Use of the protein of any one of claims 1-8, or the immunogenic composition of any one of claims 9-12, or the vaccine of any one of claims 13-16, for the preparation of a medicament for the treatment or prevention of acute exacerbations of chronic obstructive pulmonary disease (AECOPD).

A TYPICAL FERMENTATION PROFILE WITH THE HIGH CELL DENSITY INDUCTION (HCDI) PROCESSES AND THE PARAMETERS MONITERED DURING 20L - SCALE FED-BATCH FERMENTATION.

BATCH: MCA114_00/RECIPE: CLFABLR060508 BATCH STARTED AT 16/11/2010 16:22:00 AND STOPPED AT 19/11/2010 09:24:13

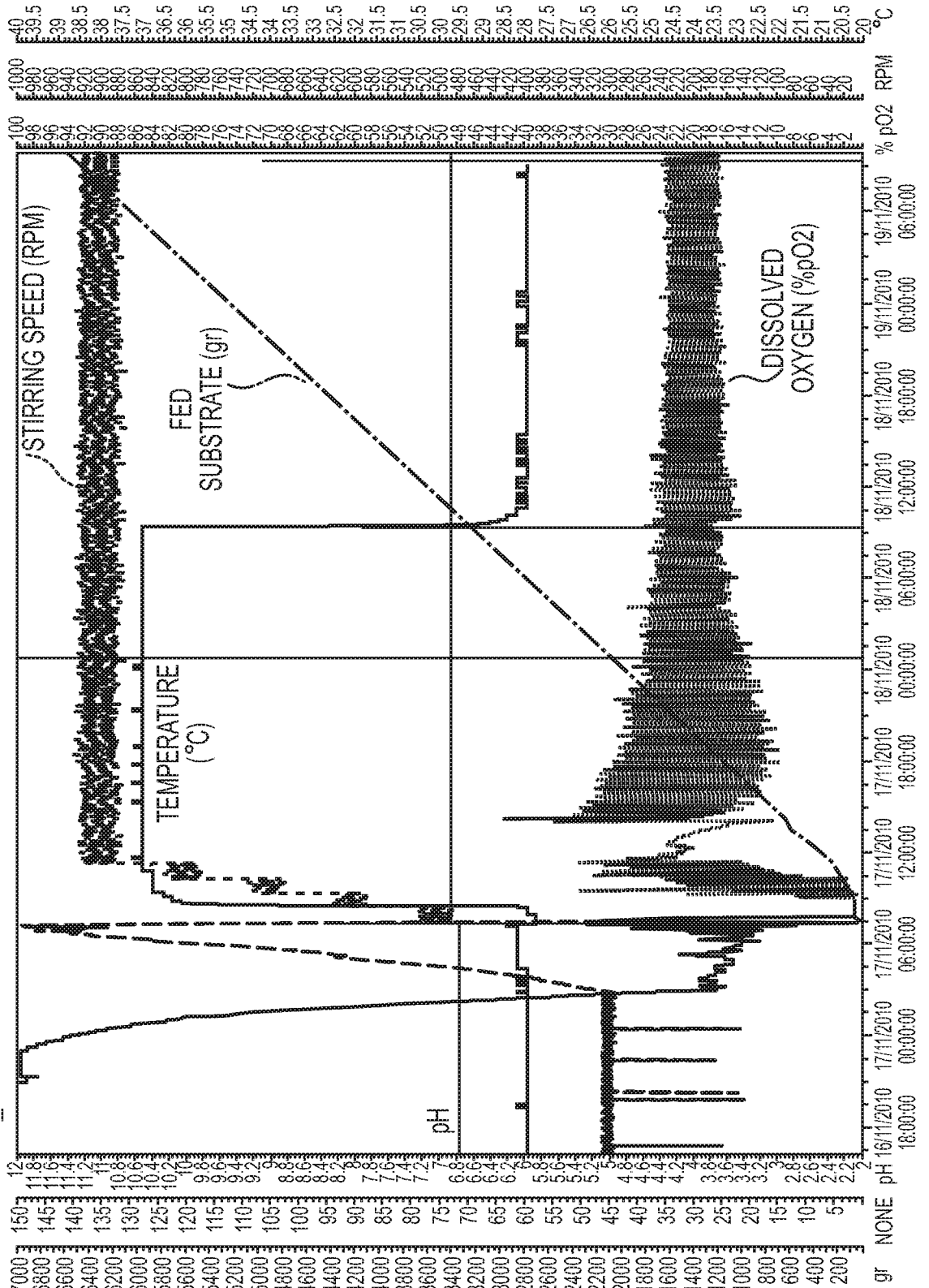
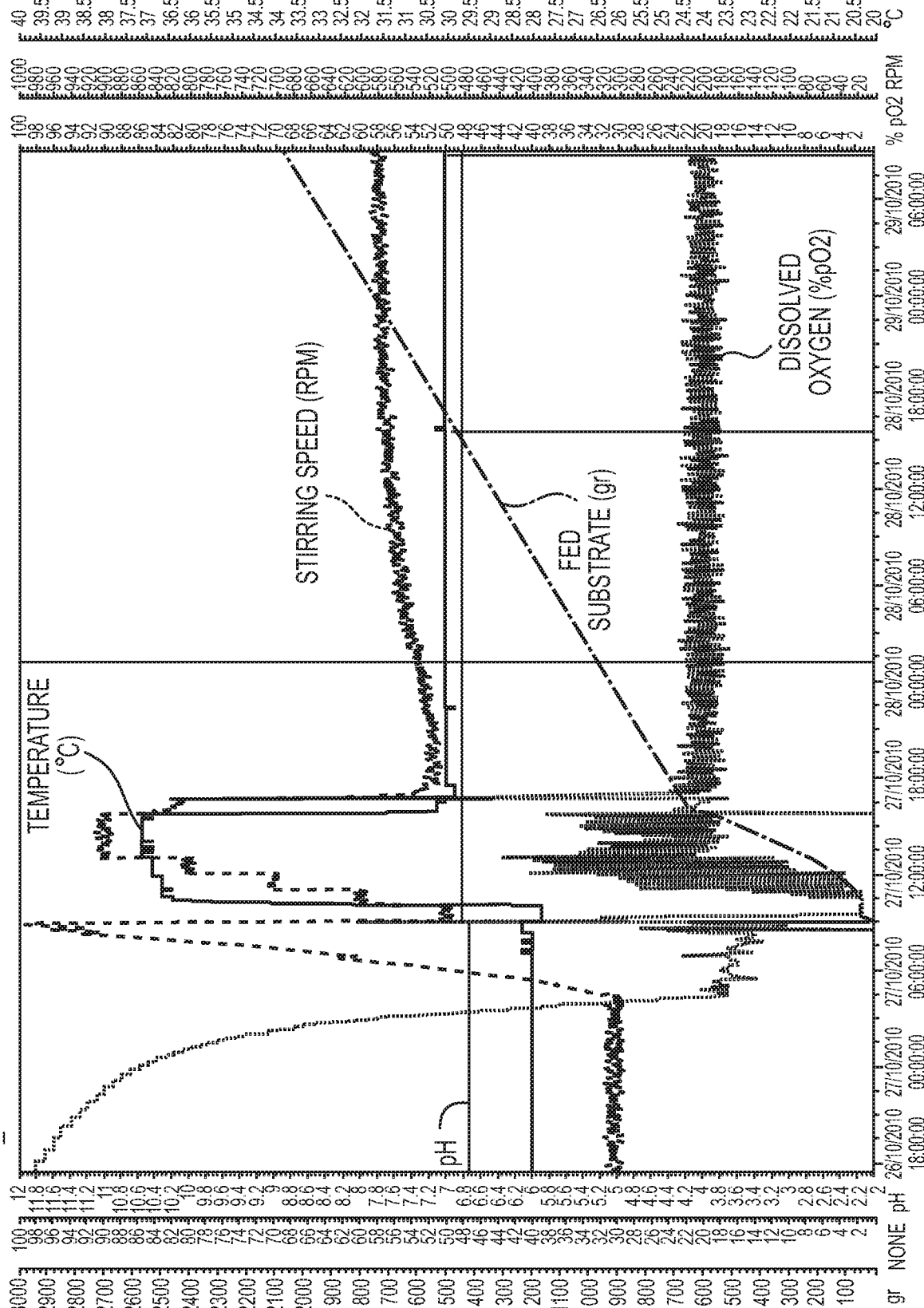


FIG. 2

A TYPICAL FERMENTATION PROFILE WITH THE LOW CELL DENSITY INDUCTION (LCDI) PROCESSES AND THE PARAMETERS MONITERED DURING 20L - SCALE FED-BATCH FERMENTATION.

BATCH: MCA109_00/RECIPE: CLFABLR060508 BATCH STARTED AT 26/10/2010 17:30:31 AND STOPPED AT 29/10/2010 09:02:11



UspA2 YIELD FROM PROTEIN CONSTRUCTS MC-001, MC-002, MC-004, MC-005, MC-006, MC-007, MC-008 AND MC-010 EVALUATED IN FERMENTER; DATA FROM TABLE 4. His = HISTIDINE.

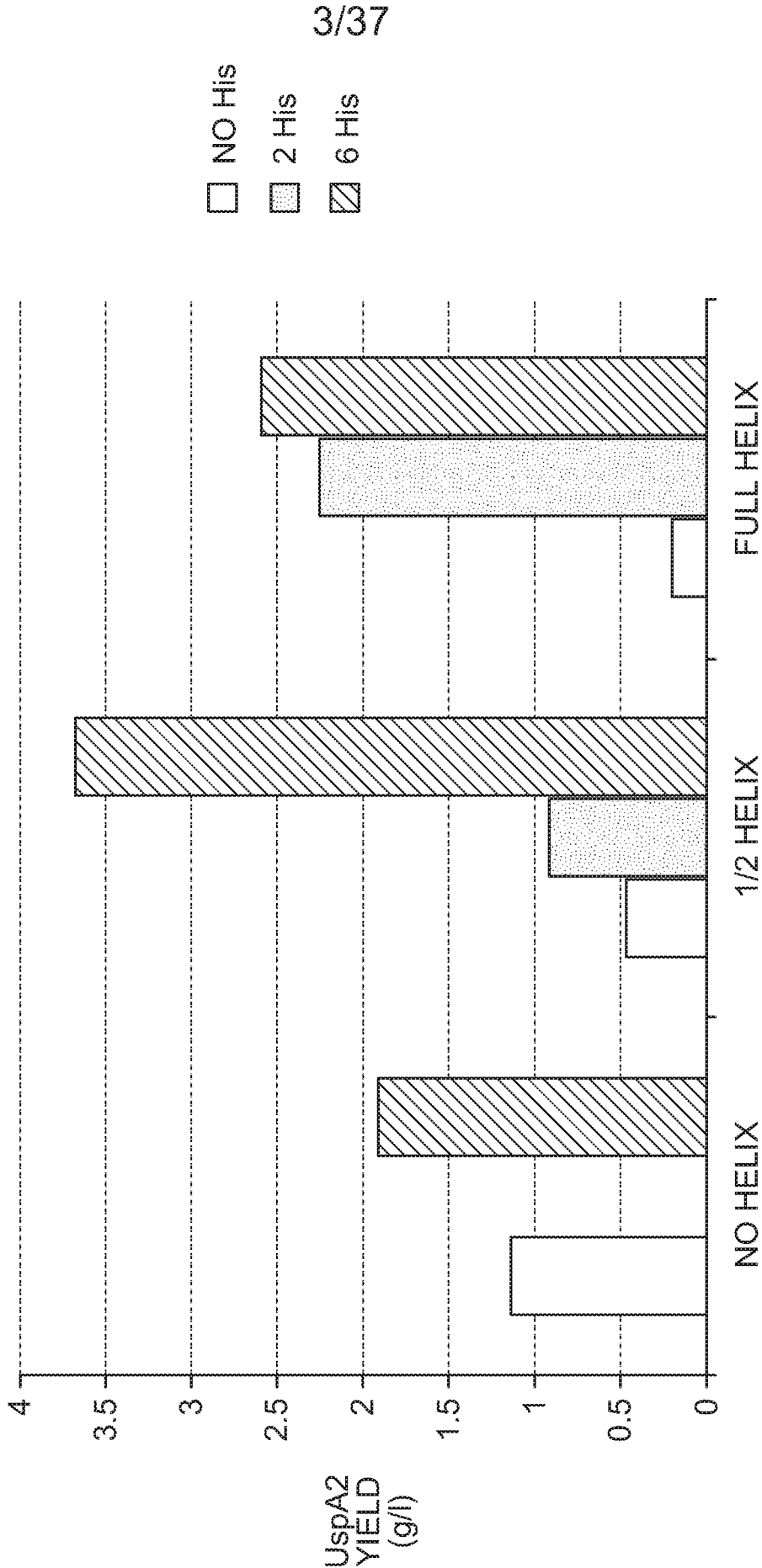


FIG. 3

MOLECULAR WEIGHT DISTRIBUTION OF PURIFIED MC-005 DETERMINED BY SEDIMENTATION VELOCITY ANALYTICAL ULTRACENTRIFUGATION. THE MAJORITY OF PROTEIN IS FOUND AS A TRIMER, WITH A SMALL PROPORTION OF A HIGHER MOLECULAR WEIGHT OLIGMER THAT MAY CORRESPOND TO DIMER OF TRIMER. MW = MOLECULAR WEIGHT. kDa = KILODALTON.

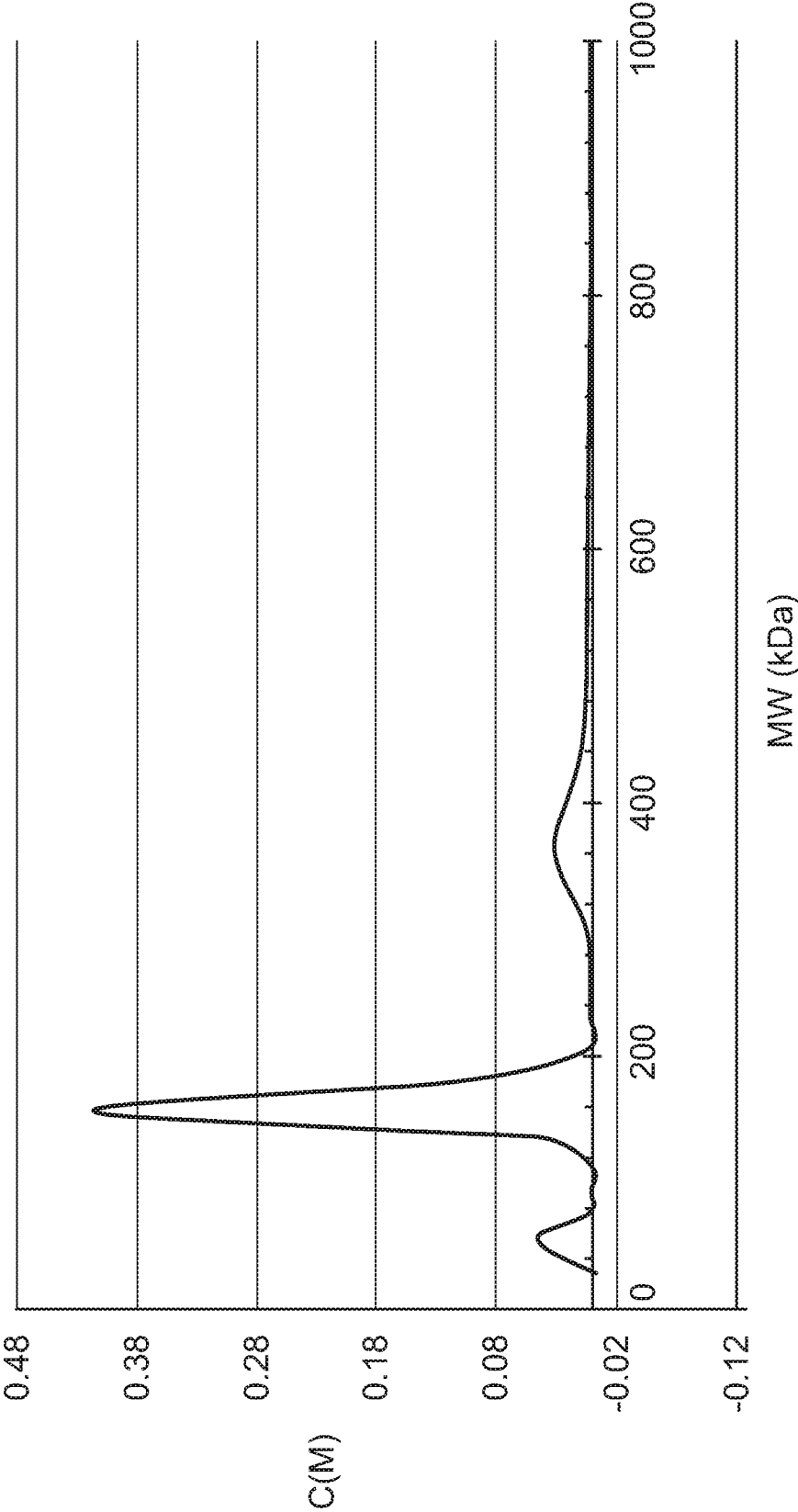


FIG. 4

MOLECULAR WEIGHT DISTRIBUTION OF PURIFIED MC-001 DETERMINED
BY SEDIMENTATION VELOCITY ANALYTICAL ULTRACENTRIFUGATION.
MAJORITY OF PROTEIN IS FOUND AS A TRIMER.

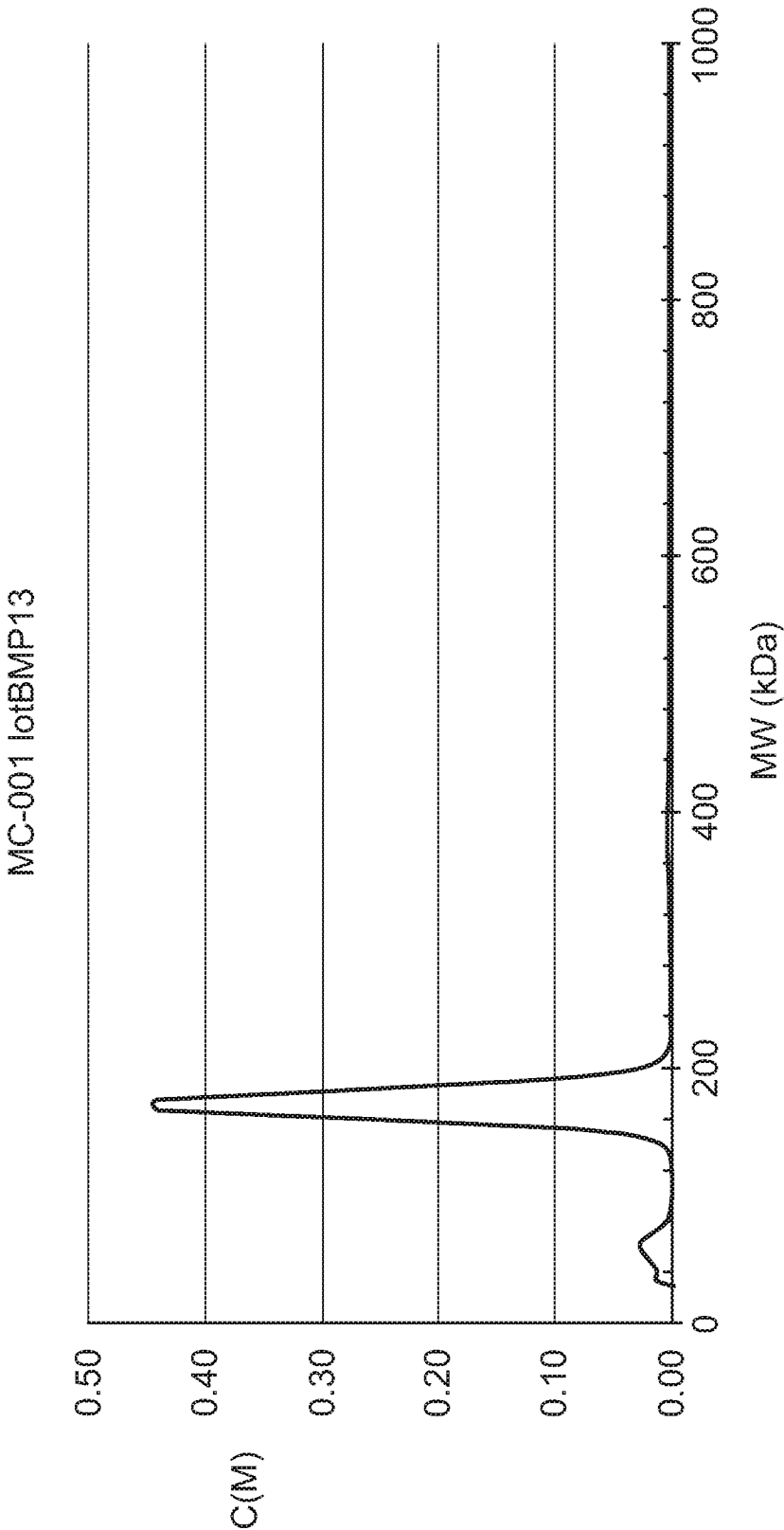


FIG. 5

MOLECULAR WEIGHT DISTRIBUTION OF PURIFIED MC-001 DETERMINED BY SEDIMENTATION VELOCITY ANALYTICAL ULTRACENTRIFUGATION. THE SAMPLE PRESENTS MULTIPLE SPECIES AND IS HIGHLY POLYDISPERSE. THE SEDIMENTATION COEFFICIENT OF THE MAJOR SPECIES DETECTED DOESN'T CORRESPOND TO THE ONE OF THE TRIMERS NORMALLY DETECTED IN THE OTHER LOTS.

MC-001 lotBMP14

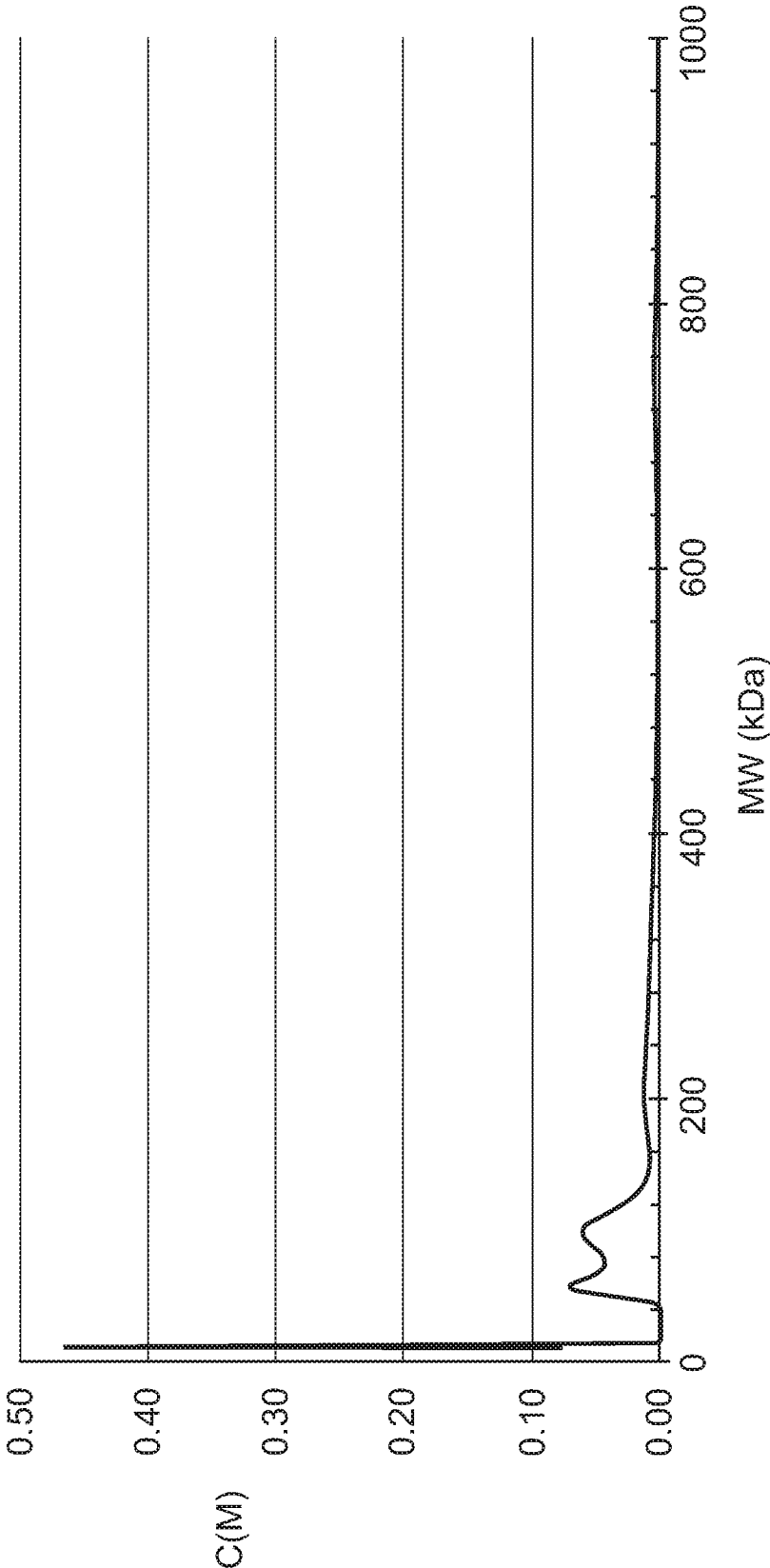


FIG. 6

MOLECULAR WEIGHT DISTRIBUTION OF PURIFIED MC-001 DETERMINED
BY SEDIMENTATION VELOCITY ANALYTICAL ULTRACENTRIFUGATION.
MAJORITY OF PROTEIN IS FOUND AS A TRIMER.

