

MODIFIED TUBERCULOSIS ANTIGENS

FIELD OF THE INVENTION

5 The present invention relates to modified *Mycobacterium tuberculosis* Rv3616c proteins, associated polynucleotides and the use of such proteins and polynucleotides in the treatment or prevention of tuberculosis, in particular use in the treatment or prevention of latent tuberculosis and in the prevention or delay of reactivation of tuberculosis.

BACKGROUND OF THE INVENTION

10 Tuberculosis (TB) is a chronic infectious disease caused by infection with *Mycobacterium tuberculosis* and other *Mycobacterium* species. It is a major disease in developing countries, as well as an increasing problem in developed areas of the world. More than 2 billion people are believed to be infected with TB bacilli, with about 9.2 million new cases of TB and 1.7 million deaths each year. 10% of those infected with TB bacilli will develop active TB, each person with active TB infecting an average of 10 to 15 others per year. While annual incidence rates have peaked globally, the number of deaths and cases is still rising due to population growth (World Health Organisation *Tuberculosis Facts* 2008).

20 *Mycobacterium tuberculosis* infects individuals through the respiratory route. Alveolar macrophages engulf the bacterium, but it is able to survive and proliferate by inhibiting phagosome fusion with acidic lysosomes. A complex immune response involving CD4+ and CD8+ T cells ensues, ultimately resulting in the formation of a granuloma. Central to the success of *Mycobacterium tuberculosis* as a pathogen is the fact that the isolated, but not eradicated, bacterium may persist for long periods, leaving an individual vulnerable to the later development of active TB.

30 Fewer than 5% of infected individuals develop active TB in the first years after infection. The granuloma can persist for decades and is believed to contain live *Mycobacterium tuberculosis* in a state of dormancy, deprived of oxygen and nutrients. However, recently it has been suggested that the majority of the bacteria in the dormancy state are located in non-macrophage cell types spread throughout the body (Locht et al, *Expert Opin. Biol. Ther.* 2007 7(11):1665-1677). The development of active TB occurs when the balance between the host's natural immunity and the pathogen changes, for example as a result of an immunosuppressive

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event (Anderson P *Trends in Microbiology* 2007 15(1):7-13; Ehlers S *Infection* 2009 37(2):87-95).

A dynamic hypothesis describing the balance between latent TB and active TB has also been proposed (Cardana P-J *Inflammation & Allergy – Drug Targets* 2006 6:27-39; Cardana P-J *Infection* 2009 37(2):80-86).

Although an infection may be asymptomatic for a considerable period of time, the active disease is most commonly manifested as an acute inflammation of the lungs, resulting in tiredness, weight loss, fever and a persistent cough. If untreated, serious complications and death typically result.

Tuberculosis can generally be controlled using extended antibiotic therapy, although such treatment is not sufficient to prevent the spread of the disease. Actively infected individuals may be largely asymptomatic, but contagious, for some time. In addition, although compliance with the treatment regimen is critical, patient behaviour is difficult to monitor. Some patients do not complete the course of treatment, which can lead to ineffective treatment and the development of drug resistance.

Multidrug-resistant TB (MDR-TB) is a form which fails to respond to first line medications. 5% of all TB cases are MDR-TB, with an estimated 490,000 new MDR-TB cases occurring each year. Extensively drug-resistant TB (XDR-TB) occurs when resistance to second line medications develops on top of MDR-TB. It is estimated that 40,000 new cases of the virtually untreatable XDR-TB arise annually (World Health Organisation *Tuberculosis Facts* 2008).

Even if a full course of antibiotic treatment is completed, infection with *M. tuberculosis* may not be eradicated from the infected individual and may remain as a latent infection that can be reactivated.

In order to control the spread of tuberculosis, an effective vaccination programme and accurate early diagnosis of the disease are of utmost importance.

Currently, vaccination with live bacteria is the most widely used method for inducing protective immunity. The most common *Mycobacterium* employed for this purpose is *Bacillus Calmette-Guerin* (BCG), an avirulent strain of *M. bovis* which was first developed over 60 years ago. However, the safety and efficacy of BCG is a source of controversy - while protecting against

severe disease manifestation in children, BCG does not prevent the establishment of latent TB or the reactivation of pulmonary disease in adult life. Additionally, some countries, such as the United States, do not vaccinate the general public with this agent.

- 5 Almost all new generation TB vaccines which are currently in clinical development have been designed as pre-exposure vaccines. These include subunit vaccines, which have been particularly effective in boosting immunity induced by prior BCG vaccination, and advanced live mycobacterial vaccines which aim to replace BCG with more efficient and/or safer strains. Although these vaccines aim to improve resistance to infection, they are likely to be less effective as post-exposure or therapeutic vaccines in latent TB cases (Lin MY et al *Endocrine, Metabolic & Immune Disorders – Drug Targets* 2008 8:15-29).

Example 2 of US20080269151 discloses the cloning, construction and expression of certain modified Rv3616c proteins, including: Δ TM-1, an Rv3616c polypeptide wherein residues 150 to 160 have been deleted (SEQ ID No: 22 of US20080269151); Δ TM-2, an Rv3616c polypeptide wherein residues 101 to 203 have been deleted (SEQ ID No: 24 of US20080269151); and a sequence wherein residues 150 to 160 of Rv3616c have been replaced by the antigen TbH9 (SEQ ID No: 60 of US20080269151).

20 BRIEF SUMMARY OF THE INVENTION

The present invention relates generally to the use of modified Rv3616c polypeptides, or polynucleotides encoding them, in the field of latent *Mycobacterial* infections. Additionally, the present invention relates to particular modified Rv3616c proteins. The inventors have surprisingly discovered that disrupting the hydrophobicity of a particular region of a Rv3616c sequence can lead to improved expression without detrimental impact to immunogenic properties. The modified Rv3616c proteins are of use as TB antigens, in particular as latent TB antigens.

30 In its broadest aspect the present invention provides a modified Rv3616c protein in which the hydrophobicity of the amino acid residues corresponding to residues 134-183 of the H37Rv sequence has been disrupted, suitably a modified Rv3616c protein in which the hydrophobicity of the amino acid residues corresponding to residues 135-154 of the H37Rv sequence is disrupted.

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In one aspect of the invention there is provided a modified Rv3616c protein, said modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the C-terminus of the modified Rv3616c protein relative to the second polypeptide, and wherein:

- 5 (i) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked.

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In a second aspect of the invention there is provided a modified Rv3616c protein, said modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the C-terminus of the modified Rv3616c protein relative to the second polypeptide, and wherein:

- 15 (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked.

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In a third aspect of the invention there is provided a modified Rv3616c protein, said protein comprising or, alternatively, consisting essentially or consisting of, a Rv3616c sequence in which at least one amino acid (e.g. at least 2) has been deleted from the region corresponding to residues 134-183 in SEQ ID No:1.

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A fourth aspect of the invention provides a modified Rv3616c protein, said protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- 30 (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked via a third polypeptide, said third polypeptide corresponding to residues 134-183 in SEQ ID No:1 in which
 35 at least 1 amino acid (e.g. at least 2) has been deleted.

A fifth aspect of the invention provides modified Rv3616c proteins comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least 1 amino acid (e.g. at least 2) has been deleted.

A sixth aspect of the invention provides a modified Rv3616c protein, said protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 90% identity to a sequence corresponding to residues 134-183 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

A seventh aspect of the invention provides modified Rv3616c proteins comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 80% identity to a sequence corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

In an eighth aspect of the invention there is provided a modified Rv3616c protein, said protein comprising a Rv3616c sequence in which a contiguous portion of at least 3 amino acids (e.g. at least 4) from the region corresponding to residues 134-183 in SEQ ID No: 1 has been substituted with hydrophilic residues.

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Modified Rv3616c proteins may be based on a wild-type Rv3616c protein sequence from any strain of *M. tuberculosis*. For example, any one of SEQ ID Nos: 3-7, in particular any one of SEQ ID Nos: 3-6, may be substituted for SEQ ID No:1 in the foregoing embodiments.

10 Exemplary modified Rv3616c proteins according to the present invention are those comprising the amino acid sequences provided in SEQ ID Nos: 161-169, 179 and 180 (such as those consisting of the amino acid sequences provided in SEQ ID Nos: 161-169, 179 and 180). Of particular interest are those comprising the amino acid sequences provided in SEQ ID Nos: 161, 163-169, 179 and 180 (such as those consisting of the amino acid sequences provided in
15 SEQ ID Nos: 161, 163-169, 179 and 180).

Also provided are such modified Rv3616c proteins for use as medicaments.

20 A further aspect of the invention relates to a method for inducing an immune response in a subject, comprising the administration of a modified Rv3616c protein.

A further aspect of the invention relates to a method for the treatment, amelioration or prevention of TB comprising the administration of an effective amount of a modified Rv3616c protein to a subject in need thereof, wherein said polypeptide induces an immune response. In
25 a further aspect, the method further comprises inducing an immune response against *Mycobacterium tuberculosis*.

The use of a modified Rv3616c protein in the manufacture of a medicament for the treatment, amelioration or prevention of TB, represents another aspect of the invention.

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The present invention provides a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein. Exemplary polynucleotides comprising a nucleic acid sequence encoding modified Rv3616c proteins are those comprising the nucleotide sequences provided in SEQ ID Nos: 170-178, such as those consisting of the nucleotide sequences provided in
35 SEQ ID Nos: 170-178. Other exemplary polynucleotides comprising a nucleic acid sequence encoding modified Rv3616c proteins are those comprising (e.g. consisting of) a nucleotide

sequence encoding an amino acid sequences provided in SEQ ID Nos: 161-169, 179 or 180, such as SEQ ID Nos: 161, 163-169, 179 or 180.

Also provided is a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein for use as a medicament.

A further aspect of the invention relates to a method for inducing an immune response in a subject, comprising the administration of a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein.

A further aspect of the invention relates to a method for the treatment, amelioration, delaying or prevention of tuberculosis reactivation comprising the administration of an effective amount of a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein to a subject in need thereof, wherein said polypeptide induces and immune response. In a further aspect, the method further comprises inducing an immune response against *Mycobacterium tuberculosis*.

Use of a polynucleotide comprising a nucleic acid sequence encoding a polypeptide comprising a modified Rv3616c protein in the manufacture of a medicament for the treatment, amelioration or prevention of TB, represents another aspect of the invention.

Additionally, there is provided a pharmaceutical composition comprising:

- (a) a modified Rv3616c protein; or
- (b) a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein;
- and
- (c) a pharmaceutically acceptable carrier or excipient.

Further, there is provided an immunogenic composition comprising:

- (a) a modified Rv3616c protein; or
- (b) a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein;
- and
- (c) a non-specific immune response enhancer.

Also provided is an expression vector comprising a nucleic acid sequence encoding a modified Rv3616c protein.

Host cells, transformed with said expression vector, form a further aspect of the invention.

5 Additionally provided is a host cell which recombinantly expresses a modified Rv3616c protein.

Further, there is provided a method for the production of a modified Rv3616c protein; said method comprising the step of recombinantly expressing said polypeptide within a host cell.

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Also provided are diagnostic kits comprising:

- (a) a modified Rv3616c protein;
- (b) apparatus sufficient to contact said modified Rv3616c protein with a sample (e.g. whole blood or more suitably PBMC) from an individual; and
- 15 (c) means to quantify the T cell response of the sample.

Another aspect of the invention relates to a diagnostic kit comprising:

- (a) a modified Rv3616c protein; and
- (b) apparatus sufficient to contact said modified Rv3616c protein with the dermal
- 20 cells of a patient.

A further aspect of the invention relates to a method for detecting *Mycobacterium tuberculosis* infection in a subject comprising:

- (a) contacting a sample from said subject with a modified Rv3616c protein; and
- 25 (b) detecting in the biological sample the presence of antibodies that bind to the modified Rv3616c protein.

The invention also provides a diagnostic kit comprising:

- (a) a modified Rv3616c protein, which protein is optionally immobilised on a solid
- 30 support; and
- (b) a detection reagent.

In one embodiment the subject receiving a modified Rv3616c protein, polynucleotide or composition according the invention may have active tuberculosis (e.g. active infection by *M. tuberculosis*). In a second embodiment the subject may have latent tuberculosis (e.g. dormant

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infection by *M. tuberculosis*). In a third embodiment the subject may be free from tuberculosis (e.g. free from infection by *M. tuberculosis*).

A subject receiving a modified Rv3616c protein, polynucleotide or composition according to the invention may have previously been vaccinated for tuberculosis (e.g. vaccinated against infection by *M. tuberculosis*), such as having been vaccinated with a *Bacillus* Calmette-Guerin (BCG). Alternatively, a subject receiving a polypeptide, polynucleotide or composition of the invention may not have previously been vaccinated for tuberculosis (e.g. not vaccinated against infection by *M. tuberculosis*), such as not having been vaccinated with a *Bacillus* Calmette-Guerin (BCG).

A modified Rv3616c protein, polynucleotide or composition according the invention may be provided for the purpose of:

- treating active tuberculosis;
- preventing active tuberculosis (such as by administering to a subject who is uninfected, or alternatively a subject who has a latent infection);
- treating latent tuberculosis;
- preventing latent tuberculosis; or
- preventing or delaying reactivation of tuberculosis (especially the delay of TB reactivation, for example by a period of months, years or even indefinitely).

There is also provided a method for the treatment of latent TB comprising the steps:

- (i) identifying a subject as having a latent TB infection (e.g. by PPD or T cell based assays); and
- (ii) administering to said subject a safe and effective amount of a modified Rv3616c protein or polynucleotide encoding a modified Rv3616c protein (such as in the form of a pharmaceutical composition or immunogenic composition).

Also provided is the use of a polypeptide of the present invention in the manufacture of a diagnostic kit for the identification of TB (e.g. latent TB) in a test subject.

DESCRIPTION OF THE FIGURES

Figure 1: Rv3616c peptide alignment with full length sequence

Figure 2: PBMC responses to Rv3616c peptides.

Figure 3	Percentage of CD4 and CD8 cells from immunised CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at day 21 (i.e. 7 days post second immunisation).
Figure 4	Cytokine profile at day 21 (i.e. 7 days post second immunisation) of the antigen specific CD4 response in immunised CB6F1 mice.
Figure 5	Cytokine profile at day 21 (i.e. 7 days post second immunisation) of the antigen specific CD8 response in immunised CB6F1 mice.
Figure 6	Percentage of CD4 and CD8 cells from immunised CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at day 35 (i.e. 7 days post third immunisation).
Figure 7	Cytokine profile at day 35 (i.e. 7 days post third immunisation) of the antigen specific CD4 response in immunised CB6F1 mice.
Figure 8	Cytokine profile at day 35 (i.e. 7 days post third immunisation) of the antigen specific CD8 response in immunised CB6F1 mice.
Figure 9	Percentage of CD4 and CD8 cells from immunised C57BL/6 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at day 21 (i.e. 7 days post second immunisation).
Figure 10	Cytokine profile at day 21 (i.e. 7 days post second immunisation) of the antigen specific CD4 response in immunised C57BL/6 mice.
Figure 11	Percentage of CD4 and CD8 cells from immunised C57BL/6 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at day 35 (i.e. 7 days post third immunisation).
Figure 12	Cytokine profile at day 35 (i.e. 7 days post third immunisation) of the antigen specific CD4 response in immunised C57BL/6 mice.
Figure 13	Cytokine profile at day 35 (i.e. 7 days post third immunisation) of the antigen specific CD8 response in immunised C57BL/6 mice.
Figure 14	Antigen-specific CD4 T cell responses in naive and latently infected humans.
Figure 15	Alignment of wild-type Rv3616c protein sequences.
Figure 16A and 16B	Alignment of exemplary modified Rv3616c protein sequences.
Figure 17	SDS-PAGE results of initial antigen expression experiments.
Figure 18	SDS-PAGE results of further antigen expression experiments.
Figure 19	SDS-PAGE results of additional antigen expression experiments.
Figure 20	Percentage of CD4 cells from immunised mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 7 days post second and 7 days post third immunisations with Rv3616Δ138-145.

- Figure 21: Cytokine profile of the Rv3616 specific CD4 T cell response at 7 days post second immunisation with Rv3616Δ138-145.
- Figure 22: Cytokine profile of the Rv3616 specific CD4 T cell response at 7 days post third immunisation with Rv3616Δ138-145.
- 5 Figure 23: Percentage of CD8 cells from immunised mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 7 days post second and 7 days post third immunisations with Rv3616Δ138-145.
- Figure 24: Cytokine profile of the Rv3616 specific CD8 T cell response at 7 days post second immunisation with Rv3616Δ138-145.
- 10 Figure 25: Cytokine profile of the Rv3616 specific CD8 T cell response at 7 days post third immunisation with Rv3616Δ138-145.

DESCRIPTION OF THE LISTED SEQUENCES

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- SEQ ID No: 1: polypeptide sequence of Rv3616c from *M. tuberculosis* H37Rv strain.
- SEQ ID No: 2: polynucleotide sequence of Rv3616c from *M. tuberculosis* H37Rv strain.
- SEQ ID No: 3: polypeptide sequence of Rv3616c from *M. tuberculosis* CDC1551 strain.
- SEQ ID No: 4: polypeptide sequence of Rv3616c from *M. tuberculosis* F11 strain.
- 20 SEQ ID No: 5: polypeptide sequence of Rv3616c from *M. tuberculosis* Haarlem A strain.
- SEQ ID No: 6: polypeptide sequence of Rv3616c from *M. tuberculosis* C strain.
- SEQ ID No: 7: polypeptide sequence of Rv3616c from BCG.
- SEQ ID No: 8: polypeptide sequence of Mtb8.4.
- 25 SEQ ID No: 9: polypeptide sequence of Mtb9.8.
- SEQ ID No: 10: polypeptide sequence of Mtb9.9.
- SEQ ID No: 11: polypeptide sequence of Ra12.
- SEQ ID No: 12: polypeptide sequence of Ra35.
- SEQ ID No: 13: polypeptide sequence of TbH9.
- 30 SEQ ID No: 14: polypeptide sequence of Mtb41.
- SEQ ID No: 15: polypeptide sequence of ESAT-6.
- SEQ ID No: 16: polypeptide sequence of Ag85A.
- SEQ ID No: 17: polypeptide sequence of Ag85B.
- SEQ ID No: 18: polypeptide sequence of alpha-crystallin.
- 35 SEQ ID No: 19: polypeptide sequence of MPT64.
- SEQ ID No: 20: polypeptide sequence of Mtb32A.

	SEQ ID No: 21:	polypeptide sequence of Ser/Ala mutated mature Mtb32A.
	SEQ ID No: 22:	polypeptide sequence of TB10.4.
	SEQ ID No: 23:	polypeptide sequence of Mtb72f.
	SEQ ID No: 24:	polypeptide sequence of M72.
5	SEQ ID No: 25:	polypeptide sequence of Mtb71f.
	SEQ ID No: 26:	polypeptide sequence of M92 fusion.
	SEQ ID No: 27:	polypeptide sequence of M103 fusion.
	SEQ ID No: 28:	polypeptide sequence of M114 fusion.
	SEQ ID No: 29:	putative human CD4 cell epitope 1.
10	SEQ ID No: 30:	putative human CD4 cell epitope 2.
	SEQ ID No: 31:	putative human CD4 cell epitope 3.
	SEQ ID No: 32:	putative human CD4 cell epitope 4.
	SEQ ID No: 33:	putative human CD4 cell epitope 5.
	SEQ ID No: 34:	putative human CD4 cell epitope 6.
15	SEQ ID No: 35:	putative human CD4 cell epitope 7.
	SEQ ID No: 36:	putative human CD4 cell epitope 8.
	SEQ ID No: 37:	putative human CD4 cell epitope 9.
	SEQ ID No: 38:	putative human CD4 cell epitope 10.
	SEQ ID No: 39:	putative human CD4 cell epitope 11.
20	SEQ ID No: 40:	putative human CD4 cell epitope 12.
	SEQ ID No: 41:	putative human CD4 cell epitope 13.
	SEQ ID No: 42:	putative human CD4 cell epitope 14.
	SEQ ID No: 43:	putative human CD4 cell epitope 15.
	SEQ ID No: 44:	putative human CD4 cell epitope 16.
25	SEQ ID No: 45:	putative human CD4 cell epitope 17.
	SEQ ID No: 46:	putative human CD4 cell epitope 18.
	SEQ ID No: 47:	putative human CD4 cell epitope 19.
	SEQ ID No: 48:	putative human CD8 cell epitope 1.
	SEQ ID No: 49:	putative human CD8 cell epitope 2.
30	SEQ ID No: 50:	putative human CD8 cell epitope 3.
	SEQ ID No: 51:	putative human CD8 cell epitope 4.
	SEQ ID No: 52:	putative human CD8 cell epitope 5.
	SEQ ID No: 53:	putative human CD8 cell epitope 6.
	SEQ ID No: 54:	putative human CD8 cell epitope 7.
35	SEQ ID No: 55:	putative human CD8 cell epitope 8.
	SEQ ID No: 56:	putative human CD8 cell epitope 9.

	SEQ ID No: 57:	putative human CD8 cell epitope 10.
	SEQ ID No: 58:	putative human CD8 cell epitope 11.
	SEQ ID No: 59:	putative human CD8 cell epitope 12.
	SEQ ID No: 60:	putative human CD8 cell epitope 13.
5	SEQ ID No: 61:	putative human CD8 cell epitope 14.
	SEQ ID No: 62:	putative human CD8 cell epitope 15.
	SEQ ID No: 63:	putative human CD8 cell epitope 16.
	SEQ ID No: 64:	putative human CD8 cell epitope 17.
	SEQ ID No: 65:	putative human CD8 cell epitope 18.
10	SEQ ID No: 66:	putative human CD8 cell epitope 19.
	SEQ ID No: 67:	putative human CD8 cell epitope 20.
	SEQ ID No: 68:	putative human CD8 cell epitope 21.
	SEQ ID No: 69:	putative human CD8 cell epitope 22.
	SEQ ID No: 70:	putative human CD8 cell epitope 23.
15	SEQ ID No: 71:	putative human CD8 cell epitope 24.
	SEQ ID No: 72:	putative human CD8 cell epitope 25.
	SEQ ID No: 73:	putative human CD8 cell epitope 26.
	SEQ ID No: 74:	putative human CD8 cell epitope 27.
	SEQ ID No: 75:	putative human CD8 cell epitope 28.
20	SEQ ID No: 76:	putative human CD8 cell epitope 29.
	SEQ ID No: 77:	putative human CD8 cell epitope 30.
	SEQ ID No: 78:	putative human CD8 cell epitope 31.
	SEQ ID No: 79:	putative human CD8 cell epitope 32.
	SEQ ID No: 80:	putative human CD8 cell epitope 33.
25	SEQ ID No: 81:	putative human CD8 cell epitope 34.
	SEQ ID No: 82:	putative human CD8 cell epitope 35.
	SEQ ID No: 83:	putative human CD8 cell epitope 36.
	SEQ ID No: 84:	putative human CD8 cell epitope 37.
	SEQ ID No: 85:	putative human CD8 cell epitope 38.
30	SEQ ID No: 86:	putative human CD8 cell epitope 39.
	SEQ ID No: 87:	putative human CD8 cell epitope 40.
	SEQ ID No: 88:	putative human CD8 cell epitope 41.
	SEQ ID No: 89:	putative human CD8 cell epitope 42.
	SEQ ID No: 90:	putative human CD8 cell epitope 43.
35	SEQ ID No: 91:	putative human CD8 cell epitope 44.
	SEQ ID No: 92:	putative human CD8 cell epitope 45.

	SEQ ID No: 93:	putative human CD8 cell epitope 46.
	SEQ ID No: 94:	putative human CD8 cell epitope 47.
	SEQ ID No: 95:	putative human CD8 cell epitope 48.
	SEQ ID No: 96:	putative human CD8 cell epitope 49.
5	SEQ ID No: 97:	putative human CD8 cell epitope 50.
	SEQ ID No: 98:	putative human CD8 cell epitope 51.
	SEQ ID No: 99:	putative human CD8 cell epitope 52.
	SEQ ID No: 100:	putative human CD8 cell epitope 53.
	SEQ ID No: 101:	putative human CD8 cell epitope 54.
10	SEQ ID No: 102:	putative human CD8 cell epitope 55.
	SEQ ID No: 103:	putative human CD8 cell epitope 56.
	SEQ ID No: 104:	putative human CD8 cell epitope 57.
	SEQ ID No: 105:	putative human CD8 cell epitope 58.
	SEQ ID No: 106:	putative human CD8 cell epitope 59.
15	SEQ ID No: 107:	putative human CD8 cell epitope 60.
	SEQ ID No: 108:	putative human CD8 cell epitope 61.
	SEQ ID No: 109:	putative human CD8 cell epitope 62.
	SEQ ID No: 110:	putative human CD8 cell epitope 63.
	SEQ ID No: 111:	putative human CD8 cell epitope 64.
20	SEQ ID No: 112:	putative human CD8 cell epitope 65.
	SEQ ID No: 113:	putative human CD8 cell epitope 66.
	SEQ ID No: 114:	putative human CD8 cell epitope 67.
	SEQ ID No: 115:	putative human CD8 cell epitope 68.
	SEQ ID No: 116:	putative human CD8 cell epitope 69.
25	SEQ ID No: 117:	putative human CD8 cell epitope 70.
	SEQ ID No: 118:	putative human CD8 cell epitope 71.
	SEQ ID No: 119:	putative human CD8 cell epitope 72.
	SEQ ID No: 120:	putative human CD8 cell epitope 73.
	SEQ ID No: 121:	putative human CD8 cell epitope 74.
30	SEQ ID No: 122:	putative human CD8 cell epitope 75.
	SEQ ID No: 123:	putative human CD8 cell epitope 76.
	SEQ ID No: 124:	putative human CD8 cell epitope 77.
	SEQ ID No: 125:	putative human CD8 cell epitope 78.
	SEQ ID No: 126:	putative human CD8 cell epitope 79.
35	SEQ ID No: 127:	peptide 1.
	SEQ ID No: 128:	peptide 2.

