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(71) Applicant: **GLAXOSMITHKLINE BIOLOGICALS S.A.** [BE/BE]; rue de l'Institut 89, B-1330 Rixensart (BE).

(72) Inventors: **DEMOITIÉ, Marie-Ange**; GlaxoSmithKline, rue de l'Institut 89, B-1330 Rixensart (BE). **DONNER, Marie-Noëlle**; GlaxoSmithKline, rue de l'Institut 89, B-1330 Rixensart (BE). **OUAKED, Nadia**; GlaxoSmithKline, rue de l'Institut 89, B-1330 Rixensart (BE).

(74) Agent: **BAKER, Suzanne Jane**; GlaxoSmithKline, Global Patents CN925.1, 980 Great West Road, Brentford Middlesex TW8 9GS (GB).

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(54) Title: NOVEL METHODS FOR INDUCING AN IMMUNE RESPONSE

(57) Abstract: The present invention relates to methods for inducing an immune response, in particular methods for inducing an immune response against mycobacterial infections or disease comprising (i) at least one administration of a polypeptide Rv1196 related antigen and at least one administration of an adenovirus encoding a Rv1196 related antigen or (ii) at least one administration of a polypeptide Rv0125 related antigen and at least one administration of an adenovirus encoding a Rv0125 related antigen. Associated compositions, adenoviral constructs and polynucleotide sequences are also provided.

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# NOVEL METHODS FOR INDUCING AN IMMUNE RESPONSE

## TECHNICAL FIELD

The present invention relates to methods for inducing an immune response, in particular methods for inducing an immune response against mycobacterial infections or disease comprising (i) at least one administration of a polypeptide Rv1196 related antigen and at least one administration of an adenovirus encoding a Rv1196 related antigen or (ii) at least one administration of a polypeptide Rv0125 related antigen and at least one administration of an adenovirus encoding a Rv0125 related antigen. Associated compositions, adenoviral constructs and polynucleotide sequences are also provided.

## BACKGROUND OF THE INVENTION

Vaccination is one of the most effective methods for preventing infectious diseases. However, a single administration of an antigen is often not sufficient to confer optimal immunity and/or a long-lasting response. Approaches for establishing strong and lasting immunity to specific pathogens include addition of adjuvants to vaccines and/or repeated vaccination, i.e. boosting an immune response by administration of one or more further doses of antigen. Such further administrations may be performed with the same vaccine (homologous boosting) or with a different vaccine (heterologous boosting).

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.

Mtb72f and M72 are fusion protein antigens derived from the *Mycobacterium tuberculosis* proteins Rv1196 and Rv0125. Mtb72f and M72 (described, for example, in international patent applications WO2006/117240, WO2012/080369 and WO2012/080370 which are incorporated herein by reference) or fragments or derivatives thereof are protein antigens of potential benefit for the treatment or prevention of tuberculosis.

Preclinical and clinical investigations have led to M72 being administered in humans in conjunction with the immunostimulants 3-O-deacylated monophosphoryl lipid A (3D-MPL) and QS21 in a liposomal formulation and in a 0,1 month schedule using 10 ug M72 polypeptide, 25 ug 3D-MPL and 25 ug QS21 (Leroux-Roels et al *Vaccine* 2013 31 2196-2206, Montoya et al *J. Clin. Immunol.* 2013 33(8): 1360-1375; Thacher EG et al *AIDS* 2014 28(12):1769-1781; Idoko OT et al *Tuberculosis (Edinb)* 2014 94(6):564-578; Penn-Nicholson A, et al *Vaccine* 2015 33(32):4025-4034 doi:10.1016/j.vaccine.2015.05.088). A candidate vaccine utilising the M72 antigen is currently in a Phase IIB trial (ClinicalTrials.gov Identifier: NCT01755598) to evaluate the protective efficacy of two doses of adjuvanted protein against pulmonary TB, as compared to placebo, in adults aged 18 - 50 living in TB endemic countries.