MC-001 lotBMP54

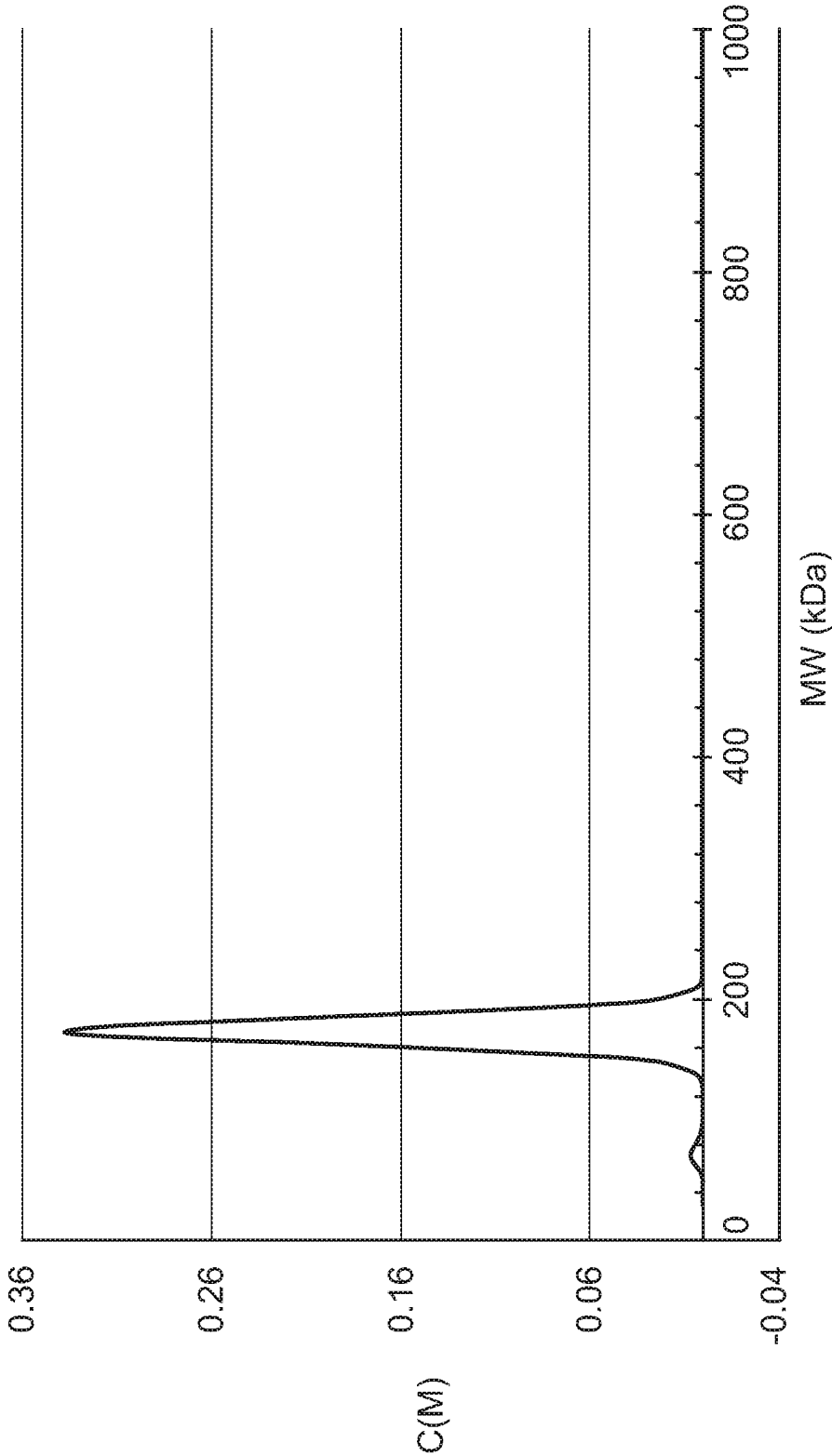


FIG. 7

MOLECULAR WEIGHT DISTRIBUTION OF PURIFIED MC-007 DETERMINED
BY SEDIMENTATION VELOCITY ANALYTICAL ULTRACENTRIFUGATION.
MAJORITY OF PROTEIN IS FOUND AS A TRIMER.

MC-007

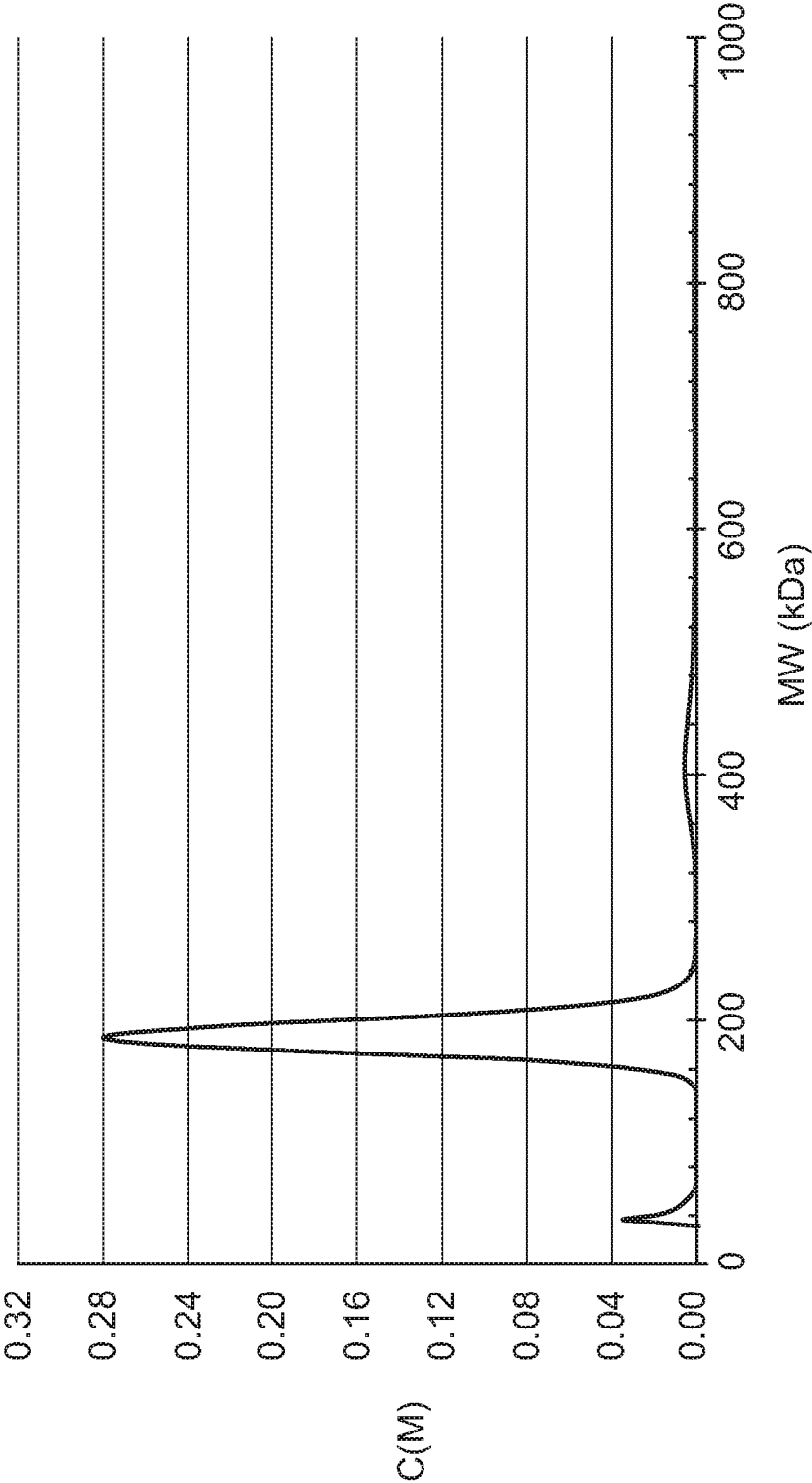


FIG. 8

FAR-UV CIRCULAR DICHROISM (CD) SPECTRA OF UspA2 CONSTRUCTS GIVING AN INDICATION OF PROTEIN SECONDARY STRUCTURES.

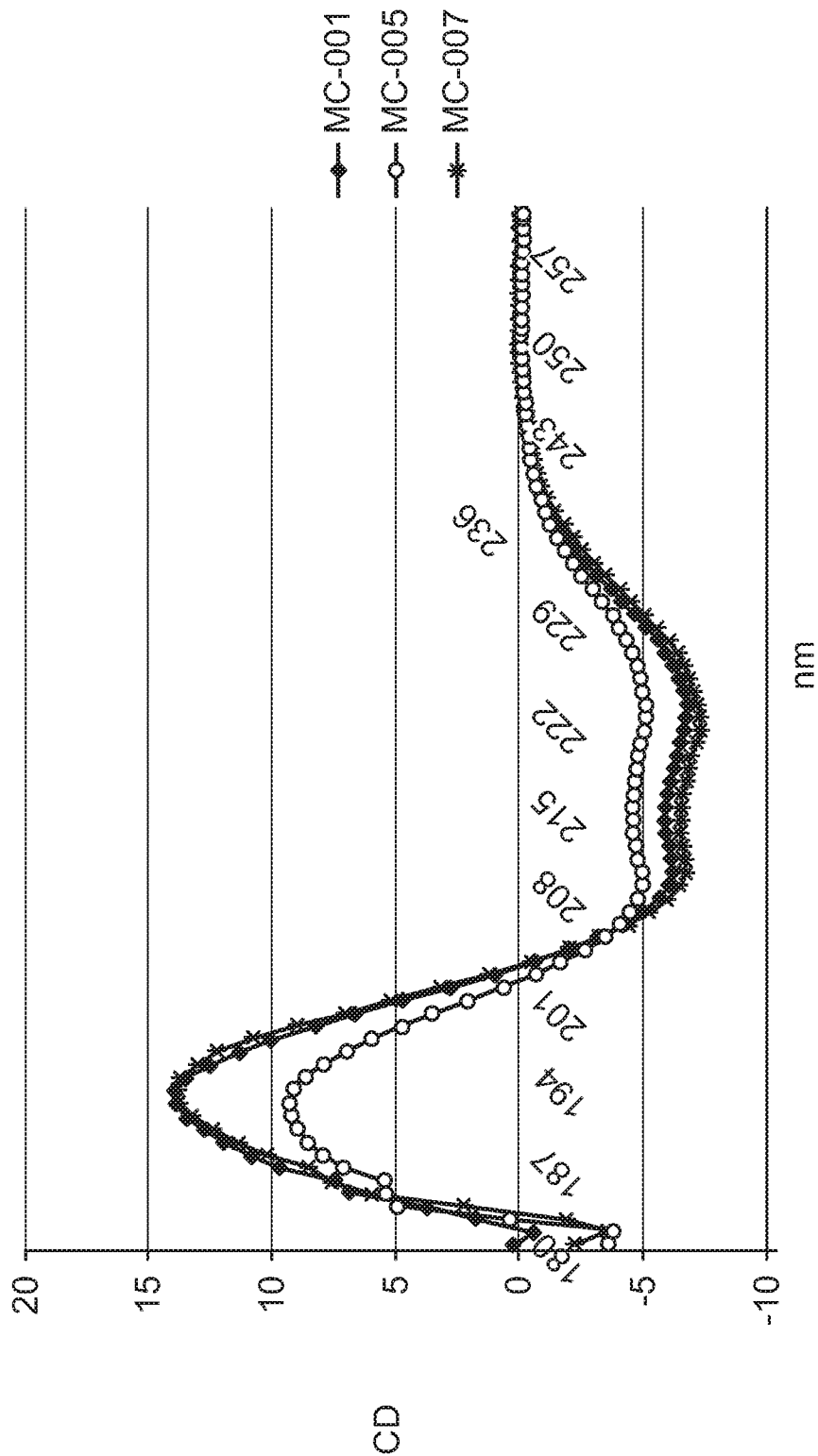


FIG. 9

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SECONDARY STRUCTURES MONITORING BY CIRCULAR DICHROISM (CD) DURING THERMAL UNFOLDING OF MC-005 (UspA2 Δ HELIX+6HIS). VISUAL ANALYSIS OF THE SPECTRA CLEARLY SHOWS THAT PROTEIN LOSES MOST OF ITS SECONDARY STRUCTURES AT 33 °C.

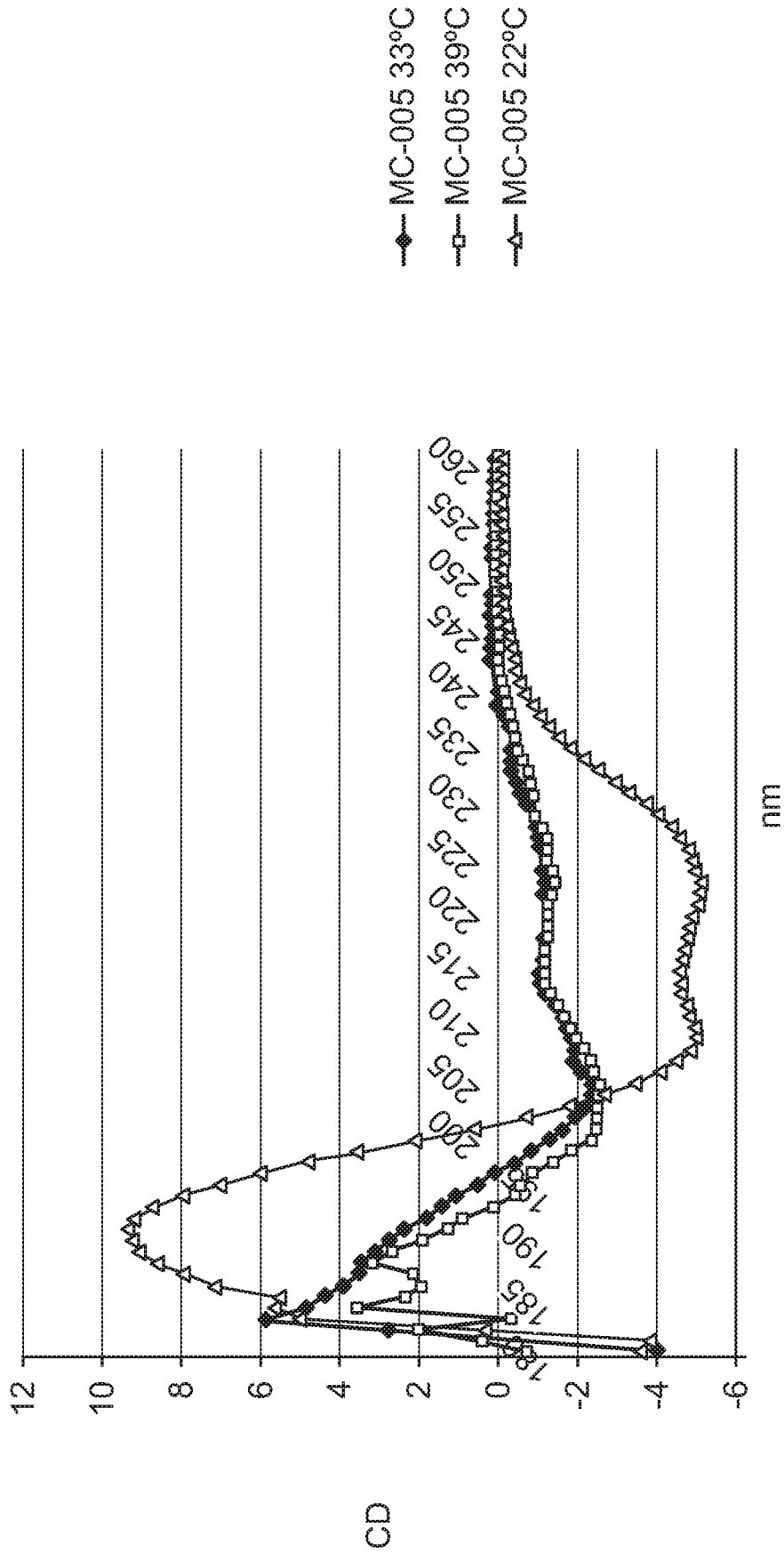


FIG. 10

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SECONDARY STRUCTURES MONITORING BY CIRCULAR DICHROISM (CD) DURING THERMAL UNFOLDING OF MC-007 (UspA2 FULL HELIX + 6HIS). VISUAL ANALYSIS OF THE SPECTRA SHOWS THAT LOSS OF SECONDARY STRUCTURE IS SLOWER COMPARED TO THE CONSTRUCT WITHOUT HELIX. STRUCTURAL CHANGES ARE DETECTABLE UPON HEATING TO 33°C, BUT COMPLETE UNFOLDING SEEMS TO OCCUR BETWEEN 35°C AND 37°C.

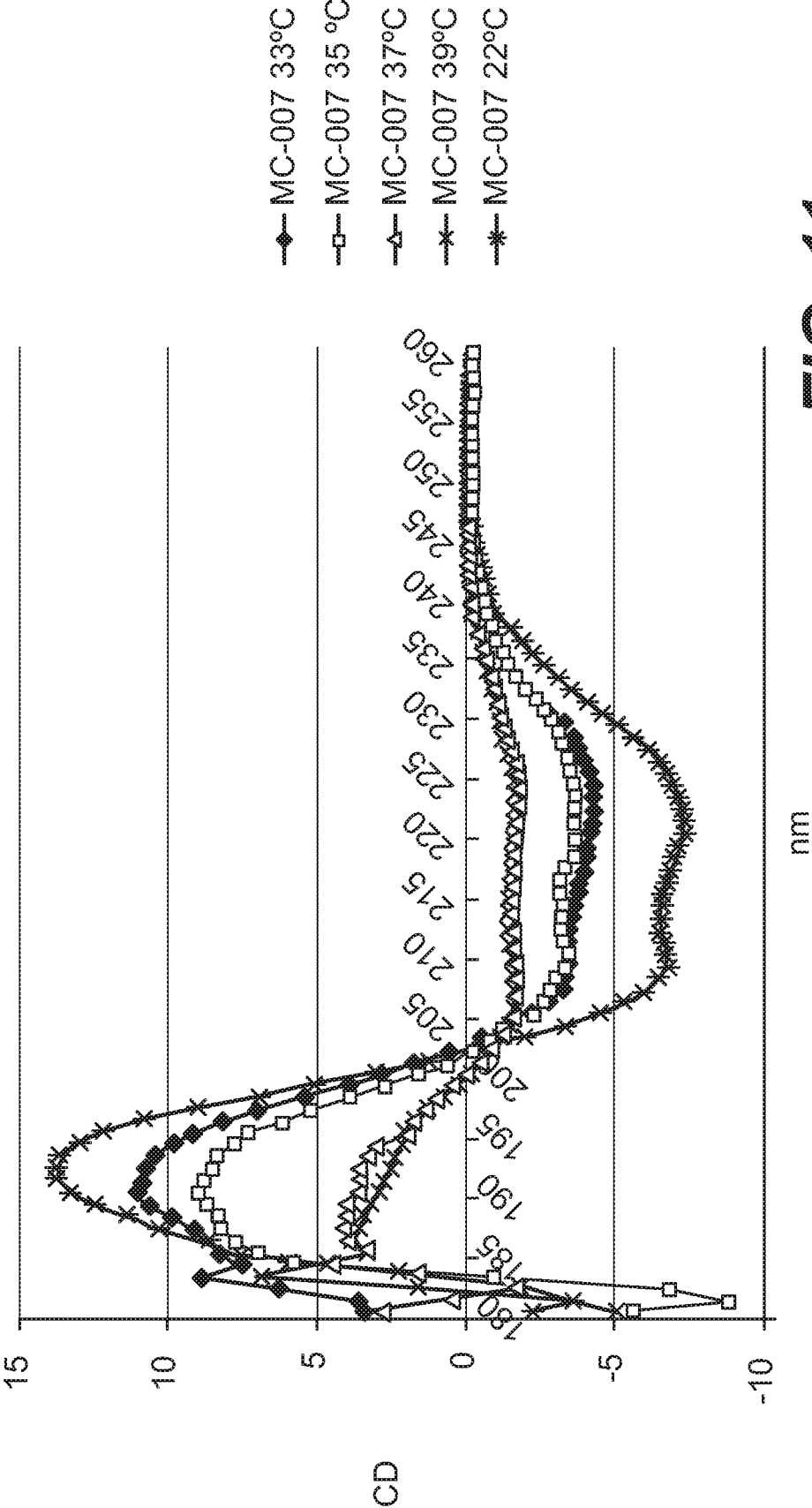
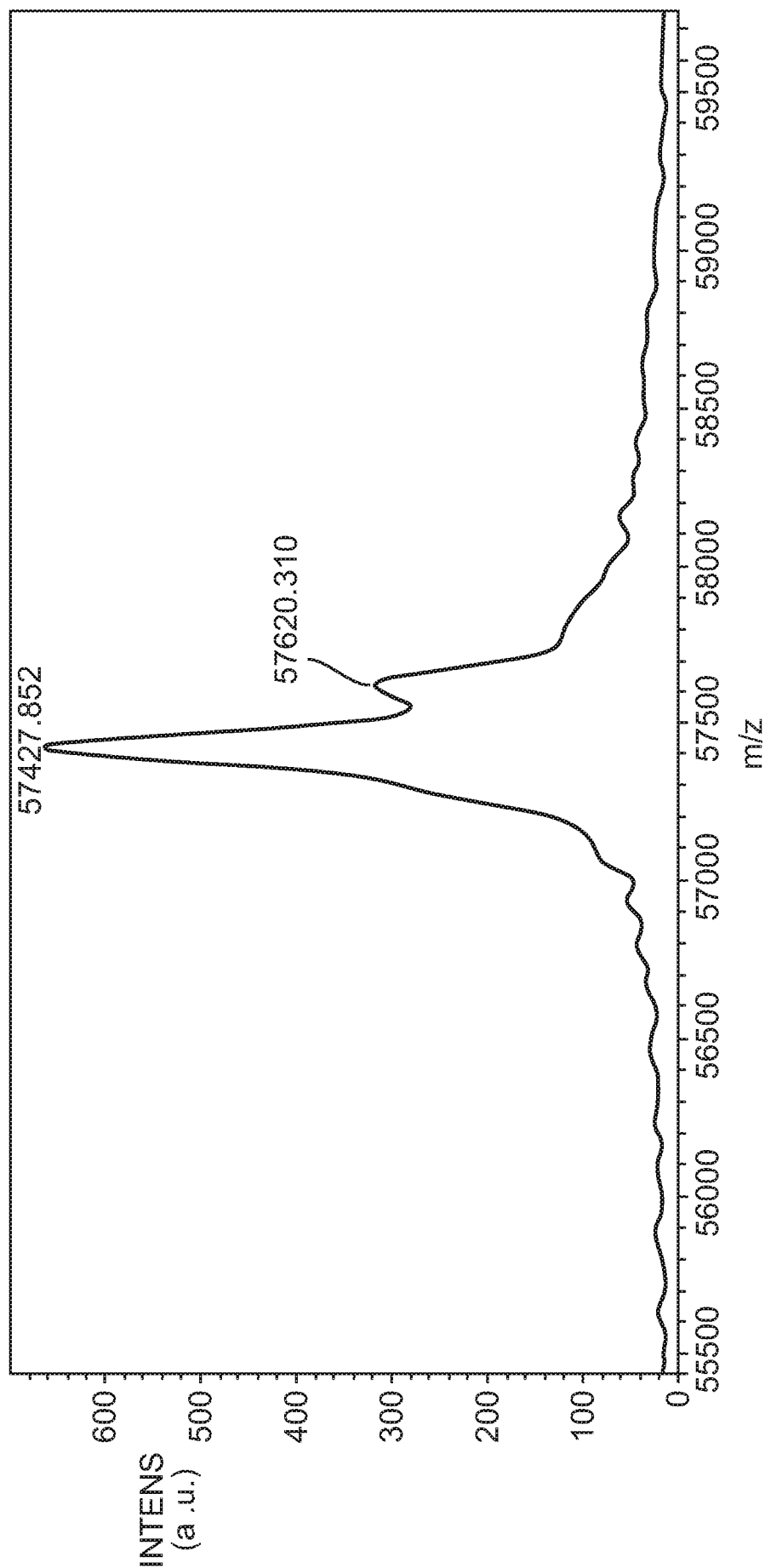


FIG. 11

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MALDI SPECTRUM OF MC-001 LOT opt-01. THE MASS OBSERVED AT 57427Da MAY BE COHERENT WITH THE DEMETHIONYLATED PROTEIN, WHILE THE PEAK AT 57620Da COULD CORRESPOND TO THE COMPLETE PROTEIN.

COMMENT 1 UspA2 opt-His lot opt 01 bm_CHCl3/MeOH_Sin
COMMENT 2

**FIG. 12**

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MALDI SPECTRUM OF MC-011 LOT BMP37. THE MASS OBSERVED MAY BE
COHERENT WITH THE DEMETHIONYLATED PROTEIN. THE TWO OTHER PEAKS
AT +186Da AND +366Da ARE UNIDENTIFIED.

COMMENT 1 Uspa2_BMP37
COMMENT 2

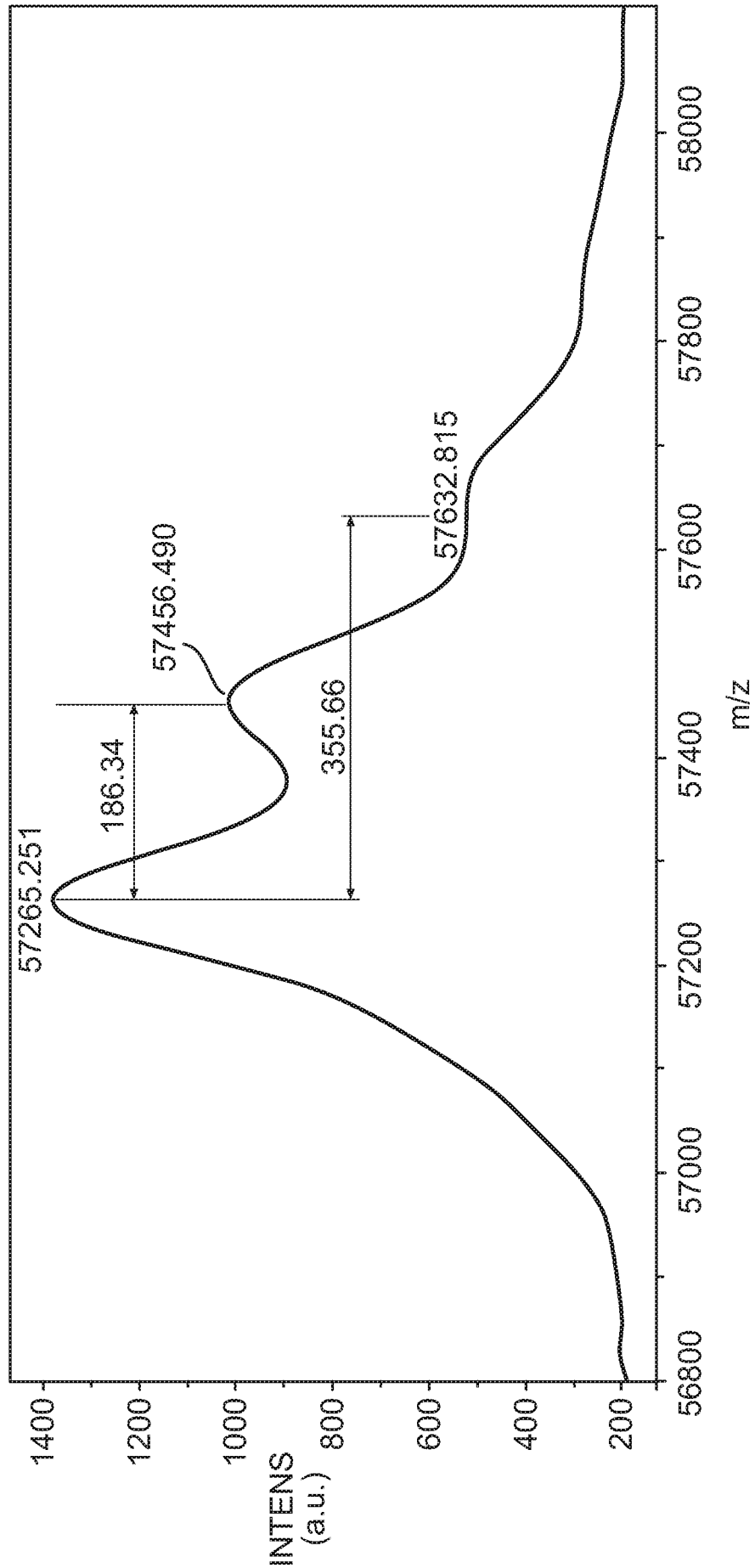


FIG. 13

PROTECTIVE EFFICACY OF MC-001 AND MC-007 IN A MOUSE MODEL OF LUNG COLONIZATION.