	SEQ ID No: 129:	peptide 3.
	SEQ ID No: 130:	peptide 4.
	SEQ ID No: 131:	peptide 5.
	SEQ ID No: 132:	peptide 6.
5	SEQ ID No: 133:	peptide 7.
	SEQ ID No: 134:	peptide 8.
	SEQ ID No: 135:	peptide 9.
	SEQ ID No: 136:	peptide 10.
	SEQ ID No: 137:	peptide 11.
10	SEQ ID No: 138:	peptide 12.
	SEQ ID No: 139:	peptide 13.
	SEQ ID No: 140:	peptide 14.
	SEQ ID No: 141:	peptide 15.
	SEQ ID No: 142:	peptide 16.
15	SEQ ID No: 143:	peptide 17.
	SEQ ID No: 144:	peptide 18.
	SEQ ID No: 145:	peptide 19.
	SEQ ID No: 146:	peptide 20.
	SEQ ID No: 147:	peptide 21.
20	SEQ ID No: 148:	peptide 22.
	SEQ ID No: 149:	peptide 23.
	SEQ ID No: 150:	peptide 24.
	SEQ ID No: 151:	peptide 25.
	SEQ ID No: 152:	peptide 26.
25	SEQ ID No: 153:	peptide 27.
	SEQ ID No: 154:	peptide 28.
	SEQ ID No: 155:	peptide 29.
	SEQ ID No: 156:	peptide 30.
	SEQ ID No: 157:	polypeptide sequence of Rv1753c from <i>M. tuberculosis</i> H37Rv strain.
30	SEQ ID No: 158:	polypeptide sequence of Rv2386c from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 159:	polypeptide sequence of Rv2707c from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 160:	<i>E. coli</i> codon optimised polynucleotide sequence for Rv3616c from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 161:	polypeptide sequence of Rv3616c Δ 136-183 derived from <i>M. tuberculosis</i> H37Rv strain.
35		

	SEQ ID No: 162:	polypeptide sequence of Rv3616cΔ150-160 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 163:	polypeptide sequence of Rv3616cΔ136-154 derived from <i>M. tuberculosis</i> H37Rv strain.
5	SEQ ID No: 164:	polypeptide sequence of Rv3616cΔ166-182 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 165:	polypeptide sequence of Rv3616cΔ135-139 derived from <i>M. tuberculosis</i> H37Rv strain.
10	SEQ ID No: 166:	polypeptide sequence of Rv3616cΔ142-145 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 167:	polypeptide sequence of Rv3616cΔ138-145 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 168:	polypeptide sequence of Rv3616cΔ145-152 derived from <i>M. tuberculosis</i> H37Rv strain.
15	SEQ ID No: 169:	polypeptide sequence of Rv3616cΔ149-154 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 170:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ136-183 derived from <i>M. tuberculosis</i> H37Rv strain.
20	SEQ ID No: 171:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ150-160 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 172:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ136-154 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 173:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ166-182 derived from <i>M. tuberculosis</i> H37Rv strain.
25	SEQ ID No: 174:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ135-139 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 175:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ142-145 derived from <i>M. tuberculosis</i> H37Rv strain.
30	SEQ ID No: 176:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ138-145 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 177:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ145-152 derived from <i>M. tuberculosis</i> H37Rv strain.
	SEQ ID No: 178:	<i>E. coli</i> codon optimised polynucleotide sequence encoding Rv3616cΔ149-154 derived from <i>M. tuberculosis</i> H37Rv strain.

SEQ ID No: 179 polypeptide sequence of modified Rv3616c protein based on separating and rearrangement around the residues 137-139 from *M. tuberculosis* H37Rv strain, including deletion of Cys138.

5 SEQ ID No: 180. polypeptide sequence of modified Rv3616c protein based on separating and rearrangement around the residues 152-153 from *M. tuberculosis* H37Rv strain.

DETAILED DESCRIPTION

10 The present invention relates generally to the use of modified Rv3616c polypeptides, or polynucleotides encoding them, in the field of latent *Mycobacterial* infections. Additionally, the present invention relates to particular modified Rv3616c proteins. The inventors have surprisingly discovered that disrupting the hydrophobicity of a particular region of a Rv3616c protein sequence can lead to improved expression without substantial detrimental impact to
15 immunogenic properties. The modified Rv3616c proteins are of use as TB antigens, in particular as latent TB antigens.

Several of the proteins which are strongly expressed during the early stages of *Mycobacterium* infection have been shown to provide strong protective efficacy in animal vaccination models.

20 However, vaccination with antigens which are highly expressed during the early stages of infection may not provide an optimal immune response for dealing with later stages of infection. Adequate control during latent infection may require T cells which are specific for the particular antigens which are expressed at that time.

25 Post-exposure vaccines which directly target the dormant persistent bacteria may aid in protecting against TB reactivation, thereby enhancing TB control, or even enabling clearance of the infection. A vaccine targeting latent TB could therefore significantly and economically reduce global TB infection rates.

30 Subunit vaccines based on late stage antigens could also be utilised in combination with early stage antigens to provide a multiphase vaccine. Alternatively, late stage antigens could be used to complement and improve BCG vaccination (either by boosting the BCG response or through the development of advanced recombinant BCG strains).

35 While macrophages have been shown to act as the principal effectors of *Mycobacterium* immunity, T cells are the predominant inducers of such immunity. The essential role of T cells

in protection against tuberculosis is illustrated by the increased rates of TB reactivation in human immunodeficiency virus infected individuals, due to the associated depletion of CD4⁺ T cells. Furthermore, adoptive transfer of CD4⁺ T cells taken at the height of the primary immune response to *M. tuberculosis* has been shown to confer protection against *M.*

5 *tuberculosis* in T cell deficient mice (Orme et al *J. Exp. Med.* 1983 158:74-83).

Mycobacterium-reactive CD4⁺ T cells have been shown to be potent producers of γ -interferon (IFN- γ), which, in turn, has been shown to trigger the anti-mycobacterial effects of macrophages in mice (Flynn et al. *J. Exp. Med.* 1993 178:2249-2254). While the role of IFN- γ

10 in humans is less clear, studies have shown that 1,25-dihydroxy-vitamin D₃, either alone or in combination with IFN- γ or tumor necrosis factor- α , activates human macrophages to inhibit *M. tuberculosis* infection. Furthermore, it is known that IFN- γ stimulates human macrophages to make 1,25-dihydroxy-vitamin D₃. Similarly, interleukin-12 (IL-12) has been shown to play a role in stimulating resistance to *M. tuberculosis* infection. For a review of the immunology of *M.*
15 *tuberculosis* infection, see Chan & Kaufmann, *Tuberculosis: Pathogenesis, Protection and Control* (Bloom ed., 1994), *Tuberculosis* (2nd ed., Rom and Garay, eds., 2003), and *Harrison's Principles of Internal Medicine*, Chapter 150, pp. 953-966 (16th ed., Braunwald, et al., eds., 2005).

20 Diagnosis of latent TB infection is commonly achieved using the tuberculin skin test, which involves intradermal exposure to tuberculin protein-purified derivative (PPD). Antigen-specific T cell responses result in measurable induration at the injection site by 48-72 hours after injection, which indicates exposure to mycobacterial antigens. Sensitivity and specificity have, however, been a problem with this test, and individuals vaccinated with BCG cannot always be
25 easily distinguished from infected individuals (this is particularly important in light of the fact that BCG does not protect against latent infection). In general, individuals who have received BCG but are not infected by *M. tuberculosis* show a PPD reaction below 10 mm in diameter whereas people who have a PPD reaction above 10 mm in diameter are considered to have been infected by *M. tuberculosis*. However, this rule is not applicable to individuals with
30 immunosuppression due to HIV infection, which may result in a PPD reaction below 10 mm in diameter); or in endemic countries, where people infected by non-tuberculosis mycobacteria can show a PPD reaction above 10 mm in diameter.

Progress over recent years has seen the development of *in vitro* T cell based assays, based
35 on interferon-gamma release and using antigens which are more specific to *M. tuberculosis* than PPD, namely ESAT-6 and CFP-10. These high specificity tests appear to be at least as

sensitive as the tuberculin skin test and also demonstrate less cross-reactivity due to BCG vaccination. See Pai M et al *Expert Rev. Mol. Diagn.* 2006 6(3):413-422 for a recent review of latent TB diagnosis. However, since ESAT-6/CFP-10 are early stage antigens, assays based on ESAT-6/CFP-10 may only perform optimally in recently infected people. Consequently, the
 5 identification of antigens specifically associated with latent tuberculosis may aid the development of more sensitive assays that could ensure detection of longer-term latent infections.

There remains a need for effective strategies for the treatment and prevention of tuberculosis,
 10 in particular the treatment and prevention of latent TB and the prevention of reactivation of TB.

Recently, a range of *M. tuberculosis* vaccine candidates have been proposed based on a bioinformatics analysis of the whole genome *M. tuberculosis* genome (Zvi et al. *BMC Medical Genetics* 2008 1:18) and on the testing of differentially expressed proteins in actively and
 15 latently infected individuals (Schuck SD et al. *PLoS ONE* 2009 4(5):e5590).

Rv3616c, also known as Mtb40, HTCC1 and EspA, is involved in the *Mycobacterium tuberculosis* ESX-1 secretion system (Woodsworth et al. *Infection and Immunity* 2008 76(9):4199-4205). Rv3616c has previously been implicated in the immune responses
 20 associated with tuberculosis (see, for example, WO98/53075). Al-Attiyah et al. *Clin. Exp. Immunol.* 2004 138:139-144 have shown that Rv3616c is well recognised (through PMBC proliferation and IFN-gamma production) by pulmonary tuberculosis patients. Mustafa et al. *Infect. Immun.* 2006 74(8):4566-4572 have investigated the recognition of Rv3616c by *M. bovis* infected and BCG vaccinated cattle.

International patent application PCT/EP2009/059580, published as WO2010/010177, describes the identification of Rv3616c as an antigen associated with the latent stage of TB infection.

International patent application WO2010/121618 proposes the use of constitutively expressed proteins and the genes encoding them for immunological compositions such as vaccines, including EspA (i.e. Rv3616c).

Vaccine antigens are desirably produced having their wild-type sequence, thus ensuring that
 35 the immunological responses solicited by the vaccine correspond closely to those required to counter infection by a pathogen. Nevertheless, efficient production of antigens is an important

factor in reducing the costs associated with vaccine manufacture. Consequently, modified antigens which are conveniently expressed at high levels but which avoid any detrimental impact on immunogenicity could provide a substantial benefit. The present invention seeks to provide modified Rv3616c antigens which address this and other issues.

5

Without being limited by theory, amino acid residues 134-183 of the *Mycobacterium tuberculosis* H37Rv strain Rv3616c are thought to correspond to a potential transmembrane region, a low complexity region and a coiled-coil. The disruption of one, two or all three of these structural elements enables the resultant modified Rv3616c protein sequence to be expressed at improved levels.

10

Consequently, in its broadest aspect the present invention provides a modified Rv3616c protein in which the hydrophobicity of the amino acid residues corresponding to residues 134-183 of the H37Rv sequence has been disrupted, suitably a modified Rv3616c protein in which the hydrophobicity of the amino acid residues corresponding to residues 135-154 of the H37Rv sequence is disrupted.

15

By the term 'disrupting the hydrophobicity' is meant a sequence modification which results in a sufficiently reduced hydrophobicity such that the modified Rv3616c protein sequence may be expressed more efficiently.

20

Desirably, the extent of modifications relative to the wild-type sequence should be kept to a minimum, to reduce the likelihood of any detrimental impact on immunogenicity.

As used herein, a 'direct peptide linkage' is a peptide linkage in which two peptides are linked via peptide bonds directly to each other and without an intervening amino acid sequence. An 'indirect peptide linkage' is a peptide linkage in which two peptides are linked via peptide bonds to a third, intervening peptide.

25

In the context of the present invention, four main approaches exist for disrupting the hydrophobicity – namely, separating hydrophobic residues, deleting hydrophobic residues, substituting hydrophobic residues with hydrophilic residues and adding hydrophilic residues. The skilled person will recognise that a combination of such approaches may also be utilised. However, as mentioned previously the extent of the sequence modifications should ideally be minimised to avoid unnecessary detrimental impact on immunogenicity.

30

35

Separating hydrophobic residues may be achieved by splitting an Rv3616c protein sequence at a location between the amino acids corresponding to residues 133 to 184 of SEQ ID No: 1 into an N-terminal and a C-terminal fragment, followed by rearranging such portions such that the N-terminal fragment is located in the C-terminal region of the modified Rv3616c protein and the C-terminal fragment is located in the N-terminal region of the modified Rv3616c protein.

In one aspect of the invention there is provided a modified Rv3616c protein, said modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the C-terminus of the modified Rv3616c protein relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked.

In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the C-terminus of the modified Rv3616c protein relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked.

The first polypeptide may be a sequence having at least 95% identity to residues 1-133 of SEQ ID No: 1, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

The second polypeptide may be a sequence having at least 95% identity to residues 184-392 of SEQ ID No: 1, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

Suitably, the first polypeptide may be a sequence having at least 90% identity to residues 1-134 of SEQ ID No: 1, in particular at least 95% identity, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

- 5 Suitably, the second polypeptide may be a sequence having at least 90% identity to residues 155-392 of SEQ ID No: 1, in particular at least 95% identity, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

10 Suitably the modified Rv3616c protein of the first aspect does not comprise a sequence having at least 90% identity to full length SEQ ID No: 1. Suitably, the modified Rv3616c protein of the first aspect is less than 500 amino acids long, such as less than 450 amino acids long, in particular less than 400 amino acids long.

The peptide linkage may be direct. The peptide linkage may alternatively be indirect.

15

In a second aspect of the invention there is provided a modified Rv3616c protein, said modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the C-terminus of the modified Rv3616c protein relative to the second polypeptide, and wherein:

- 20 (iii) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
(iv) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked.

25

In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the C-terminus of the modified Rv3616c protein relative to the second polypeptide, and wherein:

- 30 (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
(ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked.

35

The first polypeptide may be a contiguous sequence of at least 110 amino acids within residues 1-133 of SEQ ID No: 1, such as at least 120 amino acids or at least 130 amino acids, for example residues 1-133.

- 5 The second polypeptide may be a contiguous sequence of at least 180 amino acids within residues 184-392 of SEQ ID No: 1, such as at least 190 amino acids or at least 200 amino acids, for example residues 184-392.

- 10 Suitably, the first polypeptide may be a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1, in particular at least 110 amino acids, such as at least 120 amino acids or at least 130 amino acids, for example residues 1-134.

- 15 Suitably, the second polypeptide may be a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1, in particular at least 200 amino acids such as at least 210 amino acids or at least 220 amino acids, for example residues 155-392.
Embodiments wherein the second polypeptide is a contiguous sequence of at least 235 amino acids within residues 155-392 of SEQ ID No: 1 are also of interest.

- 20 Suitably the modified Rv3616c protein of the second aspect does not comprise a contiguous sequence of more than 259 amino acids from SEQ ID No: 1. Alternatively, the modified Rv3616c protein of the second aspect does not comprise a contiguous sequence of more than 257 amino acids, a contiguous sequence of more than 255 amino acids or a contiguous sequence of more than 253 amino acids. Suitably the modified Rv3616c protein of the second aspect is less than 500 amino acids long, such as less than 450 amino acids long, in particular
25 less than 400 amino acids long.

The peptide linkage may either be a direct or indirect linkage.

- 30 Examples of the first and second aspects include modified Rv3616c proteins wherein the first and second polypeptide correspond to the N-terminal and C-terminal fragments resulting from splitting an Rv3616c sequence at a location between the amino acids corresponding to residues 135-154 in SEQ ID No: 1, e.g. the residues 138-139 or 152-153, e.g. the residues 138-139 or 152-153 where the peptide linkage is direct. Suitably when the first and second polypeptides are rearranged, the start methionine is left at the N-terminus of the modified
35 Rv3616c protein. See for example SEQ ID Nos: 179 and 180 which illustrate this type of

arrangement.

Deleting hydrophobic residues may be achieved through the removal of at least one amino acid corresponding to residues 134 to 183 of SEQ ID No: 1. Deleted residues may be non-
5 contiguous, and/or contiguous.

Suitably, deleting hydrophobic residues may be achieved through the removal of at least two amino acids corresponding to residues 134 to 183 of SEQ ID No: 1. Deleting hydrophobic residues may also be achieved through the removal of at least three amino acids
10 corresponding to residues 134 to 183 of SEQ ID No: 1.

Deleted residues may be non-contiguous, and/or contiguous.

It may be noted that the wild-type Rv3616c sequences contain a Cys residue at location 138.
15 Suitably, this Cys residue is deleted or replaced (e.g. C138Q).

In a third aspect of the invention there is provided a modified Rv3616c protein, said protein comprising or, alternatively, consisting essentially or consisting of, a Rv3616c sequence in which at least one amino acid (e.g. at least 2) has been deleted from the region corresponding
20 to residues 134-183 in SEQ ID No:1.

The modified Rv3616c protein may comprise or, alternatively, consists essentially or consist of, a Rv3616c sequence in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted from the region corresponding to residues 134-183 in SEQ ID No:1.
25

Of particular interest are modified Rv3616c proteins comprising a Rv3616c sequence in which at least 1 amino acid (e.g. at least 2) has been deleted from the region corresponding to residues 135-154 in SEQ ID No:1. Other sequences of interest are modified Rv3616c proteins comprising a Rv3616c sequence in which a contiguous portion of at least 3 amino acids (e.g.
30 at least 4) has been deleted from the region corresponding to residues 135-154 in SEQ ID No:1.

The deleted contiguous portion may be at least 5 amino acids (e.g. 5 to 30, such as 5 to 20 or 5 to 15), especially at least 6 amino acids (e.g. 6 to 30, such as 6 to 20 or 6 to 15), in particular
35 at least 7 amino acids (e.g. 7 to 30, such as 7 to 20 or 7 to 15), such as at least 8 amino acids

(e.g. 8 to 30, such as 8 to 20 or 8 to 15), or at least 10 amino acids (e.g. 10 to 30, such as 10 to 20 or 10 to 15).

In certain embodiments the deleted contiguous portion may be:

- 5 - 4 amino acids, such as those corresponding to residues 142-145 in SEQ ID No:1;
- 5 amino acids, such as those corresponding to residues 135-139 in SEQ ID No:1;
- 6 amino acids, such as those corresponding to residues 149-154 in SEQ ID No:1;
- 8 amino acids, such as those corresponding to residues 138-145 in SEQ ID No:1 or residues 145-152 in SEQ ID No:1;
- 10 - 11 amino acids, such as those corresponding to residues 150-160 in SEQ ID No:1;
- 17 amino acids, such as those corresponding to residues 166-182 in SEQ ID No:1;
- 19 amino acids, such as those corresponding to residues 136-154 in SEQ ID No:1;
- 31 amino acids, such as those corresponding to residues 136-166 in SEQ ID No:1; or
- 48 amino acids, such as those corresponding to residues 136-183 in SEQ ID No:1.

15

In other embodiments the deleted contiguous portion may be 3 to 10 amino acid residues, such as 4 to 10, for example 4 to 8. The particular number of deleted amino acids may be 3, 4, 5, 6, 7, 8, 9 or 10, especially 4, 5, 6 or 8.

- 20 In other embodiments the deleted portion may be those corresponding to residues 135-138 in SEQ ID No: 1, residues 136-138 in SEQ ID No: 1, residues 137-138 in SEQ ID No: 1, residues 138-140 in SEQ ID No: 1, residues 138-141 in SEQ ID No: 1, residues 152-154 in SEQ ID No: 1 or the deletion of residues 149-151 in SEQ ID No: 1.

- 25 A fourth aspect of the invention provides a modified Rv3616c protein, said protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (iii) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- 30 (iv) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked via a third polypeptide, said third polypeptide corresponding to residues 134-183 in SEQ ID No:1 in which at least 1 amino acid (e.g. at least 2) has been deleted.

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In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked via a third polypeptide, said third polypeptide corresponding to residues 134-183 in SEQ ID No:1 in which at least 1 amino acid (e.g. at least 2) has been deleted.

Of particular interest are proteins comprising, or alternatively consisting essentially or consisting of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked via a third polypeptide, said third polypeptide corresponding to residues 134-183 in SEQ ID No:1 in which at least a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

The first polypeptide may be a contiguous sequence of at least 110 amino acids within residues 1-133 of SEQ ID No: 1, such as at least 120 amino acids or at least 130 amino acids (for example residues 1-133).

The second polypeptide may be a contiguous sequence of at least 180 amino acids within residues 184-392 of SEQ ID No: 1, such as at least 190 amino acids or at least 200 amino acids (for example residues 184-392).

The deleted contiguous portion from the residues corresponding to 134-183 in SEQ ID No:1 may be at least 5 amino acids (e.g. 5 to 30, such as 5 to 20 or 5 to 15), especially at least 6 amino acids (e.g. 6 to 30, such as 6 to 20 or 6 to 15), in particular at least 7 amino acids (e.g. 7 to 30, such as 7 to 20 or 7 to 15), such as at least 8 amino acids (e.g. 8 to 30, such as 8 to 20 or 8 to 15), or at least 10 amino acids (e.g. 10 to 30, such as 10 to 20 or 10 to 15).

In certain embodiments the deleted contiguous portion from the residues corresponding to 134-183 in SEQ ID No:1 may be:

- 4 amino acids, such as those corresponding to residues 142-145 in SEQ ID No:1;
- 5 amino acids, such as those corresponding to residues 135-139 in SEQ ID No:1;
- 5 - 6 amino acids, such as those corresponding to residues 149-154 in SEQ ID No:1;
- 8 amino acids, such as those corresponding to residues 138-145 in SEQ ID No:1 or residues 145-152 in SEQ ID No:1;
- 11 amino acids, such as those corresponding to residues 150-160 in SEQ ID No:1;
- 17 amino acids, such as those corresponding to residues 166-182 in SEQ ID No:1;
- 10 - 19 amino acids, such as those corresponding to residues 136-154 in SEQ ID No:1;
- 31 amino acids, such as those corresponding to residues 136-166 in SEQ ID No:1; or
- 48 amino acids, such as those corresponding to residues 136-183 in SEQ ID No:1.

15 In other embodiments the deleted contiguous portion from the residues corresponding to 134-183 in SEQ ID No:1 may be may be 3 to 10 amino acid residues, such as 4 to 10, for example 4 to 8. The particular number of deleted amino acids may be 3, 4, 5, 6, 7, 8, 9 or 10, especially 4, 5, 6 or 8.

20 In other embodiments the deleted contiguous portion from the residues corresponding to 134-183 in SEQ ID No:1 may be those corresponding to residues 135-138 in SEQ ID No: 1, residues 136-138 in SEQ ID No: 1, residues 137-138 in SEQ ID No: 1, residues 138-140 in SEQ ID No: 1, residues 138-141 in SEQ ID No: 1, residues 152-154 in SEQ ID No: 1 or the deletion of residues 149-151 in SEQ ID No: 1.

25 The first polypeptide and second polypeptide will in some embodiments be directly linked. In other embodiments the first polypeptide and second polypeptide will be indirectly linked via a third polypeptide. The third polypeptide may correspond to residues 134-183 in SEQ ID No: 1 wherein deletion has occurred at a single contiguous portion of at least 3 amino acids (e.g. at least 4). Additionally, the third polypeptide may correspond to residues 134-183 in SEQ ID No: 30 1 wherein deletions have occurred at a plurality of distinct locations (e.g. 1-10, such as 1-5, in particular 1 or 2 locations), each deletion being of 1-10, such as 1-5 amino acid residues.