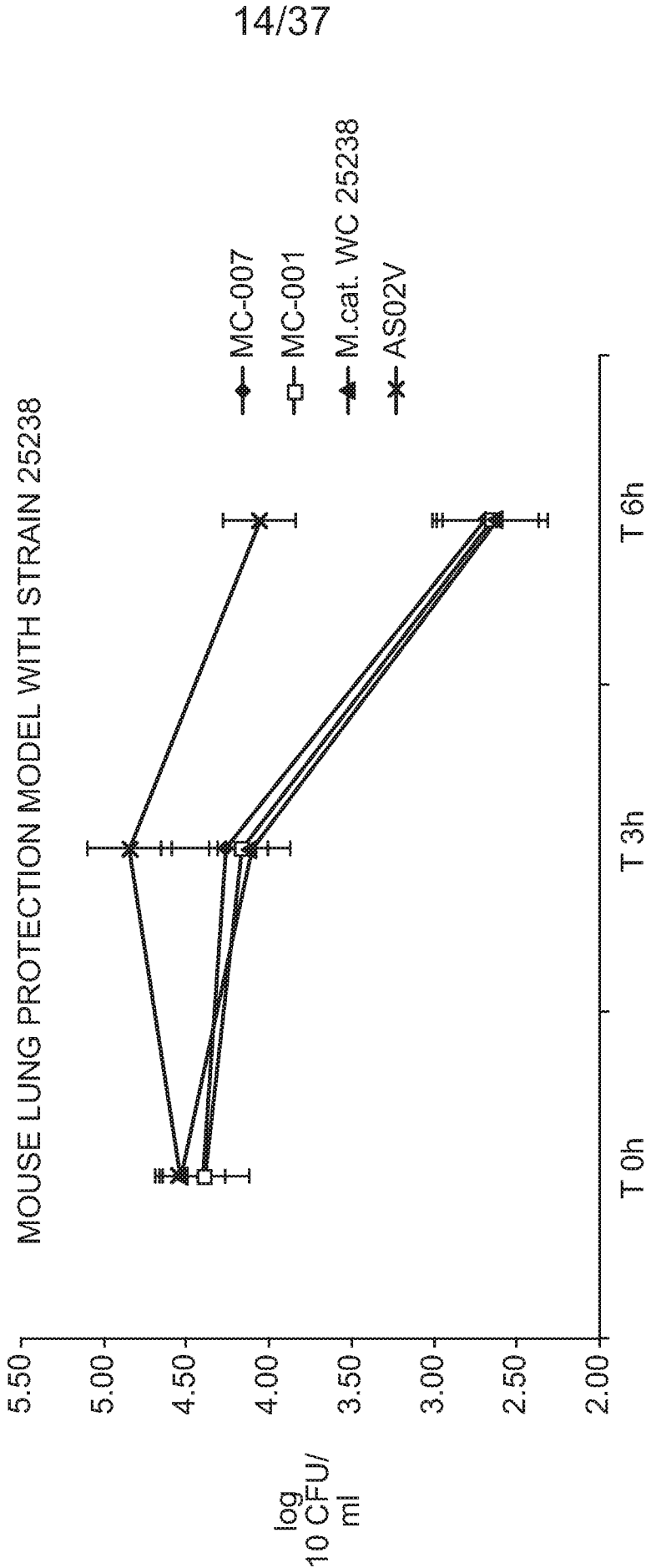


FIG. 14

ANTIBODY RESPONSE DIRECTED AGAINST UspA2 INDUCED AFTER INTRAMUSCULAR ADMINISTRATION IN MICE, WHERE PII AND PIII INDICATE, RESPECTIVELY, ANTI-IgG LEVELS IN SERA COLLECTED AT DAY 28 (POST II) AND DAY 42 (POST III).

IMMUNOGENICITY OF VARIOUS UspA2 FORMULATIONS IN MICE

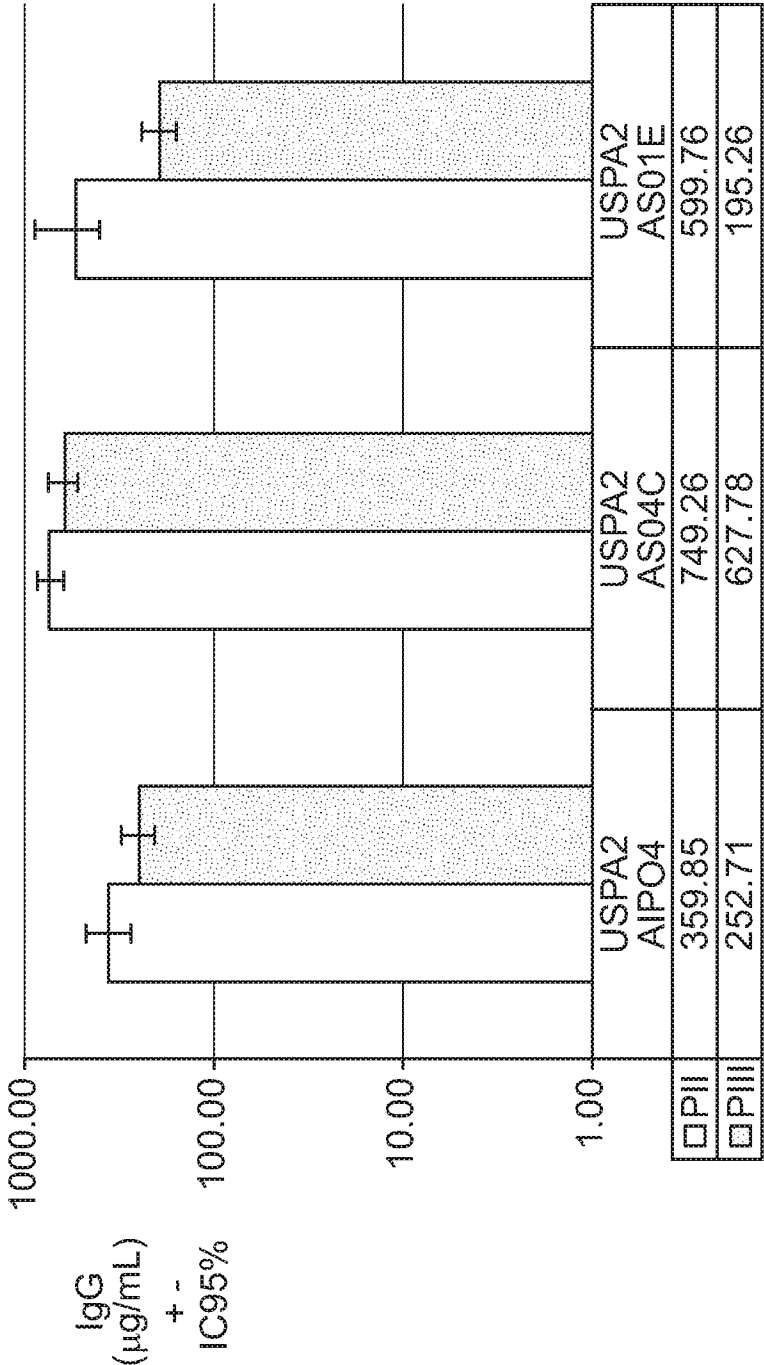


FIG. 15

BACTERICIDAL TITERS INDUCED BY UspA2 AGAINST A HOMOLOGOUS STRAIN, FORMULATED WITH DIFFERENT ADJUVANTS (AS01E, AS04C AND AIPO4). **= FIVE POOLS TESTED (5 POOLS OF FIVE SERA WERE TESTED).

BACTERICIDAL RESPONSES INDUCED BY UspA2 FORMULATED IN AS01E, AS04C, AND AIPO4

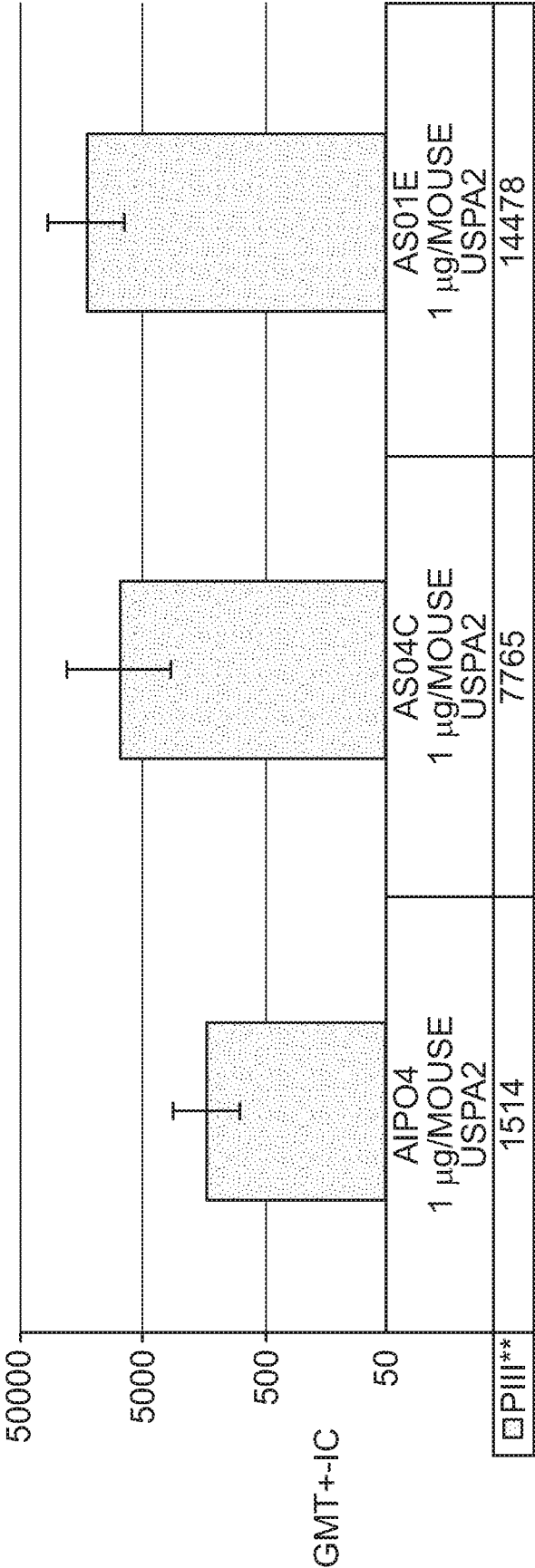


FIG. 16

ANTIBODY RESPONSE DIRECTED AGAINST UspA2 INDUCED AFTER INTRAMUSCULAR ADMINISTRATION IN MICE, USING DIFFERENT FORMULATIONS OF ANTIGENS AND ADJUVANTS.

IMMUNOGENICITY OF VARIOUS UspA2 FORMULATIONS IN MICE

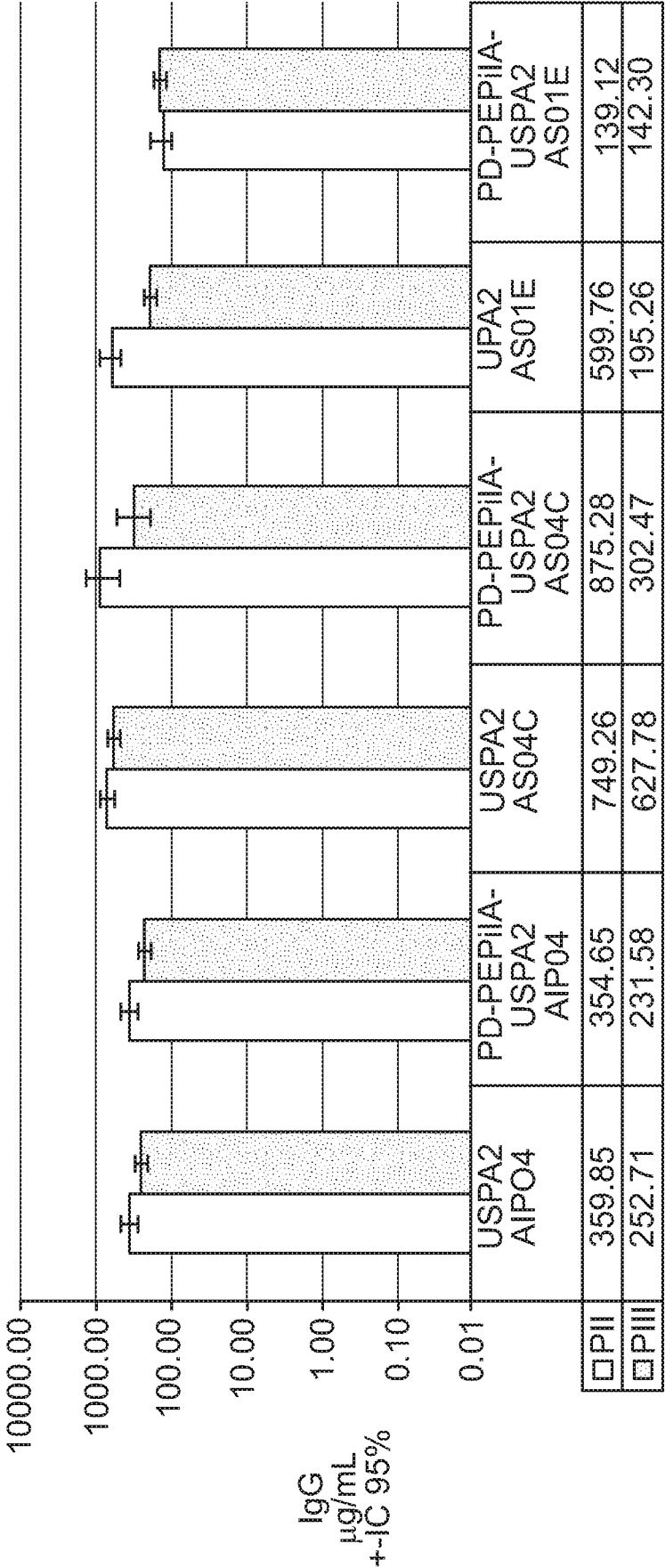


FIG. 17

BACTERICIDAL TITERS INDUCED BY UspA2 AGAINST A HOMOLOGOUS STRAIN, USING
DIFFERENT FORMULATIONS OF ANTIGENS AND ADJUVANTS. **= FIVE POOLS TESTED
(5 POOLS OF FIVE SERA WERE TESTED)

BACTERICIDAL RESPONSES INDUCED BY UspA2 FORMULATED IN AS01E, AS04C, AND AIPO4

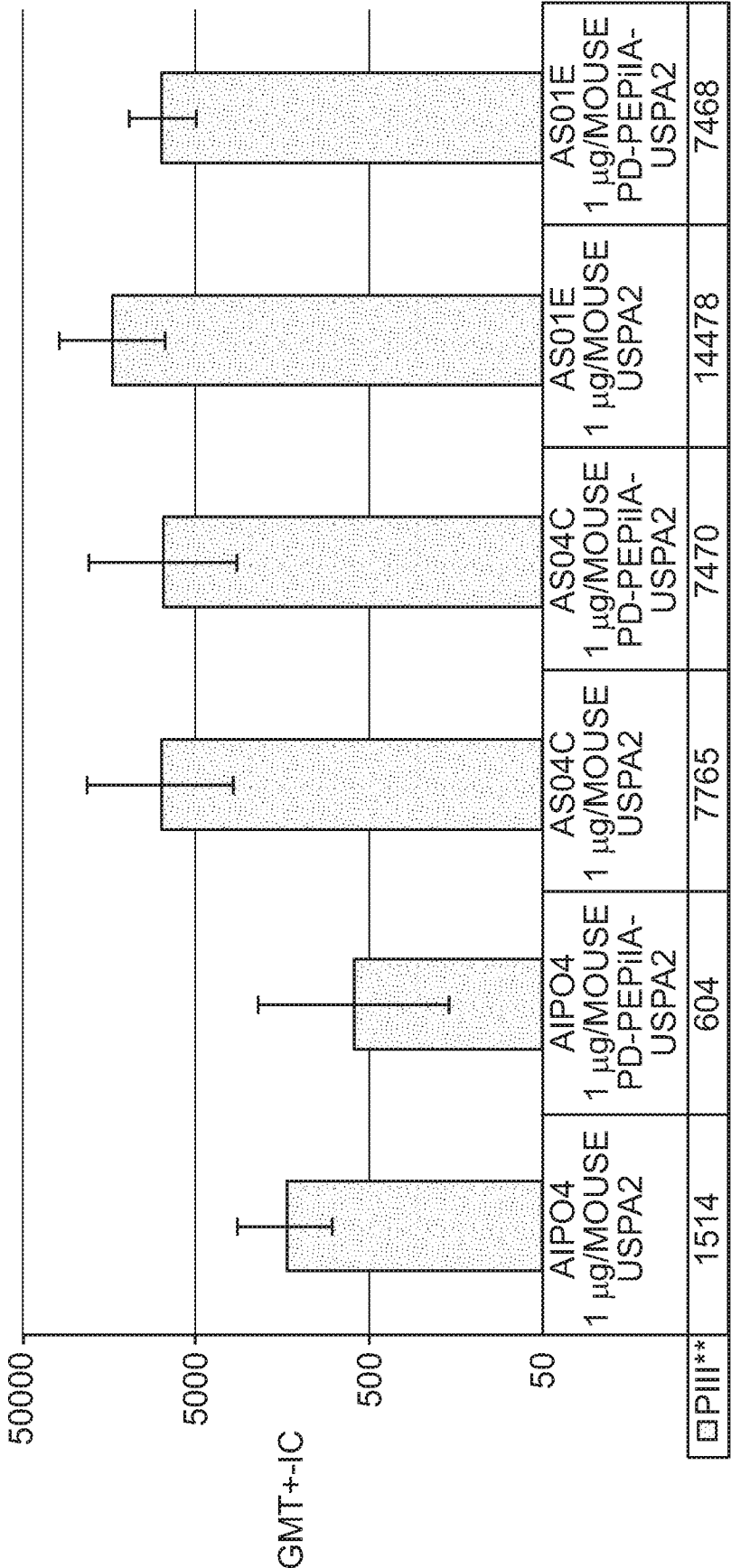


FIG. 18

IgG RESPONSE INDUCED AGAINST PD IN MICE BY PD-PEPiiA-USpA2 VACCINE
(A TRIVALENT NTHi-M.cat. VACCINE), FORMULATED WITH DIFFERENT ADJUVANTS.

IgG RESPONSE INDUCED AGAINST PD IN MICE BY TRIVALENT
NTHi-M.cat.VACCINE FORMULATIONS

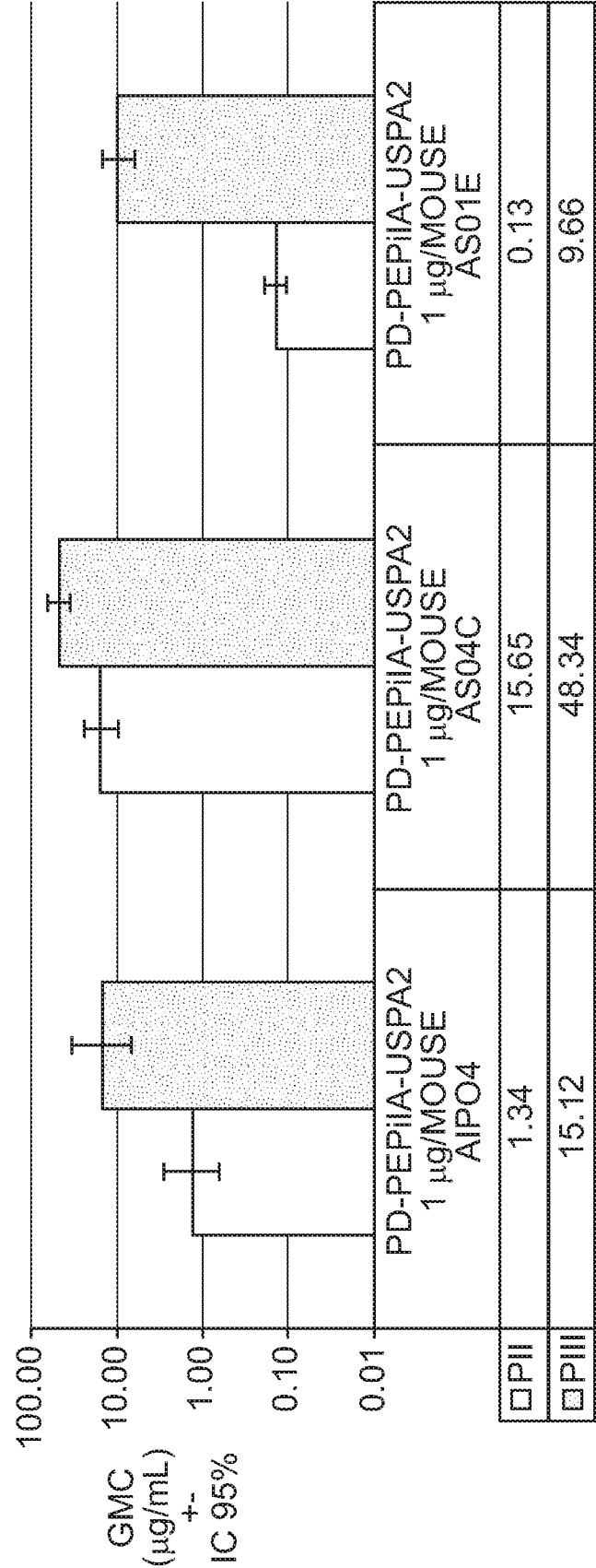


FIG. 19

IgG RESPONSE INDUCED AGAINST PE IN MICE BY PD-PEPIA-USpA2 VACCINE,
(A TRIVALENT NTHi-M.cat. VACCINE), FORMULATED WITH DIFFERENT ADJUVANTS.

IgG RESPONSE INDUCED AGAINST PE IN MICE BY TRIVALENT
NTHi-M.cat. VACCINE FORMULATIONS

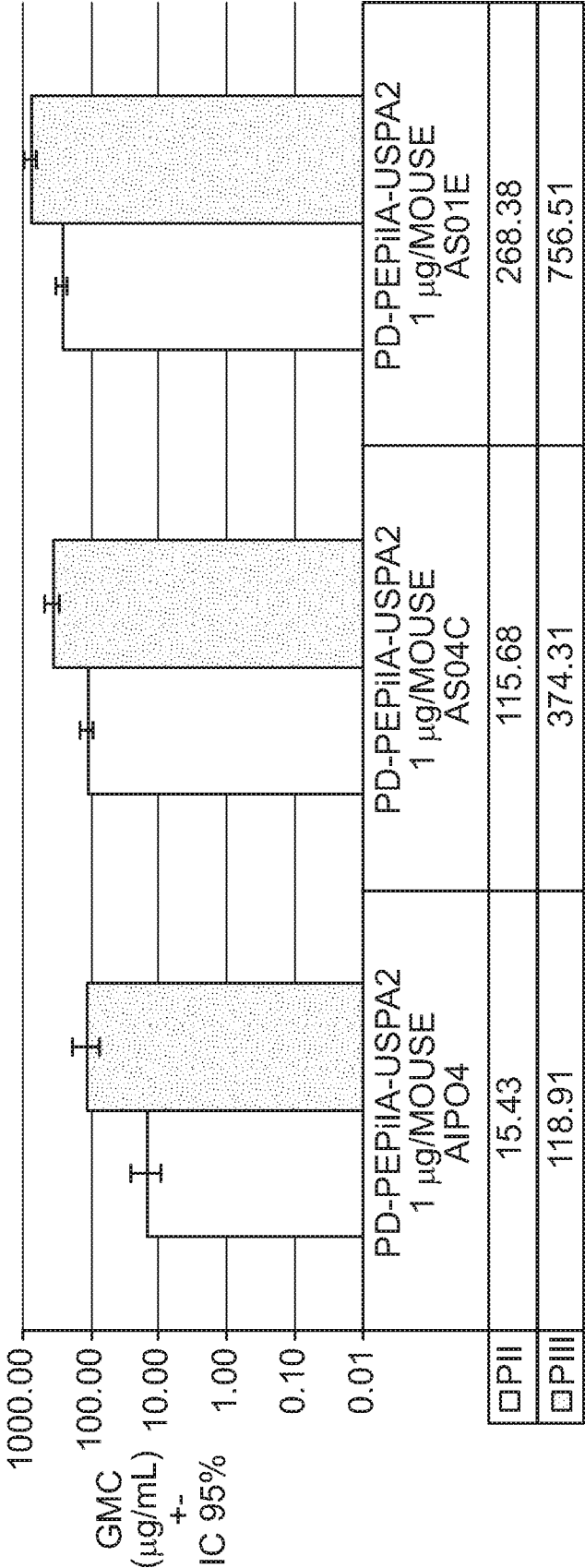


FIG. 20

IgG RESPONSE INDUCED AGAINST PIIA IN MICE BY PD-PEPIIA-USpA2 VACCINE
(A TRIVALENT NTHi-M.cat. VACCINE), FORMULATED WITH DIFFERENT ADJUVANTS.

IgG RESPONSE INDUCED AGAINST PIIA IN MICE BY TRIVALENT
NTHi-Mcat VACCINE FORMULATIONS

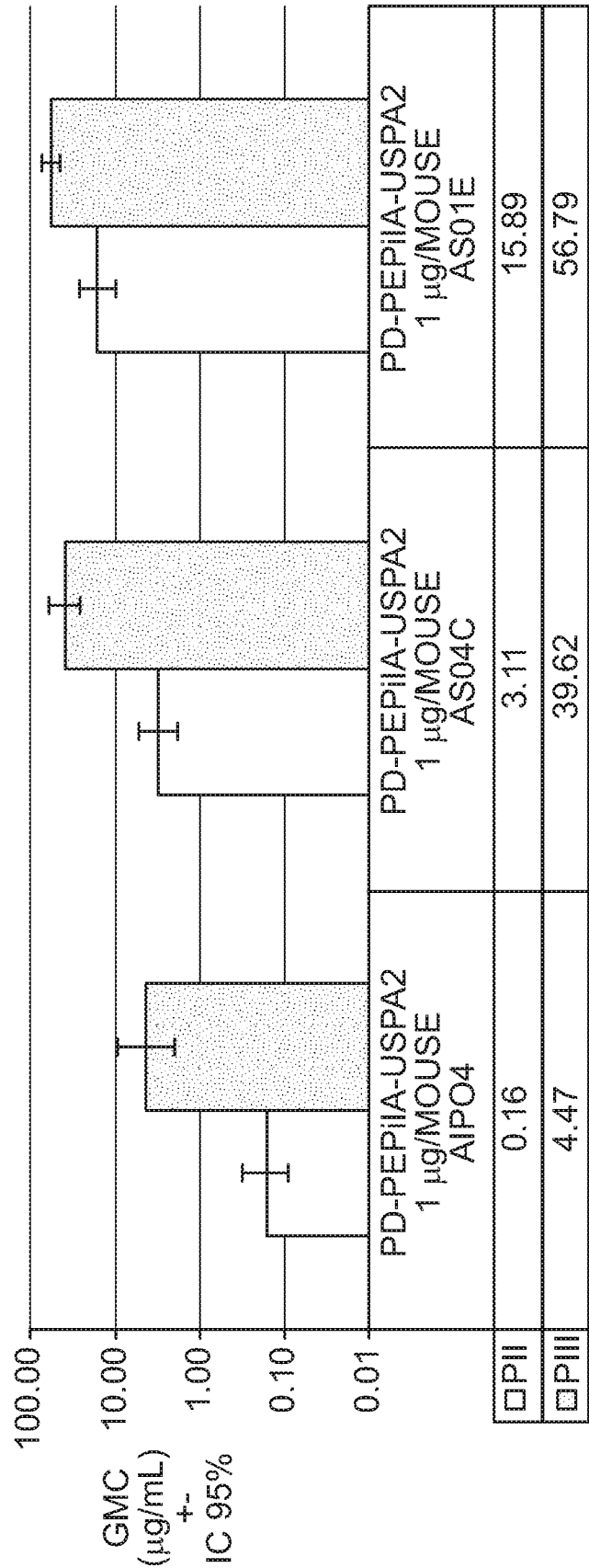


FIG. 21

IMMUNGENICITY OF PE IN THE BIVALENT NTHi PD-PEPiA AND TRIVALENT NTHi-M.cat. PD-PEPiA-USpA2 FORMULATIONS WITH AS01E.

IMPACT OF THE ADDITION OF UspA2 ON THE IMMUNGENICITY OF PD, PE AND P*i*A. ANTI-PE TITERS, 14P*II* - P*III*

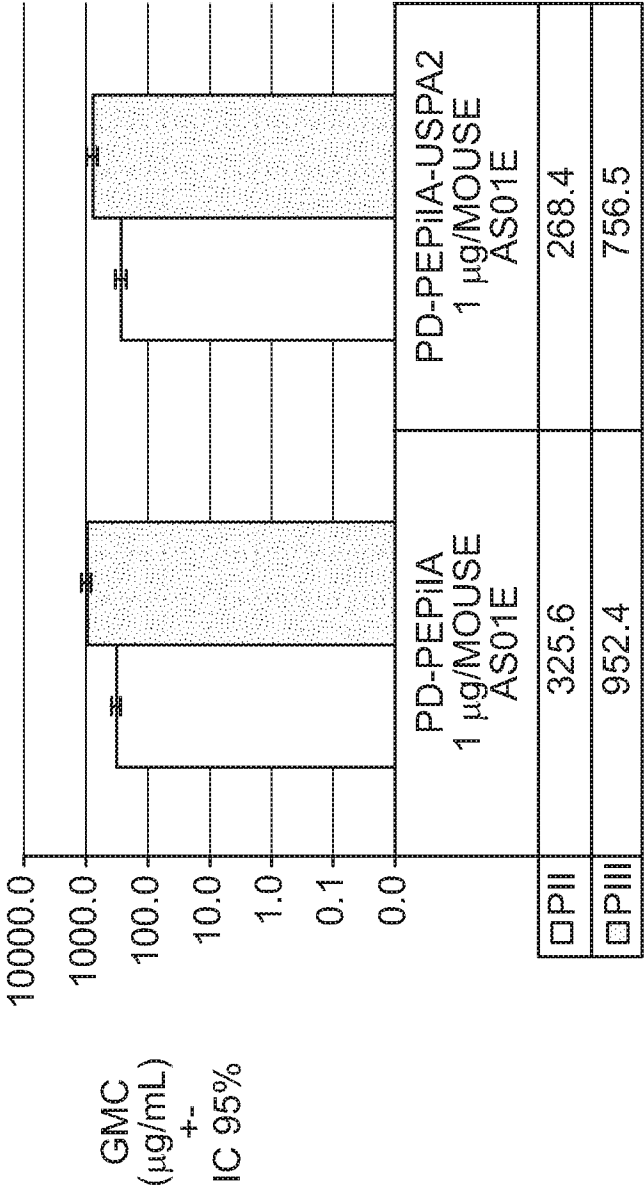


FIG. 22

IMMUNOGENICITY OF PIIA IN THE BIVALENT NTHi PD-PEPIA AND TRIVALENT NTHi-M.cat. PD-PEPIA-USpA2 FORMULATIONS WITH AS01E.

IMPACT OF THE ADDITION OF UspA2 ON THE IMMUNOGENICITY OF PD, PE AND PIIA. ANTI-PIIA TITERS, 14PII - PIII

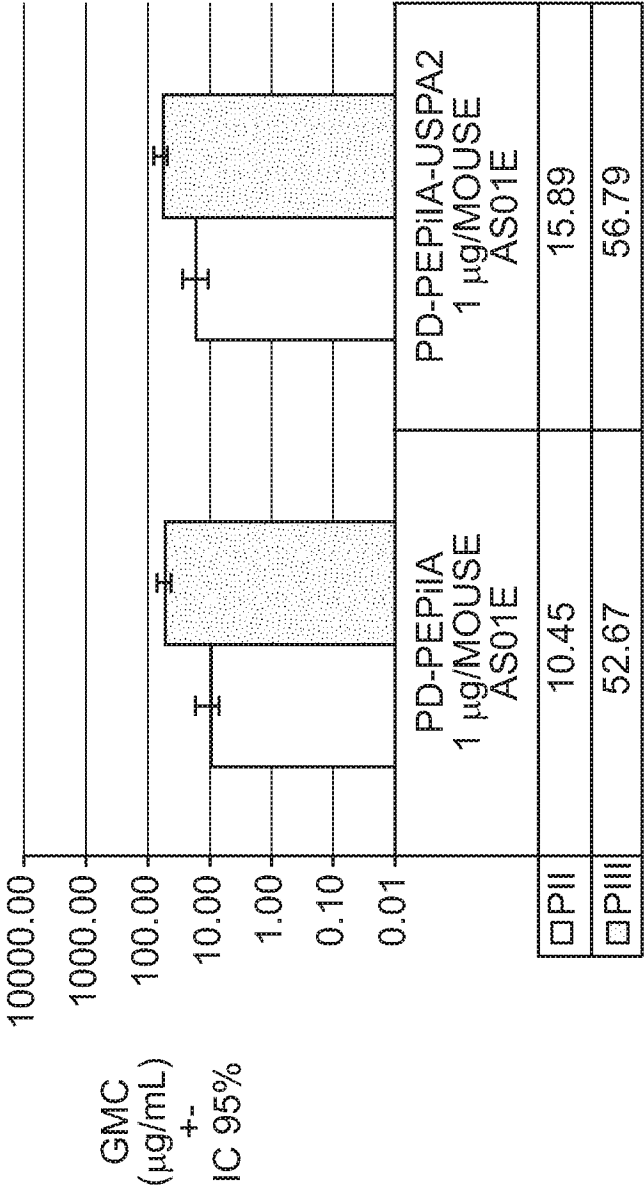


FIG. 23

IMMUNOGENICITY OF PD IN THE BIVALENT NTHi PD-PEPIIA AND TRIVALENT NTHi-M.cat. PD-PEPIIA-UspA2 FORMULATIONS WITH AS01E.

IMPACT OF THE ADDITION OF UspA2 ON THE IMMUNOGENICITY OF PD, PE AND PIIA. ANTI-PD TITERS, 14PII - PIII

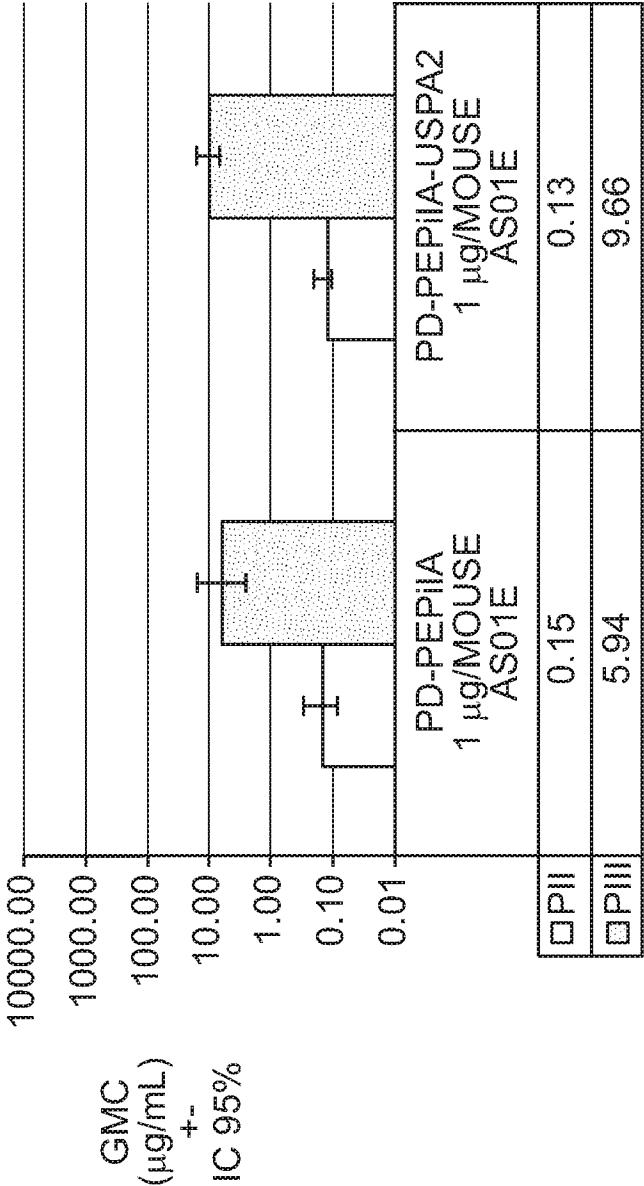
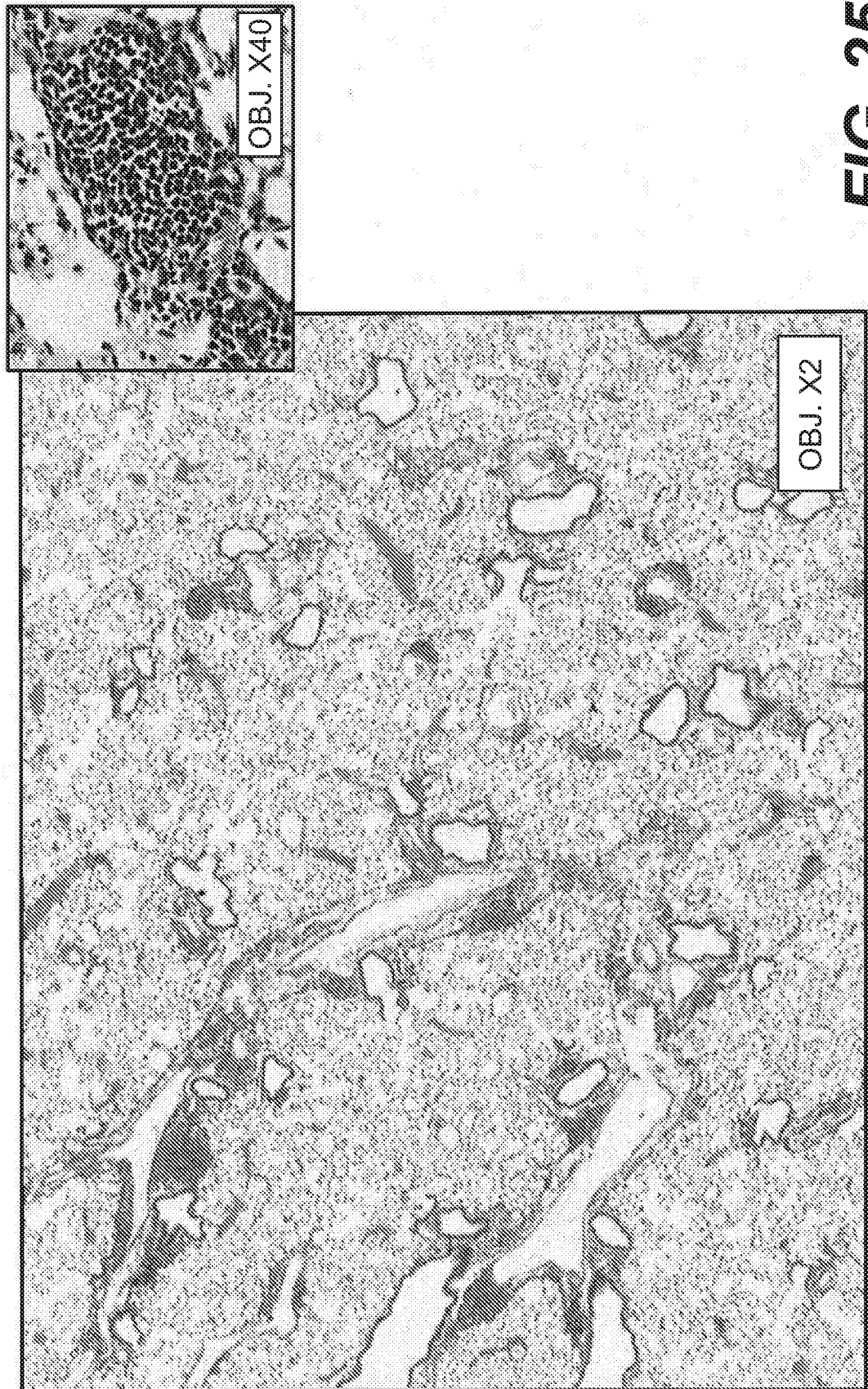


FIG. 24

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EFFECT OF THE TETRAVALENT PD/PEP1IA/ UspA2/ AS01E VACCINE FORMULATION ON MOUSE LUNGS
PRE-SENSITIZED WITH HEAT INACTIVATED M. cat. - PERIVASCULARITIS AND PERIBRONCHIOLITIS
IN PBS IMMUNIZED MICE.

**FIG. 25**

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EFFECT OF THE TETRAVALENT PD/ PEPIIA/ UspA2/ AS01E VACCINE FORMULATION ON MOUSE LUNGS PRE-SENSITIZED WITH HEAT INACTIVATED M. cat. - DAY 2 POST-IMMUNIZATION

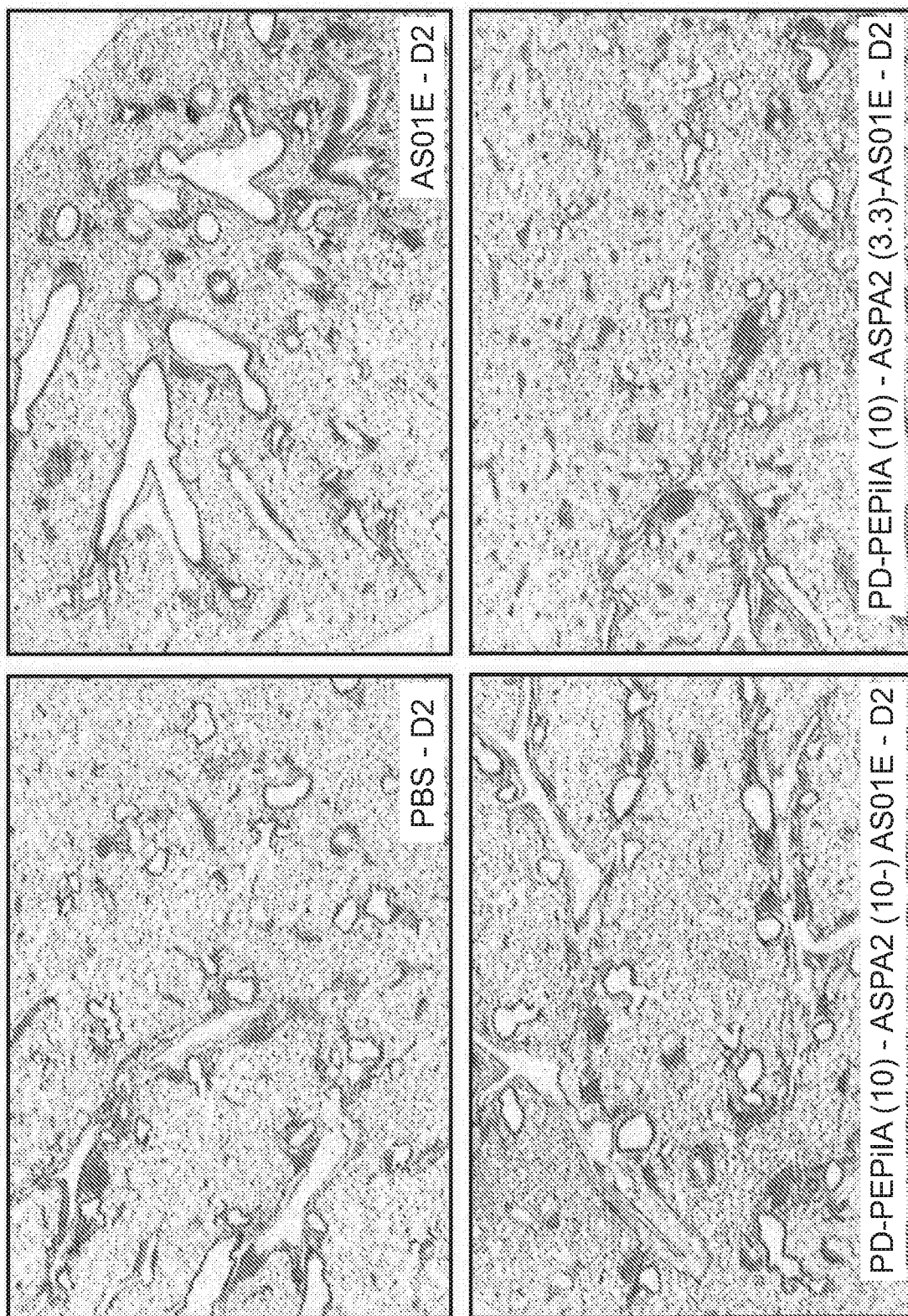
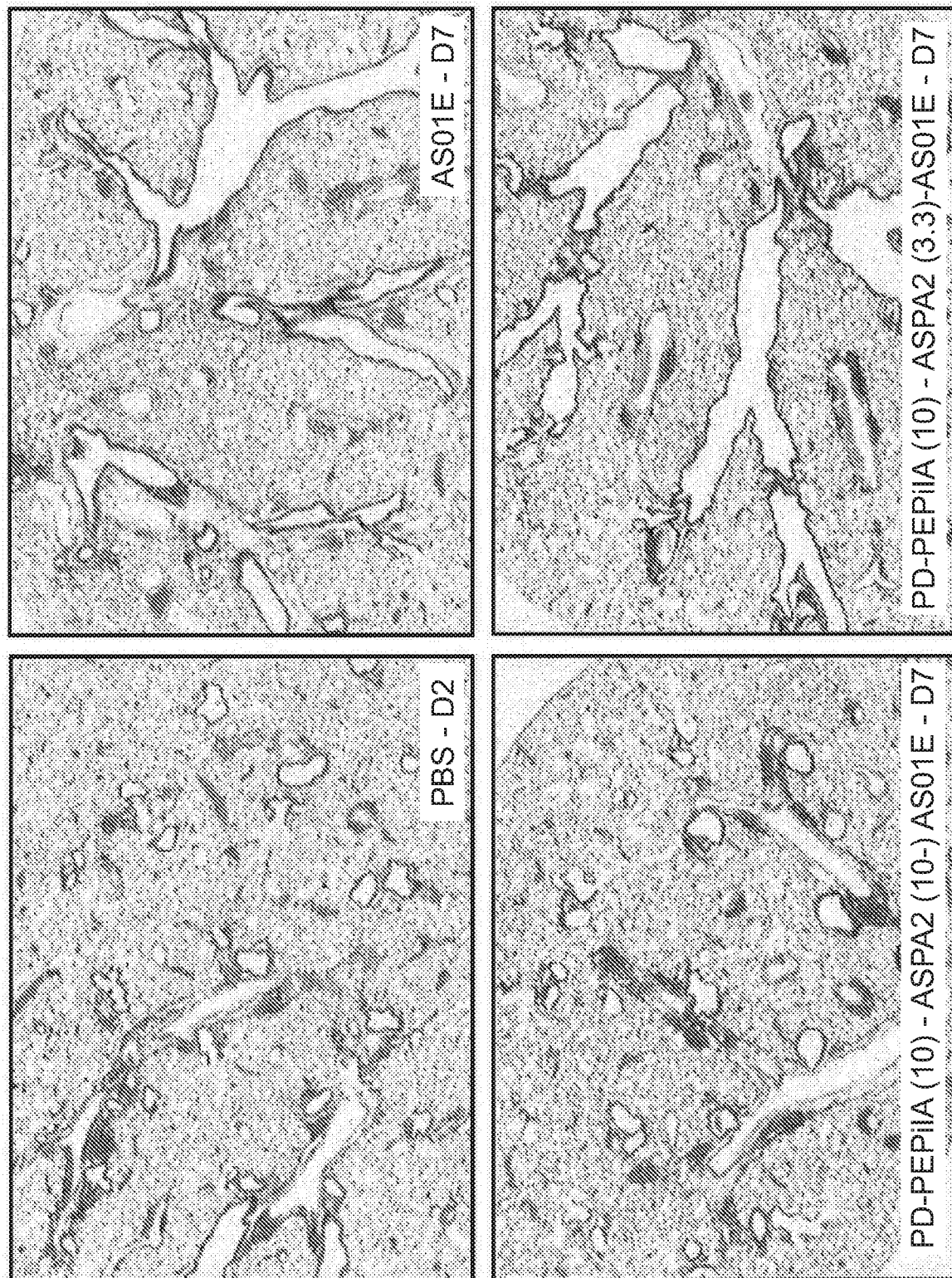


FIG. 26

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EFFECT OF THE TETRAVALENT PD/PEPIA/ UspA2/ AS01E VACCINE FORMULATION ON MOUSE LUNGS PRE-SENSITIZED WITH HEAT INACTIVATED M. cat. - DAY 7 POST-IMMUNIZATION

**FIG. 27**

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EFFECT OF THE TETRAVALENT PD/ PEPiIA/ UspA2/ AS01E VACCINE FORMULATION ON MOUSE LUNGS PRE-SENSITIZED WITH HEAT INACTIVATED M. cat. - DAY 14 POST-IMMUNIZATION

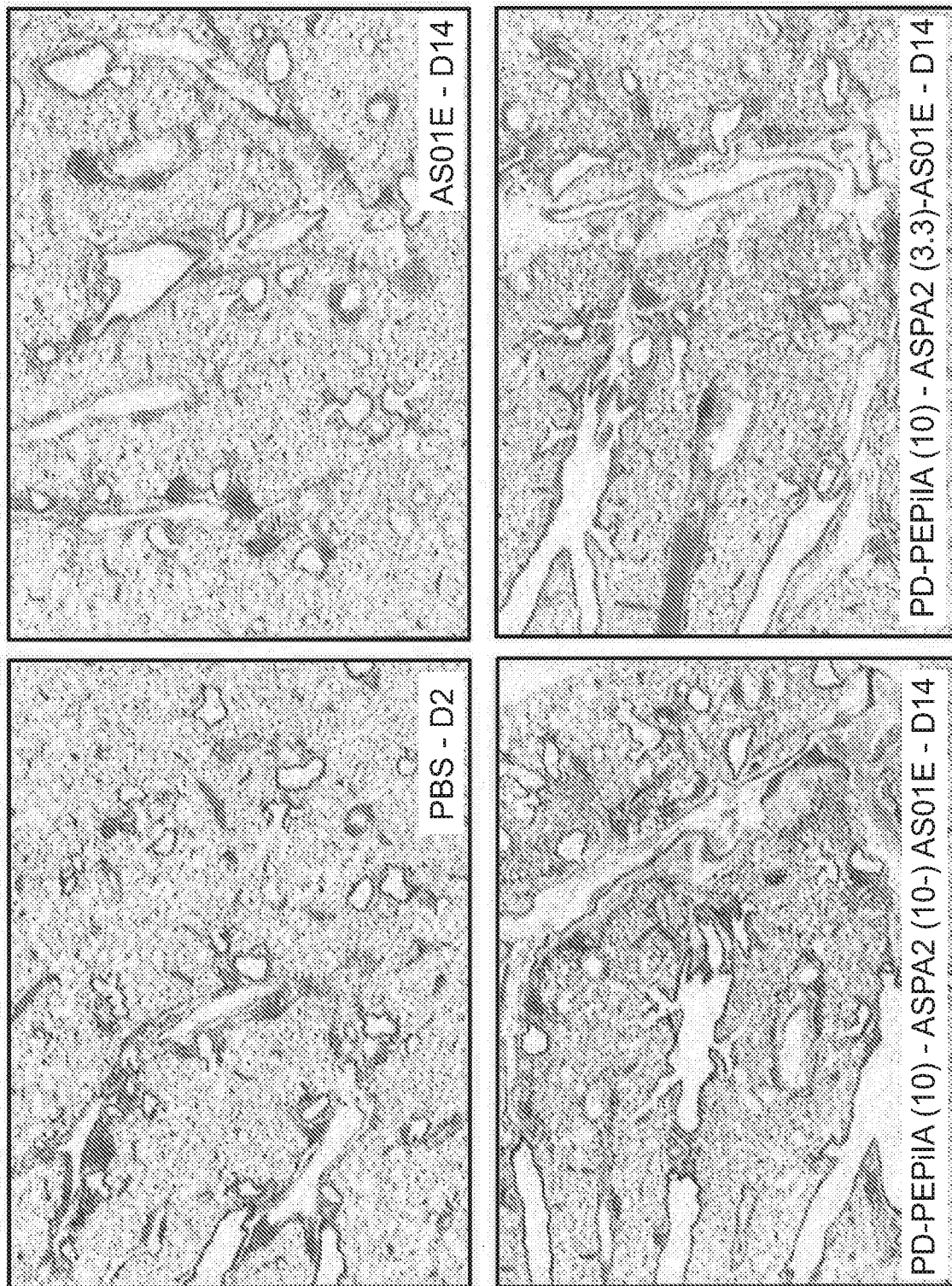


FIG. 28

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FIG. 29

EFFECT OF THE TETRAVALENT PD/PEPIIA/USPA2/AS01E VACCINE FORMULATION ON MOUSE LUNGS PRE-SENSITIZED WITH HEAT INACTIVATED M. cat. - DETAILED RESULTS

		PERIVASCULITIS/PERIBRONCHIOLITIS				
	AN. #	1	2	3	4	5
D2	PBS	3F L+M	3D L+M	3D L+M	3D L+M	A
	PD:PE-PiIA- USPA2 (10)	2D L+M	2-3D L+M	3D L+M	2-3D L+M	3D L+M
	PD:PE-PiIA- USPA2 (3.3)	2-3D L+M	2-3D L+M	2-3D L+M	3D L+M	3D L+M
	AS01E-3	3D L+M	2-3D L+M	2-3D L+M	2D L+M	3D L+M
D7	PD:PE-PiIA- USPA2 (10)	2-3D L+M	3D L+M	3D L+M	2-3D L+M	2-3D L+M
	PD:PE-PiIA- USPA2 (3.3)	3D L+M	2-3D L+M	2-3D L+M	2-3D L+M	2-3D L+M
	AS01E-3	3D L+M	2-3D L+M	2-3D L+M	2-3D L+M	2-3D L+M
	PD:PE-PiIA- USPA2 (10)	2D L+M	2-3D L+M	2-3D L+M	2-3D L+M	A
D14	PD:PE-PiIA- USPA2 (3.3)	2-3D L+M	2D L+M	2-3D L+M	2-3D L+M	A
	AS01E-3	2D L+M	2-3D L+M	2-3D L+M	2-3D L+M	2D L+M

LEGEND:

- THE FIRST LINE IN EACH BOX GIVES INFORMATION ABOUT THE INFLAMMATION SEVERITY: A = ABSENT; 1 = MINIMAL; 2 = SLIGHT; 3 = MODERATE; 4 = MARKED; 5 = SEVERE, AND THE ALTERATION DISTRIBUTION: F = FOCAL; M = MULTIFOCAL; D = DIFFUSE.
- THE SECOND LINE REFERS TO THE NATURE OF THE CELLS OBSERVED: L = LYMPHOCYTES; M = MACROPHAGES.