35 Suitably the third polypeptide is 48 amino acids or fewer (e.g. 10-48, such as 20-48 or 30-48 residues), such as 46 amino acids or fewer (e.g. 10-46, such as 20-46 or 30-46 residues), 44 amino acids or fewer (e.g. 10-44, such as 20-44 or 30-44 residues), or 42 amino acids or fewer (e.g. 10-42, such as 20-42 or 30-42 residues).

A fifth aspect of the invention provides modified Rv3616c proteins comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- 5 (iii) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (iv) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;

10 wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least 1 amino acid (e.g. at least 2) has been deleted.

15 In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;

20 wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least 1 amino acid (e.g. at least 2) has been deleted.

25 Of particular interest are proteins comprising, or alternatively consisting essentially or consisting of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;

30 wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

35

The first polypeptide may also be a contiguous sequence of at least 110 amino acids within residues 1-134 of SEQ ID No: 1, such as at least 120 amino acids or at least 130 amino acids, for example residues 1-134.

- 5 The second polypeptide may also be a contiguous sequence of at least 200 amino acids within residues 155-392 of SEQ ID No: 1, such as at least 210 amino acids or at least 220 amino acids, for example residues 155-392. Embodiments wherein the second polypeptide is a contiguous sequence of at least 235 amino acids within residues 155-392 of SEQ ID No: 1 are also of interest.

10

The deleted contiguous portion from the residues corresponding to 135-154 in SEQ ID No: 1 may be at least 5 amino acids (e.g. 5 to 20, such as 5 to 15 or 5 to 10), especially at least 6 amino acids (e.g. 6 to 20, such as 6 to 15 or 6 to 10), in particular at least 7 amino acids (e.g. 7 to 20, such as 7 to 15 or 7 to 10), such as at least 8 amino acids (e.g. 8 to 20, such as 8 to 15 or 8 to 10), or at least 10 amino acids (e.g. 10 to 20, such as 10 to 15).

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In certain embodiments the deleted contiguous portion from the residues corresponding to 135-154 in SEQ ID No: 1 may be:

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- 4 amino acids, such as those corresponding to residues 142-145 in SEQ ID No:1;
- 6 amino acids, such as those corresponding to residues 149-154 in SEQ ID No:1;
- 8 amino acids, such as those corresponding to residues 138-145 in SEQ ID No:1 or residues 145-152 in SEQ ID No:1;
- 11 amino acids, such as those corresponding to residues 150-160 in SEQ ID No:1; or
- 19 amino acids, such as those corresponding to residues 136-154 in SEQ ID No:1.

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In other embodiments the deleted contiguous portion from the residues corresponding to 135-154 may be 3 to 10 amino acid residues, such as 4 to 10, for example 4 to 8. The particular number of deleted amino acids may be 3, 4, 5, 6, 7, 8, 9 or 10, especially 4, 5, 6 or 8.

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In other embodiments the deleted contiguous portion from the residues corresponding to 135-154 in SEQ ID No: 1 may be those corresponding to residues 135-138 in SEQ ID No: 1, residues 136-138 in SEQ ID No: 1, residues 137-138 in SEQ ID No: 1, residues 138-140 in SEQ ID No: 1, residues 138-141 in SEQ ID No: 1, residues 152-154 in SEQ ID No: 1 or the deletion of residues 149-151 in SEQ ID No: 1.

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The first polypeptide and second polypeptide may in some embodiments be directly linked. In other embodiments the first polypeptide and second polypeptide may be indirectly linked via a third polypeptide. The third polypeptide may correspond to residues 135-154 in SEQ ID No: 1 wherein deletion has occurred at a single contiguous portion of at least 3 amino acids (e.g. at least 4). Additionally, the third polypeptide may correspond to residues 135-154 in SEQ ID No: 1 wherein deletions have occurred at a plurality of distinct locations (e.g. 1-10, such as 1-5, in particular 1 or 2 locations), each deletion being of 1-10, such as 1-5 amino acid residues.

Suitably the third polypeptide is 20 amino acids or fewer (e.g. 5-20, such as 10-20 residues), such as 18 amino acids or fewer (e.g. 5-18, such as 10-18 residues), 16 amino acids or fewer (e.g. 5-16, such as 10-16 residues), or 14 amino acids or fewer (e.g. 5-14, such as 10-14 residues).

A sixth aspect of the invention provides a modified Rv3616c protein, said protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

(iii) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and

(iv) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 90% identity to a sequence corresponding to residues 134-183 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

(i) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and

(ii) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 90% identity to a sequence corresponding to residues 134-183 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

The first polypeptide may be a sequence having at least 95% identity to residues 1-133 of SEQ ID No: 1, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

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The second polypeptide may be a sequence having at least 95% identity to residues 184-392 of SEQ ID No: 1, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

- 10 The first polypeptide and second polypeptide may in some embodiments be directly linked. In other embodiments the first polypeptide and second polypeptide will be indirectly linked via a third polypeptide. The third polypeptide may be a sequence having at least 95% identity to a sequence corresponding to residues 134-183 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

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The contiguous portion deleted from the residues corresponding to 134-183 in SEQ ID No: 1 may be at least 5 amino acids (e.g. 5 to 30, such as 5 to 20 or 5 to 15), especially at least 6 amino acids (e.g. 6 to 30, such as 6 to 20 or 6 to 15), in particular at least 7 amino acids (e.g. 7 to 30, such as 7 to 20 or 7 to 15), such as at least 8 amino acids (e.g. 8 to 30, such as 8 to 20 or 8 to 15), or at least 10 amino acids (e.g. 10 to 30, such as 10 to 20 or 10 to 15).

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In certain embodiments the contiguous portion deleted from the residues corresponding to 134-183 in SEQ ID No: 1 may be:

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- 4 amino acids, such as those corresponding to residues 142-145 in SEQ ID No:1;
- 5 amino acids, such as those corresponding to residues 135-139 in SEQ ID No:1;
- 6 amino acids, such as those corresponding to residues 149-154 in SEQ ID No:1;
- 8 amino acids, such as those corresponding to residues 138-145 in SEQ ID No:1 or residues 145-152 in SEQ ID No:1;

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- 11 amino acids, such as those corresponding to residues 150-160 in SEQ ID No:1;
- 17 amino acids, such as those corresponding to residues 166-182 in SEQ ID No:1;
- 19 amino acids, such as those corresponding to residues 136-154 in SEQ ID No:1;
- 31 amino acids, such as those corresponding to residues 136-166 in SEQ ID No:1; or
- 48 amino acids, such as those corresponding to residues 136-183 in SEQ ID No:1.

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In other embodiments the deleted contiguous portion may be 3 to 10 amino acid residues, such as 4 to 10, for example 4 to 8. The particular number of deleted amino acids may be 3, 4, 5, 6, 7, 8, 9 or 10, especially 4, 5, 6 or 8.

In other embodiments the contiguous portion deleted from the residues corresponding to 134-183 in SEQ ID No: 1 may be those corresponding to residues 135-138 in SEQ ID No: 1, residues 136-138 in SEQ ID No: 1, residues 137-138 in SEQ ID No: 1, residues 138-140 in SEQ ID No: 1, residues 138-141 in SEQ ID No: 1, residues 152-154 in SEQ ID No: 1 or the deletion of residues 149-151 in SEQ ID No: 1.

Suitably the third polypeptide is 48 amino acids or fewer (e.g. 10-48, such as 20-48 or 30-48 residues), such as 46 amino acids or fewer (e.g. 10-46, such as 20-46 or 30-46 residues), 44 amino acids or fewer (e.g. 10-44, such as 20-44 or 30-44 residues), or 42 amino acids or fewer (e.g. 10-42, such as 20-42 or 30-42 residues).

A seventh aspect of the invention provides modified Rv3616c proteins comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 80% identity to a sequence corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of, a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a sequence having at least 90% identity to residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 80% identity to a sequence

corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted.

The first polypeptide may be a sequence having at least 95% identity to residues 1-134 of SEQ ID No: 1, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

The second polypeptide may be a sequence having at least 95% identity to residues 155-392 of SEQ ID No: 1, such as at least 97% identity, at least 98% identity, at least 99% identity or even 100% identical.

The first polypeptide and second polypeptide will in some embodiments be directly linked. In other embodiments the first polypeptide and second polypeptide will be indirectly linked via a third polypeptide. The third polypeptide may be a sequence having at least 90% identity to a sequence corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids (e.g. at least 4) has been deleted, such as at least 95% identity, at least 98% identity, at least 99% identity or even 100% identical.

The contiguous portion deleted contiguous portion from the residues corresponding to 135-154 in SEQ ID No: 1 may be at least 5 amino acids (e.g. 5 to 20, such as 5 to 15 or 5 to 10), especially at least 6 amino acids (e.g. 6 to 20, such as 6 to 15 or 6 to 10), in particular at least 7 amino acids (e.g. 7 to 20, such as 7 to 15 or 7 to 10), such as at least 8 amino acids (e.g. 8 to 20, such as 8 to 15 or 8 to 10), or at least 10 amino acids (e.g. 10 to 20, such as 10 to 15).

In certain embodiments the contiguous portion deleted contiguous portion from the residues corresponding to 135-154 in SEQ ID No: 1 may be:

- 4 amino acids, such as those corresponding to residues 142-145 in SEQ ID No:1;
- 6 amino acids, such as those corresponding to residues 149-154 in SEQ ID No:1;
- 8 amino acids, such as those corresponding to residues 138-145 in SEQ ID No:1 or residues 145-152 in SEQ ID No:1;
- 11 amino acids, such as those corresponding to residues 150-160 in SEQ ID No:1; or
- 19 amino acids, such as those corresponding to residues 136-154 in SEQ ID No:1.

In other embodiments the deleted contiguous portion may be 3 to 10 amino acid residues, such as 4 to 10, for example 4 to 8. The particular number of deleted amino acids may be 3, 4, 5, 6, 7, 8, 9 or 10, especially 4, 5, 6 or 8.

In other embodiments the contiguous portion deleted contiguous portion from the residues corresponding to 135-154 in SEQ ID No: 1 may be those corresponding to residues 135-138 in SEQ ID No: 1, residues 136-138 in SEQ ID No: 1, residues 137-138 in SEQ ID No: 1, residues 138-140 in SEQ ID No: 1, residues 138-141 in SEQ ID No: 1, residues 152-154 in SEQ ID No: 1 or the deletion of residues 149-151 in SEQ ID No: 1.

Suitably the third polypeptide is 20 amino acids or fewer (e.g. 5-20, such as 10-20 residues), such as 18 amino acids or fewer (e.g. 5-18, such as 10-18 residues), 16 amino acids or fewer (e.g. 5-16, such as 10-16 residues), or 14 amino acids or fewer (e.g. 5-14, such as 10-14 residues).

Substituting hydrophobic residues may be achieved through the replacement of at least one (e.g. at least 2) amino acid corresponding to residues 134 to 183 of SEQ ID No: 1 with a hydrophilic residue. In this regard, suitable hydrophilic residues will typically be Gln (Q), Asp (D), Glu (E), Asn (N), His (H), Lys (K), Arg (R), Ser (S) or Thr (T).

Of particular interest is the replacement of at least one (e.g. at least 2) amino acid corresponding to residues 135 to 154 of SEQ ID No: 1 with a hydrophilic residue. In this regard, suitable hydrophilic residues will typically be Gln (Q), Asp (D), Glu (E), Asn (N), His (H), Lys (K), Arg (R), Ser (S) or Thr (T).

Substituted residues may be non-contiguous, although are suitably contiguous.

In a eighth aspect of the invention there is provided a modified Rv3616c protein, said protein comprising a Rv3616c sequence in which a contiguous portion of at least 3 amino acids (e.g. at least 4) from the region corresponding to residues 134-183 in SEQ ID No: 1 has been substituted with hydrophilic residues.

In some embodiments the modified Rv3616c protein consists essentially of, or alternatively consists of a Rv3616c sequence in which a contiguous portion of at least 3 amino acids (e.g. at least 4) from the region corresponding to residues 134-183 in SEQ ID No: 1 has been substituted with hydrophilic residues.

Of particular interest are modified Rv3616c proteins comprising an Rv3616c sequence in which a contiguous portion of at least 3 amino acids (e.g. at least 4) from the region

corresponding to residues 135-154 in SEQ ID No: 1 has been substituted with hydrophilic residues.

The substituted contiguous portion may be at least 5 amino acids (e.g. 5 to 30, such as 5 to 20 or 5 to 15), especially at least 6 amino acids (e.g. 6 to 30, such as 6 to 20 or 6 to 15), in particular at least 7 amino acids (e.g. 7 to 30, such as 7 to 20 or 7 to 15), such as at least 8 amino acids (e.g. 8 to 30, such as 8 to 20 or 8 to 15), or at least 10 amino acids (e.g. 10 to 30, such as 10 to 20 or 10 to 15).

10 In certain embodiments the substituted contiguous portion may be:

- 4 amino acids, such as those corresponding to residues 142-145 in SEQ ID No:1;
- 5 amino acids, such as those corresponding to residues 135-139 in SEQ ID No:1;
- 6 amino acids, such as those corresponding to residues 149-154 in SEQ ID No:1;
- 8 amino acids, such as those corresponding to residues 138-145 in SEQ ID No:1 or residues 145-152 in SEQ ID No:1;
- 11 amino acids, such as those corresponding to residues 150-160 in SEQ ID No:1;
- 17 amino acids, such as those corresponding to residues 166-182 in SEQ ID No:1;
- 19 amino acids, such as those corresponding to residues 136-154 in SEQ ID No:1;
- 31 amino acids, such as those corresponding to residues 136-166 in SEQ ID No:1; or
- 48 amino acids, such as those corresponding to residues 136-183 in SEQ ID No:1.

In other embodiments the substituted contiguous portion may be 3 to 10 amino acid residues, such as 4 to 10, for example 4 to 8. The particular number of substituted amino acids may be 3, 4, 5, 6, 7, 8, 9 or 10, especially 4, 5, 6 or 8.

In other embodiments the substituted portion may be those corresponding to residues 135-138 in SEQ ID No: 1, residues 136-138 in SEQ ID No: 1, residues 137-138 in SEQ ID No: 1, residues 138-140 in SEQ ID No: 1, residues 138-141 in SEQ ID No: 1, residues 152-154 in SEQ ID No: 1 or the deletion of residues 149-151 in SEQ ID No: 1.

Disrupting the hydrophobicity may also be achieved by adding hydrophilic residues, e.g. the addition of at least one hydrophilic amino acid residue (e.g. at least 2, such as 2-10) at a location between those residues corresponding to residues 133 to 184 of SEQ ID No: 1. Suitably, at least 3 hydrophilic residues may be added (e.g. 3 to 20, such as 3 to 15, especially 3 to 10), such as at least 4 residues (e.g. 4 to 20, such as 4 to 15, especially 4 to 10), in particular at least 5 residues (e.g. 5 to 20, such as 5 to 15, especially 5 to 10), optionally at

least 6 residues (e.g. 6 to 20, such as 6 to 15, especially 6 to 10). In this regard, suitable hydrophilic residues will typically be Gln (Q), Asp (D), Glu (E), Asn (N), His (H), Lys (K), Arg (R), Ser (S) or Thr (T).

- 5 The additional hydrophilic residues will typically be located between those residues corresponding to residues 133 to 184 of SEQ ID No: 1, especially between those residues corresponding to residues 134 to 155 of SEQ ID No: 1 (such as between those residues corresponding to residues 135 to 154 of SEQ ID No: 1).
- 10 The additional hydrophilic residues may be distributed at different positions between those residues corresponding to residues 133 to 184 of SEQ ID No: 1 (e.g. 1-10 locations, such as 1-5, in particular 1 or 2 locations), each location having 1-10 additional hydrophilic residues, such as 1-5 additional residues. The additional hydrophilic residues will suitably be located in one contiguous group.

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In particular embodiments of the modified Rv3616c proteins described in the various aspects above, the modified Rv3616c protein is not SEQ ID No: 162 (Rv3616c Δ 150-160). In other embodiments the modified Rv3616c protein does not comprise SEQ ID No: 162 (Rv3616c Δ 150-160).

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Modified Rv3616c proteins may be based on a wild-type Rv3616c protein sequence from any strain of *M. tuberculosis*. For example, any one of SEQ ID Nos: 3-7, in particular any one of SEQ ID Nos: 3-6, may be substituted for SEQ ID No:1 in the foregoing embodiments.

- 25 Proteins of the various aspects discussed above are collectively referred to herein as modified Rv3616c proteins. Also provided are such modified Rv3616c proteins for use as medicaments, such as a medicament for the treatment or prevention of TB.

- 30 A further aspect of the invention relates to a method for inducing an immune response in a subject, comprising the administration of a modified Rv3616c protein.

- 35 A further aspect of the invention relates to a method for the treatment, amelioration or prevention of TB comprising the administration of a safe and effective amount of a modified Rv3616c protein to a subject in need thereof, wherein said polypeptide induces an immune response. In a further aspect, the method further comprises inducing an immune response against *Mycobacterium tuberculosis*.

A further aspect of the invention relates to a method for the treatment, amelioration, delaying or prevention of tuberculosis reactivation comprising the administration of an effective amount of a modified Rv3616c protein to a subject in need thereof, wherein said polypeptide induces and immune response. In a further aspect, the method further comprises inducing an immune response against *Mycobacterium tuberculosis*.

The use of a modified Rv3616c protein in the manufacture of a medicament for the treatment, amelioration or prevention of TB, represents another aspect of the invention.

The present invention provides a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein. Also provided is a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein for use as a medicament, such as a medicament for the treatment, amelioration or prevention of TB.

A further aspect of the invention relates to a method for inducing an immune response in a subject, comprising the administration of a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein.

A further aspect of the invention relates to a method for the treatment, amelioration or prevention of TB comprising the administration of a safe and effective amount of a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein to a subject in need thereof, wherein said polynucleotide induces an immune response. In a further aspect, the present invention provides a method for inducing an immune response against *Mycobacterium tuberculosis*.

A further aspect of the invention relates to a method for the treatment, amelioration, delaying or prevention of tuberculosis reactivation comprising the administration of an effective amount of a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein to a subject in need thereof, wherein said polypeptide induces and immune response. In a further aspect, the method further comprises inducing an immune response against *Mycobacterium tuberculosis*.

Use of a polynucleotide comprising a nucleic acid sequence encoding a polypeptide comprising a modified Rv3616c protein in the manufacture of a medicament for the treatment, amelioration or prevention of TB, represents another aspect of the invention.

Additionally, there is provided a pharmaceutical composition comprising:

- (a) a modified Rv3616c protein; or
- (b) a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein;
- and
- (c) a pharmaceutically acceptable carrier or excipient.

Further, there is provided an immunogenic composition comprising:

- (a) a modified Rv3616c protein; or
- (b) a polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein;
- and
- (c) a non-specific immune response enhancer.

Also provided is an expression vector comprising a nucleic acid sequence encoding a modified Rv3616c protein.

Host cells, transformed with said expression vector, form a further aspect of the invention.

Additionally provided is a host cell which recombinantly expresses a modified Rv3616c protein.

Further, there is provided a method for the production of a modified Rv3616c protein; said method comprising the step of recombinantly expressing said polypeptide within a host cell.

Also provided are diagnostic kits comprising:

- (a) a modified Rv3616c protein;
- (b) apparatus sufficient to contact said modified Rv3616c protein with a sample (e.g. whole blood or more suitably PBMC) from an individual; and
- (c) means to quantify the T cell response of the sample.

Another aspect of the invention relates to a diagnostic kit comprising:

- (a) a modified Rv3616c protein; and
- (b) apparatus sufficient to contact said modified Rv3616c protein with the dermal cells of a patient.

A further aspect of the invention relates to a method for detecting *Mycobacterium tuberculosis* infection in a subject comprising:

- (a) contacting a sample from said subject with a modified Rv3616c protein; and
- (b) detecting in the biological sample the presence of antibodies that bind to the modified Rv3616c protein.

The invention also provides a diagnostic kit comprising:

- (a) a modified Rv3616c protein, which protein is optionally immobilised on a solid support; and
- (b) a detection reagent.

In one embodiment the subject receiving a modified Rv3616c protein, polynucleotide or composition according the invention may have active tuberculosis (e.g. active infection by *M. tuberculosis*). In a second embodiment the subject may have latent tuberculosis (e.g. dormant infection by *M. tuberculosis*). In a third embodiment the subject may be free from tuberculosis (e.g. free from infection by *M. tuberculosis*).

A subject receiving a modified Rv3616c protein, polynucleotide or composition according to the invention may have previously been vaccinated for tuberculosis (e.g. vaccinated against infection by *M. tuberculosis*), such as having been vaccinated with a *Bacillus Calmette-Guerin* (BCG). Alternatively, a subject receiving a polypeptide, polynucleotide or composition of the invention may have not been previously vaccinated for tuberculosis (e.g. not vaccinated against infection by *M. tuberculosis*), such as not having been vaccinated with a *Bacillus Calmette-Guerin* (BCG).

A modified Rv3616c protein, polynucleotide or composition according the invention may be provided for the purpose of:

- treating active tuberculosis;
- preventing active tuberculosis (such as by administering to a subject who is uninfected, or alternatively a subject who has latent infection);
- treating latent tuberculosis;
- preventing latent tuberculosis; or
- preventing or delaying reactivation of tuberculosis (especially the delay of TB reactivation, for example by a period of months, years or even indefinitely).

There is also provided a method for the treatment of latent TB comprising the steps:

- (i) identifying a subject as having a latent TB infection (e.g. by PPD or T cell based assays); and
- (ii) administering to said subject a safe and effective amount of a modified Rv3616c protein or polynucleotide encoding a modified Rv3616c protein (such as in the form of a pharmaceutical composition or immunogenic composition).

Also provided is the use of a polypeptide of the present invention in the manufacture of a diagnostic kit for the identification of TB (e.g. latent TB) in a test subject.

- 10 The term “*Mycobacterium* species of the tuberculosis complex” includes those species traditionally considered as causing the disease tuberculosis, as well as *Mycobacterium* environmental and opportunistic species that cause tuberculosis and lung disease in immune compromised patients, such as patients with AIDS, e.g., *M. tuberculosis*, *M. bovis*, or *M. africanum*, BCG, *M. avium*, *M. intracellulare*, *M. celatum*, *M. genavense*, *M. haemophilum*,
 15 *M. kansasii*, *M. simiae*, *M. vaccae*, *M. fortuitum*, and *M. scrofulaceum* (see, e.g., *Harrison's Principles of Internal Medicine*, Chapter 150, pp. 953-966 (16th ed., Braunwald, *et al.*, eds., 2005). The present invention is particularly directed to infection with *M. tuberculosis*.

- The term “active infection” refers to an infection (e.g. infection by *M. tuberculosis*) with
 20 manifested disease symptoms and/or lesions (suitably with manifested disease symptoms).

- The terms “inactive infection”, “dormant infection” or “latent infection” refer to an infection (e.g. infection by *M. tuberculosis*) without manifested disease symptoms and/or lesions (suitably without manifested disease symptoms). A subject with latent infection will suitably be one
 25 which tests positive for infection (e.g. by PPD or T cell based assays) but which has not demonstrated the disease symptoms and/or lesions which are associated with an active infection.

- The term “primary tuberculosis” refers to clinical illness (e.g., manifestation of disease symptoms) directly following infection (e.g. infection by *M. tuberculosis*). See, *Harrison's Principles of Internal Medicine*, Chapter 150, pp. 953-966 (16th ed., Braunwald, *et al.*, eds., 2005).

- The terms “secondary tuberculosis” or “postprimary tuberculosis” refer to the reactivation of a
 35 dormant, inactive or latent infection (e.g. infection by *M. tuberculosis*). See, *Harrison's*

Principles of Internal Medicine, Chapter 150, pp. 953-966 (16th ed., Braunwald, *et al.*, eds., 2005).

The term “tuberculosis reactivation” refers to the later manifestation of disease symptoms in an individual that tests positive for infection (e.g. in a tuberculin skin test, suitably in an *in vitro* T cell based assay) test but does not have apparent disease symptoms. Suitably the individual will not have been re-exposed to infection. The positive diagnostic test indicates that the individual is infected, however, the individual may or may not have previously manifested active disease symptoms that had been treated sufficiently to bring the tuberculosis into an inactive or latent state. It will be recognised that methods for the prevention, delay or treatment of tuberculosis reactivation can be initiated in an individual manifesting active symptoms of disease.

The term “drug resistant” tuberculosis refers to an infection (e.g. infection by *M. tuberculosis*) wherein the infecting strain is not held static or killed (i.e. is resistant to) one or more of so-called “front-line” chemotherapeutic agents effective in treating tuberculosis (e.g., isoniazid, rifampin, ethambutol, streptomycin and pyrazinamide).

The term “multi-drug resistant” tuberculosis refers to an infection (e.g. infection by *M. tuberculosis*) wherein the infecting strain is resistant to two or more of “front-line” chemotherapeutic agents effective in treating tuberculosis.