POST-VACCINATION LUNG CD4 T CELL RESPONSES UPON M. cat. WC RE-STIMULATION: LUNG CD4 CELLS EXPRESSING IL17. RESTIMULATED WITH HEAT-INACTIVATED M. cat. WHOLE CELLS (WC) OR MEDIUM.

20140268

LUNG CD4 CELLS EXPRESSING IL-17 STIM MEDIUM VS WC
DAYS 7 & 14 POST-VACCINATION

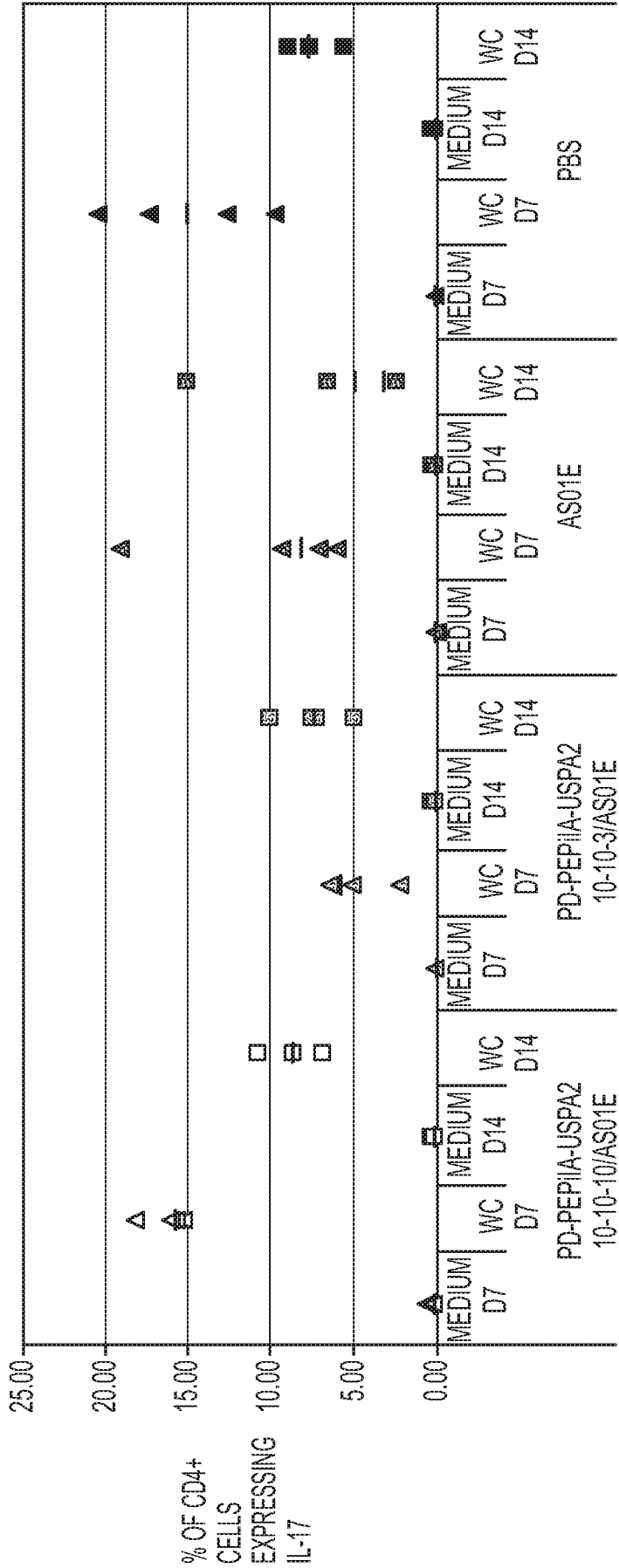


FIG. 30

POST-VACCINATION LUNG CD4 T CELL RESPONSES UPON M. cat. WC RE-STIMULATION. LUNG CD4 CELLS EXPRESSING TNF α . RESTIMULATED WITH HEAT-INACTIVATED M. cat. WHOLE CELLS (WC) OR MEDIUM.

20140268

LUNG CD4 CELLS EXPRESSING TNF α STIM MEDIUM VS WC
DAYS 7 & 14 POST-VACCINATION

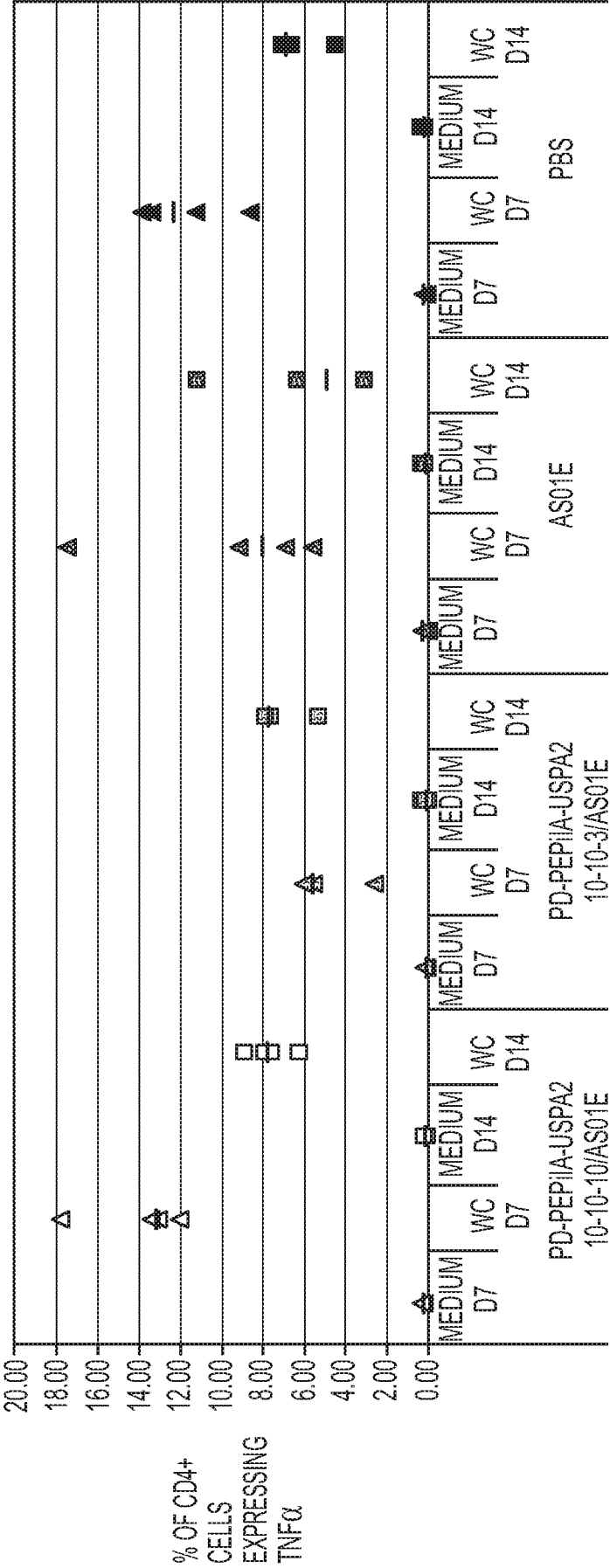


FIG. 31

POST-VACCINATION LUNG CD4 T CELL RESPONSES UPON M. cat. WC RE-STIMULATION. LUNG CD4 CELLS EXPRESSING INF γ . RESTIMULATED WITH HEAT-INACTIVATED M. cat. WHOLE CELLS (WC) OR MEDIUM.

20140268

LUNG CD4 CELLS EXPRESSING INF γ STIM MEDIUM VS WC
DAYS 7 & 14 POST-VACCINATION

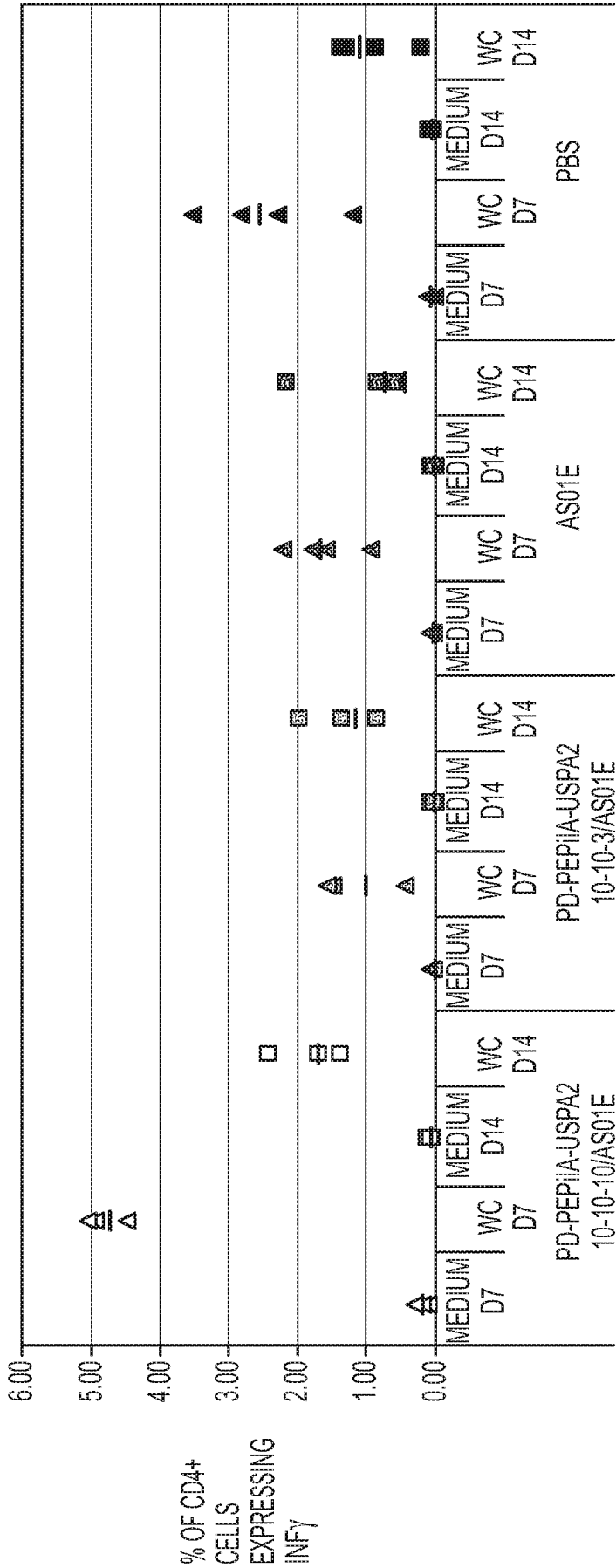


FIG. 32

POST-VACCINATION LUNG CD4 T CELL RESPONSES UPON M. cat. WC RE-STIMULATION. LUNG CD4 CELLS EXPRESSING IL-13. RESTIMULATED WITH HEAT-INACTIVATED M. cat. WHOLE CELLS (WC) OR MEDIUM.

20140268

LUNG CD4 CELLS EXPRESSING IL-13 STIM MEDIUM VS WC
DAYS 7 & 14 POST-VACCINATION

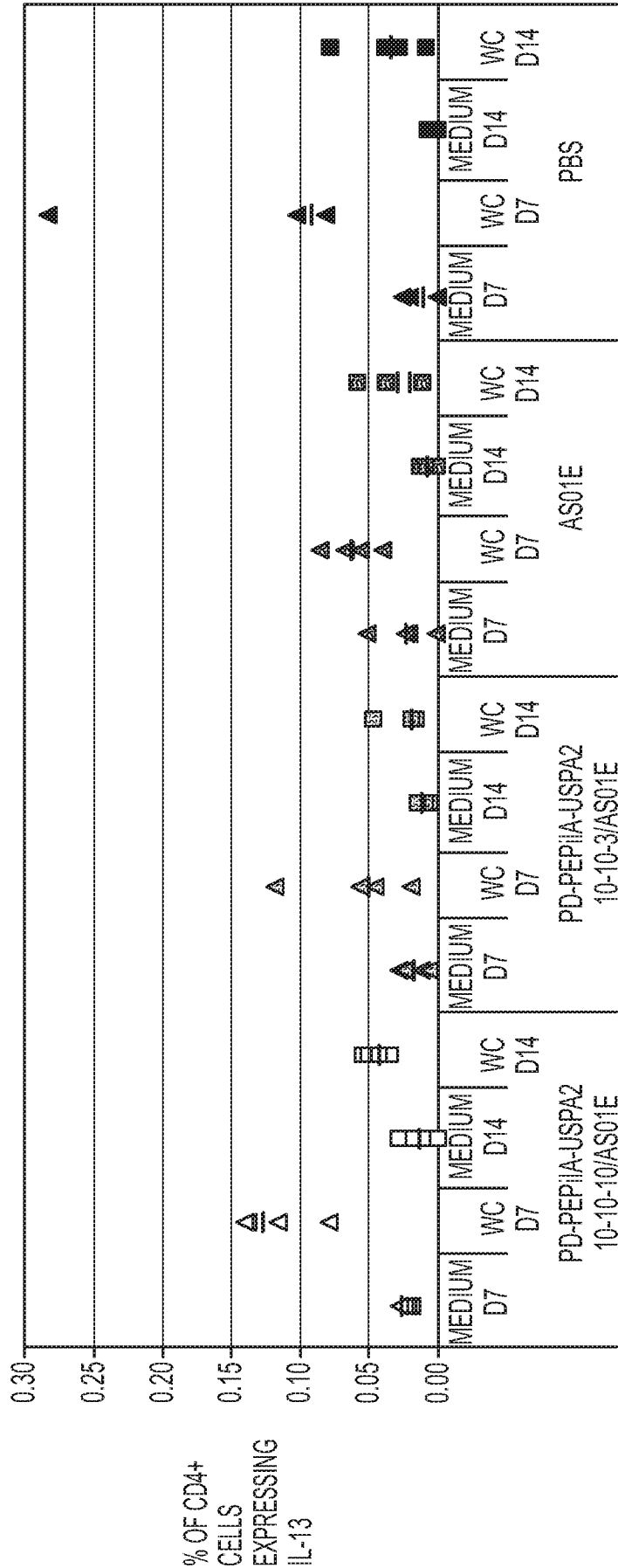


FIG. 33

POST-CHALLENGE LUNG CD4 T CELL RESPONSES UPON M. cat. WC RE-STIMULATION. LUNG CD4
CELLS EXPRESSING INF γ . RESTIMULATED WITH HEAT-INACTIVATED M. cat. WHOLE CELLS (WC) OR MEDIUM.

20140416

LUNG CD4 CELLS EXPRESSING INF γ STIM MEDIUM VS WC
DAYS 7 & 14 POST-CHALLENGE

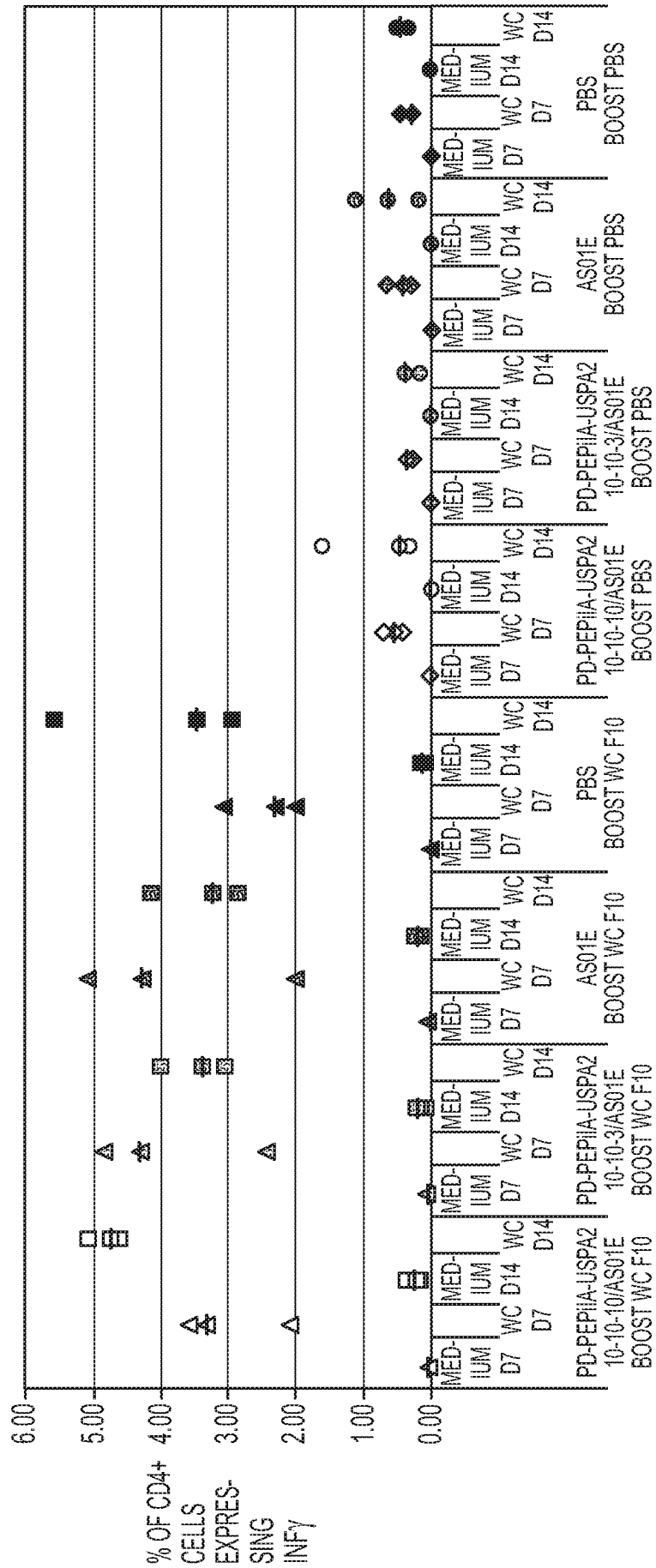


FIG. 36

POST-CHALLENGE LUNG CD4 T CELL RESPONSES UPON M. cat. WC RE-STIMULATION. LUNG CD4 CELLS EXPRESSING IL-13. RESTIMULATED WITH HEAT-INACTIVATED M. cat. WHOLE CELLS (WC) OR MEDIUM.

20140416

LUNG CD4 CELLS EXPRESSING IL-13 STIM MEDIUM VS WC
DAYS 7 & 14 POST-CHALLENGE

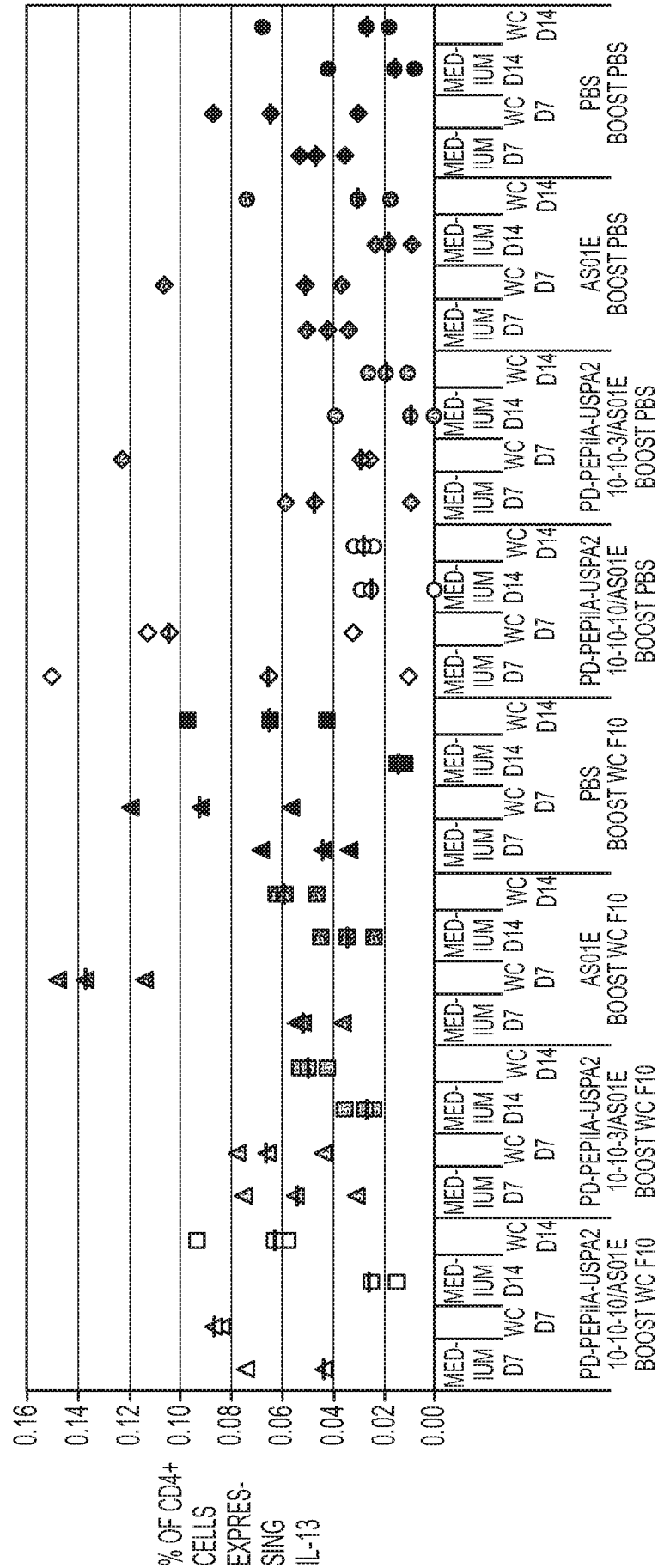


FIG. 37

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

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

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

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Page 3

35

40

45

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 100 105 110

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

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

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

Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 245 250 255

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

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

Leu Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser
 290 295 300

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln

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Lys Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
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Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
                340                345                350
Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
                355                360                365
Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
                370                375                380
Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
385                390                395                400
Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn 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 Asn Arg Ile Ala Thr Ala Glu Leu
                435                440                445
Gly Ile Ala Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala
                450                455                460
Asn Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr
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Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
                485                490                495
Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
                500                505                510
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                515                520                525
Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala
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Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe
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Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala
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Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly

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Val Asn Tyr Glu Phe
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Asp Leu Thr Asp Pro Phe Tyr His Asn Met Ile Leu Gly Asp Thr Ala
 50 55 60

Leu Leu Asp Lys Gln Asp Gly Ser Gln Pro Gln Leu Lys Phe Tyr Ser
 65 70 75 80

Asn Asp Lys Asp Ser Val Pro Asp Ser Leu Leu Phe Ser Lys Leu Leu
 85 90 95

His Glu Gln Gln Leu Asn Gly Phe Lys Lys Gly Asp Thr Ile Ile Pro
 100 105 110

Leu Asp Lys Asp Gly Lys Pro Val Tyr Gln Val Asp Tyr Lys Leu Asp
 115 120 125

Gly Lys Gly Lys Lys Gln Lys Arg Arg Gln Val Tyr Ser Val Thr Thr
 130 135 140

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

Leu Gly Lys Val Asp Asp Leu Asp Asp Glu Met Asn Phe Leu Asn His
 165 170 175

Asp Ile Thr Ser Leu Tyr Asp Val Thr Ala Asn Gln Gln Asp Ala Ile
 180 185 190

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

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Leu Asp Lys Glu Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu Asn
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 Asp Asp Val Ala Gln Asn Asn Glu Ser Ile Glu Asp Leu Tyr Asp Phe
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 Ser Gln Glu Val Ala Asp Ser Ile Gly Glu Ile His Ala His Asn Lys
 245 250 255
 Ala Gln Asn Glu Thr Leu Gln Asp Leu Ile Thr Asn Ser Val Glu Asn
 260 265 270
 Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu Asn
 275 280 285
 Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln
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 Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Ser Asn Val Glu
 305 310 315 320
 Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp
 325 330 335
 Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln
 340 345 350
 Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
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 Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln
 370 375 380
 Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
 385 390 395 400
 Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 405 410 415
 Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile
 420 425 430
 Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 435 440 445
 Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala
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 Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn
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Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
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Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
515 520 525

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

Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly
545 550 555 560

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
565 570 575

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
580 585 590

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
595 600 605

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
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Asn Tyr Glu Phe

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His Tyr His Asn Val Val Val Gly Asp Thr Ser Ile Val Ser Asp Leu
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VR65032W0-seql-000001.txt

Gln Ser Asn Ser Asp Gln Leu Lys Phe Tyr Ser Asp Asp Glu Gly Leu
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Val Pro Asp Ser Leu Leu Phe Asn Lys Met Leu His Glu Gln Leu Leu
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Asn Gly Phe Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly
100 105 110

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

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

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

Asp Phe Asp His Gln Val Thr Glu Arg Leu Thr Gln His Gly Lys Thr
165 170 175

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

Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile Glu His Ile Tyr Glu Leu
195 200 205

Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Glu Ser
210 215 220

Asn Val Glu Lys Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln
225 230 235 240

Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Ser Asn Val Glu
245 250 255

Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp
260 265 270

Leu Thr Lys Asp Ile Lys Thr Leu Glu Ser Asn Val Glu Glu Gly Leu
275 280 285

Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln
290 295 300

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

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

Asn Thr Asn Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala Glu Asn Lys
420 425 430

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

Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala
450 455 460

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

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

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

Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly
515 520 525

Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu
530 535 540

Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg
545 550 555 560

Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser
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Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
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<212> PRT

<213> Moraxella catarrhalis

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35 40 45

Asn Ile Phe Phe Asn Glu Asn His Asp Glu Leu Asp Asp Ala Tyr His
50 55 60

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

Gln Pro Gln Leu Lys Phe Tyr Ser Asn Asp Lys Asp Ser Val Pro Asp
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Ser Leu Leu Phe Ser Lys Leu Leu His Glu Gln Gln Leu Asn Gly Phe
100 105 110

Lys Lys Gly Asp Thr Ile Ile Pro Leu Asp Lys Asp Gly Lys Pro Val
115 120 125

Tyr Gln Val Asp Tyr Lys Leu Asp Gly Lys Gly Lys Lys Gln Lys Arg
130 135 140

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

Asn Ser Ala Tyr Ser Arg Gly Ile Leu Gly Lys Val Asp Asp Leu Asp
165 170 175

Asp Glu Met Asn Phe Leu Asn His Asp Ile Thr Ser Leu Tyr Asp Val
180 185 190

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

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

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

Ser Ile Glu Asp Leu Tyr Asp Phe Ser Gln Glu Val Ala Asp Ser Ile
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Gly Glu Ile His Ala His Asn Lys Ala Gln Asn Glu Thr Leu Gln Asp
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Leu Ile Thr Asn Ser Val Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
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Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
290 295 300

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

Lys Thr Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
325 330 335

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

Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu
355 360 365

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

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

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

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

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
435 440 445

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

Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu
465 470 475 480

Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala
485 490 495

Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp
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Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile
515 520 525

VR65032W0-seq1-000001.txt

Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala
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Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala
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Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser
565 570 575

Ile Thr Asp Leu Gly Thr Lys Val Asp Ala Phe Asp Gly Arg Val Thr
580 585 590

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

Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly
610 615 620

Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu
625 630 635 640

Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg
645 650 655

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

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<211> 683
<212> PRT
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<400> 6

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Met Ile Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
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Lys Ser Pro Lys Thr Glu Thr Phe Leu Pro Asn Ile Phe Phe Asn Glu
35 40 45

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

Thr Ala Ile Thr His Asp Asp Gln Tyr Lys Phe Tyr Ala Asp Asp Ala
65 70 75 80

Thr Glu Val Pro Asp Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln
Page 13

Leu Leu Tyr Gly Phe Lys Glu Gly Asp Lys Ile Ile Pro Leu Asp Glu
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 Asn Gly Lys Pro Val Tyr Lys Leu Asp Lys Arg Leu Glu Asn Gly Val
 115 120 125
 Gln Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp Asp
 130 135 140
 Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu
 145 150 155 160
 Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp
 165 170 175
 Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu Val
 180 185 190
 Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln
 195 200 205
 His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp Leu
 210 215 220
 Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala Gln
 225 230 235 240
 Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp
 245 250 255
 Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 260 265 270
 Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile Lys
 275 280 285
 Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His
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 Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu
 305 310 315 320
 Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp
 325 330 335
 Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala
 340 345 350
 Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala

355

360

365

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

Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
 385 390 395 400

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

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
 420 425 430

Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 435 440 445

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

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 465 470 475 480

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

Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn
 500 505 510

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
 515 520 525

Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys
 530 535 540

Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
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Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe
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Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr
 580 585 590

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

Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro
 610 615 620

Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly

625 630 635 640
 Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn
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 35 40 45
 Asn Thr Glu Leu Thr Asp Pro Leu Tyr His Asn Met Ile Leu Gly Asn
 50 55 60
 Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
 65 70 75 80
 Gly Asn Gly Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp
 85 90 95
 Gln Leu Leu His Gly Phe Lys Glu Gly Gly Thr Ile Ile Pro Leu Asp
 100 105 110
 Glu Asn Gly Lys Pro Val Tyr Lys Leu Asp Ser Ile Val Glu Gln Gly
 115 120 125
 Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
 130 135 140
 Asp Val Asn Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
 145 150 155 160
 Leu Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly
 165 170 175
 Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
 180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
 195 200 205
 Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
 210 215 220
 Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
 225 230 235 240
 Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
 245 250 255
 Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
 260 265 270
 Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
 275 280 285
 Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
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 His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
 305 310 315 320
 Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
 325 330 335
 Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu
 340 345 350
 Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
 355 360 365
 Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
 370 375 380
 Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
 385 390 395 400
 Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
 405 410 415
 Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
 420 425 430
 Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
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 Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
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VR65032W0-seql-000001.txt

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
465 470 475 480

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

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
500 505 510

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
515 520 525

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
530 535 540

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
545 550 555 560

Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
565 570 575

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
580 585 590

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

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
645 650 655

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Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
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<210> 8
<211> 684
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<213> Moraxella catarrhalis

<400> 8

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20 25 30

Gln Lys Thr Lys Thr Glu Val Phe Leu Pro Asn Leu Phe Asp Asn Asp
35 40 45

Tyr Tyr Asp Leu Thr Asp Pro Leu Tyr His Ser Met Ile Leu Gly Asp
50 55 60

Thr Ala Thr Leu Phe Asp Gln Gln Asp Asn Ser Lys Ser Gln Leu Lys
65 70 75 80

Phe Tyr Ser Asn Asp Lys Asp Ser Val Pro Asp Ser Leu Leu Phe Ser
85 90 95

Lys Leu Leu His Glu Gln Gln Leu Asn Gly Phe Lys Ala Gly Asp Thr
100 105 110

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

Arg Thr Lys Asp Gly Lys Val Glu Thr Val Tyr Ser Val Thr Thr Lys
130 135 140

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

Gln Gly Asp Ile Asp Asp Leu Tyr Asp Ile Asn Arg Glu Val Asn Glu
165 170 175

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

Asp Ala Leu Asn Lys Ala Ser Ser Ala Asn Thr Asp Arg Ile Asp Thr
195 200 205

Ala Glu Glu Arg Ile Asp Lys Asn Glu Tyr Asp Ile Lys Ala Leu Glu
210 215 220

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

Gln Lys Glu Asp Ile Asp Asn Asn Ile Asn His Ile Tyr Glu Leu Ala
245 250 255

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Asn Asn
260 265 270

Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
275 280 285

VR65032W0-seql-000001.txt

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305 310 315 320

Thr Lys Asp Ile Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu
325 330 335

Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln Asn
340 345 350

Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln
355 360 365

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

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

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

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

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

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
450 455 460

Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
465 470 475 480

Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser
485 490 495

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

Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp
515 520 525

Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala
530 535 540

Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile
545 550 555 560

VR65032W0-seql-000001.txt

Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp
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Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp
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Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
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Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
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Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
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Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
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 165 170 175
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 Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
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 Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
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 Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
 290 295 300
 His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
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 Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
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 Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
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Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
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 Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
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 Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
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 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 465 470 475 480
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 580 585 590
 Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
 595 600 605
 Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
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 Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
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His Tyr His Asn Val Val Val Gly Asp Thr Ser Ile Val Glu Asn Leu
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Gln Asp Ser Asp Asp Thr Gln Leu Lys Phe Tyr Ser Asn Asp Glu Tyr
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Ser Val Pro Asp Ser Leu Leu Phe Asn Lys Met Leu His Glu Gln Gln
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Leu Asn Gly Phe Lys Lys Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn
100 105 110

Gly Lys Pro Val Tyr Lys Val Asp Tyr Lys Leu Asp Gly Gln Glu Pro
115 120 125

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

Asp Asn Ser Pro Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp Leu
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Tyr Glu Ala Asn Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp
165 170 175

Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val
180 185 190

Gln Asn Asn Ile Glu Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
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His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu
Page 24

210

215

220

Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys
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490

495

Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu
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 515 520 525

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Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
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Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
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Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu
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Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala
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Gln Leu Asn Gly Phe Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu
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Asn Gly Lys Pro Val Tyr Lys Leu Asp Glu Lys Val Glu Asn Gly Val
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Lys Lys Ser Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Arg Ala Asp
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Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp Ile Asp Asp
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610 615 620

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<400> 13

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Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
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Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly
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Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn
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<400> 14

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Page 33

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 Asp Arg Leu Ile Ala Gln Asn Gln Ala Asp Ile Lys Thr Leu Glu Asn
 130 135 140
 Asn Val Val Glu Glu Leu Phe Asn Leu Ser Asp Arg Leu Ile Asp Gln
 145 150 155 160
 Glu Ala Asp Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp
 165 170 175
 Phe Asp Asn Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr
 180 185 190
 Glu Glu Val Asn Lys Thr Leu Glu Lys Leu Ile Thr Asn Ser Val Lys
 195 200 205
 Asn Thr Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu
 210 215 220
 Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp
 225 230 235 240
 Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val
 245 250 255
 Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala
 260 265 270
 Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile
 275 280 285
 Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
 290 295 300
 Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
 305 310 315 320
 Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
 325 330 335
 Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
 340 345 350
 Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
 355 360 365
 Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
 370 375 380

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

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

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr
420 425 430

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

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
450 455 460

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
465 470 475 480

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

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

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

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

Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val
545 550 555 560

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

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

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

Asn Ile Gly Val Asn Tyr Glu Phe
610 615

<210> 16
<211> 676
<212> PRT
<213> Moraxella catarrhalis

<400> 16

VR65032W0-seql-000001.txt

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Thr Glu Thr Thr
35 40 45

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

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Gln Leu Asn Gly Phe
85 90 95

Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly Lys Pro Val
100 105 110

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

Ser Val Thr Thr Lys Thr Ala Thr Arg Glu Asp Val Glu Gln Ser Ala
130 135 140

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

Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp Lys Ile Phe Ala
165 170 175

Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile
180 185 190

Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
195 200 205

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

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

Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp 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

VR65032W0-seql-000001.txt

Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
 275 280 285
 Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr
 290 295 300
 Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 305 310 315 320
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 325 330 335
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 340 345 350
 Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 355 360 365
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 370 375 380
 Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
 385 390 395 400
 Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
 405 410 415
 Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
 420 425 430
 Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
 435 440 445
 Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
 450 455 460
 Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
 465 470 475 480
 Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp
 485 490 495
 Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
 500 505 510
 Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp
 515 520 525
 Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala
 530 535 540

VR65032W0-seql-000001.txt

Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr
545 550 555 560

Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu
565 570 575

Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly
580 585 590

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
595 600 605

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
610 615 620

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
625 630 635 640

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
645 650 655

Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val
660 665 670

Asn Tyr Glu Phe
675

<210> 17
<211> 629
<212> PRT
<213> Moraxella catarrhalis

<400> 17

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Asn Gly
20 25 30

Thr Ser Thr Lys Leu Lys Asn Leu Lys Glu Tyr Ala Gln Tyr Leu Asp
35 40 45

Asn Tyr Ala Gln Tyr Leu Asp Asp Asp Ile Asp Asp Leu Asp Lys Glu
50 55 60

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

Asp Leu Asn Lys Lys Leu Ser Arg Asp Ile Asp Ser Leu Arg Glu Asp
85 90 95

VR65032W0-seq1-000001.txt

Val Tyr Asp Asn₁₀₀ Gln Tyr Glu Ile Val₁₀₅ Asn Asn Gln Ala Asp₁₁₀ Ile Glu
 Lys Asn Gln₁₁₅ Asp Asp Ile Lys Glu₁₂₀ Leu Glu Asn Asn Val₁₂₅ Gly Lys Glu
 Leu Leu₁₃₀ Asn Leu Ser Gly Arg₁₃₅ Leu Leu Asp Gln Lys₁₄₀ Ala Asp Ile Asp
 Asn₁₄₅ Asn Ile Asn Asn Ile₁₅₀ Tyr Glu Leu Ala Gln₁₅₅ Gln Gln Asp Gln His₁₆₀
 Ser Ser Asp Ile Lys₁₆₅ Thr Leu Lys Lys Asn₁₇₀ Val Glu Glu Gly Leu₁₇₅ Leu
 Glu Leu Ser Gly₁₈₀ His Leu Ile Asp Gln₁₈₅ Lys Ser Asp Ile Ala₁₉₀ Gln Asn
 Gln Thr Asp₁₉₅ Ile Gln Asp Leu Ala₂₀₀ Thr Tyr Asn Glu Leu₂₀₅ Gln Asp Gln
 Tyr Ala₂₁₀ Gln Lys Gln Thr Glu₂₁₅ Ala Ile Asp Ala Leu₂₂₀ Asn Lys Ala Ser
 Ser₂₂₅ Glu Asn Thr Gln Asn₂₃₀ Ile Glu Asp Leu Ala₂₃₅ Ala Tyr Asn Glu Leu₂₄₀
 Gln Asp Ala Tyr Ala₂₄₅ Lys Gln Gln Thr Glu₂₅₀ Ala Ile Asp Ala Leu₂₅₅ Asn
 Lys Ala Ser Ser₂₆₀ Glu Asn Thr Gln Asn₂₆₅ Ile Gln Asp Leu Ala₂₇₀ Ala Tyr
 Asn Glu Leu₂₇₅ Gln Asp Ala Tyr Ala₂₈₀ Lys Gln Gln Thr Glu₂₈₅ Ala Ile Asp
 Ala Leu₂₉₀ Asn Lys Ala Ser Ser₂₉₅ Glu Asn Thr Gln Asn₃₀₀ Ile Glu Asp Leu
 Ala₃₀₅ Ala Tyr Asn Glu Leu₃₁₀ Gln Asp Ala Tyr Ala₃₁₅ Lys Gln Gln Thr Glu₃₂₀
 Ala Ile Asp Ala Leu₃₂₅ Asn Lys Ala Ser Ser₃₃₀ Glu Asn Thr Gln Asn₃₃₅ Ile
 Glu Asp Leu Ala₃₄₀ Ala Tyr Asn Glu Leu₃₄₅ Gln Asp Ala Tyr Ala₃₅₀ Lys Gln
 Gln Thr Glu₃₅₅ Ala Ile Asp Ala Leu₃₆₀ Asn Lys Ala Ser Ser₃₆₅ Glu Asn Thr

VR65032W0-seq1-000001.txt

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

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

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

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
420 425 430

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

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

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

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

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

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

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

Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala
545 550 555 560

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

Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala
580 585 590

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

Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly
610 615 620

Val Asn Tyr Glu Phe
625

<210> 18
 <211> 683
 <212> PRT
 <213> Moraxella catarrhalis

<400> 18

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

Met Ile Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30

Arg Ser Pro Lys Thr Glu Thr Phe Leu Pro Asn Ile Phe Phe Asn Glu
 35 40 45

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

Thr Ala Ile Thr His Asp Asp Gln Tyr Lys Phe Tyr Ala Asp Asp Ala
 65 70 75 80

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

Leu Leu Tyr Gly Phe Lys Glu Gly Asp Lys Ile Ile Pro Leu Asp Glu
 100 105 110

Asn Gly Lys Pro Val Tyr Lys Leu Asp Lys Arg Leu Asp Asn Gly Val
 115 120 125

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

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

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

Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val
 180 185 190

Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln
 195 200 205

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

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

Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp

245

250

255

Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 260 265 270

Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn Arg Ile Lys
 275 280 285

Ala Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His
 290 295 300

Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu
 305 310 315 320

Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp
 325 330 335

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

Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala
 355 360 365

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

Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln
 385 390 395 400

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

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
 420 425 430

Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 435 440 445

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

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 465 470 475 480

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

Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn
 500 505 510

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr

515

520

525

Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys
 530 535 540

Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr
 545 550 555 560

Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe
 565 570 575

Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr
 580 585 590

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

Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro
 610 615 620

Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly
 625 630 635 640

Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn
 645 650 655

Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys
 660 665 670

Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 675 680

<210> 19

<211> 700

<212> PRT

<213> Moraxella catarrhalis

<400> 19

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

Met Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Gln
 20 25 30

Ser Asn Arg Ser Leu Asp Gln Val Gln Ala Leu Leu Arg Gly Ile Asp
 35 40 45

Glu Thr Lys Ile Lys Lys Glu Ile Gln Gln Ser Gln Gln Pro Glu Leu
 50 55 60

Asn Lys Tyr Leu Thr Phe Asn Gln Leu Ala Asn Ala Leu Asn Ile Glu
 65 70 75 80

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

Ala Thr Leu Tyr Gly Asp Leu Ser Lys Thr Val Pro Lys Ser Ile Lys
100 105 110

Glu Asn Lys Glu Ser Ile Lys Glu Asn Lys Glu Ser Ile Lys Glu Asn
115 120 125

Lys Glu Ser Ile Lys Glu Asn Lys Glu Ser Ile Lys Glu Asn Lys Glu
130 135 140

Ser Ile Lys Glu Asn Lys Glu Ser Ile Thr Thr Leu Thr Arg Lys Ser
145 150 155 160

Phe Gln Asn Gln Val Asp Ile Val Arg Asn Asn Ala Ser Ile Glu Asp
165 170 175

Leu Tyr Ala Tyr Gly Gln Glu Val Ala Lys Ser Ile Gly Glu Ile His
180 185 190

Ala Tyr Thr Glu Glu Val Asn Lys Thr Leu Glu Asn Leu Ile Thr Asn
195 200 205

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

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

Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr
245 250 255

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

Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile
275 280 285

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

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

Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr
325 330 335

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

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu
 355 360 365
 Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
 370 375 380
 Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
 385 390 395 400
 Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
 405 410 415
 Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
 420 425 430
 Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
 435 440 445
 Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
 450 455 460
 Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn
 465 470 475 480
 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 485 490 495
 Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile
 500 505 510
 Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
 515 520 525
 Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
 530 535 540
 Thr Ala Asn Lys Thr Val Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
 545 550 555 560
 Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
 565 570 575
 Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
 580 585 590
 Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
 595 600 605
 Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
 610 615 620

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Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
625 630 635 640

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
645 650 655

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
660 665 670

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
675 680 685

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
690 695 700

<210> 20
<211> 676
<212> PRT
<213> Moraxella catarrhalis
<400> 20

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Ile Glu Thr Thr
35 40 45

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

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Gln Leu Asn Gly Phe
85 90 95

Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly Lys Pro Val
100 105 110

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

Ser Val Thr Thr Lys Thr Ala Thr Arg Glu Asp Val Glu Gln Ser Ala
130 135 140

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

VR65032W0-seql-000001.txt

Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp Lys Ile Phe Ala
 165 170 175
 Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile
 180 185 190
 Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 195 200 205
 Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 210 215 220
 Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr
 225 230 235 240
 Leu Glu 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 Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr
 290 295 300
 Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 305 310 315 320
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 325 330 335
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 340 345 350
 Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 355 360 365
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 370 375 380
 Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
 385 390 395 400
 Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
 405 410 415
 Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
 420 425 430

VR65032W0-seql-000001.txt

Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
435 440 445

Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
450 455 460

Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
465 470 475 480

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

Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
500 505 510

Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp
515 520 525

Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala
530 535 540

Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr
545 550 555 560

Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu
565 570 575

Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly
580 585 590

Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln
595 600 605

Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn
610 615 620

Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile
625 630 635 640

Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala
645 650 655

Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val
660 665 670

Asn Tyr Glu Phe
675

<210> 21
<211> 678
<212> PRT

<213> Moraxella catarrhalis

<400> 21

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Leu Ala
20 25 30

Glu Gln Phe Phe Pro Asn Ile Phe Ser Asn His Ala Pro Val Lys Gln
35 40 45

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

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

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

Leu Asn Gly Phe Lys Lys Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn
100 105 110

Gly Lys Pro Val Tyr Lys Val Asp Tyr Lys Leu Asp Gly Gln Glu Pro
115 120 125

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

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

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

Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val
180 185 190

Gln Asn Asn Ile Glu Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
195 200 205

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

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

Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
245 250 255

VR65032W0-seq1-000001.txt

Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
260 265 270

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
275 280 285

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
290 295 300

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

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

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

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
355 360 365

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

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

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

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
420 425 430

Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
435 440 445

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

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
465 470 475 480

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

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
500 505 510

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
515 520 525

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Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
530 535 540

Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
545 550 555 560

Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp
565 570 575

Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe
580 585 590

Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala
595 600 605

Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys
610 615 620

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
625 630 635 640

Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala
645 650 655

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
660 665 670

Gly Val Asn Tyr Glu Phe
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<210> 22
<211> 613
<212> PRT
<213> Moraxella catarrhalis

<400> 22

Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg
20 25 30

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

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

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

Asn Asn Val Ile Lys Asn Thr Asn Ser Ile Glu Ala Leu Gly Asp Glu

Ile Gly Trp Leu Glu Asn Asp Ile Ala Asp Leu Glu Glu Gly Val Glu
 100 105 110
 Glu Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Glu Glu His
 115 120 125
 Asp Arg Leu Ile Ala Gln Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn
 130 135 140
 Asn Val Val Glu Glu Leu Phe Asn Leu Ser Gly Arg Leu Ile Asp Gln
 145 150 155 160
 Glu Ala Asp Ile Ala Lys Asn Asn Ala Ser Ile Glu Glu Leu Tyr Asp
 165 170 175
 Phe Asp Asn Glu Val Ala Glu Arg Ile Gly Glu Ile His Ala Tyr Thr
 180 185 190
 Glu Glu Val Asn Lys Thr Leu Glu Asn Leu Ile Thr Asn Ser Val Lys
 195 200 205
 Asn Thr Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile
 210 215 220
 Asn His Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 225 230 235 240
 Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 245 250 255
 Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala
 260 265 270
 Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu
 275 280 285
 Leu Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser
 290 295 300
 Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln
 305 310 315 320
 Lys Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
 325 330 335
 Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
 340 345 350
 Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp

355

360

365

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

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

Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn 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 Asn Arg Ile Ala Thr Ala Glu Leu
 435 440 445

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

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

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

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

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

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

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

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

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

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

Val Asn Tyr Glu Phe
 610

<210> 23

<211> 589

<212> PRT

<213> Moraxella catarrhalis

<400> 23

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

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

Asp Pro Tyr Glu Leu Arg Asp Tyr Ile Glu Tyr Pro Thr Ala Ile Glu
50 55 60

Arg Phe Leu Leu Leu Ser Gln Tyr Gly Asn Thr Leu Thr Leu Glu Glu
65 70 75 80

Phe Asp Asn Asp Ile Glu Leu Leu Asp Gln Asp Val Glu Asp Leu Glu
85 90 95

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

Gly Glu Ala Ile Lys Glu Asp Leu Gln Gly Leu Ala Asp Phe Val Glu
115 120 125

Arg Gln Glu Asp Lys Ile Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn
130 135 140

Thr Gln Arg Asn Leu Val Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp
145 150 155 160

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

His Glu Val Ala Lys Ser Ile Gly Glu Ile His Ala His Asn Glu Ala
180 185 190

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

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

Val Glu Lys Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
225 230 235 240

Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile His Glu Leu Ala Gln Gln
245 250 255

Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu
 260 265 270
 Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ser Asp
 275 280 285
 Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu
 290 295 300
 Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
 305 310 315 320
 Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
 325 330 335
 Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
 340 345 350
 Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
 355 360 365
 Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
 370 375 380
 Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
 385 390 395 400
 Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp
 405 410 415
 Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys
 420 425 430
 Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp
 435 440 445
 Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala
 450 455 460
 Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr
 465 470 475 480
 Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu
 485 490 495
 Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser
 500 505 510
 Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe
 515 520 525

Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly
530 535 540

Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn
545 550 555 560

Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn
565 570 575

Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
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<210> 24
<211> 684
<212> PRT
<213> Moraxella catarrhalis

<400> 24

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

Met Met Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
20 25 30

Lys Ser Pro Lys Thr Glu Ile Phe Leu Pro Asn Leu Phe Asp Asn Asp
35 40 45

Asn Thr Glu Leu Thr Asp Pro Leu Tyr His Asn Met Ile Leu Gly Asn
50 55 60

Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
65 70 75 80

Gly Asn Gly Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp
85 90 95

Gln Leu Leu His Gly Phe Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp
100 105 110

Glu Asn Gly Lys Pro Val Tyr Lys Leu Asp Ser Ile Val Glu Gln Gly
115 120 125

Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
130 135 140

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

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

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Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
 180 185 190
 Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
 195 200 205
 Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
 210 215 220
 Leu Leu Asp Leu Ser Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala
 225 230 235 240
 Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
 245 250 255
 Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
 260 265 270
 Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
 275 280 285
 Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
 290 295 300
 His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
 305 310 315 320
 Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
 325 330 335
 Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn Ile Gln Asp Leu
 340 345 350
 Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
 355 360 365
 Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
 370 375 380
 Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
 385 390 395 400
 Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
 405 410 415
 Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
 420 425 430
 Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
 435 440 445

VR65032W0-seql-000001.txt

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

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
465 470 475 480

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

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
500 505 510

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
515 520 525

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
530 535 540

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
545 550 555 560

Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
565 570 575

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
580 585 590

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

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
645 650 655

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
660 665 670

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680

<210> 25
<211> 650
<212> PRT
<213> Moraxella catarrhalis
<400> 25

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Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
 1 5 10 15
 Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30
 Gln Lys Thr Lys Thr Glu Val Phe Leu Pro Asn Leu Phe Tyr Asn Asp
 35 40 45
 Tyr Ile Glu Glu Thr Asp Leu Leu Tyr His Asn Met Ile Leu Gly Asp
 50 55 60
 Thr Ala Ala Leu Val Asp Arg Gln Asn Tyr Ser Asn Ser Gln Leu Lys
 65 70 75 80
 Phe Tyr Ser Asn Asp Glu Glu Ser Val Pro Asp Ser Leu Leu Phe Ser
 85 90 95
 Lys Met Leu Asn Asn Gln Gln Leu Asn Gly Phe Lys Ala Gly Asp Ile
 100 105 110
 Ile Ile Pro Val Asp Ala Asn Gly Gln Val Ile Tyr Gln Lys Asp Thr
 115 120 125
 Arg Val Glu Gly Gly Lys Thr Arg Thr Val Leu Ser Val Thr Thr Lys
 130 135 140
 Ile Ala Thr Gln Gln Asp Val Asp Ser Ala Tyr Ser Arg Gly Ile Gln
 145 150 155 160
 Gly Lys Val Asn Asp Leu Asp Asp Glu Met Asn Phe Leu Asn His Asp
 165 170 175
 Ile Thr Ser Leu Tyr Asp Val Thr Ala Asn Gln Gln Asp Asp Ile Lys
 180 185 190
 Gly Leu Lys Lys Gly Val Lys Asp Leu Lys Lys Gly Val Lys Gly Leu
 195 200 205
 Asn Lys Glu Leu Lys Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg
 210 215 220
 Asp Ile Gly Ser Leu Asn Asp Asp Val Ala Gln Asn Asn Glu Ser Ile
 225 230 235 240
 Glu Asp Leu Tyr Asp Phe Ser Gln Glu Val Ala Asp Ser Ile Gly Glu
 245 250 255
 Ile His Ala His Asn Lys Ala Gln Asn Glu Thr Leu Gln Asp Leu Ile
 260 265 270