A “chemotherapeutic agent” refers to a pharmacological agent known and used in the art to treat tuberculosis (e.g. infection by *M. tuberculosis*). Exemplified pharmacological agents used to treat tuberculosis include, but are not limited to amikacin, aminosalicylic acid, capreomycin, cycloserine, ethambutol, ethionamide, isoniazid, kanamycin, pyrazinamide, rifamycins (*i.e.*, rifampin, rifapentine and rifabutin), streptomycin, ofloxacin, ciprofloxacin, clarithromycin, azithromycin and fluoroquinolones. “First-line” or “Front-line” chemotherapeutic agents used to treat tuberculosis that is not drug resistant include isoniazid, rifampin, ethambutol, streptomycin and pyrazinamide. “Second-line” chemotherapeutic agents used to treat tuberculosis that has demonstrated drug resistance to one or more “first-line” drugs include ofloxacin, ciprofloxacin, ethionamide, aminosalicylic acid, cycloserine, amikacin, kanamycin and capreomycin. Such pharmacological agents are reviewed in Chapter 48 of *Goodman and Gilman's The Pharmacological Basis of Therapeutics*, Hardman and Limbird eds., 2001.

The terms “polypeptide”, “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Suitably a polypeptide according to the present invention will consist only of naturally occurring amino acid residues, especially those amino acids encoded by the genetic code.

“Nucleic acid” refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

By the term ‘Rv3616c protein sequence’ as used herein is meant the Rv3616c polypeptide sequence provided in SEQ ID No: 1 or a homologue thereof from a *Mycobacterium* species of the tuberculosis complex, e.g., a species such as *M. tuberculosis*, *M. bovis*, or *M. africanum*, or a *Mycobacterium* species that is environmental or opportunistic and that causes opportunistic infections such as lung infections in immune compromised hosts (e.g., patients with AIDS), e.g., *BCG*, *M. avium*, *M. intracellulare*, *M. celatum*, *M. genavense*, *M. haemophilum*, *M. kansasii*, *M. simiae*, *M. vaccae*, *M. fortuitum*, and *M. scrofulaceum* (see, e.g., *Harrison’s Principles of Internal Medicine*, Chapter 150, pp. 953-966, 16th ed., Braunwald, et al., eds., 2005).

To ensure a high efficacy rate among vaccinated hosts, the components of a vaccine should be well conserved among the strains of clinical significance. Suitably, the Rv3616c protein is derived from *M. tuberculosis* H37Rv (i.e. the polypeptide sequence provided in SEQ ID No: 1) or a homologue thereof from another *M. tuberculosis* strain (such as CDC1551, F11, Haarlem A and C strains). Strains of *M. tuberculosis* which are associated with drug resistance (e.g. MDR or especially XDR) are a particularly valuable basis for the wild-type Rv3616c protein sequence. Strains of interest include:

CDC1551 - transmissible and virulent strain

Haarlem family (such as Haarlem A) - Drug resistant strains found in crowded human populations. Members of the Haarlem family of *M. tuberculosis* strains have been found in many parts of the world. The first representative of the family was discovered in Haarlem, The Netherlands.

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KZN4207 - Drug sensitive isolate from patients in KwaZulu-Natal, South Africa

KZN1435 - Multiple drug resistant (MDR) isolate from patients in KwaZulu-Natal, South Africa

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KZN605 - Extensively drug resistant (XDR) isolate from patients in KwaZulu-Natal, South Africa

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C - Highly transmitted in New York City. In one study this strain was found to be more common among injection drug users and resistant to reactive nitrogen intermediates (Friedman et al. *J. Infect. Dis.* 1997 176(2):478-84)

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94 M4241A - Isolated in San Francisco in 1994 from a patient born in China. This strain was previously analysed by genomic deletion analysis (Gagneux et al., *PNAS* 2006 103(8):2869-2873).

25

02 1987 - Isolated in San Francisco in 2002 from a patient born in South Korea. This strain was previously analyzed by genomic deletion analysis (Gagneux et al., *PNAS* 2006 103(8):2869-2873).

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T92 - Isolated in San Francisco in 1999 from a patient born in The Philippines. This strain was published in Hirsh et al. *PNAS* 2004 101:4871–4876).

T85 - Isolated in San Francisco in 1998 from a patient born in China. This strain was published in Hirsh et al. *PNAS* 2004 101:4871–4876).

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EAS054 - Isolated in San Francisco in 1993 from a patient born in India. This strain was previously analyzed by genomic deletion analysis (Gagneux et al., *PNAS* 2006 103(8):2869-2873).

Gagneux et al., *PNAS* 2006 103(8):2869-2873 and Herbert et al. *Infect. Immun.* 2007 75(12):5798-5805 provide valuable background on the range of *M. tuberculosis* strains which are known to exist.

- 5 Most suitably, the Rv3616c protein is selected from the polypeptide sequences provided in SEQ ID Nos: 1 and 3-7, in particular SEQ ID Nos: 1 and 3-6, such as SEQ ID No: 1. An alignment of SEQ ID Nos: 1 and 3-7 is provided in Figure 15.

- Modified Rv3616c proteins of particular interest are those comprising (e.g. consisting of) SEQ
10 ID Nos: 161-169.

Polynucleotides of particular interest are those derived from the wild-type sequences corresponding to the *M. tuberculosis* strains discussed above, such as those derived from SEQ ID No: 2 or its related *E. coli* codon optimised SEQ ID No: 160.

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COMBINATIONS

- A sequence containing the modified Rv3616c proteins (or associated polynucleotides) of the present invention can further comprise other components designed to enhance their
20 immunogenicity or to improve these antigens in other respects. For example, improved isolation of the polypeptide antigens may be facilitated through the addition of a stretch of histidine residues (commonly known as a his-tag) towards one end of the antigen.

- The term "his-tag" refers to a string of histidine residues, typically six residues, that are
25 inserted within the reference sequence. To minimise disruption of the activity associated with the reference sequence, a his-tag is typically inserted at the N-terminus, usually immediately after the initiating methionine residue, or else at the C-terminus. They are usually heterologous to the native sequence but are incorporated since they facilitate isolation by improving the protein binding to immobilised metal affinity chromatography resins (IMAC). Generally
30 speaking the presence or absence of a his-tag is not of significance from the point of view of eliciting a desirable immune response against the reference protein. However, to avoid the risk of an adverse reaction against the his-tag itself, it is considered best to minimise the length of the his-tag e.g. to four or fewer residues, in particular two residues, or to exclude the use of a his-tag entirely.

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To improve the magnitude and/or breadth of the elicited immune response compositions, polypeptides (and nucleic acids encoding them) can be prepared which comprise multiple modified Rv3616c sequences and/or additional heterologous polypeptides or the polynucleotides encoding them from *Mycobacterium* species (in particular *M. tuberculosis*).

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One skilled in the art will recognise that when a number of components are utilised in combination, the precise presentation can be varied. For example, a modified Rv3616c sequence component and an additional copy of the antigen or an additional heterologous antigen component could be presented:

10

- (1) as two individual polypeptide components;
- (2) as a fusion protein comprising both polypeptide components;
- (3) as one polypeptide and one polynucleotide component;
- (4) as two individual polynucleotide components;
- (5) as a single polynucleotide encoding two individual polypeptide components; or
- (6) as a single polynucleotide encoding a fusion protein comprising both polypeptide components.

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This flexibility applies equally to situations where three or more components are used in combination. However, for convenience, it is often desirable that when a number of components are present they are contained within a single fusion protein or a polynucleotide encoding a single fusion protein. In one embodiment of the invention all antigen components are provided as polypeptides (e.g. within a single fusion protein). In an alternative embodiment of the invention all antigen components are provided as polynucleotides (e.g. a single polynucleotide, such as one encoding a single fusion protein).

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The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

35

- “Fusion polypeptide” or “fusion protein” refers to a protein having at least two heterologous polypeptides (e.g. at least two *Mycobacterium* sp. polypeptides) covalently linked, either directly or via an amino acid linker. The polypeptides forming the fusion protein are typically linked C-terminus to N-terminus, although they can also be linked C-terminus to C-terminus, N-terminus to N-terminus, or N-terminus to C-terminus. The polypeptides of the fusion protein can be in any order. This term also refers to conservatively modified variants, polymorphic variants, alleles, mutants, immunogenic fragments, and interspecies homologs of the antigens that make up the fusion protein. *Mycobacterium tuberculosis* antigens are described in Cole *et al.*, *Nature* 393:537 (1998), which discloses the entire *Mycobacterium tuberculosis* genome.
- Antigens from other *Mycobacterium* species that correspond to *M. tuberculosis* antigens can be identified, e.g., using sequence comparison algorithms, as described herein, or other methods known to those of skill in the art, e.g., hybridisation assays and antibody binding assays.
- The term “fused” refers to the covalent linkage between two polypeptides in a fusion protein. The polypeptides are typically joined via a peptide bond, either directly to each other or via an amino acid linker. Optionally, the peptides can be joined via non-peptide covalent linkages known to those of skill in the art.
- Exemplary *M. tuberculosis* antigens which may be combined with a modified Rv3616c sequence include one or more of (e.g. 1 to 5, such as 1 to 3, in particular 1) the following:
- (i) Mtb8.4 (also known as DPV and Rv1174c), the polypeptide sequence of which is described in SEQ ID No: 102 of WO97/09428 (cDNA in SEQ ID No: 101) and in Coler *et al Journal of Immunology* 1998 161:2356-2364. Of particular interest is the mature Mtb8.4 sequence which is absent the leading signal peptide (i.e. amino acid residues 15-96 from SEQ ID No: 102 of WO97/09428). The full-length polypeptide sequence of Mtb8.4 is shown in SEQ ID No: 8;
 - (ii) Mtb9.8 (also known as MSL and Rv0287), the polypeptide sequence of which is described in SEQ ID No: 109 of WO98/53075 (fragments of MSL are disclosed in SEQ ID Nos: 110-124 of WO98/53075, SEQ ID Nos: 119 and 120 being of particular interest) and also in Coler *et al Vaccine* 2009 27:223-233 (in particular the reactive fragments shown in Figure 2 therein). The full-length polypeptide sequence for Mtb9.8 is shown in SEQ ID No: 9;

(iii) Mtb9.9 (also known as Mtb9.9A, MTI, MTI-A and Rv1793) the polypeptide sequence of which is described in SEQ ID No: 19 of WO98/53075 and in Alderson et al *Journal of Experimental Medicine* 2000 7:551-559 (fragments of MTI are disclosed in SEQ ID Nos: 17 and 51-66 of WO98/53075, SEQ ID Nos: 17, 51, 52, 53, 56 and 62-65 being of particular interest). A number of polypeptide variants of MTI are described in SEQ ID Nos: 21, 23, 25, 27, 29 and 31 of WO98/53075 and in Alderson et al *Journal of Experimental Medicine* 2000 7:551-559. The full-length polypeptide sequence for Mtb9.9 is shown in SEQ ID No: 10;

(iv) Ra12 (also known as Mtb32A C-terminal antigen) the polypeptide sequence of which is described in SEQ ID No: 10 of WO01/98460 and in Skeiky et al *Journal of Immunology* 2004 172:7618-7682. The full-length polypeptide sequence for Ra12 is shown in SEQ ID No: 11;

(v) Ra35 (also known as Mtb32A N-terminal antigen) the polypeptide sequence of which is described in SEQ ID No: 8 of WO01/98460 and in Skeiky et al *Journal of Immunology* 2004 172:7618-7682. The full-length polypeptide sequence for Ra35 is shown in SEQ ID No: 12;

(vi) TbH9 (also known as Mtb39, Mtb39A, TbH9FL and Rv1196) the polypeptide sequence of which is described in SEQ ID No: 107 of WO97/09428, and also in Dillon et al *Infection and Immunity* 1999 67(6):2941-2950 and Skeiky et al *Journal of Immunology* 2004 172:7618-7682. The full-length polypeptide sequence for TbH9 is shown in SEQ ID No: 13;

(vii) Mtb41 (also known as MTCC2 and Rv0915c) the polypeptide sequence of which is described in SEQ ID No: 142 of WO98/53075 (cDNA in SEQ ID No: 140) and in Skeiky et al *Journal of Immunology* 2000 165:7140-7149. The full-length polypeptide sequence for Mtb41 is shown in SEQ ID No: 14;

(viii) ESAT-6 (also known as esxA and Rv3875) the polypeptide sequence of which is described in SEQ ID No: 103 of WO97/09428 (cDNA in SEQ ID No: 104) and in Sorensen et al *Infection and Immunity* 1995 63(5):1710-1717. The full-length polypeptide sequence for ESAT-6 is shown in SEQ ID No: 15;

(ix) Ag85 complex antigens (e.g. Ag85A, also known as fbpA and Rv3804c; or Ag85B, also known as fbpB and Rv1886c) which are discussed, for example, in Content et al *Infection and Immunity* 1991 59:3205-3212 and in Huygen et al *Nature Medicine* 1996 2(8):893-898. The full-length polypeptide sequence for Ag85A is shown in SEQ ID No: 16 (the mature protein of residues 43-338, i.e. lacking the signal peptide, being of particular interest). The full-length polypeptide sequence for Ag85B is shown in SEQ ID No: 17 (the mature protein of residues 41-325, i.e. lacking the signal peptide, being of particular interest);

(x) Alpha-crystallin (also known as hspX and Rv2031c) which is described in Verbon et al *Journal of Bacteriology* 1992 174:1352-1359 and Friscia et al *Clinical and Experimental Immunology* 1995 102:53-57 (of particular interest are the fragments corresponding to residues 71-91, 21-40, 91-110 and 111-130)). The full-length polypeptide sequence for alpha-crystallin is shown in SEQ ID No: 18;

(xi) Mpt64 (also known as Rv1980c) which is described in Roche et al *Scandinavian Journal of Immunology* 1996 43:662-670. The full-length polypeptide sequence for MPT64 is shown in SEQ ID No: 19 (the mature protein of residues 24-228, i.e. lacking the signal peptide, being of particular interest):

(xii) Mtb32A, the polypeptide sequence of which is described in SEQ ID No: 2 (full-length) and residues 8-330 of SEQ ID No: 4 (mature) of WO01/98460, especially variants having at least one of the catalytic triad mutated (e.g. the catalytic serine residue, which may for example be mutated to alanine). The full-length polypeptide sequence for Mtb32A is shown in SEQ ID No: 20. The mature form of Mtb32A having a Ser/Ala mutation is shown in SEQ ID No: 21;

(xiii) TB10.4, the full-length polypeptide sequence for TB10.4 is shown in SEQ ID No: 22;

(xiv) Rv1753c, the full-length polypeptide sequence for Rv1753c from *Mycobacterium tuberculosis* H37Rv is shown in SEQ ID No: 157;

(xv) Rv2386c, the full-length polypeptide sequence for Rv2386c from *Mycobacterium tuberculosis* H37Rv is shown in SEQ ID No: 158; and/or

(xvi) Rv2707c, the full-length polypeptide sequence for Rv2707c from *Mycobacterium tuberculosis* H37Rv is shown in SEQ ID No: 159.

or combinations thereof, such as:

5

(a) a combination of Ra12, TbH9 and Ra35 components, for example in the form of a fusion protein, such as Mtb72f. The polypeptide sequence of Mtb72f is described in SEQ ID No: 6 of WO2006/117240 (cDNA in SEQ ID No: 5) and in Skeiky et al *Journal of Immunology* 2004 172:7618-7682 (where it incorporates an optional His-tag to aid purification, when utilised in the present invention suitably Mtb72f is absent the optional histidine residues). The polypeptide sequence for Mtb72f is shown in SEQ ID No: 23;

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(b) a combination of Ra12, TbH9 and Ser/Ala mutated Ra35 (i.e. where the catalytic serine residue has been replaced with alanine) components, for example in the form of a fusion protein, such as M72. The polypeptide sequence of M72 is described in SEQ ID No: 4 of WO2006/117240 (cDNA in SEQ ID No: 3) where it incorporates an optional double histidine to aid manufacture, when utilised in the present invention M72 may also incorporate a double histidine though suitably M72 is absent the optional double histidine (i.e. residues 4-725 from SEQ ID No: 4 of WO2006/117240 are of particular interest). The polypeptide sequence for M72 is shown in SEQ ID No: 24;

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(c) a combination of Mtb8.4, Mtb9.8, Mtb9.9 and Mtb41 components, for example in the form of a fusion protein, such as Mtb71f. The polypeptide sequence of Mtb71f is described in SEQ ID No: 16 of WO99/051748 (cDNA in SEQ ID No: 15), where it incorporates an optional His-tag to aid purification, when utilised in the present invention suitably Mtb71f corresponds to amino acid residues 9-710 of SEQ ID NO: 16 from WO99/051748. The polypeptide sequence for Mtb71f is shown in SEQ ID No: 25;

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(d) a combination of Mtb72f or M72 (suitably without optional histidine residues to aid expression) with Mtb9.8 and Mtb9.9, for example in a fusion protein. The polypeptide sequence for an M72-Mtb9.9-Mtb9.8 fusion is shown in SEQ ID No: 26 (M92 fusion), when used in the present invention, the M72-Mtb9.9-Mtb9.8 fusion may optionally incorporate a double histidine following the initiating methionine residue to aid manufacture;

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(e) a combination of Mtb72f or M72 (suitably without optional histidine residues to aid expression) with Ag85B, for example in a fusion protein, such Mtb103f. The polypeptide sequence of Mtb103f is described in SEQ ID No: 18 of WO03/070187 (cDNA in SEQ ID No: 10), where it incorporates an optional His-tag to aid purification, when utilised in the present invention suitably Mtb103f corresponds to amino acid residues 8-1016 of SEQ ID No: 18 from WO03/070187. Also of particular interest is M103, i.e. Mtb103f incorporating a Ser/Ala mutation in the Ra35 component, when utilised in the present invention suitably M103 corresponds to amino acid residues 8-1016 of SEQ ID No: 18 from WO03/070187 wherein the Ser residue at position 710 has been replaced with Ala. The polypeptide sequence for M103 is shown in SEQ ID No: 27, when used in the present invention, the M72-Mtb9.9-Mtb9.8 fusion may optionally incorporate a double histidine following the initiating methionine residue to aid manufacture;

(f) a combination of Mtb72f or M72 (suitably without optional histidine residues to aid expression) with Mtb41, for example in a fusion protein, such Mtb114f. The polypeptide sequence of Mtb114f is described in SEQ ID No: 16 of WO03/070187 (cDNA in SEQ ID No: 9), where it incorporates an optional His-tag to aid purification, when utilised in the present invention suitably Mtb114f corresponds to amino acid residues 8-1154 of SEQ ID No: 16 from WO03/070187. Also of particular interest is M114, i.e. Mtb114f incorporating a Ser/Ala mutation in the Ra35 component, when utilised in the present invention suitably M114 corresponds to amino acid residues 8-1154 of SEQ ID No: 16 from WO03/070187 wherein the Ser residue at position 710 has been replaced with Ala. The polypeptide sequence for M114 is shown in SEQ ID No: 28, when used in the present invention, the M72-Mtb9.9-Mtb9.8 fusion may optionally incorporate a double histidine following the initiating methionine residue to aid manufacture;

(g) a combination of Ag85B and ESAT-6 components, such as in a fusion described in Doherty et al *Journal of Infectious Diseases* 2004 190:2146–2153; and/or

(h) a combination of Ag85B and TB10.4 components, such as in a fusion described in Dietrich et al *Journal of Immunology* 2005 174(10):6332-6339 190:2146–2153.

Combinations of a modified Rv3616c sequence component and an Rv1753c component are of particular interest. Obviously such combinations could optionally contain other additional antigen components (e.g. an M72 component).

Another combination of interest comprises a modified Rv3616c sequence component and an M72 component.

- 5 A further combination of interest comprises a modified Rv3616c sequence component and an Rv2386c component.

Other combinations of interest include those comprising a modified Rv3616c sequence component and an Rv2707c component.

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An additional combination of interest comprises a modified Rv3616c sequence component and an alpha-crystallin component.

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The skilled person will recognise that combinations need not rely upon the specific sequences described in above in (i)-(xvi) and (a)-(h), and that conservatively modified variants (e.g. having at least 70% identity, such as at least 80% identity, in particular at least 90% identity and especially at least 95% identity) or immunogenic fragments (e.g. at least 20% of the full length antigen, such as at least 50% of the antigen, in particular at least 70% and especially at least 80%) of the described sequences can be used to achieve the same practical effect.

20

Each of the above individual antigen sequences is also disclosed in Cole et al *Nature* 1998 393:537-544 and Camus *Microbiology* 2002 148:2967-2973. The genome of *M. tuberculosis* H37Rv is publicly available, for example at the Wellcome Trust Sanger Institute website (www.sanger.ac.uk/Projects/M_tuberculosis/) and elsewhere.

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Many of the above antigens are also disclosed in U.S. patent application numbers 08/523,435, 08/523,436, 08/658,800, 08/659,683, 08/818,111, 08/818,112, 08/942,341, 08/942,578, 08/858,998, 08/859,381, 09/056,556, 09/072,596, 09/072,967, 09/073,009, 09/073,010, 09/223,040, 09/287,849 and in PCT patent applications PCT/US98/10407, PCT/US98/10514, 30 PCT/US99/03265, PCT/US99/03268, PCT/US99/07717, WO97/09428 and WO97/09429, WO98/16645, WO98/16646, each of which is herein incorporated by reference.

35

The compositions, polypeptides, and nucleic acids of the invention can also comprise additional polypeptides from other sources. For example, the compositions and fusion proteins of the invention can include polypeptides or nucleic acids encoding polypeptides, wherein the

polypeptide enhances expression of the antigen, e.g., NS1, an influenza virus protein (see, e.g. WO99/40188 and WO93/04175).

The nucleic acids of the invention can be engineered based on codon preference in a species of choice, e.g., humans (in the case of *in vivo* expression) or a particular bacterium (in the case of polypeptide production). SEQ ID No: 160 for example, provides a codon optimised polynucleotide for the expression of Rv3616c from H37Rv in *E. coli*.

The modified Rv3616c sequence component may also be administered with one or more chemotherapeutic agents effective against tuberculosis (e.g. *M. tuberculosis* infection). Examples of such chemotherapeutic agents include, but are not limited to, amikacin, aminosalicylic acid, capreomycin, cycloserine, ethambutol, ethionamide, isoniazid, kanamycin, pyrazinamide, rifamycins (*i.e.*, rifampin, rifapentine and rifabutin), streptomycin, ofloxacin, ciprofloxacin, clarithromycin, azithromycin and fluoroquinolones. Such chemotherapy is determined by the judgment of the treating physician using preferred drug combinations. "First-line" chemotherapeutic agents used to treat tuberculosis (e.g. *M. tuberculosis* infection) that is not drug resistant include isoniazid, rifampin, ethambutol, streptomycin and pyrazinamide. "Second-line" chemotherapeutic agents used to treat tuberculosis (e.g. *M. tuberculosis* infection) that has demonstrated drug resistance to one or more "first-line" drugs include ofloxacin, ciprofloxacin, ethionamide, aminosalicylic acid, cycloserine, amikacin, kanamycin and capreomycin.

Conventional chemotherapeutic agents are generally administered over a relatively long period (ca. 9 months). Combination of conventional chemotherapeutic agents with the administration of a modified Rv3616c sequence component according to the present invention may enable the chemotherapeutic treatment period to be reduced (e.g. to 8 months, 7 months, 6 months, 5 months, 4 months, 3 months or less) without a decrease in efficacy.

Of particular interest is the use of a modified Rv3616c sequence component in conjunction with *Bacillus Calmette-Guerin* (BCG). For example, in the form of a modified BCG which recombinantly expresses a modified Rv3616c protein. Alternatively, the modified Rv3616c sequence component may be used to enhance the response of a subject to BCG vaccination, either by co-administration or by boosting a previous BCG vaccination. When used to enhance the response of a subject to BCG vaccination, the modified Rv3616c sequence component may obviously be provided in the form of a polypeptide or a polynucleotide (optionally in conjunction with additional antigenic components as described above).

The skilled person will recognise that combinations of components need not be administered together and may be applied: separately or in combination; at the same time, sequentially or within a short period; though the same or through different routes. Nevertheless, for
 5 convenience it is generally desirable (where administration regimes are compatible) to administer a combination of components as a single composition.

The polypeptides, polynucleotides and compositions of the present invention will usually be administered to humans, but may be expected to be effective in other mammals including
 10 domestic mammals (e.g., dogs, cats, rabbits, rats, mice, guinea pigs, hamsters, chinchillas) and agricultural mammals (e.g., cows, pigs, sheep, goats, horses).