VR65032W0-seq1-000001.txt

Thr Asn Ser Val Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp
275 280 285

Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu Ser
290 295 300

Gly Arg Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr
305 310 315 320

Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu
325 330 335

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

Asn Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
355 360 365

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

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

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

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
420 425 430

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

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

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

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

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Glu Asn Lys
500 505 510

Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys
515 520 525

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

Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys
545 550 555 560

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

Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr
580 585 590

Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser
595 600 605

Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu
610 615 620

Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly
625 630 635 640

Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
645 650

<210> 26
<211> 616
<212> PRT
<213> Moraxella catarrhalis

<400> 26

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

Leu Ile Val Gly Leu Gly Ala Val Ser Thr Thr Asn Ala Gln Ala Gln
20 25 30

Ser Arg Ser Leu Asp Gln Ile Gln Thr Lys Leu Ala Asp Leu Ala Gly
35 40 45

Lys Ile Ala Ala Gly Lys Asn Gly Gly Gly Gln Asn Asn Gln Asn Asn
50 55 60

Gln Asn Asp Ile Asn Lys Tyr Leu Phe Leu Ser Gln Tyr Ala Asn Ile
65 70 75 80

Leu Thr Met Glu Glu Leu Asn Asn Asn Val Val Lys Asn Ser Ser Ser
85 90 95

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

Asp Leu Glu Asp Gly Val Glu Glu Leu Thr Lys Asn Gln Asn Thr Leu
115 120 125

Ile Glu Lys Asp Glu Glu His Asp Arg Leu Ile Ala Gln Asn Gln Ala
Page 64

130

135

140

Asp Ile Gln Thr Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
 145 150 155 160

Ser Asp Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala
 165 170 175

Asp Ile Ala Gln Asn Asn Glu Ser Ile Glu Glu Leu Tyr Asp Phe Asp
 180 185 190

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

Val Asn Lys Thr Leu Gln Asp Leu Ile Thr Asn Ser Val Lys Asn Thr
 210 215 220

Asp Asn Ile Asp Lys Asn Lys Ala Asp Ile Asp Asn Asn Ile Asn His
 225 230 235 240

Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys
 245 250 255

Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His
 260 265 270

Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu
 275 280 285

Asn Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp
 290 295 300

Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln
 305 310 315 320

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

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

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
 355 360 365

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

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

Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln

405

410

415

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

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

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
 450 455 460

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

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

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

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

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

Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val
 545 550 555 560

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

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

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

Asn Ile Gly Val Asn Tyr Glu Phe
 610 615

<210> 27

<211> 668

<212> PRT

<213> Moraxella catarrhalis

<400> 27

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

Leu Ile Val Gly Leu Gly Thr Ala Ser Thr Ala Asn Ala Gln Val Ala
 20 25 30

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Ser Pro Ala Asn Gln Lys Ile Gln Gln Lys Ile Lys Lys Val Arg Lys
35 40 45

Glu Leu Arg Gln Asp Ile Lys Ser Leu Arg Asn Asp Ile Asp Ser Asn
50 55 60

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

Asp Ile Leu Asp Asn Gln Ala Asp Ile Ala Lys Asn Gln Asp Asp Ile
85 90 95

Glu Lys Asn Gln Ala Asp Ile Lys Glu Leu Asp Lys Glu Val Gly Val
100 105 110

Leu Ser Arg Glu Ile Gly Ser Leu Asn Asp Asp Ile Ala Asp Asn Tyr
115 120 125

Thr Asp Ile Ile Asp Asn Tyr Thr Asp Ile Ile Asp Asn Gln Ala Asn
130 135 140

Ile Ala Lys Asn Gln Asp Asp Ile Glu Lys Asn Gln Ala Asp Ile Lys
145 150 155 160

Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg Glu Ile Gly Ser Leu
165 170 175

Asn Asp Asp Val Ala Asp Asn Gln Asp Asp Ile Ala Lys Asn Gln Ala
180 185 190

Asp Ile Gln Thr Leu Glu Asn Asn Val Glu Glu Gly Leu Leu Glu Leu
195 200 205

Ser Gly His Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
210 215 220

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

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

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

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Glu
275 280 285

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

VR65032W0-seql-000001.txt

Gln Asn Ile Ala Lys Asn Ser Asn Arg Ile Lys Ala Leu Glu Ser Asn
305 310 315 320

Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
325 330 335

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

Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Ile
355 360 365

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

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

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

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
420 425 430

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
435 440 445

Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
450 455 460

Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser
465 470 475 480

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

Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp
500 505 510

Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala
515 520 525

Asn Lys Val Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile
530 535 540

Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp
545 550 555 560

Leu Gly Thr Lys Val Asp Ala Phe Asp Ser Arg Val Thr Ala Leu Asp
565 570 575

Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys
580 585 590

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
595 600 605

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
610 615 620

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
625 630 635 640

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
645 650 655

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
660 665

<210> 28
<211> 674
<212> PRT
<213> Moraxella catarrhalis
<400> 28

Met Lys Thr Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala
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Met Ile Val Gly Leu Gly Ala Thr Ser Thr Val Asn Ala Gln Val Val
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
305 310 315 320

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

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

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

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

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

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

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Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala
 420 425 430
 Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln
 435 440 445
 Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln
 450 455 460
 Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala
 465 470 475 480
 Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser
 485 490 495
 Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys
 500 505 510
 Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn
 515 520 525
 Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr
 530 535 540
 Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu
 545 550 555 560
 Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr
 565 570 575
 Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile
 580 585 590
 Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala
 595 600 605
 Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr
 610 615 620
 Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala
 625 630 635 640
 Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile
 645 650 655
 Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr
 660 665 670
 Glu Phe

<210> 29
 <211> 613
 <212> PRT
 <213> Moraxella catarrhalis

<400> 29

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Asn Tyr Glu Phe
610

<210> 30
<211> 576
<212> PRT
<213> Moraxella catarrhalis

<400> 30

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

Met Ile Val Gly Leu Gly Ala Thr Ser Thr Val Asn Ala Gln Val Val
20 25 30

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

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

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

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

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

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

Val Glu Thr Val Tyr Ser Val Thr Thr Lys Ile Ala Thr Gln Asp Asp

130

135

140

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

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

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

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

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

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

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

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

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

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

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

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

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

Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
 355 360 365

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

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

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His

405

410

415

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

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

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

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

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

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

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

Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr
 530 535 540

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

Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 565 570 575

<210> 31

<211> 684

<212> PRT

<213> Moraxella catarrhalis

<400> 31

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

Met Met Val Gly Leu Gly Met Ala Ser Thr Ala Asn Ala Gln Gln Gln
 20 25 30

Lys Ser Pro Lys Thr Glu Ile Phe Leu Pro Asn Leu Phe Asp Asn Asp
 35 40 45

Asn Thr Glu Leu Thr Asp Pro Leu Tyr His Asn Met Ile Leu Gly Asn
 50 55 60

Thr Ala Leu Leu Thr Gln Glu Asn Gln Tyr Lys Phe Tyr Ala Asp Asp
 65 70 75 80

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Gly Asn Gly Val Pro Asp Ser Leu Leu Phe Asn Lys Ile Leu His Asp
85 90 95

Gln Leu Leu His Gly Phe Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp
100 105 110

Glu Asn Gly Lys Pro Val Tyr Lys Leu Asp Ser Ile Val Glu Gln Gly
115 120 125

Lys Thr Lys Thr Val Tyr Ser Val Thr Thr Lys Thr Ala Thr Ala Asp
130 135 140

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

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

Asp Lys Ile Phe Ala Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu
180 185 190

Val Gln Asn Asn Ile Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp
195 200 205

Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Lys Asp
210 215 220

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

Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln
245 250 255

Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
260 265 270

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile
275 280 285

Lys Thr Leu Glu Asn Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly
290 295 300

His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu
305 310 315 320

Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
325 330 335

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

VR65032W0-seql-000001.txt

Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu
355 360 365

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

Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln
385 390 395 400

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

Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
420 425 430

Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
435 440 445

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

Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
465 470 475 480

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

Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
500 505 510

Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile
515 520 525

Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr
530 535 540

Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile
545 550 555 560

Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly
565 570 575

Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp
580 585 590

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

Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln
610 615 620

VR65032W0-seql-000001.txt

Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr
625 630 635 640

Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro
645 650 655

Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys
660 665 670

Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680

<210> 32
<211> 686
<212> PRT
<213> Moraxella catarrhalis

<400> 32

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Thr Glu Thr Thr
35 40 45

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

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Gln Leu Asn Gly Phe
85 90 95

Lys Glu Gly Asp Thr Ile Ile Pro Leu Asp Glu Asn Gly Lys Pro Val
100 105 110

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

Ser Val Thr Thr Lys Thr Ala Thr Arg Glu Asp Val Glu Gln Ser Ala
130 135 140

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

Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp Lys Ile Phe Ala
165 170 175

VR65032W0-seql-000001.txt

Asn Glu Glu Ser Val Gln Tyr Leu Asn Lys Glu Val Gln Asn Asn Ile
 180 185 190
 Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 195 200 205
 Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 210 215 220
 Gly Arg Leu Ile Ala Gln Lys Glu Asp Ile Ala Gln Asn Gln Thr Asp
 225 230 235 240
 Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
 245 250 255
 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
 260 265 270
 Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile Lys Thr Leu Glu Asn
 275 280 285
 Asn Ile Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln
 290 295 300
 Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu
 305 310 315 320
 Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp
 325 330 335
 Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln
 340 345 350
 Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln
 355 360 365
 Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln
 370 375 380
 Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
 385 390 395 400
 Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 405 410 415
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 420 425 430
 Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 435 440 445

VR65032W0-seql-000001.txt

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

Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
465 470 475 480

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

Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu
500 505 510

Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys
515 520 525

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

Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn
545 550 555 560

Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val
565 570 575

Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala
580 585 590

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

Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu
610 615 620

Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly
625 630 635 640

Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val
645 650 655

Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly
660 665 670

Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
675 680 685

<210> 33
<211> 630
<212> PRT
<213> Moraxella catarrhalis
<400> 33

VR65032W0-seq1-000001.txt

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Lys
20 25 30

Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys Ile Asp
35 40 45

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

Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu Glu Glu Leu
65 70 75 80

Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn Gln Asn
85 90 95

Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr Lys Asn Gln
100 105 110

Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu Gln Gly
115 120 125

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

Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly Phe Glu
145 150 155 160

Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser Ile Glu
165 170 175

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

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

Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala Asp Ile
210 215 220

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

Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile
245 250 255

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

VR65032W0-seq1-000001.txt

Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu
275 280 285

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

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

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

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

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

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

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

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

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
420 425 430

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

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

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

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

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

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

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

VR65032W0-seq1-000001.txt

Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala
545 550 555 560

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

Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val
580 585 590

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

Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile
610 615 620

Gly Val Asn Tyr Glu Phe
625 630

<210> 34
<211> 616
<212> PRT
<213> Moraxella catarrhalis

<400> 34

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

Leu Ile Val Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ala Gln
20 25 30

Asp Arg Ser Leu Glu Gln Ile Gln Asp Lys Leu Ala Asn Leu Val Glu
35 40 45

Lys Ile Glu Gln Ala Lys Ser Gln Asn Gly Gln Ser Gln Lys Asp Ile
50 55 60

Asn Gln Tyr Leu Leu Leu Ser Gln Tyr Ala Asn Val Leu Thr Met Glu
65 70 75 80

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

Asp Asn Asp Ile Ala Trp Leu Asn Asp Asp Leu Ile Asp Leu Asp Lys
100 105 110

Glu Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp Asp Val
115 120 125

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

Glu Leu Phe Asn Leu Ser Asp Arg Leu Ile Asp Gln Glu Ala Asp Ile

145					150					155					160
Ala	Gln	Asn	Asn	Glu	Ser	Ile	Glu	Asp	Leu	Tyr	Asp	Phe	Gly	Arg	Glu
				165					170					175	
Val	Ala	Glu	Ser	Ile	Gly	Glu	Ile	His	Ala	His	Asn	Glu	Ala	Gln	Asn
			180					185					190		
Glu	Thr	Leu	Lys	Asp	Leu	Ile	Thr	Asn	Ser	Val	Lys	Asn	Thr	Asp	Asn
		195					200					205			
Ile	Thr	Lys	Asn	Lys	Ala	Asp	Ile	Gln	Ala	Leu	Glu	Asn	Asp	Val	Gly
	210					215					220				
Lys	Glu	Leu	Leu	Asn	Leu	Ser	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Ala	Asp
225					230					235					240
Ile	Asp	Asn	Asn	Ile	Asn	His	Ile	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp
				245					250					255	
Gln	His	Ser	Ser	Asp	Ile	Lys	Thr	Leu	Lys	Asn	Asn	Val	Glu	Glu	Gly
			260					265					270		
Leu	Leu	Glu	Leu	Ser	Gly	His	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Leu	Thr
		275					280					285			
Lys	Asp	Ile	Lys	Ala	Leu	Glu	Ser	Asn	Val	Glu	Glu	Gly	Leu	Leu	Asp
	290					295					300				
Leu	Ser	Gly	Arg	Leu	Leu	Asp	Gln	Lys	Ala	Asp	Ile	Ala	Gln	Asn	Gln
305					310					315					320
Ala	Asn	Ile	Gln	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	Tyr
				325					330					335	
Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser
			340					345					350		
Glu	Asn	Thr	Gln	Asn	Ile	Glu	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln
		355					360					365			
Asp	Ala	Tyr	Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys
	370					375					380				
Ala	Ser	Ser	Glu	Asn	Thr	Gln	Asn	Ile	Ala	Lys	Asn	Gln	Ala	Asp	Ile
385					390					395					400
Ala	Asn	Asn	Ile	Asn	Asn	Ile	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln
				405					410					415	
His	Ser	Ser	Asp	Ile	Lys	Thr	Leu	Ala	Lys	Ala	Ser	Ala	Ala	Asn	Thr

420

425

430

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

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
 450 455 460

Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
 465 470 475 480

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

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

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

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

Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val
 545 550 555 560

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

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

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

Asn Ile Gly Val Asn Tyr Glu Phe
 610 615

<210> 35
 <211> 614
 <212> PRT
 <213> Moraxella catarrhalis

<400> 35

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

Met Ile Ile Gly Leu Gly Ala Thr Ser Thr Val Asn Ala Gln Val Val
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Asn Ile Asn His Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
245 250 255

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

Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp
275 280 285

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

Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln Asn Gln Ala Asn
305 310 315 320

VR65032W0-seql-000001.txt

Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
325 330 335

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

Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
355 360 365

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

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

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

Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg
420 425 430

Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
435 440 445

Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
450 455 460

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

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

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

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

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

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

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

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

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

Gly Val Asn Tyr Glu Phe
610

<210> 36
<211> 679
<212> PRT
<213> Moraxella catarrhalis
<400> 36

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

Met Ile Ile Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Thr Thr
20 25 30

Glu Thr Phe Leu Pro Asn Leu Phe Asp Asn Asp Tyr Thr Glu Thr Thr
35 40 45

Asp Pro Leu Tyr His Gly Met Ile Leu Gly Asp Thr Ala Ile Thr Gln
50 55 60

Asp Thr Gln Tyr Lys Phe Tyr Ala Glu Asn Gly Asn Glu Val Pro Asp
65 70 75 80

Ser Leu Phe Phe Asn Lys Ile Leu His Asp Gln Leu Leu Asn Gly Phe
85 90 95

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

Tyr Lys Leu Asp Glu Arg Thr Glu Asn Gly Val Lys Arg Lys Val Tyr
115 120 125

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

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

Lys Glu Asn Val Asn Arg Leu Ile Glu His Gly Asp Lys Ile Phe Ala
165 170 175

Asn Glu Glu Ser Val Gln Tyr Leu Asn Arg Glu Val Gln Asn Asn Ile
180 185 190

Glu Asn Ile His Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
195 200 205

VR65032W0-seql-000001.txt

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

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

Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
245 250 255

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

Thr Gln Asn Ile Ala Lys Asn Ser Asn His Ile Lys Thr Leu Glu Asn
275 280 285

Asn Ile Glu Glu Cys Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln
290 295 300

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

Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp
325 330 335

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

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

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

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

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

Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
420 425 430

Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
435 440 445

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

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

VR65032W0-seql-000001.txt

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

Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu
500 505 510

Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr
515 520 525

Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr
530 535 540

Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys
545 550 555 560

Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val
565 570 575

Thr Ala Leu Asp Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala
580 585 590

Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met
595 600 605

Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly
610 615 620

Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala
625 630 635 640

Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys
645 650 655

Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn
660 665 670

Ile Gly Val Asn Tyr Glu Phe
675

<210> 37
<211> 724
<212> PRT
<213> Moraxella catarrhalis

<400> 37

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

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

VR65032W0-seq1-000001.txt

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

VR65032W0-seq1-000001.txt

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

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

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

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

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

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

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

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

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

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

Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala
465 470 475 480

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

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

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
515 520 525

Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala
530 535 540

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

Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr
565 570 575

VR65032W0-seq1-000001.txt

Ala Asn Lys Thr 580 Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys 590

Phe Ala Ala Thr 595 Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr 605

Lys Asn Ala Lys Ser Ile Thr 615 Asp Leu Gly Thr Lys Val Asp Gly Phe 620

Asp Ser Arg Val Thr 630 Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly 640

Arg Ile Thr Ala 645 Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln 655

Ala Ala Leu Ser 660 Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn 670

Ala Thr Ala 675 Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile 685

Gly Ala Gly Tyr Arg Val 695 Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala 700

Ala Ile Asn Thr Ser 710 Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val 720

Asn Tyr Glu Phe

<210> 38
<211> 611
<212> PRT
<213> Moraxella catarrhalis

<400> 38

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

Leu Ile Val Gly 20 Leu Gly Ala Ala Ser 25 Thr Ala Asn Ala Gln Ala Gln 30

Ala Arg Asp 35 Arg Ser Leu Glu Asp 40 Ile Gln Ala Leu Ile Gly Asn Ile 45

Asp Val Asp Lys Ile Arg Ser 55 Gln Lys Gln Lys Asn Pro Glu Ile Phe 60

Gln Tyr Leu Leu Leu 70 Asn Gln Leu Ser Asn 75 Thr Leu Ile Thr Asp Glu 80

Leu Asn Asn Asn Val Ile Lys Asn Thr Asn Ser Ile Glu Thr Leu Asp

Asn Asp Ile Ala Trp Leu Asn Asp Asp Leu Ile Asp Leu Asp Lys Glu
 100 105 110
 Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp Asp Val Ala
 115 120 125
 Gln Asn Gln Ala Asp Ile Lys Thr Leu Glu Asn Asn Val Val Glu Glu
 130 135 140
 Leu Phe Asn Leu Ser Asp Arg Leu Ile Asp Gln Glu Ala Glu Ile Ala
 145 150 155 160
 Gln Asn Asn Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly Arg Glu Val
 165 170 175
 Ala Glu Ser Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu
 180 185 190
 Thr Leu Lys Asp Leu Ile Thr Asn Ser Val Lys Asn Thr Asp Asn Ile
 195 200 205
 Asp Lys Asn Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Glu Glu
 210 215 220
 Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu
 225 230 235 240
 Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu
 245 250 255
 Asp Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Ala Lys Asn
 260 265 270
 Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala
 275 280 285
 Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile
 290 295 300
 Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp
 305 310 315 320
 Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr
 325 330 335
 Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn
 340 345 350
 Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys

355

360

365

Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
 370 375 380
 Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn
 385 390 395 400
 Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
 405 410 415
 Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys
 420 425 430
 Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln
 435 440 445
 Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala
 450 455 460
 Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe
 465 470 475 480
 Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys
 485 490 495
 Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp
 500 505 510
 Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg
 515 520 525
 Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala
 530 535 540
 Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala
 545 550 555 560
 Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly
 565 570 575
 Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala
 580 585 590
 Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn
 595 600 605
 Tyr Glu Phe
 610

<210> 39

<211> 511

<212> PRT

<213> Moraxella catarrhalis

<400> 39

Gln Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys
1 5 10 15

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

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

Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
245 250 255

Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
 260 265 270
 Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
 275 280 285
 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
 290 295 300
 Thr Gln Asn Ile Glu 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 Glu Asp Leu Ala Ala Tyr Asn Glu Leu
 340 345 350
 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
 355 360 365
 Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
 370 375 380
 Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
 385 390 395 400
 Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
 405 410 415
 Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
 420 425 430
 Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
 435 440 445
 Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
 450 455 460
 Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
 465 470 475 480
 Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
 485 490 495
 Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys
 500 505 510

<210> 40
 <211> 510

<212> PRT

<213> Moraxella catarrhalis

<400> 40

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys
 1 5 10 15

Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala Leu
 20 25 30

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

Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn
 50 55 60

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

Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu
 85 90 95

Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu Gln
 100 105 110

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

Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser
 130 135 140

Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly
 145 150 155 160

Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu
 165 170 175

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

Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
 195 200 205

Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
 210 215 220

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

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

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

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
275 280 285

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

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

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

Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
340 345 350

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
370 375 380

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

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
405 410 415

Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr
420 425 430

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
435 440 445

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

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

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

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

<210> 41
<211> 490
<212> PRT

<213> Moraxella catarrhalis

<400> 41

Gln Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys
1 5 10 15

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
130 135 140

Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
145 150 155 160

Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
165 170 175

Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
180 185 190

Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
195 200 205

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
210 215 220

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

Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
245 250 255

VR65032W0-seq1-000001.txt

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

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

Thr Gln Asn Ile Glu 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 Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

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

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

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

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
420 425 430

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
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Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
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<210> 42

<211> 535

<212> PRT

<213> Moraxella catarrhalis

<400> 42

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      50      55      60
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      65      70      75      80
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      115      120      125
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Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
      145      150      155      160
Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
      165      170      175
Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
      180      185      190
Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
      195      200      205
Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
      210      215      220
Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
      225      230      235      240
Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
      245      250      255
Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
      260      265      270
Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln

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275

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 Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
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 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
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 Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
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<210> 43

<211> 534
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<400> 43

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

Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly
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Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser
 130 135 140

Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly
 145 150 155 160

Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu
 165 170 175

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

Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
 195 200 205

Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
 210 215 220

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
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Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
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 290 295 300
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 450 455 460
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 465 470 475 480
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 485 490 495
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<213> Moraxella catarrhalis

<400> 44

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Leu Glu Lys Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu
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Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

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Ser Ile Glu Asp
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<210> 45
<211> 154
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Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
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 100 105 110

Val Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys
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<400> 46

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Leu Glu Lys Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu
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Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
 50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
 85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
 100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
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115

120

125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
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 Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
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 Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
 180 185 190
 Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
 195 200 205
 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
 210 215 220
 Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 225 230 235 240
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 Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
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 Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
 340 345 350
 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
 355 360 365
 Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
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385 390 395 400
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 450 455 460
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 Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
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 Asn Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr
 65 70 75 80
 Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
 85 90 95
 Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
 100 105 110
 Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
 115 120 125

Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
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 Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
 145 150 155 160
 Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
 165 170 175
 Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
 180 185 190
 Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
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 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
 210 215 220
 Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 225 230 235 240
 Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 245 250 255
 Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
 260 265 270
 Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
 275 280 285
 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
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 Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
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 Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
 340 345 350
 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
 355 360 365
 Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
 370 375 380
 Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
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Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
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Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
420 425 430

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
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<211> 490
<212> PRT
<213> Moraxella catarrhalis
<400> 48

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
115 120 125

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 Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
 145 150 155 160
 Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
 165 170 175
 Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
 180 185 190
 Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
 195 200 205
 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
 210 215 220
 Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 225 230 235 240
 Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 245 250 255
 Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
 260 265 270
 Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
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 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
 290 295 300
 Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala
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 Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
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 340 345 350
 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
 355 360 365
 Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
 370 375 380
 Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
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Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
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Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
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Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
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Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser
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<210> 49
<211> 535
<212> PRT
<213> Moraxella catarrhalis

<400> 49

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp
85 90 95

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
100 105 110

Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
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 Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
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 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
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 225 230 235 240
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 245 250 255
 Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
 260 265 270
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 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
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 Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
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 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
 355 360 365
 Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
 370 375 380
 Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
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Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
420 425 430

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

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

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

Lys Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val
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Gly Met Ala Ala Gln Ala Ala
530 535

<210> 50

<211> 534

<212> PRT

<213> Moraxella catarrhalis

<400> 50

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Glu Lys Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu Glu
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Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn
50 55 60

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

Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu
85 90 95

Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu Gln
100 105 110

Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly
Page 116

115

120

125

Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser
 130 135 140

Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly
 145 150 155 160

Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu
 165 170 175

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

Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
 195 200 205

Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
 210 215 220

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

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

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

Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
 275 280 285

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

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

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

Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
 370 375 380

Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln
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385 390 395 400
 His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
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 Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr
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 Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
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 Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser
 450 455 460
 Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly
 465 470 475 480
 Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys
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 Val Asp Gly Phe Asp Ser Arg Val Thr Ala Leu Asp Thr Lys Val Asn
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 Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly
 515 520 525
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 530

<210> 51
 <211> 510
 <212> PRT
 <213> Moraxella catarrhalis

<400> 51

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile Lys Lys
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 Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala Leu
 20 25 30
 Glu Lys Tyr Leu Ala Leu Ser Gln Tyr Gly Asn Ile Leu Ala Leu Glu
 35 40 45
 Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp Asn
 50 55 60
 Gln Asn Asp Ile Ala Asn Leu Glu Asp Asp Val Glu Thr Leu Thr Lys
 65 70 75 80
 Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp Leu
 85 90 95

Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu Gln
 100 105 110
 Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn Gly
 115 120 125
 Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu Ser
 130 135 140
 Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile Gly
 145 150 155 160
 Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly Leu
 165 170 175
 Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys Ala
 180 185 190
 Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn Leu
 195 200 205
 Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
 210 215 220
 Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
 225 230 235 240
 Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly
 245 250 255
 His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn Ile
 260 265 270
 Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys
 275 280 285
 Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr
 290 295 300
 Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Ala Tyr
 305 310 315 320
 Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser
 325 330 335
 Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln
 340 345 350
 Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys
 355 360 365

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Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp Ile
370 375 380