VARIANTS

15 T cell epitopes are short contiguous stretches of amino acids which are recognised by T cells (e.g. CD4+ or CD8+ T cells). Identification of T cell epitopes may be achieved through epitope mapping experiments which are well known to the person skilled in the art (see, for example, Paul, *Fundamental Immunology*, 3rd ed., 243-247 (1993); Beißbarth et al *Bioinformatics* 2005
 21(Suppl. 1):i29-i37). Alternatively, epitopes may be predicted or mapped using the
 20 approaches discussed in the Examples.

In a diverse out-bred population, such as humans, different HLA types mean that particular epitopes may not be recognised by all members of the population. As a result of the crucial involvement of the T cell response in tuberculosis, to maximise the level of recognition and
 25 scale of immune response, an optimal modified Rv3616c protein is one which contains the majority (or suitably all) T cell epitopes intact.

“Variants” or “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified
 30 variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences.

Due to the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all
 35 encode the amino acid alanine. Thus, at every position where an alanine is specified by a

codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations lead to "silent" or "degenerate" variants, which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognise that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid that encodes a polypeptide is implicit in each described sequence.

Non-silent variations are those which result in a change in the encoded amino acid sequence (either through the substitution, deletion or addition of amino acid residues). Those skilled in the art will recognise that a particular polynucleotide sequence may contain both silent and non-silent conservative variations.

In respect of variants of a protein sequence, the skilled person will recognise that individual substitutions, deletions or additions to polypeptide, which alters, adds or deletes a single amino acid or a small percentage of amino acids is a "conservatively modified variant" where the alteration(s) results in the substitution of an amino acid with a functionally similar amino acid or the substitution/deletion/addition of residues which do not substantially impact the biological function of the variant.

Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

In general, such conservative substitutions will fall within one of the amino-acid groupings specified below, though in some circumstances other substitutions may be possible without substantially affecting the immunogenic properties of the antigen. The following eight groups each contain amino acids that are typically conservative substitutions for one another:

- 1) Alanine (A), Glycine (G);
- 2) Aspartic acid (D), Glutamic acid (E);
- 3) Asparagine (N), Glutamine (Q);
- 4) Arginine (R), Lysine (K);
- 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V);
- 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W);
- 7) Serine (S), Threonine (T); and

8) Cysteine (C), Methionine (M)
 (see, e.g., Creighton, *Proteins* 1984).

5 Suitably such substitutions do not occur in the region of an epitope, and do not therefore have a significant impact on the immunogenic properties of the antigen.

Protein variants may also include those wherein additional amino acids are inserted compared to the reference sequence. Suitably such insertions do not occur in the region of an epitope, and do not therefore have a significant impact on the immunogenic properties of the antigen.

10 One example of insertions includes a short stretch of histidine residues (e.g. 2-6 residues) to aid expression and/or purification of the antigen in question.

Protein variants include those wherein amino acids have been deleted compared to the reference sequence. Suitably such deletions do not occur in the region of an epitope, and do

15 not therefore have a significant impact on the immunogenic properties of the antigen.

The skilled person will recognise that a particular protein variant may comprise substitutions, deletions and additions (or any combination thereof).

20 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or sub-sequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., 70% identity, optionally 75%, 80%, 85%, 90%, 95%, 98% or 99% identity over a specified region), when compared and aligned for maximum correspondence over a comparison

25 window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Such sequences are then said to be "substantially identical." This definition also refers to the complement of a test sequence. Optionally, the identity exists over a region that is at least about 25 to about 50 amino acids or nucleotides in length, or optionally over a region that is 75-100 amino acids or nucleotides in

30 length. Suitably, the comparison is performed over a window corresponding to the entire length of the reference sequence (as opposed to the variant sequence).

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference

35 sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program

parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

- 5 A "comparison window", as used herein, references to a segment in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the
10 homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., *Current*
15 *Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

- One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a tree or dendrogram showing the clustering
20 relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J. Mol. Evol.* 35:351-360 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most
25 similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for
30 regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g., version 7.0 (Devereaux *et al.*, *Nuc. Acids Res.*
35 12:387-395 (1984).

Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (website at www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

In any event, variants of a polypeptide sequence will have essentially the same activity as the reference sequence (in the case of polynucleotides, variant polynucleotide sequences will encode a polypeptide which has essentially the same activity as the reference sequence). By essentially the same activity is meant at least 50%, suitably at least 75% and especially at least 90% activity of the reference sequence in an *in vitro* restimulation assay of PBMC or whole blood with specific antigens (e.g. restimulation for a period of between several hours to up to two weeks, such as up to one day, 1 day to 1 week or 1 to 2 weeks) that measures the activation of the cells via lymphoproliferation, production of cytokines in the supernatant of culture (measured by ELISA, CBA etc) or characterisation of T and B cell responses by intra and extracellular staining (e.g. using antibodies specific to immune markers, such as CD3, CD4, CD8, IL2, TNFa, IFNg, CD40L, CD69 etc) followed by analysis with a flowcytometer. Suitably, by essentially the same activity is meant at least 50%, suitably at least 75% and especially at least 90% activity of the reference sequence in a T cell proliferation and/or IFN-gamma production assay.

As will be understood by those skilled in the art, the polynucleotides of use in this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be recognised by the skilled artisan, polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (i.e., an endogenous sequence that encodes a *Mycobacterium* antigen or a portion thereof) or may comprise a variant, or a biological or functional equivalent of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions, such that the immunogenicity of the encoded polypeptide is not diminished relative to the reference protein.

POLYNUCLEOTIDE IDENTIFICATION AND CHARACTERISATION

Polynucleotides may be identified, prepared and/or manipulated using any of a variety of well established techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs. Such screens may be performed, for example, using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena *et al.*, *Proc. Natl. Acad. Sci. USA* 93:10614-10619 (1996) and Heller *et al.*, *Proc. Natl. Acad. Sci. USA* 94:2150-2155 (1997)). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as *M. tuberculosis* cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesised.

An amplified portion of a polynucleotide may be used to isolate a full length gene from a suitable library (e.g., a *M. tuberculosis* cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridisation techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridising filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (2000)). Hybridising colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

- 10 One such amplification technique is inverse PCR (see Triglia *et al.*, *Nucl. Acids Res.* 16:8186 (1988)), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularised by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE.
- 20 This technique involves the use of an internal primer and an external primer, which hybridises to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom *et al.*, *PCR Methods Applic.* 1:111-19 (1991)) and walking PCR (Parker *et al.*, *Nucl. Acids. Res.* 19:3055-60 (1991)). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.
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In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

POLYNUCLEOTIDE EXPRESSION IN HOST CELLS

Polynucleotide sequences or fragments thereof which encode polypeptides, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences.

In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

Natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognised by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesised, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. *et al.*, *Nucl. Acids Res. Symp. Ser.* pp. 215-223 (1980), Horn *et al.*, *Nucl. Acids Res. Symp. Ser.* pp. 225-232 (1980)).

Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis

can be performed using various solid-phase techniques (Roberge *et al.*, *Science* 269:202-204 (1995)) and automated synthesis may be achieved, for example, using the ABL 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

- 5 A newly synthesised peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, *Proteins, Structures and Molecular Principles* (1983)) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may
10 be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

- In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into an appropriate expression vector, i.e., a vector
15 which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such
20 techniques are described in Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2000), and Ausubel *et al.*, *Current Protocols in Molecular Biology* (updated annually).

- A variety of expression vector/host systems may be utilised to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as
25 bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

- 30 The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host
35 utilised, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems,

inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPO1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β -galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke & Schuster, *J. Biol. Chem.* 264:5503-5509 (1989)); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. Other vectors containing constitutive or inducible promoters include GAP, PGK, GAL and ADH. For reviews, see Ausubel *et al.* (*supra*) and Grant *et al.*, *Methods Enzymol.* 153:516-544 (1987) and Romas *et al.* *Yeast* 8 423-88 (1992).

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, *EMBO J.* 6:307-311 (1987)). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi *et al.*, *EMBO J.* 3:1671-1680 (1984); Broglie *et al.*, *Science* 224:838-843 (1984); and Winter *et al.*, *Results Probl. Cell Differ.* 17:85-105 (1991)). These constructs can be

introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, e.g., Hobbs in *McGraw Hill Yearbook of Science and Technology* pp. 191-196 (1992)).

- 5 An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia larvae*. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of
10 the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia larvae* in which the polypeptide of interest may be expressed (Engelhard et al., *Proc. Natl. Acad. Sci. U.S.A.* 91 :3224-3227 (1994)).
- 15 In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is
20 capable of expressing the polypeptide in infected host cells (Logan & Shenk, *Proc. Natl. Acad. Sci. U.S.A.* 81:3655-3659 (1984)). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. Methods and protocols for working with adenovirus vectors are reviewed in Wold, *Adenovirus Methods and Protocols*, 1998. Additional references regarding use of adenovirus vectors can
25 be found in *Adenovirus: A Medical Dictionary, Bibliography, and Annotated Research Guide to Internet References*, 2004.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent
30 sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon
35 should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and

synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf. *et al.*, *Results Probl. Cell Differ.* 20:125-162 (1994)).

- 5 In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.
- 15 For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.
- 25 Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, *Cell* 11:223-32 (1977)) and adenine phosphoribosyltransferase (Lowy *et al.*, *Cell* 22:817-23 (1990)) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 77:3567-70 (1980)); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin *et al.*, *J. Mol. Biol.* 150:1-14 (1981)); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilise indole in place of tryptophan, or hisD, which allows cells to utilise histinol in place of histidine (Hartman

& Mulligan, *Proc. Natl. Acad. Sci. U.S.A.* 85:8047-51 (1988)). Recently, the use of visible markers has gained popularity with such markers as anthocyanins, β -glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes *et al.*, *Methods Mol. Biol.* 55:121-131 (1995)).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells which contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridisations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilising monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton *et al.*, *Serological Methods, a Laboratory Manual* (1990) and Maddox *et al.*, *J. Exp. Med.* 158:1211-1216 (1983).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labelled hybridisation or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labelling or PCR amplification using a labelled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available,

and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath *et al.*, *Prot. Exp. Purif.* 3:263-281 (1992) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll *et al.*, *DNA Cell Biol.* 12:441-453 (1993)).

IN VIVO POLYNUCLEOTIDE DELIVERY TECHNIQUES

In additional embodiments, genetic constructs comprising one or more of the polynucleotides of the invention are introduced into cells *in vivo*. This may be achieved using any of a variety of well known approaches, several of which are outlined below for the purpose of illustration.

1. ADENOVIRUS

One of the preferred methods for *in vivo* delivery of one or more nucleic acid sequences involves the use of an adenovirus expression vector. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct and (b) to express a polynucleotide that has been cloned therein in a sense or antisense orientation. Of course, in the context of an antisense construct, expression does not require that the gene product be synthesised.

The expression vector comprises a genetically engineered form of an adenovirus. Knowledge of the genetic organisation of adenovirus, a 36 kb, linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kb (Grunhaus & Horwitz, 1992). In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification. Adenovirus can infect virtually all epithelial cells regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titre, wide target-cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990).

The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNA's issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNA's for translation.

In a current system, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of the current adenovirus vectors, which are replication deficient, depend on a unique helper cell line, designated 293, which was transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones & Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the D3 or both regions (Graham & Prevec, 1991). In nature, adenovirus can package approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kB of DNA. Combined with the approximately 5.5 kB of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of the current adenovirus vector is under 7.5 kB, or about 15% of the total length of the vector. More than 80% of the adenovirus viral genome remains in the vector backbone and is the source of vector-borne cytotoxicity. Also, the replication deficiency of the E1-deleted virus is incomplete. For example, leakage of viral gene expression has been observed with the currently available vectors at high multiplicities of infection (MOI) (Mulligan, 1993).

Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, e.g., Vero cells or other monkey embryonic mesenchymal or epithelial cells. As stated above, the currently preferred helper cell line is 293.

Racher *et al.* (1995) have disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 litre siliconised spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) is employed as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells are

allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

5

Other than the requirement that the adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may be of any of the 42 different known serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain a conditional replication-defective adenovirus vector for use in the present invention, since Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

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As stated above, the typical vector according to the present invention is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the polynucleotide encoding the gene of interest at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors as described by Karlsson *et al.* (1986) or in the E4 region where a helper cell line or helper virus complements the E4 defect.

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Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titres, e.g., 10^9 - 10^{11} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

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Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus & Horwitz, 1992; Graham & Prevec, 1992). Recently, animal studies suggested that recombinant adenovirus could be used for gene therapy (Stratford-Perricaudet & Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1990; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues

include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993), peripheral intravenous injections (Herz & Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993).

- 5 Adenovirus vectors may originate from human adenovirus. Alternatively they may originate from adenovirus of other species e.g. chimpanzee which may have the advantage that the viral vectors are not neutralised by antibodies against human adenovirus circulating in many human subjects (see e.g.: Tatsis N *et al* *Gene Therapy* 2006 13:421-429).
- 10 Adenovirus type 35, which is relatively uncommon and therefore there are low levels of pre-existing immunity to the vector itself, has been used as a delivery system in certain tuberculosis vaccines which are being developed (see for example, Radosevic *et al* *Infection and Immunity* 2007 75(8):4105-4115). Adenovirus type 35 may also be of particular value in the present invention as a delivery vector.

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2. RETROVIRUSES

- The retroviruses are a group of single-stranded RNA viruses characterised by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-
- 20 transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream
 - 25 from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5' and 3' ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).
 - 30 In order to construct a retroviral vector, a nucleic acid encoding one or more oligonucleotide or polynucleotide sequences of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is constructed (Mann *et al.*, 1983). When a recombinant plasmid containing a
 - 35 cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA

transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas & Rubenstein, 1988; Temin, 1986; Mann *et al.*, 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.*, 1975).

A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification could permit the specific infection of hepatocytes *via* sialoglycoprotein receptors.

A different approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled *via* the biotin components by using streptavidin (Roux *et al.*, 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.*, 1989).

3. ADENO-ASSOCIATED VIRUSES

AAV (Ridgeway, 1988; Hermonat & Muzyczka, 1984) is a parovirus, discovered as a contamination of adenoviral stocks. It is a ubiquitous virus (antibodies are present in 85% of the US human population) that has not been linked to any disease. It is also classified as a dependovirus, because its replication is dependent on the presence of a helper virus, such as adenovirus. Five serotypes have been isolated, of which AAV-2 is the best characterised. AAV has a single-stranded linear DNA that is encapsidated into capsid proteins VP1, VP2 and VP3 to form an icosahedral virion of 20 to 24 nm in diameter (Muzyczka & McLaughlin, 1988).

The AAV DNA is approximately 4.7 kilobases long. It contains two open reading frames and is flanked by two ITRs. There are two major genes in the AAV genome: *rep* and *cap*. The *rep* gene codes for proteins responsible for viral replications, whereas *cap* codes for capsid protein VP1-3. Each ITR forms a T-shaped hairpin structure. These terminal repeats are the only essential *cis* components of the AAV for chromosomal integration. Therefore, the AAV can be used as a vector with all viral coding sequences removed and replaced by the cassette of genes for delivery. Three viral promoters have been identified and named p5, p19, and p40,

according to their map position. Transcription from p5 and p19 results in production of rep proteins, and transcription from p40 produces the capsid proteins (Hermonat & Muzyczka, 1984).

- 5 There are several factors that prompted researchers to study the possibility of using rAAV as an expression vector. One is that the requirements for delivering a gene to integrate into the host chromosome are surprisingly few. It is necessary to have the 145-bp ITRs, which are only 6% of the AAV genome. This leaves room in the vector to assemble a 4.5-kb DNA insertion. While this carrying capacity may prevent the AAV from delivering large genes, it is
10 amply suited for delivering antisense constructs.

- AAV is also a good choice of delivery vehicles due to its safety. There is a relatively complicated rescue mechanism: not only wild type adenovirus but also AAV genes are required to mobilise rAAV. Likewise, AAV is not pathogenic and not associated with any
15 disease. The removal of viral coding sequences minimises immune reactions to viral gene expression, and therefore, rAAV does not evoke an inflammatory response.

4. OTHER VIRAL VECTORS AS EXPRESSION CONSTRUCTS

- 20 Other viral vectors may be employed as expression constructs in the present invention for the delivery of oligonucleotide or polynucleotide sequences to a host cell. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Coupar *et al.*, 1988), lentiviruses, polio viruses and herpes viruses may be employed. Other poxvirus derived vectors, such as fowl-pox derived vectors, may also be expected to be of use. They offer several attractive features
25 for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Coupar *et al.*, 1988; Horwich *et al.*, 1990).

- With the recent recognition of defective hepatitis B viruses, new insight was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the
30 virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwich *et al.*, 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. The hepatotropism and persistence (integration) were particularly attractive properties for liver-directed gene transfer. Chang *et al.* (1991) introduced the chloramphenicol acetyltransferase (CAT) gene
35 into duck hepatitis B virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was cotransfected with wild-type virus into an avian hepatoma cell line.

Culture media containing high titres of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days after transfection (Chang *et al.*, 1991).

- 5 Additional 'viral' vectors include virus like particles (VLPs) and phages.

5. NON-VIRAL VECTORS

10 In order to effect expression of the oligonucleotide or polynucleotide sequences of the present invention, the expression construct must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cells lines, or *in vivo* or *ex vivo*, as in the treatment of certain disease states. As described above, one preferred mechanism for delivery is *via* viral infection where the expression construct is encapsulated in an infectious viral particle.

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Once the expression construct has been delivered into the cell the nucleic acid encoding the desired oligonucleotide or polynucleotide sequences may be positioned and expressed at different sites. In certain embodiments, the nucleic acid encoding the construct may be stably integrated into the genome of the cell. This integration may be in the specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronisation with the host cell cycle. How the expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed.

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In certain embodiments of the invention, the expression construct comprising one or more oligonucleotide or polynucleotide sequences may simply consist of naked recombinant DNA or plasmids. Transfer of the construct may be performed, for example, by any method which physically or chemically permeabilises the cell membrane. This is particularly applicable for transfer *in vitro* but it may be applied to *in vivo* use as well. Dubensky *et al.* (1984) successfully injected polyomavirus DNA in the form of calcium phosphate precipitates into liver and spleen of adult and newborn mice demonstrating active viral replication and acute infection. Benvenisty & Reshef (1986) also demonstrated that direct intraperitoneal injection of calcium phosphate-precipitated plasmids results in expression of the transfected genes. It is

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envisioned that DNA encoding a gene of interest may also be transferred in a similar manner *in vivo* and express the gene product.

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, 1987). Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

Selected organs including the liver, skin, and muscle tissue of rats and mice have been bombarded *in vivo* (Yang *et al.*, 1990; Zelenin *et al.*, 1991). This may require surgical exposure of the tissue or cells, to eliminate any intervening tissue between the gun and the target organ, i.e., *ex vivo* treatment. Again, DNA encoding a particular gene may be delivered *via* this method and still be incorporated.

Bacteria may also be utilised as a delivery method (e.g. listeria, see WO2004/11048) and in particular BCG.

POLYPEPTIDE COMPOSITIONS

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells, such as mammalian cells and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Shorter polypeptides may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesised using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase
5 synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

10 Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple modified Rv3616c proteins as described herein, or that comprises at least one modified Rv3616c proteins as described herein and an unrelated sequence such as those described in (i) to (xvi) and (a) to (g) above.

15 A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognised by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing
20 fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical
25 conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA
30 sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the fusion partners by a distance
35 sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques

well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea *et al.*, *Gene* 40:39-46 (1985); Murphy *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8258-8262 (1986); U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza* B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292 (1986)). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798 (1992)). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a

fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

PHARMACEUTICAL COMPOSITIONS

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In additional embodiments, the polynucleotide or polypeptide compositions disclosed herein may be formulated in pharmaceutically-acceptable or physiologically-acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy. Compositions may be presented in powder form (e.g. freeze-dried) for reconstitution shortly before use, such dry compositions generally are more stable during storage.

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Pharmaceutical compositions may comprise a fusion protein or a polynucleotide encoding a fusion protein, in combination with a pharmaceutically-acceptable carrier or excipient.

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It will also be understood that, if desired, the nucleic acid segment (e.g., RNA or DNA) that expresses a polypeptide as disclosed herein may be administered in combination with other agents as well, such as, e.g., other proteins or polypeptides or various pharmaceutically-active agents, including chemotherapeutic agents effective against a *M. tuberculosis* infection. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesised as described herein.

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Likewise, such compositions may further comprise substituted or derivatised RNA or DNA compositions.

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Formulation of pharmaceutically-acceptable excipients and carrier solutions is well-known to those of skill in the art, as is the development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including e.g., oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation. Other routes of administration include via the mucosal surfaces.

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Typically, formulations comprising a therapeutically effective amount deliver about 0.01 ug to about 1000 ug of modified Rv3616c polypeptide per administration, more typically about 0.1 ug to about 100 ug of polypeptide per administration (e.g. 0.5 to 50 ug). In respect of

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polynucleotide compositions, these typically deliver about 10 ug to about 20 mg of the inventive polynucleotide per administration, more typically about 0.1 mg to about 10 mg of the inventive polynucleotide per administration

- 5 Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as
10 such, a variety of dosages and treatment regimens may be desirable.

1. ORAL DELIVERY

- 15 In certain applications, the pharmaceutical compositions disclosed herein may be delivered via oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

- 20 The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (Mathiowitz *et al.*, 1997; Hwang *et al.*, 1998; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451, each specifically incorporated herein by reference in its entirety). The tablets, troches, pills, capsules and the like may also contain the following: a
25 binder, as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavouring agent, such as peppermint, oil of wintergreen, or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to
30 materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. A syrup or elixir may contain the active component, sucrose as a sweetening agent methyl and propylparabens as preservatives, a dye and flavouring, such as cherry or orange flavour. Of course, any material
35 used in preparing any dosage unit form should be pharmaceutically pure and substantially

non-toxic in the amounts employed. In addition, the active components may be incorporated into sustained-release preparation and formulations.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. For example, a mouthwash may be prepared incorporating the active ingredient in the required amount in an appropriate solvent, such as a sodium borate solution (Dobell's Solution). Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

2. INJECTABLE DELIVERY

In general it may be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, intradermally, or even intraperitoneally as described in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363 (each specifically incorporated herein by reference in its entirety). Solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (U. S. Patent 5,466,468, specifically incorporated herein by reference in its entirety). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle

size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it may be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion (see, e.g., *Remington's Pharmaceutical Sciences*, 15th Edition, pp. 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The compositions disclosed herein may be formulated in a neutral or salt form.

Pharmaceutically-acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic

bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug-release capsules, and the like.

As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a protein as an active ingredient is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified.

3. NASAL AND BUCCAL DELIVERY

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, buccal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs eg *via* nasal and buccal aerosol sprays has been described e.g., in U. S. Patent 5,756,353 and U. S. Patent 5,804,212 (each specifically incorporated herein by reference in its entirety). Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, 1998) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871, specifically incorporated herein by reference in its entirety) are also well-known in the pharmaceutical arts. Likewise, transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045 (specifically incorporated herein by reference in its entirety).

4. LIPOSOME-, NANOCAPSULE-, AND MICROPARTICLE-MEDIATED DELIVERY

In certain embodiments, the inventors contemplate the use of liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the compositions of the present invention into suitable host cells. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like.

Such formulations may be preferred for the introduction of pharmaceutically-acceptable formulations of the nucleic acids or constructs disclosed herein. The formation and use of liposomes is generally known to those of skill in the art (see for example, Couvreur *et al.*, 1977; Couvreur, 1988; Lasic, 1998; which describes the use of liposomes and nanocapsules in the targeted antibiotic therapy for intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-times (Gabizon & Papahadjopoulos, 1988; Allen and Choun, 1987; U. S. Patent 5,741,516, specifically incorporated herein by reference in its entirety). Further, various methods of liposome and liposome like preparations as potential drug carriers have been reviewed (Takakura, 1998; Chandran *et al.*, 1997; Margalit, 1995; U. S. Patent 5,567,434; U. S. Patent 5,552,157; U. S. Patent 5,565,213; U. S. Patent 5,738,868 and U. S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, 1990; Muller *et al.*, 1990). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs (Heath & Martin, 1986; Heath *et al.*, 1986; Balazsovits *et al.*, 1989; Fresta & Puglisi, 1996), radiotherapeutic agents (Pikul *et al.*, 1987), enzymes (Imaizumi *et al.*, 1990a; Imaizumi *et al.*, 1990b), viruses (Faller & Baltimore, 1984), transcription factors and allosteric effectors (Nicolau & Gersonde, 1979) into a variety of cultured cell lines and animals. In addition, several successful clinical trials examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein *et al.*, 1985a; 1985b; Coune, 1988; Sculier *et al.*, 1988). Furthermore, several studies suggest that the use of liposomes is not associated with autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori & Fukatsu, 1992).

Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)). MLVs generally have diameters of from 25 nm to 4 μ m. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core.

Liposomes bear resemblance to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely suitable as both water- and lipid-soluble substances can be entrapped, i.e. in the aqueous spaces and within the bilayer itself, respectively. It is possible that the drug-bearing liposomes may even be employed for site-specific delivery of active agents by selectively modifying the liposomal formulation.

In addition to the teachings of Couvreur *et al.* (1977; 1988), the following information may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in water, depending on the molar ratio of lipid to water. At low ratios the liposome is the preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a phase transition which markedly alters their permeability. The phase transition involves a change from a closely packed, ordered structure, known as the gel state, to a loosely packed, less-ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature and results in an increase in permeability to ions, sugars and drugs.

In addition to temperature, exposure to proteins can alter the permeability of liposomes. Certain soluble proteins, such as cytochrome c, bind, deform and penetrate the bilayer, thereby causing changes in permeability. Cholesterol inhibits this penetration of proteins, apparently by packing the phospholipids more tightly. It is contemplated that the most useful liposome formations for antibiotic and inhibitor delivery will contain cholesterol.

The ability to trap solutes varies between different types of liposomes. For example, MLVs are moderately efficient at trapping solutes, but SUVs are extremely inefficient. SUVs offer the advantage of homogeneity and reproducibility in size distribution, however, and a compromise between size and trapping efficiency is offered by large unilamellar vesicles (LUVs). These are prepared by ether evaporation and are three to four times more efficient at solute entrapment than MLVs.

In addition to liposome characteristics, an important determinant in entrapping compounds is the physicochemical properties of the compound itself. Polar compounds are trapped in the aqueous spaces and nonpolar compounds bind to the lipid bilayer of the vesicle. Polar compounds are released through permeation or when the bilayer is broken, but nonpolar compounds remain affiliated with the bilayer unless it is disrupted by temperature or exposure to lipoproteins. Both types show maximum efflux rates at the phase transition temperature.

Liposomes interact with cells via four different mechanisms: endocytosis by phagocytic cells of the reticuloendothelial system such as macrophages and neutrophils; adsorption to the cell surface, either by nonspecific weak hydrophobic or electrostatic forces, or by specific interactions with cell-surface components; fusion with the plasma cell membrane by insertion of the lipid bilayer of the liposome into the plasma membrane, with simultaneous release of liposomal contents into the cytoplasm; and by transfer of liposomal lipids to cellular or subcellular membranes, or vice versa, without any association of the liposome contents. It often is difficult to determine which mechanism is operative and more than one may operate at the same time.

The fate and disposition of intravenously injected liposomes depend on their physical properties, such as size, fluidity, and surface charge. They may persist in tissues for h or days, depending on their composition, and half lives in the blood range from min to several h. Larger liposomes, such as MLVs and LUVs, are taken up rapidly by phagocytic cells of the reticuloendothelial system, but physiology of the circulatory system restrains the exit of such large species at most sites. They can exit only in places where large openings or pores exist in the capillary endothelium, such as the sinusoids of the liver or spleen. Thus, these organs are the predominate site of uptake. On the other hand, SUVs show a broader tissue distribution but still are sequestered highly in the liver and spleen. In general, this *in vivo* behavior limits the potential targeting of liposomes to only those organs and tissues accessible to their large size. These include the blood, liver, spleen, bone marrow, and lymphoid organs.

Targeting is generally not a limitation in terms of the present invention. However, should specific targeting be desired, methods are available for this to be accomplished. Antibodies may be used to bind to the liposome surface and to direct the antibody and its drug contents to specific antigenic receptors located on a particular cell-type surface. Carbohydrate determinants (glycoprotein or glycolipid cell-surface components that play a role in cell-cell recognition, interaction and adhesion) may also be used as recognition sites as they have

potential in directing liposomes to particular cell types. Mostly, it is contemplated that intravenous injection of liposomal preparations would be used, but other routes of administration are also conceivable.

5 Alternatively, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland *et al.*, 1987; Quintanar-Guerrero *et al.*, 1998; Douglas *et al.*, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) should be designed using polymers able to be
10 degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present invention. Such particles may be easily made, as described (Couvreux *et al.*, 1980; 1988; zur Muhlen *et al.*, 1998; Zambaux *et al.* 1998; Pinto-Alphandry *et al.*, 1995 and U. S. Patent 5,145,684, specifically incorporated herein by reference in its entirety).

15

Skin patches may also be utilised for transcutaneous delivery.

IMMUNOGENIC COMPOSITIONS

20 In certain embodiments of the present invention, immunogenic compositions are provided. The immunogenic compositions will comprise one or more modified Rv3616c sequences (polypeptides or polynucleotides) as those discussed above, in combination with an immunostimulant.

25 Immunogenic compositions may also comprise a fusion protein or a polynucleotide encoding a fusion protein, in combination with a pharmaceutically-acceptable carrier or excipient.

An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants
30 include adjuvants.

Preparation of immunogenic compositions is generally described in, for example, Powell & Newman, eds., *Vaccine Design* (the subunit and adjuvant approach) (1995). Pharmaceutical compositions and immunogenic compositions within the scope of the present invention may
35 also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other *M. tuberculosis* antigens may be present, either

incorporated into a fusion polypeptide or as a separate component, within the pharmaceutical or immunogenic composition.

Illustrative immunogenic compositions may contain a polynucleotide (e.g. DNA) encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ* (thereby eliciting an immune response). As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198 (1998), and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium host cell (*for example*, a *Mycobacterium*, *Bacillus* or *Lactobacillus* strain, including *Bacillus-Calmette-Guerrin* or *Lactococcus lactis*) that expresses the polypeptide (e.g. on its cell surface or secretes the polypeptide) (*see, for example*, Ferreira, *et al.*, *An Acad Bras Cienc* (2005) 77:113-124; and Raha, *et al.*, *Appl Microbiol Biotechnol* (2005) PubMedID 15635459). In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch *et al.*, *Proc. Natl. Acad. Sci. USA* 86:317-321 (1989); Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86-103 (1989); Flexner *et al.*, *Vaccine* 8:17-21 (1990); U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627 (1988); Rosenfeld *et al.*, *Science* 252:431-434 (1991); Kolls *et al.*, *Proc. Natl. Acad. Sci. USA* 91:215-219 (1994); Kass-Eisler *et al.*, *Proc. Natl. Acad. Sci. USA* 90:11498-11502 (1993); Guzman *et al.*, *Circulation* 88:2838-2848 (1993); and Guzman *et al.*, *Cir. Res.* 73:1202-1207 (1993). Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer *et al.*, *Science* 259:1745-1749 (1993) and reviewed by Cohen, *Science* 259:1691-1692 (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells. It will be apparent that a immunogenic composition may comprise both a polynucleotide and a polypeptide component. Such immunogenic composition may provide for an enhanced immune response.

It will be apparent that an immunogenic composition may contain pharmaceutically acceptable salts of the polynucleotides and polypeptides provided herein. Such salts may be prepared

from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

5 While any suitable carrier known to those of ordinary skill in the art may be employed in the immunogenic compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral
10 administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the
15 pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344 and 5,942,252. One may also employ a carrier comprising the particulate-protein complexes described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

20 Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that render
25 the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

30 Any of a variety of immunostimulants may be employed in the immunogenic compositions of this invention. For example, an adjuvant may be included. An adjuvant refers to the components in a vaccine or therapeutic composition that increase the specific immune response to the antigen (see, e.g., Edelman, *AIDS Res. Hum Retroviruses* 8:1409-1411 (1992)). Adjuvants induce immune responses of the Th1-type and Th-2 type response. Th1-
35 type cytokines (e.g., IFN- γ , IL-2, and IL-12) tend to favour the induction of cell-mediated

immune response to an administered antigen, while Th-2 type cytokines (e.g., IL-4, IL-5, IL-6, IL-10) tend to favour the induction of humoral immune responses.

Within the immunogenic compositions provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type.

Suitable adjuvant compositions include oil in water emulsions. In particular an oil in water emulsion which comprises 0.5 - 10 mg metabolisable oil (e.g. squalene), 0.5 - 11 mg tocol (e.g. alpha-tocopherol) and 0.1 - 4 mg emulsifying agent (e.g. polyoxyethylene sorbitan monooleate) per human dose. See, for example, WO2008/043774 which is hereby incorporated by reference.

An alternative adjuvant comprises an immunologically active saponin fraction derived from the bark of *Quillaja Saponaria Molina* (such as the HPLC purified fraction known as QS21, as described in US5,057,540) presented in the form of a liposome and a lipopolysaccharide (such as 3-de-O-acylated monophosphoryl lipid A). These compositions may further comprise a sterol (e.g. cholesterol), such as wherein the ratio of saponin:sterol is from 1:1 to 1:100 w/w (e.g. the ratio of saponin:sterol is from 1:1 to 1:10 w/w). Particularly suitable are those adjuvants wherein said QS21 and said 3-de-O-acylated monophosphoryl lipid A are present at ratio of QS21:3D-MPL of 1:1 w/w and both are present in a human dose at a level of below 30 ug. Such adjuvant compositions are described, for example, in WO2007/068907 and US2008279926, which are hereby incorporated by reference.

Other adjuvant systems of interest include those based on aluminium salts in conjunction with the lipopolysaccharide 3-de-O-acylated monophosphoryl lipid A. The antigen and 3-de-O-acylated monophosphoryl lipid A may be co-adsorbed to the same metallic salt particles or may be adsorbed to distinct metallic salt particles. See, for example, WO00/23105, US7357936 and US20080226672A1, which are hereby incorporated by reference, which describe immunogenic compositions comprising an antigen bound to a first metallic salt particle (in particular aluminium phosphate or aluminium hydroxide) and 3-de-O-acylated monophosphoryl lipid A which is bound to a second metallic salt particle (in particular aluminium phosphate or aluminium hydroxide).

Any immunogenic composition provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient (as necessary).

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and immunogenic compositions to facilitate production of an antigen-specific immune response.

- 5 Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response and/or to be immunologically compatible with the receiver (i.e., matched HLA haplotype). APCs may
10 generally be isolated from any of a variety of biological fluids and organs, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau & Steinman,
15 *Nature* 392:245-251 (1998)) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic immunity (see Timmerman & Levy, *Ann. Rev. Med.* 50:507-529 (1999)). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T
20 cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within an immunogenic composition (see Zitvogel *et al.*, *Nature Med.* 4:594-600 (1998)).

25 Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood.
30 Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

35 Dendritic cells are conveniently categorised as “immature” and “mature” cells, which allows a simple way to discriminate between two well characterised phenotypes. However, this

nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterised as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a protein (or portion or other variant thereof) such that the polypeptide, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition or immunogenic composition comprising such transfected cells may then be used, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi *et al.*, *Immunology and Cell Biology* 75:456-460 (1997). Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Immunogenic compositions and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, an immunogenic composition or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

In some embodiments, a "priming" or first administration of a modified Rv3616c protein (including fusion proteins), or polynucleotide encoding said protein, is followed by one or more "boosting" or subsequent administrations of a modified Rv3616c protein (including fusion proteins) or polynucleotide encoding said protein ("prime and boost" method). For instance, a

first administration with a modified Rv3616c polypeptide (including fusion proteins) or polynucleotide encoding said protein is followed by one or more subsequent administrations of a modified Rv3616c polypeptide (including fusion proteins) or polynucleotide encoding said polypeptide.

5

In one embodiment, a first administration with a modified Rv3616c protein or polynucleotide is followed by one or more subsequent administrations of a modified Rv3616c protein. In one embodiment, a first administration with a modified Rv3616c protein or polynucleotide is followed by one or more subsequent administrations of a modified Rv3616c polynucleotide.

10

Usually the first or "priming" administration and the second or "boosting" administration are given about 2-12 weeks apart, or up to 4-6 months apart. Subsequent "booster" administrations are given about 6 months apart, or as long as 1, 2, 3, 4 or 5 years apart. Conventional booster treatment (e.g., a protein priming administration followed by a protein boosting administration) may also useful be in preventing or treating tuberculosis (e.g. preventing or treating latent tuberculosis, in particular preventing or delay tuberculosis reactivation).

15

DIAGNOSTICS

20

In another aspect, this invention provides methods for using one or more of the modified Rv3616c proteins described above to diagnose tuberculosis, such as latent tuberculosis (for example using T cell response based assays or antibody based assays of conventional format).

25

For example, there is provided a method for determining latent *M. tuberculosis* infection in an individual comprising:

- (a) obtaining a sample from the individual;
- (b) contacting said sample with a modified Rv3616c protein;
- (c) quantifying the sample response.

30

The sample may for example be whole blood or purified cells. Suitably the sample will contain peripheral blood mononucleated cells (PBMC). In one embodiment of the invention the individual will be seropositive. In a second embodiment of the invention the individual will be seronegative.

35

Suitably the individual will not previously have been vaccinated against *M. tuberculosis* infection (e.g. suitably the individual will not previously have been vaccinated with a BCG)

The sample response may be quantified by a range of means known to those skilled in the art, including the monitoring of lymphocyte proliferation or the production of specific cytokines or antibodies. For example, T-cell ELISPOT may be used to monitor cytokines such as interferon gamma (IFN γ), interleukin 2 (IL2) and interleukin 5 (IL5). B-cell ELISPOT may be used to monitor the stimulation of *M. tuberculosis* specific antigens. The cellular response may also be characterised by the use of by intra- and extra-cellular staining and analysis by a flow cytometer.

Methods of quantifying a sample proliferation response include:

- (i) pulsing cultured cells with a radiolabel (e.g. tritiated thymidine) and monitoring tritium uptake (e.g. gas scintillation);
- (ii) carboxyfluorescein diacetate succinimidyl ester (CFSE) labelling and fluorescence monitoring of cell division using flow cytometry.

Quantifying a sample cytokine response includes in particular the monitoring of interferon gamma production.

When using such quantification methods, a positive response to an antigen may be defined by a signal to noise ratio (S/N ratio) of at least 2:1 (for example, at least 3:1 or at least 5:1).

In a further aspect of the present invention methods are provided to diagnose latent *M. tuberculosis* infection using a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of a modified Rv153c protein as described above. Such injection may be achieved using any suitable device sufficient to contact the antigen combinations with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. The reaction is measured after a period of time, for example at least 48 hours after injection, especially 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater in patients that have been exposed previously to the test antigen. The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, especially greater

than about 1.0 cm in diameter, is a positive response, indicative of prior *M. tuberculosis* infection, which may or may not be manifested as an active disease.

For use in a skin test, the modified Rv3616c protein component is suitably formulated as a pharmaceutical composition containing a physiologically acceptable carrier. Suitably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80™.

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a modified Rv3616c protein. Such protein may be provided attached to a support material. Such kits may also, contain a detection reagent that contains a reporter group suitable for direct or indirect detection of antibody binding.

Other diagnostics kits include those designed for the detection of cell mediated responses (which may, for example, be of use in the diagnostic methods of the present invention). Such kits will typically comprise:

- (i) apparatus for obtaining an appropriate cell sample from a subject;
- (ii) means for stimulating said cell sample with an Rv3616c polypeptide (or variant thereof, immunogenic fragments thereof, or DNA encoding such polypeptides);
- (iii) means for detecting or quantifying the cellular response to stimulation.

Suitable means for quantifying the cellular response include a B-cell ELISPOT kit or alternatively a T-cell ELISPOT kit, which are known to those skilled in the art.

One possible kit comprises:

- (a) a polypeptide of the invention; and
- (b) a detection reagent suitable for direct or indirect detection of antibody binding.

Of particular interest are diagnostic kits tailored for quantifying T cell responses:

A diagnostic kit comprising:

- (a) a polypeptide of the invention; and

- (b) apparatus sufficient to contact said polypeptide with the dermal cells of an individual.

A diagnostic kit comprising:

- (a) a polypeptide of the invention;
- (b) apparatus sufficient to contact said polypeptide with a sample (e.g. whole blood or more suitably PBMC) from an individual; and
- (c) means to quantify the T cell response (e.g. proliferation or IFN-gamma production).

EXAMPLES

The following examples are provided by way of illustration only and not by way of limitation. Those of skill in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield essentially similar results.

EXAMPLE 1 – IDENTIFICATION OF Rv3616c AS A LATENT TB VACCINE TARGET

The gene Rv3616c encodes for a conserved hypothetical alanine and glycine rich protein.

Rv3616c was selected based on a genome-wide analysis of *Mycobacterium tuberculosis* genes associated with dormancy phase maintenance and infectivity as in Murphy and Brown *BMC.Infect. Dis.* 2007 7:84-99. Potential dormancy phase gene targets in *Mycobacterium tuberculosis* were prioritised through a bioinformatics meta-analysis of published genome-wide DNA microarray datasets of bacterial gene expression under simulated dormancy conditions. Subcellular localisation of *M. tuberculosis* proteins encoded by genes, was subsequently carried out on the entire genome to identify vaccine targets.

Briefly, experimental conditions in the dormancy models were quite varied so a zero to five scoring system was developed to normalise these data based upon two criteria: 1) the relevance of the experimental conditions to the dormant state and 2) the rank order of expression. The maximum score for a particular experimental dataset was adjusted based on potential relevance to the clinical occurrence of dormancy phase *M. tuberculosis* infections. Table 1 shows the data sets collected for Step 1 together with the adjusted maximum scores for each dataset. Additional datasets on gene essentiality for growth were obtained from

published studies using transposon-based knockout experiments (TraSH). Genes which had no effect on growth received a score of zero.

5 **Table 1 – Sources, experimental models, and scoring criteria for *M. tuberculosis* DNA microarray gene expression and genome-wide gene knock-out (growth phase essentiality).**

Reference	Experimental model	Timepoint: Maximum score ^a
Betts JC et al. <i>Mol. Microbiol.</i> 2002 43:717-731	Starvation under controlled O ₂	96h: 3 24h: 2 4h: 1
Hampshire T et al. <i>Tuberculosis.(Edinb.)</i> 2004 84:228-238	Nutrient depletion under controlled O ₂	62 and 75d: 5 49d: 4 18d: 2
Muttucumaru DG et al. <i>Tuberculosis.(Edinb.)</i> 2004 84:239-246	Wayne model of hypoxia [#]	14d (NRP-2): 4 7d (NRP-1): 2
Voskuil MI et al. <i>Tuberculosis.(Edinb.)</i> 2004 84:218-227	Wayne model of hypoxia [#]	30 and 80d: 5 14 and 20d: 4 10 and 12d: 3 6 and 8d: 2
Schnappinger D et al. <i>J. Exp. Med.</i> 2003 198:693-704	Infection of mouse macrophages, +/- γ -INF	24 and 48h: 5
Karakousis PC et al. <i>J. Exp. Med.</i> 2004 200:647-657	Hollow fiber subcutaneous implant in mice	10d: 3
Talaat AM et al. <i>Proc. Natl. Acad. Sci. U.S.A</i> 2004, 101:4602-4607	Infection of mice. MTB harvested from lung ^b	28d: 3
Sasseti CM et al. <i>Mol. Microbiol.</i> 2003 48:77-84	TraSH mutated libraries grown on solid media	14d:5
Rengarajan J et al. <i>Proc.Natl.Acad.Sci.U.S.A</i> 2005, 102:8327-8332	Infection of mouse macrophages, +/- γ -INF with TraSH mutated libraries of <i>M. tuberculosis</i>	7d:5

Reference	Experimental model	Timepoint: Maximum score ^a
Sassetti CM et al. <i>Proc.Natl.Acad.Sci.U.S.A</i> 2003 100:12989-12994	C57BL/6J mice infected with TraSH mutated libraries of <i>M.</i> <i>tuberculosis</i>	7, 14, 28 and 56d:5

^aMaximum score based on relevance as a dormancy model; h = hour ; d = day..

^bRatio of *M. tuberculosis* from Balb/c lung to MTB in aerated culture for 28d.

Wayne LG and Hayes LG *Infect. Immun.* 1996 64:2062-2069

5 Step 2 - In applying the second criterion, the rank order of gene expression, gene scores from each dataset were ordered from highest to lowest based on expression ratio (fold expression in the experimental condition versus cells in log-phase liquid culture). The highest scoring gene received the maximum score for that particular dataset (listed in column 3 of Table 1. (e.g. 5, 4 ..., 1 point)). The score was decreased by 0.005 points for each gene in order until zero, or the
10 end of the data set was reached. Thus when the maximum score was 4 points, the 100th ranked gene would receive a score of 3.500. For a maximum score of 5 points, 1000 genes or 25% of the *M. tuberculosis* genome received a score. For experiments where data from multiple time points were collected, the maximum score across all time points was used as the final score.

15

In Step 3 scores for each gene in each of the experimental conditions were collected into a Microsoft Access database. Reference fields were added to facilitate prioritisation, such as the Refseq ID, Genbank function, Genbank note, Tuberculist classification, and KEGG and Sanger Center links. By combining the data from different studies and sources, a consensus view was
20 reached about the particular genes and pathways most critical for survival in the dormant state.

In Step 4, a prioritised list of therapeutic targets was derived utilising the top 400 scoring genes (~10% of the genome) supplemented by expert computational and manual analysis of biochemical pathways, enzymology, drug tractability, homology to human genes and other
25 prior knowledge. The great majority of the high scoring genes come from the subset where two or three of the groups intersect.

In Step 5, the identification of subcellular localisation of *M. tuberculosis* proteins encoded by genes, was carried out on the entire genome. The heuristic used for membrane protein
30 prediction is described in Chalker et al. *J. Bacteriol.* 2001 183:1259-1268. Average hydropathy profiles (H) (von Heijne G *J. Mol. Biol.* 1992 225:487-494) were generated using GES

hydropathy values (Engelman DM et al. *Annu. Rev. Biophys. Biophys. Chem.* 1986 15:321-353) weighted using a trapezoid window. Using a process similar to the initial steps of the TopPred II algorithm (Claros MG et al. *Comput. Appl. Biosci.* 1994 10:685-686), helical transmembrane segments (TMS) were predicted for each peptide sequence by selecting 19 amino acids centered on the highest H value (MaxH), masking these from further consideration, and repeating the process until no peaks with a H of >0.5 remained. Subcellular locations were assigned based on the peak MaxH value, number of segments with a H of >1.0, and distribution and peak H values of the putative TMS. A MaxH cutoff of 1.15 was chosen to maximize the discrimination between two SwissProtein release 34 test datasets containing transmembrane and cytoplasmic proteins, respectively (Boyd D et al. *Protein Sci.* 1998 7:201-205). Proteins with a MaxH of <1.15 were classified as cytoplasmic, while those with a MaxH of >1.15 and at least three possible TMS were classified as membrane proteins. Anchored proteins were defined as having exactly two TMS, one starting before amino acid (aa) 35 and one having a H of >1.15 with the other having a H not lower than 0.5. SignalP with Gram positive settings was specifically used for *M. bacterium* to identify secreted proteins amongst those classified as either cytoplasmic or "unknown" in the heuristic analysis (Nielsen H et al. *Protein Eng.* 1997 10:1-6).

Rv3616c ranked very high as a vaccine antigen according to several criteria:

(i) Rv3616c is consistently up-regulated across all models of dormancy. Among the entire suite of 3999 genes scored in the meta-analysis, Rv3616c was ranked in the top quartile of overexpressed genes across all dormancy models. The up-regulated score for Rv3616c was 6.52 which favourably compared with the top gene score of 22.28.

(ii) Rv3616c ranked as being highly essential for survival in the mouse spleen infection model (scoring 4.945, out of a possible scoring of 5).

(iii) Subcellular localisation predicted that Rv3616c protein is a membrane bound protein and thus has significant extracellular exposure, indicating suitability as a vaccine target.