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

His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr
405 410 415

Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr
420 425 430

Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp
435 440 445

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

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

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

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

<210> 52
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-001 construct

<400> 52
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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
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aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt 420
gccaaaaaca acgaaagcat tgaagatctg tatgatattg gtcattgaagt tgccgaaagc 480
attggtgaaa ttcattgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
aataatgttg tggaagaact gtttaatctg agcggctcgtc tgattgatca gaaagccgat 660

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atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat      840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa      900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat      960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac     1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag     1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc     1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag     1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt     1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac     1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt     1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattaccaaa     1440
aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctggggcac caaagttgat     1500
ggttttgata gccgtgtgac cgactggat accaaagcaa gccatcatca tcaccaccac     1560
taa                                                                    1563

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<210> 53
 <211> 520
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-001 construct

<400> 53

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 1 5 10 15

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
 85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110
 Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125
 Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140
 Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160
 Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175
 Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190
 Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205
 Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220
 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 225 230 235 240
 Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255
 Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270
 Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 290 295 300
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320
 Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350
 Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

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Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

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

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

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

Ala Ser His His His His His His
515 520

<210> 54
<211> 1539
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-002 construct
<400> 54

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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat	180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg	240
accaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt	300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa	360
aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt	420
gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc	480
attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc	540

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aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat 660
atcgataata acattaacaa cttttatgaa ctggcacagc agcaggatca gcatagcagc 720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg 780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa 900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa ggcgagcaaa taccgatcgt 1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac 1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
gatgcaaata aagccagcgc agatacaaaa tttgcagcaa ccgcagatgc aattacaaaa 1440
aatggcaatg ccatcaccaa aaatgccaaa agcattaccg atctgggcac caaagttgat 1500
ggttttgata gccgtgtgac cgactggat accaaataa 1539

<210> 55

<211> 512

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein sequence for MC-002 construct

<400> 55

Met Gln Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile
1 5 10 15

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

VR65032W0-seql-000001.txt

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110
 Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125
 Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140
 Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160
 Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175
 Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190
 Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205
 Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220
 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 225 230 235 240
 Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255
 Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270
 Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 290 295 300
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320
 Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350
 Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

VR65032W0-seql-000001.txt

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

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

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

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

<210> 56
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for construct

<400> 56
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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
acaaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt 420
gccaaaaaca acgaaagcat tgaagatctg tatgatattg gtcattgaagt tgccgaaagc 480
attggtgaaa ttcattgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat 660

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gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg 780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa 900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020
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cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt 1260
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accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
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ggttttgata gccgtgtgac cgactggat accaaagtta atgcatttga tggtcgtatt 1560
accgctctgg atagtaaagt tgaaaatgga atggcagcac aagcagcaca ctaa 1614

<210> 57

<211> 537

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein sequence for construct

<400> 57

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1 5 10 15

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile

100

105

110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220

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

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285

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

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

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

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
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370

375

380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
 405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
 435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
 450 455 460

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

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

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

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

Asn Gly Met Ala Ala Gln Ala Ala His
 530 535

<210> 58
 <211> 1545
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-004 construct

<400> 58
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 agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
 gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
 accaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
 ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
 aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt 420
 gccaaaaaca acgaaagcat tgaagatctg tatgatattg gtcatgaagt tgccgaaagc 480

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aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat 660
atcgataata acattaacaa cttttatgaa ctggcacagc agcaggatca gcatagcagc 720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg 780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
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gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
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aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
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accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattaccaaa 1440
aatggcaatg ccatcaccaa aaatgcaaaa agcattaccg atctgggcac caaagttgat 1500
ggttttgata gccgtgtgac cgactggat accaaacatc attaa 1545

<210> 59
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein sequence for MC-004 construct
<400> 59

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1 5 10 15

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
Page 130

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110
 Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125
 Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140
 Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160
 Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175
 Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190
 Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205
 Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220
 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 225 230 235 240
 Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255
 Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270
 Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 290 295 300
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320
 Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350
 Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu

355

360

365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
 370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
 405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
 435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
 450 455 460

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

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

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

His His

<210> 60

<211> 1500

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence for MC-005 construct

<400> 60

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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180

gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240

acaaaaatc agaatgcact ggacagaacag ggtgaagcaa ttaaagaaga tctgcagggt 300

ctggcagatt ttgttggaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360

aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt 420

gccaaaaaca acgaaagcat tgaagatctg tatgatattg gtcatagaagt tgccgaaagc 480

VR65032W0-seq1-000001.txt

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aataatgttg tggaagaact gtttaatctg agcggtcgctc tgattgatca gaaagccgat      660
atcgataata acattaacaa cttttatgaa ctggcacagc agcaggatca gcatagcagc      720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg      780
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accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt     1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattaccaaa     1440
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<210> 61

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein sequence for MC-005 construct

<400> 61

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Lys  Lys  Ile  Asp  Gln  Asn  Glu  Leu  Glu  Ala  Asp  Ile  Gly  Asp  Ile  Thr
          20           25           30

```

```

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

```

```

Leu  Glu  Glu  Leu  Asn  Lys  Ala  Leu  Glu  Glu  Leu  Asp  Glu  Asp  Val  Gly
50           55           60

```

```

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

```

```

Thr  Lys  Asn  Gln  Asn  Ala  Leu  Ala  Glu  Gln  Gly  Glu  Ala  Ile  Lys  Glu
          85           90           95

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Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110
 Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125
 Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140
 Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160
 Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175
 Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190
 Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205
 Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220
 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 225 230 235 240
 Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255
 Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270
 Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 290 295 300
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320
 Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350
 Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

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Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

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

Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ala Ser His His His
485 490 495

His His His

<210> 62
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-006 construct

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agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
gaagatgttg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
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gccaaaaaca acgaaagcat tgaagatctg tatgatattg gtcattgaagt tgccgaaagc 480
attggtgaaa ttcattgaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat 660

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aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa      900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat      960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac     1020
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cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc     1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag     1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt     1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac     1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt     1380
gatgcaaata aagccagcgc agataccaaa tttgcagcaa ccgcagatgc aattaccaaa     1440
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<210> 63
<211> 491
<212> PRT
<213> Artificial Sequence

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<220>
<223> Protein sequence for MC-006 construct

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<400> 63

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1          5          10          15

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Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
20          25          30

```

```

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

```

```

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
50          55          60

```

```

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

```

```

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
85          90          95

```

```

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
100         105         110

```

```

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
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```

115

120

125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220

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

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285

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

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

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

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
 370 375 380

Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
 Page 137

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aaaaacaccc	agcgta	ggtgaatgg	tttgaaattg	aaaaaaaa	agatgccatt	420
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aataatgttg	tggaaga	gtttaatct	agcggtcg	tgattgatca	gaaagccgat	660
atcgataata	acattaaca	catttatgaa	ctggcacagc	agcaggatca	gcatagcagc	720
gatatcaaaa	ccctgaaaa	aaacgttgaa	gaaggtctgc	tggaactgtc	tggtcacctg	780
atcgatcaga	aaactgat	tgcccagaat	caggcaaata	ttcaggatct	ggccacctat	840
aatgaactgc	aggatcag	tgcacagaaa	cagaccgaag	caattgatgc	cctgaataaa	900
gcgagcagcg	aaaacaccca	gaatatcgaa	gatctggcag	catacaacga	actgcaggat	960

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cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
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catcaccacc actaa 1635
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<210> 65
 <211> 544
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-007 construct

<400> 65

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 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
 85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 Page 139

130

135

140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220

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

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255

Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270

Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285

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

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

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

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
 370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
 Page 140

405

410

415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
 435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
 450 455 460

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

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

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

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

Asn Gly Met Ala Ala Gln Ala Ala Ala Ser His His His His His His
 530 535 540

<210> 66
 <211> 1617
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-008 construct

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 gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
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 aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat 660
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<210> 67

<211> 538

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein sequence for MC-008 construct

<400> 67

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
 85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110

VR65032W0-seql-000001.txt

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125
 Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140
 Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160
 Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175
 Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190
 Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205
 Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220
 Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser
 225 230 235 240
 Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255
 Ser Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala
 260 265 270
 Asn Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 275 280 285
 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu
 290 295 300
 Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp
 305 310 315 320
 Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala
 325 330 335
 Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
 340 345 350
 Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
 355 360 365
 Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
 370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

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

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

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

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

Asn Gly Met Ala Ala Gln Ala Ala His His
530 535

<210> 68
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-009 construct

<400> 68
atggcgaaaa atgatattac cctggaagat ctgccgtatc tgatcaaaaa aatcgatcag 60
aacgaactgg aagccgatat tggatgatatt accgcactgg aaaaatatct ggcactgagc 120
cagtatggaa atattctggc cctggaagaa ctgaataaag ctctggaaga gctggatgaa 180
gatgtgggtt ggaatcagaa tgatatcgcc aatctggaag atgatgttga aaccctgacc 240
aaaaatcaga atgcactggc agaacagggt gaagcaatta aagaagatct gcagggtctg 300
gcagattttg ttgaaggta ggaaggcaaa attctgcaga acgaaaccag catcaaaaaa 360
aacaccagc gtaatctggt gaatggcttt gaaattgaaa aaaacaaaga tgccattgcc 420
aaaaacaacg aaagcattga agatctgtat gattttgggtc atgaagttgc cgaaagcatt 480
ggtgaaattc atgcacataa cgaagcacag aatgaaaccc tgaaaggtct gattaccaac 540

VR65032W0-seql-000001.txt

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agcatcgaat ataccaataa cattaccaa aacaaagcag atattcaggc gctggaaaat 600
aatgttgtgg aagaactgtt taatctgagc ggtcgtctga ttgatcagaa agccgatatc 660
gataataaca ttaacaacat ttatgaactg gcacagcagc aggatcagca tagcagcgat 720
atcaaaaccc tgaaaaaaa cgttgaagaa ggtctgtctgg aactgtctgg tcacctgac 780
gatcagaaaa ctgatattgc ccagaatcag gcaaatatc aggatctggc cacctataat 840
gaactgcagg atcagtatgc acagaaacag accgaagcaa ttgatgccct gaataaagcg 900
agcagcgaat acaccagaa tatcgaagat ctggcagcat acaacgaact gcaggatgcc 960
tatgcaaac agcagactga agccatcgac gcaactgaaca aggcaagctc tgaaaacacg 1020
cagaacattg aagatctggc tgcctataat gaattacagg atgcgtatgc caaacagcag 1080
accgaagcga ttgatgcgct gaacaaagcc tcttctgaaa atacacagaa tatcgccaaa 1140
aatcaggccg atattgccaa caatatcaat aatatctatg aactggccca gcagcaggat 1200
cagcactctt ctgatataaa aacactggca aaagcaagcg cagcaaatac cgatcgtatt 1260
gcgaaaaaca aagccgatgc agatgcaagc tttgaaacac tgacgaaaaa ccagaacacc 1320
ctgattgaaa aagataaaga acatgataaa ctgatcaccg ccaataaaaac cgcaattgat 1380
gcaaataaag ccagcgcaga taccaaattt gcagcaaccg cagatgcaat taccaaaaat 1440
ggcaatgcca tcaccaaaaa tgccaaaagc attaccgatc tgggcaccaa agttgatggt 1500
tttgatagcc gtgtgaccgc actggatacc aaagttaatg cttttgatgg tcgtattacc 1560
gctctggata gtaaagttga aaatggatat gcagcacagg cagcacacca ctaa 1614

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<210> 69
 <211> 537
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-009 construct

<400> 69

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

Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
 20 25 30

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

Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly Trp
 50 55 60

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

Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu Asp

Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile Leu
 100 105 110
 Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val Asn
 115 120 125
 Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn Glu
 130 135 140
 Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser Ile
 145 150 155 160
 Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys Gly
 165 170 175
 Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn Lys
 180 185 190
 Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe Asn
 195 200 205
 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile
 210 215 220
 Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp
 225 230 235 240
 Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu Ser
 245 250 255
 Gly His Leu Ile Asp Gln Lys Thr Asp Ile Ala Gln Asn Gln Ala Asn
 260 265 270
 Ile Gln Asp Leu Ala Thr Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
 275 280 285
 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn
 290 295 300
 Thr Gln Asn Ile Glu 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 Glu Asp Leu Ala Ala Tyr Asn Glu Leu
 340 345 350
 Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn

355

360

365

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
 370 375 380

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

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
 405 410 415

Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
 420 425 430

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
 435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
 450 455 460

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

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

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

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

Gly Met Ala Ala Gln Ala Ala His His
 530 535

<210> 70

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence for MC-010 construct

<400> 70

atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat 60

cagaacgaac tggaagccga tattggtgat attaccgcac tggaaaaata tctggcactg 120

agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180

gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240

accaaaaatc agaatgcact ggcagaacag ggtgaagcaa ttaaagaaga tctgcagggt 300

ctggcagatt ttgttgaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360

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aaaaacaccc agcgtaatct ggtgaatggc ttgaaattg aaaaaaaca agatgccatt      420
gccaaaaaca acgaaagcat tgaagatctg tatgatattg gtcataagtg tgccgaaagc      480
attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc      540
aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa      600
aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat      660
atcgataata acattaacaa ctttatgaa ctggcacagc agcaggatca gcatagcagc      720
gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg      780
atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat      840
aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa      900
gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat      960
gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac     1020
acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag     1080
cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc     1140
aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag     1200
gatcagcact cttctgatat caaaacactg gcaaaagcaa ggcagcaaaa taccgatcgt     1260
attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac     1320
accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt     1380
gatgcaaata aagccagcgc agatacaaaa ttgacagcaa ccgcagatgc aattacaaaa     1440
aatggcaatg ccatcaccaa aaatgcaaaa agcattaccg atctgggcac caaagttgat     1500
ggttttgata gccgtgtgac cgactggat accaaagtta atgcatttga tggtcgtatt     1560
accgctctgg atagtaaagt tgaaaatggg atggcagcac aggcagcata a              1611

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<210> 71
 <211> 536
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein sequence for MC-010 construct

<400> 71

Met Gln Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro Tyr Leu Ile
 1 5 10 15

Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

VR65032W0-seql-000001.txt

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

VR65032W0-seql-000001.txt

Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu
340 345 350

Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu
355 360 365

Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala
370 375 380

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

Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala
405 410 415

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

Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu
435 440 445

His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys
450 455 460

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

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

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

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

Asn Gly Met Ala Ala Gln Ala Ala
530 535

<210> 72
<211> 1560
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for MC-011 construct

<400> 72
atggcgaaaa atgatattac cctggaagat ctgccgtatc tgatcaaaaa aatcgatcag 60
aacgaactgg aagccgatat tgggtgatatt accgcactgg aaaaatatct ggcactgagc 120
cagtatggaa atattctggc cctggaagaa ctgaataaag ctctggaaga gctggatgaa 180

VR65032W0-seq1-000001.txt

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gatgtgggtt ggaatcagaa tgatatcgcc aatctggaag atgatgttga aaccctgacc      240
aaaaatcaga atgcaactggc agaacagggt gaagcaatta aagaagatct gcaggggtctg      300
gcagattttt ttgaagggtca ggaaggcaaa attctgcaga acgaaaccag catcaaaaaa      360
aacacccagc gtaatctggt gaatggcttt gaaattgaaa aaaacaaaga tgccattgcc      420
aaaaacaacg aaagcattga agatctgtat gatttttggtc atgaagttgc cgaaagcatt      480
ggtgaaattc atgcacataa cgaagcacag aatgaaaccc tgaaagggtct gattaccaac      540
agcatcgaaa ataccaataa cattaccaa aacaaagcag atattcaggc gctggaaaat      600
aatgtttgtg aagaactgtt taatctgagc ggtcgtctga ttgatcagaa agccgatatc      660
gataataaca ttaacaacat ttatgaactg gcacagcagc aggatcagca tagcagcgat      720
atcaaaaccc tgaaaaaaaa cgttgaagaa ggtctgctgg aactgtctgg tcacctgatc      780
gatcagaaaa ctgatattgc ccagaatcag gcaaataattc aggatctggc cacctataat      840
gaactgcagg atcagtatgc acagaaacag accgaagcaa ttgatgccct gaataaagcg      900
agcagcgaaa acaccagaa tatcgaagat ctggcagcat acaacgaact gcaggatgcc      960
tatgcaaaac agcagactga agccatcgac gcaactgaaca aggcaagctc tgaaaacacg     1020
cagaacattg aagatctggc tgcctataat gaattacagg atgcgtatgc caaacagcag     1080
accgaagcga ttgatgcgt gaacaaagcc tcttctgaaa atacacagaa tatcgccaaa     1140
aatcaggccg atattgccaa caatatcaat aatatctatg aactggccca gcagcaggat     1200
cagcactctt ctgatatcaa aacactggca aaagcaagcg cagcaaatac cgatcgtatt     1260
gcgaaaaaca aagccgatgc agatgcaagc tttgaaacac tgacgaaaaa ccagaacacc     1320
ctgattgaaa aagataaaga acatgataaa ctgatcaccg ccaataaaaac cgcaattgat     1380
gcaaataaag ccagcgcaga taccaaattt gcagcaaccg cagatgcaat taccaaaaat     1440
ggcaatgcca tcacaaaaaa tgccaaaagc attaccgatc tgggcaccaa agttgatggt     1500
tttgatagcc gtgtgaccgc actggatacc aaagcaagcc atcatcatca ccaccactaa     1560

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<210> 73
<211> 519
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Protein sequence for MC-011 construct
<400> 73

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

```

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Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr Ala
20           25           30

```

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

```

VR65032W0-seql-000001.txt

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

VR65032W0-seql-000001.txt

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 Glu Asp Leu Ala Ala Tyr Asn Glu Leu
340 345 350

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

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
370 375 380

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

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
405 410 415

Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
420 425 430

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
435 440 445

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
450 455 460

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

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

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

Ser His His His His His His
515

<210> 74
<211> 1893
<212> DNA
<213> Moraxella catarrhalis

<400> 74
atgaaaacca tgaaacttct ccctctaaaa atcgctgtaa ccagtgccat gattattggc 60
ttgggtgcgg catctactgc gaatgcgcag gctaaaaatg atataacttt agaggattta 120
ccatatttaa taaaaaagat tgacaaaat gaattggaag cagatatcgg agatattact 180
gctcttgaaa agtatctagc acttagccag tatggcaata ttttagctct agaagagctc 240
aacaaggctc tagaagagct cgacaggat gttggatgga atcagaatga tattgcaaac 300

VR65032W0-seql-000001.txt

ttggaagatg atgttgaaac gctcaccaaa aatcaaaatg ctttggctga acaaggtgag	360
gcaattaaag aagatcttca agggcttgca gattttgtag aagggcaaga gggtaaaatt	420
ctacaaaatg aaacttcaat taaaaaaaaat actcagagaa accttgtcaa tgggtttgag	480
attgagaaaa ataaagatgc tattgctaaa aacaatgagt ctatcgaaga tctttatgat	540
tttggctcatg aggttgacaga aagtataggc gagatacatg ctcataatga agcgcaaaat	600
gaaactctta aaggcttgat aacaaacagt attgagaata ctaataatat taccaaaaac	660
aaagctgaca tccaagcact tgaaaacaat gtcgtagaag aactattcaa tctaagcggc	720
cgcctaattg atcaaaaagc agatattgat aataacatca acaatatcta tgagctggca	780
caacagcaag atcagcatag ctctgatatc aaaacactta aaaaaaatgt cgaagaaggt	840
ttgttgagc taagcggcga cctaattgat caaaaaacag atattgctca aaaccaagct	900
aacatccaag atctggccac ttacaacgag ctacaagacc agtatgctca aaagcaaacc	960
gaagcgattg acgctctaaa taaagcaagc tctgagaata cacaaaacat cgaagatctg	1020
gccgcttaca acgagctaca agatgcctat gccaaacagc aaaccgaagc aattgacgct	1080
ctaaataaag caagctctga gaatacaca aacatcgaag atctggccgc ttacaacgag	1140
ctacaagatg cctatgccaa acagcaaacc gaagccattg acgctctaaa taaagcaagc	1200
tctgagaata cacaaaacat tgctaaaaac caagcggata ttgctaataa catcaacaat	1260
atctatgagc tggcacacaa gcaagatcag catagctctg atatcaaaac cttggcaaaa	1320
gcaagtgctg ccaatactga tcgtattgct aaaaacaaag ccgatgctga tgcaagtttt	1380
gaaacgctca ccaaaaatca aaatactttg attgaaaaag ataaagagca tgacaaatta	1440
attactgcaa acaaaaactgc gattgatgcc aataaagcat ctgcggtac caagtttgca	1500
gcgacagcag acgccattac caaaaatgga aatgctatca ctaaaaacgc aaaatctatc	1560
actgatttgg gcactaaagt ggatggtttt gacagtcgtg taactgcatt agacaccaaa	1620
gtcaatgcct ttgatggcgc tatcacagct ttagacagta aagttgaaaa cggatatggc	1680
gccaagctg ccctaagtgg tctattccag ctttatagcg ttggtaagtt taatgcgacc	1740
gctgcacttg gtggctatgg ctcaaaatct gcggttgcta tcggtgctgg ctatcgtgtg	1800
aatccaaatc tggcgtttaa agctggtgcg gcgattaata ccagtggtaa taaaaaaggc	1860
tcttataaca tcggtgtgaa ttacgagttc taa	1893

<210> 75

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence

<400> 75

gaattcttaa ttaacatatg caggccaaaa atgatattac cctg

44

<210> 76
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 76
 ggcgcgccctc gagttattat ttggtatcca gtgcgggtcac acg 43

 <210> 77
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 77
 ggcgcgccctc gagttagtgt ttggtatcca gtgcgggtcac acg 43

 <210> 78
 <211> 46
 <212> DNA
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 <220>
 <223> Primer sequence

 <400> 78
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 <210> 79
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 tggcat 66

 <210> 80
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence

 <400> 80
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 <210> 81
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer sequence

<400> 81
ggaattccat atggcgaaaa atgatattac cctggaagat ctg 43

<210> 82
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 82
ggcgcgcctc gagttatggt tgtgctgcct gtgctgcat accatt 46

<210> 83
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 83
ggcgcgcctc gagttatgct gcctgtgctg ccataccatt 40

<210> 84
<211> 27
<212> DNA
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<220>
<223> Primer sequence

<400> 84
cagttcatta taggtggcca gacctg 27

<210> 85
<211> 4
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<220>
<223> N terminal amino acids of MC-001

<400> 85

Met Gln Ala Lys
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<210> 86
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> N terminal amino acid sequence

<400> 86

Ala Lys Asn Asp Ile Thr Leu Glu Asp Leu Pro
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<210> 87
 <211> 1542
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence for MC-003 Construct

<400> 87
 atgcaggcca aaaatgatat taccctggaa gatctgccgt atctgatcaa aaaaatcgat 60
 cagaacgaac tggaagccga tattggtgat attaccgcac tggaaaaata tctggcactg 120
 agccagtatg gaaatattct ggccctggaa gaactgaata aagctctgga agagctggat 180
 gaagatgtgg gttggaatca gaatgatatc gccaatctgg aagatgatgt tgaaaccctg 240
 accaaaaatc agaatgcact ggacagaacag ggtgaagcaa ttaaagaaga tctgcagggt 300
 ctggcagatt ttgttggaagg tcaggaaggc aaaattctgc agaacgaaac cagcatcaaa 360
 aaaaacaccc agcgtaatct ggtgaatggc tttgaaattg aaaaaaaca agatgccatt 420
 gccaaaaaca acgaaagcat tgaagatctg tatgattttg gtcatagaagt tgccgaaagc 480
 attggtgaaa ttcatgcaca taacgaagca cagaatgaaa ccctgaaagg tctgattacc 540
 aacagcatcg aaaataccaa taacattacc aaaaacaaag cagatattca ggcgctggaa 600
 aataatgttg tggaagaact gtttaatctg agcggtcgtc tgattgatca gaaagccgat 660
 atcgataata acattaacaa ctttatgaa ctggcacagc agcaggatca gcatagcagc 720
 gatatcaaaa ccctgaaaaa aaacgttgaa gaaggtctgc tggaactgtc tggtcacctg 780
 atcgatcaga aaactgatat tgcccagaat caggcaaata ttcaggatct ggccacctat 840
 aatgaactgc aggatcagta tgcacagaaa cagaccgaag caattgatgc cctgaataaa 900
 gcgagcagcg aaaacaccca gaatatcgaa gatctggcag catacaacga actgcaggat 960
 gcctatgcaa aacagcagac tgaagccatc gacgcactga acaaggcaag ctctgaaaac 1020
 acgcagaaca ttgaagatct ggctgcctat aatgaattac aggatgcgta tgccaaacag 1080
 cagaccgaag cgattgatgc gctgaacaaa gcctcttctg aaaatacaca gaatatcgcc 1140
 aaaaatcagg ccgatattgc caacaatatc aataatatct atgaactggc ccagcagcag 1200
 gatcagcact cttctgatat caaaacactg gcaaaagcaa gcgcagcaaa taccgatcgt 1260
 attgcgaaaa acaaagccga tgcagatgca agctttgaaa cactgacgaa aaaccagaac 1320
 accctgattg aaaaagataa agaacatgat aaactgatca ccgccaataa aaccgcaatt 1380
 gatgcaataa aagccagcgc agatacaaaa tttgcagcaa ccgcagatgc aattaccaaa 1440
 aatggcaatg ccatcaccaa aaatgcaaaa agcattaccg atctgggcac caaagttgat 1500
 ggttttgata gccgtgtgac cgactggat accaaacact aa 1542

<210> 88
 <211> 513
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Protein sequence for MC-003 Construct

<400> 88

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Lys Lys Ile Asp Gln Asn Glu Leu Glu Ala Asp Ile Gly Asp Ile Thr
 20 25 30

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

Leu Glu Glu Leu Asn Lys Ala Leu Glu Glu Leu Asp Glu Asp Val Gly
 50 55 60

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

Thr Lys Asn Gln Asn Ala Leu Ala Glu Gln Gly Glu Ala Ile Lys Glu
 85 90 95

Asp Leu Gln Gly Leu Ala Asp Phe Val Glu Gly Gln Glu Gly Lys Ile
 100 105 110

Leu Gln Asn Glu Thr Ser Ile Lys Lys Asn Thr Gln Arg Asn Leu Val
 115 120 125

Asn Gly Phe Glu Ile Glu Lys Asn Lys Asp Ala Ile Ala Lys Asn Asn
 130 135 140

Glu Ser Ile Glu Asp Leu Tyr Asp Phe Gly His Glu Val Ala Glu Ser
 145 150 155 160

Ile Gly Glu Ile His Ala His Asn Glu Ala Gln Asn Glu Thr Leu Lys
 165 170 175

Gly Leu Ile Thr Asn Ser Ile Glu Asn Thr Asn Asn Ile Thr Lys Asn
 180 185 190

Lys Ala Asp Ile Gln Ala Leu Glu Asn Asn Val Val Glu Glu Leu Phe
 195 200 205

Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn
 210 215 220

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

Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu Gly Leu Leu Glu Leu
 245 250 255

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

His

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