(iv) Rv3616c can elicit a protective response against initial tuberculosis challenge

(v) Rv3616c is broadly recognised as an antigen

EXAMPLE 2 – Rv3616c EPI TOPE PREDICTIONMethod

- 5 T cell epitope prediction was based on the following approaches:

Prediction	Name	URL/References
CD4 and CD8	Multipred	website: antigen.i2r.a-star.edu.sg/multipred/ Zhang,G.L., Khan,A.M., Srinivasan,K.N., August,J.T. and Brusic,V. (2005) "MULTIPRED: a computational system for prediction of promiscuous HLA binding peptides" <i>Nucleic Acids Res.</i> 33, W172 - W179.
	SVMHC	website: www-bs.informatik.uni-tuebingen.de/SVMHC "Prediction of MHC class I binding peptides, using SVMHC." Pierre Dönnes and Arne Elofsson in: <i>BMC Bioinformatics</i> 2002 3: 25
CD4	ProPred	website: www.imtech.res.in/raghava/propred/ Singh,H. and Raghava,G.P.S.(2001) "ProPred: Prediction of HLA-DR binding sites." <i>Bioinformatics</i> ,17(12), 1236-37.
	Tepitope2	In house program based on : H. Bian, J. Hammer (2004) "Discovery of promiscuous HLA-II-restricted T cell epitopes with TEPITOPE." <i>Methods</i> 34 : 468-75
CD8	nHLA	website: www.imtech.res.in/raghava/nhlapred/ Bhasin M. and Raghava G P S (2006) "A hybrid approach for predicting promiscuous MHC class I restricted T cell epitopes"; <i>J. Biosci.</i> 32:31-42

Prediction	Name	URL/References
	NetCTL	website: www.cbs.dtu.dk/services/NetCTL/ "An integrative approach to CTL epitope prediction. A combined algorithm integrating MHC-I binding, TAP transport efficiency, and proteasomal cleavage predictions." Larsen M.V., Lundegaard C., Kasper Lamberth, Buus S., Brunak S., Lund O., and Nielsen M. <i>European Journal of Immunology</i>. 35(8): 2295-303. 2005
	EpiJen	website: www.jenner.ac.uk/EpiJen/ Doytchinova, I. A., P. Guan, D. R. Flower. "EpiJen: a server for multi-step T cell epitope prediction." <i>BMC Bioinformatics</i>, 2006, 7, 131.
	Syfpeithi	website: www.syfpeithi.de/Scripts/MHCServer.dll/EpitopePrediction.htm Hans-Georg Rammensee, Jutta Bachmann, Niels Nikolaus Emmerich, Oskar Alexander Bachor, Stefan Stevanovic: "SYFPEITHI: database for MHC ligands and peptide motifs." <i>Immunogenetics</i> (1999) 50: 213-219
	PredTAP	website: antigen.i2r.a-star.edu.sg/predTAP/ Zhang,G.L., Petrovsky,N., Kwoh,C.K., August,J.T. and Brusic,V. (2006) "PRED^{TAP}: a system for prediction of peptide binding to the human transporter associated with antigen processing." <i>Immunome Res.</i> 2(1), 3.

Prediction	Name	URL/References
	PAPROC	http://www.paproc2.de/paproc1/paproc1.html C. Kuttler, A.K. Nussbaum, T.P. Dick, H.-G. Rammensee, H. Schild, K.P. Haderler, "An algorithm for the prediction of proteasomal cleavages", J. Mol. Biol. 298 (2000), 417-429 A.K. Nussbaum, C. Kuttler, K.P. Haderler, H.-G. Rammensee, H. Schild, "PAPROC: A Prediction Algorithm for Proteasomal Cleavages available on the WWW", Immunogenetics 53 (2001), 87-94

Results

5

Table 2 – Putative Rv3616c human CD4+ T cell epitopes

Putative CD4 epitope number	Amino acid position	Epitope sequence	SEQ ID No:	HLA allele
1	5	FIIDPTISA	SEQ ID No: 29	DRB1_0301, DRB1_0401, DRB1_1101
2	31	ILYSSLEYF	SEQ ID No: 30	DRB1_0301
3	36	LEYFEKALE	SEQ ID No: 31	DRB1_1301
4	63	YAGKNRNVH	SEQ ID No: 32	DRB1_0801
5	87	LIHDQANAV	SEQ ID No: 33	DRB1_0301, DRB1_0401
6	111	FVRPVAVDL	SEQ ID No: 34	DRB1_0101
7	119	LYIPVVGH	SEQ ID No: 35	DRB1_0401
8	121	YIPVVGHAL	SEQ ID No: 36	DRB1_0101
9	151	YLVVKTLIN	SEQ ID No: 37	DRB1_0401
10	152	LVVVKTLINA	SEQ ID No: 38	DRB1_1301
11	154	VKTLINATQ	SEQ ID No: 39	DRB1_0401
12	164	LKLLAKLAE	SEQ ID No: 40	DRB1_0301, DRB1_0801, DRB1_1101, DRB1_1301
13	173	LVAAAIADI	SEQ ID No: 41	DRB1_0301, DRB1_1101, DRB1_1301
14	181	IISDVADII	SEQ ID No: 42	DRB1_0301
15	197	WEFITNALN	SEQ ID No: 43	DRB1_0401
16	252	LFGAAGLSA	SEQ ID No: 44	DRB1_1501
17	264	LAHADSLAS	SEQ ID No: 45	DRB1_0401
18	270	LASSASLPA	SEQ ID No: 46	DRB1_0401
19	288	FGGLPSLAQ	SEQ ID No: 47	DRB1_0401

Table 3 – Putative Rv3616c human CD8+ T cell epitopes

Putative CD8 epitope number	Amino acid position	Epitope sequence	SEQ ID No:	HLA allele
1	5	FIIDPTISA	SEQ ID No: 48	A2
2	6	IIDPTISAI	SEQ ID No: 49	A_0101, A2
3	9	PTISAIIDGL	SEQ ID No: 50	A2, A_0201, B7, B8
4	10	TISAIIDGLY	SEQ ID No: 51	A1, A_0101, A3, A_0301
5	12	SAIDGLYDL	SEQ ID No: 52	A2, B_3501
6	13	AIDGLYDLL	SEQ ID No: 53	A_0101, A_0201, B44
7	17	LYDLLGIGI	SEQ ID No: 54	A24
8	25	IPNQGGILY	SEQ ID No: 55	B7, A_0101, B_3501, B51
9	30	GILYSSLEY	SEQ ID No: 56	A1, A_0101, A3, A_0301
10	33	YSSLEYFEK	SEQ ID No: 57	A1, A_0301
11	35	SLEYFEKAL	SEQ ID No: 58	A_0201, B7, Cw_0401, Cw_0602
12	38	YFEKALEEL	SEQ ID No: 59	A24, A_2402, B8, Cw_0401, Cw_0602
13	39	FEKALEELA	SEQ ID No: 60	B44, B_4403
14	69	NHVNFFQEL	SEQ ID No: 61	A24, Cw_0602
15	76	ELADLDRQL	SEQ ID No: 62	A_0201
16	77	LADLDRQLI	SEQ ID No: 63	A_0101, B51
17	79	DLDRQLISL	SEQ ID No: 64	A_0101, A_0201
18	80	LDRQLISLI	SEQ ID No: 65	A24, B7, B51
19	94	AVQTTRDIL	SEQ ID No: 66	B7
20	103	EGAKKGLEF	SEQ ID No: 67	A24, B7
21	107	KGLEFVRPV	SEQ ID No: 68	A_0201, B51
22	108	GLEFVRPVA	SEQ ID No: 69	A_0101, A_0301
23	109	LEFVRPVAV	SEQ ID No: 70	B44
24	111	FVRPVAVDL	SEQ ID No: 71	B7, B8, B_3501
25	113	RPVAVDLTY	SEQ ID No: 72	B7, A_0101, B_3501, B51
26	116	AVDLTYIPV	SEQ ID No: 73	A2, A_0201
27	120	TYIPVVGHA	SEQ ID No: 74	A24
28	121	YIPVVGHAL	SEQ ID No: 75	A_0101, A2, A_0201, B7, B8
29	129	LSAAFQAPF	SEQ ID No: 76	A1, B7, B_3501
30	130	SAAFQAPFC	SEQ ID No: 77	A_0201
31	131	AAFQAPFCA	SEQ ID No: 78	A_0301, B_3501
32	133	FQAPFCAGA	SEQ ID No: 79	A2, A_0201
33	135	APFCAGAMA	SEQ ID No: 80	B7, B_3501
34	136	PFCAGAMAV	SEQ ID No: 81	A3
35	141	AMAVVGGAL	SEQ ID No: 82	A2, A_0201, A24, B7
36	143	AVVGGALAY	SEQ ID No: 83	A1, A3, A_0301, B7
37	147	GALAYLVVK	SEQ ID No: 84	A3, A_0301
38	149	LAYLVVKTL	SEQ ID No: 85	B8, B44, B51
39	150	AYLVVKTLI	SEQ ID No: 86	A24
40	155	KTLINATQL	SEQ ID No: 87	A_0201, A2, A_0301, A24
41	156	TLINATQLL	SEQ ID No: 88	A2, A_0201, A3, A_0101, Cw_0401
42	158	INATQLLKL	SEQ ID No: 89	B7, B8, Cw_0602

Putative CD8 epitope number	Amino acid position	Epitope sequence	SEQ ID No:	HLA allele
43	159	NATQLLKLL	SEQ ID No: 90	A_2402, B7, B_3501, B44, Cw_0401, Cw_0602
44	162	QLLKLLAKL	SEQ ID No: 91	A2, A_0201, A_0301, A_2402, B8, Cw_0401, Cw_0602
45	165	KLLAKLAEL	SEQ ID No: 92	A2, A_0201, A_0301, B7, B8, Cw_0602
46	166	LLAKLAELV	SEQ ID No: 93	A2, A_0201, A_0101, B8
47	169	KLAELVAAA	SEQ ID No: 94	A2
48	170	LAELVAAAI	SEQ ID No: 95	A1, A24, B51
49	173	LVAAAIADI	SEQ ID No: 96	B7, B51
50	177	AIADIISDV	SEQ ID No: 97	A2, A_0201, Cw_0602
51	178	IADIISDVA	SEQ ID No: 98	A_0101, B_3501
52	182	ISDVADIIK	SEQ ID No: 99	A1, A_0301
53	192	TLGEVWEFI	SEQ ID No: 100	A2, A_0201
54	199	FITNALNGL	SEQ ID No: 101	A2
55	202	NALNGLKEL	SEQ ID No: 102	B51, A_2402, B_3501, Cw_0602
56	213	KLTGWVTGL	SEQ ID No: 103	A2, A_0201
57	214	LTGWVTGLF	SEQ ID No: 104	A1, A_0101, A24
58	225	GWSNLESFF	SEQ ID No: 105	A24
59	228	NLESFFAGV	SEQ ID No: 106	A2, A_0201
60	231	SFFAGVPGL	SEQ ID No: 107	A2, A_0201, A24, Cw_0401
61	238	GLTGATSGL	SEQ ID No: 108	A2, A_0201
62	246	LSQVTGLFG	SEQ ID No: 109	A1, B8
63	247	SQVTGLFGA	SEQ ID No: 110	A2
64	258	LSASSGLAH	SEQ ID No: 111	A1, A3, B7, B8
65	260	ASSGLAHAD	SEQ ID No: 112	A1, A3, A_0301
66	262	SGLAHADSL	SEQ ID No: 113	A_0201
67	263	GLAHADSLA	SEQ ID No: 114	A_0101, A_0201, A_0301
68	269	SLASSASLP	SEQ ID No: 115	A_0201, A_0301
69	271	ASSASLPAL	SEQ ID No: 116	B7
70	286	SGFGGLPSL	SEQ ID No: 117	A2, A_0201, B51
71	291	LPSLAQVHA	SEQ ID No: 118	B7, B_3501, B51
72	298	HAASTRQAL	SEQ ID No: 119	B7, B8, B_3501
73	301	STRQALRPR	SEQ ID No: 120	A3, A_0301
74	307	RPRADGPVG	SEQ ID No: 121	B7, B_0702, B8, B51
75	319	EQVGGQSQL	SEQ ID No: 122	B7, B44
76	350	GASKGTTTK	SEQ ID No: 123	A3, A_0301
77	351	ASKGTTTKK	SEQ ID No: 124	A3, A_0301
78	353	KGTTTKKYS	SEQ ID No: 125	A_0301, B8
79	368	TEDAERAPV	SEQ ID No: 126	B44

As can be seen from Tables 2 and 3, Rv3616c contains a number of predicted CD4+ and CD8 T cell epitopes. Furthermore, this information suggests that the protein carries epitopes that can be recognised by HLAs which occur worldwide (that is HLAs from Caucasian, African, Asian or Latin-American individuals – see website at www.allele frequencies.net).

EXAMPLE 3 – Rv3616c EPITOPE IDENTIFICATION

A range of 30 overlapping peptides covering the full length of Rv3616c were prepared (see Figure 1 for details and SEQ ID Nos: 127-156) and tested for their ability to stimulate PBMC from four PPD+ donors.

The data, shown in Figure 2, reveals that peptides 1-7 and 17-30 were immunogenic for these individuals. These peptides are suitably present within the sequence of the modified Rv3616c proteins of the invention.

It should be noted that peptides 8-16 (amino acid residues 92-215) may be immunogenic in other individuals of differing HLA type.

EXAMPLE 4 – Rv3616c H37Rv HOMOLOGUES

Rv3616c sequences from a number of *M. tuberculosis* strains and BCG were identified using BLASTP searches of GenBank (H37Rv reference sequence accession number NP_218133.1):

Strain	Accession Number	% identity
CDC1551	NP_338263.1	99
F11	YP_001289574.1	99
Haarlem	ZP_02248979.1	99
C	ZP_00877472.1	99
BCG	YP_979759.1	99

Alignment of the homologue sequences indicates a high level of identity.

BIOLOGICAL ASSAYS

Quantification of T cell responses to Rv3616c

Polypeptides may be screened for their ability to activate T-cells (induction of proliferation and/or production of cytokines) in peripheral blood mononuclear cell (PBMC) or in whole blood preparations from infected (such as latently infected) individuals.

Latently infected individuals are usually identified by a skin test that has a diameter above 10mm and without symptoms, with no Mtb positive culture, with a negative sputum negative and with no lesion (as detected by chest X-Ray).

A range of *in vitro* assays can be used based on PBMC samples or whole blood: after

5 restimulation in presence of the antigen (or variant/immunogenic fragment thereof as appropriate) the proliferation of the cells may be determined (as measured by CFSE/flow cytometry) or the production of cytokines quantified (present in the supernatant of cultured cells and measured by ELISA, or, after intracellular staining of CD4 and CD8 T cells and analysis by flow cytometry).

10 For example, PBMC samples may be obtained from heparinised whole blood by Ficoll-Hypaque density gradient centrifugation following standard procedures. The cells may then be washed and cryopreserved in liquid nitrogen until testing (for further details see Lalvani A et al. *J. Infect. Dis.* 1999 180:1656-1664).

T cell proliferation

15

The specific immune response may be characterised by performing lymphocyte proliferation analysis using the tritiated thymidine. This technique assesses the cellular expansion upon *in vitro* stimulation to an antigen. In practice, cell proliferation is determined by estimating incorporation of tritiated-thymidine into DNA, a process closely related to underlying changes

20 in cell number.

More suitably, lymphocyte proliferation may be performed using the succinimidyl ester of carboxyfluorescein diacetate (CFSE). CFSE spontaneously and irreversibly couples to both intracellular and cell surface proteins by reaction with lysine side chains and other available

25 amine groups. When lymphocyte cells divide, CFSE labelling is distributed equally between the daughter cells, which are therefore half as fluorescent as the parents. As a result, halving of cellular fluorescence intensity marks each successive generation in a population of proliferating cells and is readily followed by flow cytometry (for further details see Hodgkins, PD et al *J. Exp. Med.* 1996 184:277-281).

30

Practically, after thawing, PMBC may be washed and stained with CFSE before being cultivated (2×10^5 cells) for 72 hrs with 10 ug/ml of antigen in culture media (RPMI-1640 supplemented with glutamine, non essential amino acid, pyruvate and heat inactivated human

AB serum). Cells may then then harvested and their phenotype characterised using surface staining to identify memory CD8 and CD4+ T-Cells. Subsequently, flow cytometry analysis can be used to indicate the extent of lymphocyte proliferation in response to each antigen (proportion of cells with decreased CFSE intensity upon *in vitro* stimulation).

5

Cytokine production

IFN- γ production (or the production of other cytokines such as e.g. IL2, TNF-alpha, IL5, IL12 etc) may be measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates may be coated with a mouse monoclonal antibody directed to human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are then washed, for example, six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN- γ serum, for example, diluted 1:3000 in PBS/10% normal goat serum may be added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) may be added, for example, at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction may be stopped after 20 min with 1 N sulfuric acid. Optical density can then be determined at 450 nm using 570 nm as a reference wavelength. Typically, fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone may be considered positive.

EXAMPLE 5 – IMMUNOGENICITY OF Rv3616c IN CB6F1 MICE

The immunogenicity of the antigen was evaluated in CB6F1 mice (first generation cross of BALB/c and C57BL/6 mice).

CB6F1 mice were immunised intramuscularly three times (on day 0, day 14 and day 28) with 0.5 ug of protein antigen in combination with the Adjuvant System AS01E (a liposomal adjuvant formulation comprising 3D-MPL and QS21).

The experimental design was as follows:

Group	Day 0	Day 14	Day 28
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1	0.5 ug Rv3616c/AS01E	0.5 ug Rv3616c/AS01E	0.5 ug Rv3616c/AS01E
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A total of 24 mice were used in the protocol group

- Peripheral blood lymphocytes (PBL) were collected and pooled on day 21 (i.e. 7 days post second immunisation) and day 35 (i.e. 7 days post third immunisation) and the antigen-specific CD4 & CD8 T cell responses (as determined by CD4 or CD8 T cells producing IL-2 and/or IFN-gamma and/or TNF-alpha) were measured by flow cytometry after overnight *in vitro* restimulation with pools of 15mer peptides covering the sequences of interest.
- The detection of mouse T cells that express IL-2 and/or IFN-gamma and/or TNF-alpha was done by using short-term antigen-driven *in vitro* amplification of cytokine expression.

- Briefly, PharmLyse solution (BD-Pharmingen) was added to heparinised mouse peripheral blood in order to lyse the red blood cells. The PBLs (Peripheral Blood Lymphocytes) obtained were washed and then incubated in the presence of a pool of 15-mer peptides - overlapping by 11 amino acids - covering the sequence of the antigen of interest and of 1 ug/ml of antibodies to CD28 and CD49d (BD-Pharmingen). Each 15-mer peptide was used at a final concentration of 1 ug/ml. Medium controls were also stimulated with antibodies to CD28 and CD49d.

- The cytokine secretion blocking compound brefeldin-A (BD-Pharmingen) was added 2 h after the onset of the cultures at 37°C, 5% CO₂ and the cells maintained at 37°C, 5% CO₂ for 4 additional hours followed by overnight incubation at +4°C.

- Cells were then harvested and stained with Pacific Blue-coupled anti-CD4 (BD – clone RM4-5, BD-Pharmingen) and peridinin chlorophyll A protein (PerCp) cyanin5.5 (Cy5.5)-coupled anti-CD8 alpha (clone 53-6.7, BD-Pharmingen) antibodies.

- Cells were then washed, fixed, permeabilised (Cytofix-cytoperm kit, BD-Pharmingen) and stained with allophycocyanin-coupled anti-IFN-g antibodies (clone XMG1.2, BDPharmingen), fluorescein isothiocyanate (FITC)-coupled anti-IL-2 antibodies (clone JES 6-5H4, Beckman Coulter) and phycoerythrin (PE)-coupled anti-TNF alpha antibodies (clone MP6-XT22, BD-Pharmingen). After final washes, stained cells were analysed on a LSR II flow cytometer (Beckton-Dickinson). A minimum number of 10,000 cells were acquired in the CD8+ subset.

For further background see Walzer T et al *Cell Immunol.* 2000 206(1):16-25 and Maecker HT et al *J. Immunol. Methods* 2001 255(1-2):27-40.

As negative controls, some cells were also cultured overnight *in vitro* in culture medium (unstimulated). The antigen-specific responses were calculated by subtracting the average cytokine response produced by unstimulated cells from the average cytokine response produced by the peptide-stimulated cells.

At each timepoint and for each group, the data was collected from 4 pools of 6 mice each. The data below is presented as the % of CD4 or CD8 T cells producing IL-2 and/or IFN-gamma and/or TNF-alpha. Each individual pool of mice is plotted (triangles) as well as the average value of the group (bar).

Figure 3 shows that on day 21 (i.e. 7 days post second immunisation), Rv3616c-specific CD4 and CD8 T cell responses are detected in mice immunised with 0.5 ug of Rv3616c/AS01E.

Figure 4 shows the cytokine profile of CD4 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 21 (i.e. 7 days post second immunisation).

Figure 5 shows the cytokine profile of CD8 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 21 (i.e. 7 days post second immunisation).

Figure 6 shows that on day 35 (i.e. 7 days post third immunisation), Rv3616c-specific CD4 and CD8 T cell responses are detected in mice immunised with 0.5 ug of Rv3616c/AS01E. The third dose increases the CD4 T cell response but not the CD8 T cell response. Due to technical difficulties, data was only available for a single pool.

Figure 7 shows the cytokine profile of CD4 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 35 (i.e. 7 days post third immunisation). Due to technical difficulties, data was only available for a single pool.

Figure 8 shows the cytokine profile of CD8 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 35 (i.e. 7 days post third immunisation). Due to technical difficulties, data was only available for a single pool.

EXAMPLE 6 – IMMUNOGENICITY OF Rv3616c IN C57BL/6 MICE

The immunogenicity of the antigen was also evaluated in C57BL/6 mice.

C57BL/6 mice were immunised intramuscularly three times (on day 0, day 14 and day 28) with 1 ug protein antigen in combination with a the Adjuvant System AS01E (a liposomal adjuvant formulation comprising 3D-MPL and QS21).

The experimental design was the following:

Group	Day 0	Day 14	Day 28
1	1 ug Rv3616c/AS01E	1 ug Rv3616c/AS01E	1 ug Rv3616c/AS01E

Peripheral blood lymphocytes (PBL) were collected and pooled on day 21 (i.e. 7 days post second immunisation) and day 35 (i.e. 7 days post third immunisation) and the antigen-specific CD4 & CD8 T cell responses (as determined by CD4 or CD8 T cells producing IL-2 and/or IFN-gamma and/or TNF-alpha) were measured by flow cytometry after overnight *in vitro* restimulation with pools of 15mer peptides covering the sequences of interest. The procedure followed was as described previously.

As negative controls, some cells were also cultured overnight *in vitro* in culture medium (unstimulated). The antigen-specific responses were calculated by subtracting the average cytokine response produced by unstimulated cells from the average cytokine response produced by the peptide-stimulated cells.

At each timepoint and for each group, the data was collected from 4 pools of 6 mice each. The data below is presented as the % of CD4 or CD8 T cells producing IL-2 and/or IFN-gamma and/or TNF-alpha. Each individual pool of mice is plotted (triangles) as well as the average value of the group (bar).

Figure 9 shows that on day 21 (i.e. 7 days post second immunisation), Rv3616c-specific CD4 and CD8 T cell responses are detected in mice immunised with 1 ug of Rv3616c/AS01E, although the antigen-specific CD8 T cell response is very low (cytokine profile data is therefore not shown).

Figure 10 shows the cytokine profile of CD4 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 21 (i.e. 7 days post second immunisation).

Figure 11 shows that on day 35 (i.e. 7 days post third immunisation), Rv3616c-specific CD4 and CD8 T cell responses are detected in mice immunised with 1 ug of Rv3616c/AS01E. A third immunisation dose increases the CD4 T cell responses but only slightly the CD8 T cell response.

Figure 12 shows the cytokine profile of CD4 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 35 (i.e. 7 days post third immunisation).

Figure 13 shows the cytokine profile of CD8 T cell response from the Rv3616c peptide pool-stimulated PBL (not medium removed) on day 35 (i.e. 7 days post third immunisation).

EXAMPLE 7 – IN VITRO RECOGNITION OF Rv3616c BY PBMC FROM HUMANS WITH LATENT TB

Experiments were performed in order to assess the peripheral T cell response specific to the inventive antigen in 4 TB naïve healthy adults (PPD skin test = 0 mm) and 8 TB latently Infected healthy adults (PPD skin test = 15 mm or above) from South Africa

PPD Skin Test Data

Individual ID Number	Induration diameter (mm)
4	0
5	0
33	0
38	0
36	15
46	15
13	15
7	16
58	25
74	26
8	53
60	55

The cell-mediated immune (CMI) response was assessed by measuring cytokines on isolated peripheral blood mononuclear cells (PBMCs) by intracellular cytokine staining (ICS) assay.

ICS carried out was an adaptation of previously described methodology (see Von Eschen et al, *Hum. Vaccin.* 2009 5(7)). PBMCs were stimulated *in vitro* by one pool of 15-mer peptides - overlapping by 11 amino acids - covering the entire sequence of the antigen of interest. Cells were stimulated with peptides for 2 hours, further cultured overnight in the presence of Brefeldin A, processed for ICS and analysed using flow cytometry. The frequencies of the antigen-specific CD3+CD4+ or CD3+CD8+ T cells expressing IFN-gamma and/or TNF-alpha and/or IL-17 were measured. Medium-stimulated cell responses were subtracted from the responses obtained in peptide pools stimulated cells.

ICS: antibodies

Anti-CD3 PO (Invitrogen – cat CD0330)
 Anti-CD4 PB (BD - cat 558116)
 Anti-CD8 APC-H7 (BD – cat 641400)
 Anti-IFNg AF700 (BD-Pharmingen – cat 557995)
 Anti-TNF PE-Cy7 (BD-Pharmingen – cat 557647)
 Anti-IL17 AF647 (BD-Pharmingen – cat 51-7178-71)

The results are presented as number of antigen-specific CD3+CD4+ T cells expressing TNF-alpha and IFN-gamma, per million of CD3+CD4+ T cells since these cells represent the main population of the antigen-specific CD4 T cells (the background response level due to the medium is removed). No antigen-specific CD3+CD8+ T cells were detected. Figure 14 shows that an antigen-specific CD4 T cell response is measured in 6 out of 8 latently infected individuals (not in individuals number 7 and 74) when compared to the non-specific CD4 T cell response measured in the naïve individuals.

EXAMPLE 8 – PRODUCTION OF MODIFIED Rv3616c SEQUENCES

(i) Cloning

The *Mycobacterium tuberculosis* H37Rv Rv3616 nucleotide sequence was codon-optimized for expression in *E. coli* and gene synthesised. The insert obtained following subcloning was cloned into pET21b+ (Novagen) using a NdeI restriction site at the N-terminus and a XhoI restriction site at the C-terminus. To generate the modified Rv3616c constructs, a series of

PCR amplications using different primers was performed in order to delete specific nucleotide residues within the Rv3616c. The modified inserts were then cloned into pET26b+ and/or pET19b (Novagen).

Clone to be generated	Primers used
pET26_Rv3616Δ136-183His	CAN1001/1004 CAN1003/1002
pET26_Rv3616Δ150-160His	CAN1001/1006 CAN1005/1002
pET26_Rv3616Δ136-154His	CAN1001/1008 CAN1007/1002
pET26_Rv3616Δ166-182His	CAN1001/1010 CAN1009/1002
pET19_Rv3616Δ136-183His	CAN1001/1004 CAN1003/1002
pET19_Rv3616Δ150-160His	CAN1001/1006 CAN1005/1002
pET19_Rv3616Δ136-154His	CAN1001/1008 CAN1007/1002
pET19_Rv3616Δ166-182His	CAN1001/1010 CAN1009/1002
pET26_Rv3616Δ135-139His	CAN1001/1065 CAN1064/1002
pET26_Rv3616Δ142-145His	CAN1001/1067 CAN1066/1002
pET26_Rv3616Δ145-152His	CAN1001/1069 CAN1068/1002
pET26_Rv3616Δ138-145His	CAN1001/1071 CAN1070/1002
pET26_Rv3616Δ149-154His	CAN1001/1073 CAN1072/1002

5

Primer	primer sequence	Restriction site
CAN1001	ggaattccatatgagccgtgcctttattattgatccgac	Nde1
CAN1002	ccg ctc gag cac cac att gcg aac cag aac	Xho1
CAN1003	ctg agc gca gca ttt cag gca ccg atg tgg ccg ata tta tta aag	nil

CAN1004	ctttaataatatcgccacatcggtgctgaaatgctgcgctcag	nil
CAN1005	gtttggggtggtgctctgacccagctgctgaaactg	nil
CAN1006	cagtttcagcagctgggtcagagcaccacccacaac	nil
CAN1007	ctgagcgcagcatttcaggcgaaaaccctgattaatgcaac	nil
CAN1008	gttgcattaatcagggttttcgctgaaatgctgcgctcag	nil
CAN1009	gcaaccagctgctgaaatccgatgtggccgatattattaaag	nil
CAN1010	ctttaataatatcgccacatcggttttcagcagctgggttg	nil
CAN1064	ctgagcgcagcatttcagggtgcaatggcagttgtg	nil
CAN1065	cacaactgccattgcacctgaaatgctgcgctcag	nil
CAN1066	caatggcagttgtgggtggtgctaaaaccctgattaatgcaac	nil
CAN1067	gttgcattaatcagggttttagcaccacccacaactgccattg	nil
CAN1068	ccgttttggtgcgggtgcagggtggtgctctggcatatc	nil
CAN1069	gatatgccagagcaccacctgcaccggcacaaaacgg	nil
CAN1070	gccggtgcaatggcagttgtgtgaaaaccctgattaatg	nil
CAN1071	cattaatcagggttttcacaacaactgccattgcaccggc	nil
CAN1072	gcatttcaggcaccggtttggtggtgctctggcatatc	nil
CAN1073	gatatgccagagcaccaccaaacggtgctgaaatgc	nil

(ii) Expression of the recombinant proteins

Host strain: T7 Express competent *E.coli* (New England Biolabs): enhanced BL21 derivative.

5

Transformation of *Escherichia coli* T7 Express with plasmid DNA was carried out by standard methods with CaCl₂-treated cells (Hanahan D. « Plasmid transformation by Simanis. » in Glover, D. M. (Ed), DNA cloning. IRL Press London. (1985): p. 109-135).

Recombinant plasmids ID	Host strain	Plate agar
pET21_Rv3616His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Carbenicillin ^B
pET26_Rv3616Δ136-183His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET26_Rv3616Δ150-160His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET26_Rv3616Δ136-154His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET26_Rv3616Δ166-182His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET19_Rv3616Δ136-183His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Carbenicillin ^B
pET19_Rv3616Δ150-160His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Carbenicillin ^B
pET19_Rv3616Δ136-154His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Carbenicillin ^B
pET19_Rv3616Δ166-182His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Carbenicillin ^B
pET26_Rv3616Δ135-139His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C

Recombinant plasmids ID	Host strain	Plate agar
pET26_Rv3616Δ142-145His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET26_Rv3616Δ145-152His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET26_Rv3616Δ138-145His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C
pET26_Rv3616Δ149-154His	T7 Express ^A	LB agar plate with phytone and 100 µg/ml Kanamycin ^C

A: NEB (catalogue number: C2566H)

B: Teknova, CA, USA (catalogue number L1092)

C: Teknova, CA, USA (catalogue number L1096)

- 5 Confluent agar plate inoculated with transformed *E. coli* T7 Express + plasmid was used to inoculate 800 ml of LB broth APS + 50 µg/ml of antibiotic to obtain O.D._{600nm} between 0.05 - 0.1. Cultures were incubated at 37°C, 250 RPM to an O.D._{600nm} around 0.8.

- 10 Expression of the recombinant protein was induced by addition of 1 mM final of isopropyl β-D-1-thiogalactopyranoside (IPTG; EMD Chemicals Inc) to the growing culture medium. Induction was maintained for 3 hours at 37°C (or overnight at 16°C).

(iii) Purification

- 15 Bacterial culture was centrifuged 15 min, 4°C at 8000g. Bacterial culture pellets were resuspended in Lysis buffer (20 mM Tris buffer (pH 8.0) and a mixture of protease inhibitors cocktail (Complete EDTA-free). Bacteria were lysed with the Constant Cell disruption system (Constant System). Soluble (supernatant) and insoluble (pellet) components were separated by centrifugation at 20000g for 20 min at 4°C.

20

The insoluble components (pellets) were resolubilised in 20mM HEPES buffer containing 6M guanidine HCl, 500mM NaCl, 10mM imidazole pH8.0. The supernatant was then loaded on a 5ml IMAC column (BioRad). After washes, elution was performed using a 20mM HEPES buffer (pH 8.0) containing 6M Guanidine-HCl, 500mM NaCl, and 250 mM imidazole.

25

Two dialysis steps were performed in membrane 12-14000 MWCO (SpectraPor): primary in a 8M urea buffer containing 20mM HEPES, 150mM NaCl at pH 8.0 followed by a second dialysis in PBS, 4M urea pH7.4.

30

(iv) SDS-PAGE

Samples from non-induced and induced cultures were collected to determine the expression profile and analyzed by SDS-PAGE.

5 Briefly, samples were treated with NUPAGE 4X LDS Sample buffer (Invitrogen), reduced using 0.05M DTT and heated at 70°C for 10 min. Samples were then centrifuged at maximum speed for 2 minutes and loaded on NUPAGE Novex 4-12% Bis-Tris gel (Invitrogen). The migration was performed at 200V for 35 minutes in 1X NUPAGE MES Running Buffer (Invitrogen) and the gel was stained to allow visualization of the separated proteins, the results of which are
10 shown in Figures 17 and 18.

When compared to the H37Rv wild-type expression, the constructs Rv3616Δ138-145, Rv3616Δ136-154, Rv3616Δ150-160, Rv3616Δ166-182, Rv3616Δ149-154 and Rv3616Δ135-139 are notably improved.

15 The construct Rv3616Δ136-183 contained an erroneous STOP codon within the sequence, consequently expression of the sequence did not proceed as intended.

EXAMPLE 9 – FURTHER PRODUCTION OF MODIFIED Rv3616c SEQUENCES

20 Using analogous methodology to that described in Example 8, wherein the BL21 (DE3) strain was used in place of T7Express and confluent agar plate was used to inoculate 25 ml of LB broth APS with antibiotic, three expression runs were performed (starting from the same transformation plate) in respect of a range of modified Rv3616c constructs.

25 The products of the expression runs were analysed by SDS-PAGE and a representative gel from one of the expression runs is provided in Figure 19. Rv3616Δ138-145 was found to offer the best protein expression, followed closely by Rv3616Δ149-154 and Rv3616Δ136-154, with Rv3616Δ135-139 also showing good expression.

30 Quantification of the band corresponding to the target protein was performed using ImageQuant TL software. Briefly, the SDS-PAGE gels were stained using InstantBlue staining (Novexin) and scanned with a UVP BioImaging System in TIFF files format. The bands were then analysed using ImageQuantTL 7.0 software from GE Healthcare. The Rv3616 non-
35 induced protein being used as control for negative expression as no reactivity with anti-his tag Ab was observed.

Construct	Band % : Gel 1	Band % : Gel 2	Band % : Gel 3	Band % average
non induced Rv3616	9	8	7	8
Rv3616	8	8	8	8
Rv3616Δ150-160	8	10	12	10
Rv3616Δ136-154	22	28	29	26
Rv3616Δ166-182	10	10	9	10
Rv3616Δ135-139	15	16	17	16
Rv3616Δ142-145	9	9	8	9
Rv3616Δ145-152	10	9	10	10
Rv3616Δ149-154	26	28	31	28
Rv3616Δ138-145	23	25	21	23

Band %: measure of the band's Volume divided by the Total Volume of all the bands in the lane.

In band percentage, the Rv3616Δ149-154, Rv3616Δ138-145 and Rv3616Δ136-154 proteins are all expressed at notably higher levels compared to the natural sequence or the known

5 Rv3616Δ150-160 construct. Rv3616Δ135-139 was also expressed at a high level.

Example 10 – IMMUNOGENICITY OF Rv3616Δ138-145 IN CB6F1 MICE

The immunogenicity of Rv3616Δ138-145 was evaluated in CB6F1 mice.

10

CB6F1 mice were immunised intramuscularly three times (on day 0, day 14 and day 28) with 50 ul of test vaccine containing a dose range (8 ug, 2 ug and 0.5 ug) of Rv3616Δ138-145 in combination with the Adjuvant System AS01E (a liposomal adjuvant formulation comprising 3D-MPL and QS21). The formulations also contained urea (4M) and arginine (500 mM).

15

The experimental design was the following:

Group	Day 0	Day 14	Day 28
1	8 ug Rv3616Δ138-145 /AS01E	8 ug Rv3616Δ138-145 /AS01E	8 ug Rv3616Δ138-145 /AS01E
2	2 ug Rv3616Δ138-145 /AS01E	2 ug Rv3616Δ138-145 /AS01E	2 ug Rv3616Δ138-145 /AS01E
3	0.5 ug Rv3616Δ138-145 /AS01E	0.5 ug Rv3616Δ138-145 /AS01E	0.5 ug Rv3616Δ138-145 /AS01E

A total of 20 mice were used in each immunisation group. 10 mice received saline as a negative control group (data not shown).

Peripheral blood lymphocytes (PBL) were collected & pooled on days 21 (i.e. 7 days post second immunisation) and 35 (i.e. 7 days post third immunisation) and the antigen-specific CD4 & CD8 T cell responses (as determined by CD4 or CD8 T cells producing IL-2 and/or IFN-gamma and/or TNF-alpha) were measured by flow cytometry after a 6 hour *in vitro* restimulation with pools of 15mer peptides covering the full Rv3616c antigen sequence. The detection of mouse T cells that express IL-2 and/or IFN-gamma and/or TNF-alpha was done by using short-term antigen-driven *in vitro* amplification of cytokine expression.

Briefly, PharmLyse solution (BD-Pharmingen) was added to heparinised mouse peripheral blood in order to lyse red blood cells. The PBLs (Peripheral Blood Lymphocytes) obtained were washed and then incubated in the presence of a pool of 15-mer peptides - overlapping by 11 amino acids - covering the sequence of the antigen of interest and of 1 ug/ml of antibodies to CD28 and CD49d (BD-Pharmingen). Each 15-mer peptide was used at a final concentration of 1 ug/ml. Medium controls wells were also stimulated with antibodies to CD28 and CD49d.

The cytokine secretion blocking compound brefeldin-A (BD-Pharmingen) was added 2 h after the onset of the cultures at 37°C, 5% CO₂ and the cells maintained at 37°C, 5% CO₂ for 4 additional hours followed by overnight storage at +4°C.

Cells were then harvested and stained with Pacific Blue-coupled anti-CD4 (clone RM4-5, BD-Pharmingen) and peridinin chlorophyll A protein (PerCp) cyanin5.5 (Cy5.5)-coupled anti-CD8 alpha (clone 53-6.7, BD-Pharmingen) antibodies.

Cells were then washed, fixed, permeabilised (Cytofix-cytoperm kit, BD-Pharmingen) and stained with allophycocyanin-coupled anti IFN-gamma antibodies (clone XMG1.2, BD-Pharmingen), fluorescein isothiocyanate (FITC)-coupled anti IL-2 antibodies (clone JES 6-5H4, BD-Pharmingen) and phycoerythrin (PE)-coupled anti-TNF alpha antibodies (clone MP6-XT22, BD-Pharmingen). After final washes, stained cells were analysed on a LSRII flow cytometer (Becton-Dickinson). A minimum of 10,000 cells were acquired in the CD8+ subset.

As negative controls, some cells were also cultured for 6 h *in vitro* in culture medium (unstimulated). The antigen-specific responses were calculated by subtracting the average

cytokine response produced by unstimulated cells from the average cytokine response produced by the peptide-stimulated cells.

At each timepoint and for each group, the data was collected from 4 pools of 5 mice each and the data presented as the % of CD4 or CD8 T cells producing IL-2 and/or IFN-gamma and/or TNF-alpha. Each individual pool of mice is plotted (closed diamonds) as well as the median value of the group (bar).

The results are shown in Figures 20 to 25.

Figure 20 shows that at both timepoints (7dPII & 7dPIII), Rv3616c-specific CD4 T cell responses are detected in mice immunised with either dose of Rv3616 Δ 138-145/AS01E. The levels of Rv3616c-specific T cell responses are higher at the 7dPIII timepoint when compared to the 7dPII timepoint. Cytokine profiles of the CD4 T cell response from the Rv3616c peptide pool-stimulated PBL (medium removed) are shown in Figures 21 (7dPII) and 22 (7dPIII).

Figure 23 shows that at both timepoints (7dPII & 7dPIII), Rv3616c-specific CD8 T cell responses are detected in mice immunised with either dose of Rv3616 Δ 138-145/AS01E. The levels of Rv3616c-specific T cell responses are higher at the 7dPII timepoint when compared to the 7dPIII timepoint. Cytokine profiles of the CD8 T cell response from the Rv3616c peptide pool-stimulated PBL (medium removed) are shown in Figures 24 (7dPII) and 25 (7dPIII).

In conclusion it may be noted that the Rv3616c antigen is capable of eliciting an immune response in both CB6F1 and C57BL/6 mice. Furthermore, the profile of cytokine production indicates that a large proportion of antigen-specific T-cells express a plurality of Th1 associated cytokines (i.e. a polyfunctional T-cell response is elicited). Importantly both CD4 and CD8 antigen-specific T-cells are present after immunisation, CD8 cells may be particularly important in a latent TB scenario. The relevance of Rv3616c to human infection is confirmed by the high level of recognition in latently infected individuals from South Africa and the absence of responses in naive subjects. Rv3616c may therefore be expected to be of substantial value in the prevention, treatment and diagnosis of tuberculosis infection (especially latent tuberculosis infection).

A number of modified Rv3616c proteins have been prepared which clearly demonstrate expression equal to or better than the corresponding H37Rv wild-type sequence, or to the Rv3616 Δ 150-160 sequence of the prior art. The immunogenicity of Rv3616 Δ 138-145/AS01E was confirmed in CB6F1 mice.

5

Constructs demonstrating good expression characteristics while maintaining the immunogenicity of the wild-type sequence are key to the production of commercially viable vaccine products. The new modified Rv3616c proteins may be of great value in the commercial production of Rv3616c compositions, such as vaccines.

10

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

15

All references referred to in this application, including patents and patent applications, are incorporated herein by reference to the fullest extent possible as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

20

Throughout the 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, step, group of integers or group of steps but not to the exclusion of any other integer, step, group of integers or group of steps.

25

30

CLAIMS

- 5 1 A modified Rv3616c protein, said protein comprising:
 (a) the amino acid sequence of SEQ ID No: 164, 179 or 180; or
 (b) a first polypeptide and a second polypeptide, the first polypeptide being located
 towards the N-terminus relative to the second polypeptide, and wherein:
 (i) the first polypeptide is a sequence having at least 98% identity to residues 1-
 10 134 of SEQ ID No: 1; and
 (ii) the second polypeptide is a sequence having at least 98% identity to residues
 155-392 of SEQ ID No: 1;
 wherein the first and second polypeptides are directly linked or indirectly linked via a
 third polypeptide, said third polypeptide having at least 80% identity to a sequence
 15 corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of
 at least 3 amino acids has been deleted.
2. The modified Rv3616c protein according to claim 1, said protein comprising a first
 polypeptide and a second polypeptide, the first polypeptide being located towards the
 20 N-terminus relative to the second polypeptide, and wherein:
 (iii) the first polypeptide is a sequence having at least 98% identity to residues 1-
 134 of SEQ ID No: 1; and
 (iv) the second polypeptide is a sequence having at least 98% identity to residues
 155-392 of SEQ ID No: 1;
 25 wherein the first and second polypeptides are directly linked or indirectly linked via a
 third polypeptide, said third polypeptide having at least 80% identity to a sequence
 corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of
 at least 3 amino acids has been deleted.
- 30 3. The modified Rv3616c protein according to claim 2, wherein the first polypeptide has
 100% identity to residues 1-134 of SEQ ID No: 1.
- 4 The modified Rv3616c protein according to claim 2 or 3, wherein the second
 polypeptide has at least 99% identity to residues 155-392 of SEQ ID No: 1.
 35
- 5 The modified Rv3616c protein according to claim 4, wherein the second polypeptide
 has 100% identity to residues 155-392 of SEQ ID No: 1
- 6 The modified Rv3616c protein according to any one of claims 2 to 5, wherein the
 40 peptide linkage is direct.

7 The modified Rv3616c protein according to any one of claims 2 to 5, wherein the peptide linkage is indirect.

5

8 The modified Rv3616c protein according to claim 7, wherein the third polypeptide is a sequence having at least 90% identity to a sequence corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids has been deleted.

10

9. The modified Rv3616c protein according to claim 8, wherein the third polypeptide is a sequence having at least 95% identity to a sequence corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids has been deleted.

15

10. The modified Rv3616c protein according to any one of claims 2 to 9, in which the contiguous portion deleted from the residues corresponding to 134-154 in SEQ ID No: 1 is least 4 amino acids.

20

11 The modified Rv3616c protein according to claim 10, in which the contiguous portion deleted from the residues corresponding to 134-154 in SEQ ID No: 1 is least 5 amino acids.

25

12. The modified Rv3616c protein according to any one of claims 7 to 11, in which the third polypeptide is 20 amino acids or fewer in length.

13. The modified Rv3616c protein according to any one of claims 1 to 12, said protein being fewer than 500 amino acid residues in length.

30

14. The modified Rv3616c protein according to claim 13, said protein being fewer than 400 amino acid residues in length.

15. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 163.

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16. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 164.

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17. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 165.

18. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 166.

10

19. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 167.

15

20. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 168.

21. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 169.

20

22. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 179.

23. The modified Rv3616c protein according to any one of claims 1, 13 or 14, comprising the amino acid sequence of SEQ ID No: 180.

25

24. The modified Rv3616c protein according to any one of claims 1 to 23, said protein consisting of:

(a) the amino acid sequence of SEQ ID No: 164, 179 or 180; or

30

(b) a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

(i) the first polypeptide is a sequence having at least 98% identity to residues 1-134 of SEQ ID No: 1; and

(ii) the second polypeptide is a sequence having at least 98% identity to residues 155-392 of SEQ ID No: 1;

35

wherein the first and second polypeptides are directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 80% identity to a sequence corresponding to residues 135-154 in SEQ ID No: 1 in which a contiguous portion of at least 3 amino acids has been deleted.

40

25. A polynucleotide comprising a nucleic acid sequence encoding a modified Rv3616c protein according to any one of claims 1 to 24.

5

26. The polynucleotide according to claim 25, consisting of a nucleic acid sequence encoding a modified Rv3616c protein according to any one of claims 1 to 24.

27. The polynucleotide according to either claim 25 or 26, comprising a sequence encoding a polypeptide according to any one of SEQ ID Nos: 163 to 169.

10

28. The polynucleotide according to either claim 25 or 26, comprising a sequence encoding a polypeptide according to either of SEQ ID Nos: 179 or 180.

15

29. A fusion protein comprising a modified Rv3616c protein according to any one of claims 1 to 23 and an additional heterologous polypeptide.
- 5
30. A polynucleotide encoding a fusion protein according to claim 29
31. A host cell which recombinantly expresses a modified Rv3616c protein according to any one of claims 1 to 24 or a fusion protein according to claim 29.
- 10
32. Use of a modified Rv3616c protein according to any one of claims 1 to 24 in the manufacture of a medicament for the treatment, prevention or amelioration of TB.
33. Use of a modified Rv3616c protein, or a polynucleotide comprising a nucleic acid sequence encoding it, in the manufacture of a medicament for the treatment of latent TB, wherein said modified Rv3616c protein is selected from:
- 15
- (a) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:
- 20
- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;
- wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least 1 amino acid has been deleted; or
- 25
- (b) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein.
- 30
- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;
- wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least a contiguous portion of at least 3 amino acids has been deleted; or
- 35
- (c) a modified Rv3616c protein comprising a Rv3616c sequence in which at least one amino acid has been deleted from the region corresponding to residues 134-183 in SEQ ID No:1; or
- 40

(d) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked via a third polypeptide, said third polypeptide corresponding to residues 134-183 in SEQ ID No:1 in which at least 1 amino acid has been deleted; or

(e) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-133 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 155 amino acids within residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly or indirectly linked via a third polypeptide, said third polypeptide corresponding to residues 134-183 in SEQ ID No:1 in which at least a contiguous portion of at least 3 amino acids has been deleted; or

(f) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and
- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least 1 amino acid has been deleted; or

(g) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a contiguous sequence of at least 100 amino acids within residues 1-134 of SEQ ID No: 1; and

- (ii) the second polypeptide is a contiguous sequence of at least 175 amino acids within residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are either directly linked or indirectly linked via a third polypeptide, wherein said third polypeptide corresponds to residues 135-154 in SEQ ID No:1 in which at least a contiguous portion of at least 3 amino acids has been deleted; or

- (h) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-133 of SEQ ID No: 1; and

- (ii) the second polypeptide is a sequence having at least 90% identity to residues 184-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 90% identity to a sequence corresponding to residues 134-183 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids has been deleted; or

- (i) a modified Rv3616c protein comprising a first polypeptide and a second polypeptide, the first polypeptide being located towards the N-terminus relative to the second polypeptide, and wherein:

- (i) the first polypeptide is a sequence having at least 90% identity to residues 1-134 of SEQ ID No: 1; and

- (ii) the second polypeptide is a sequence having at least 90% identity to residues 155-392 of SEQ ID No: 1;

wherein the first and second polypeptides are directly linked or indirectly linked via a third polypeptide, said third polypeptide having at least 80% identity to a sequence corresponding to residues 135-154 in SEQ ID No:1 in which a contiguous portion of at least 3 amino acids has been deleted.

- 34 The use according to claim 33 wherein the modified Rv3616c protein is fewer than 500 amino acid residues in length.
- 5 35 The use according to any one of claims 33 or 34, wherein a modified Rv3616c protein is used in the manufacture of the medicament.
- 36 The use according to any one of claims 33 or 34, wherein a polynucleotide comprising a nucleic acid sequence encoding the modified Rv3616c protein is used
- 10 in the manufacture of the medicament.

37 The use according to any one of claims 33 to 36 in the manufacture of a medicament for the prevention of reactivation of tuberculosis.

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38 The use according to any one of claims 33 to 36, in the manufacture of a medicament for the delay of reactivation of tuberculosis.

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MODIFIED TUBERCULOSIS ANTIGENS

ABSTRACT

- 5 Modified Rv3616c proteins and their use as medicaments, particularly for the prevention of reactivation of tuberculosis.

No figure