WO2008107370A1 (incorporated herein by reference) describes the concomitant administration of a polypeptide antigen and an adenovirus encoding a polypeptide antigen.

WO2010023260 (incorporated herein by reference) describes the concomitant administration of a polypeptide antigen and viral vector encoding a polypeptide antigen.

There remains a need for novel methods of immunising against diseases, including tuberculosis, which are highly efficacious, safe, convenient, cost-effective, long-lasting and induce a broad spectrum of immune responses.

## SUMMARY OF THE INVENTION

It has now surprisingly been found that, priming with a polypeptide Rv1196/Rv0125 related antigen and boosting with a non-human simian adenovirus encoding a Rv1196/Rv0125 related antigen, or priming with a non-human simian adenovirus encoding a Rv1196/Rv0125 related antigen with and boosting with a polypeptide Rv1196/Rv0125 related antigen can provide immune responses which are substantially improved relative to other potential approaches.

Accordingly, in a first aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a polypeptide Rv1196 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv1196 related antigen.

In a second aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a non-human simian adenovirus encoding a Rv1196 related antigen, followed by administration of a polypeptide Rv1196 related antigen to the subject.

Suitably the polypeptide Rv1196 related antigen is provided in a composition which also comprises an adjuvant. Optionally, the adjuvant comprises a TLR agonist and/or an immunologically active saponin. The TLR agonist is suitably a TLR4 agonist.

Suitably the polypeptide Rv1196 related antigen is provided in a composition which does not comprise a non-human simian adenovirus encoding a Rv1196 related antigen.

Suitably the non-human simian adenovirus encoding a Rv1196 related antigen is provided in a composition which does not comprise a polypeptide Rv1196 related antigen.

In a third aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a polypeptide Rv0125 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv0125 related antigen.

In a fourth aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a non-human simian adenovirus encoding a

Rv0125 related antigen, followed by administration of a polypeptide Rv0125 related antigen to the subject.

Suitably the polypeptide Rv0125 related antigen is provided in a composition which also comprises an adjuvant. Optionally, the adjuvant comprises a TLR agonist and/or an immunologically active saponin. The TLR agonist is suitably a TLR4 agonist.

Suitably the polypeptide Rv0125 related antigen is provided in a composition which does not comprise a non-human simian adenovirus encoding a Rv0125 related antigen.

Suitably the non-human simian adenovirus encoding a Rv0125 related antigen is provided in a composition which does not comprise a polypeptide Rv0125 related antigen.

## BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Median percentage of M72-specific CD4 T cell response from CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 7, 14 and 21 days post immunisation using ChAd3 in a range of doses.

Figure 2: Median percentage of M72-specific CD4 T cell response from CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 7, 14 and 21 days post immunisation using ChAd63 in a range of doses.

Figure 3: Median percentage of M72-specific CD8 T cell response from CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 7, 14 and 21 days post immunisation using ChAd3 in a range of doses.

Figure 4: Median percentage of M72-specific CD8 T cell response from CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 7, 14 and 21 days post immunisation using ChAd63 in a range of doses.

Figure 5: Percentage of M72-specific CD4 T cell response from whole blood of CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 14 PI and 14PII using heterologous (ChAd/Prot and Prot/ChAd) prime-boost vaccination strategies.

Figure 6: Percentage of M72-specific CD4 T cell response from whole blood of CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 14 PI and 14PII using homologous (ChAd/ChAd) and in combination with M72/AS01E (admixture or co-administration) prime-boost vaccination strategies.

Figure 7: Percentage of M72-specific CD8 T cell response from whole blood of CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 14 PI and 14PII using heterologous (ChAd/Prot and Prot/ChAd) prime-boost vaccination strategies.

Figure 8: Percentage of M72-specific CD8 T cell response from whole blood of CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 14 PI and 14PII

using homologous (ChAd/ChAd) and in combination with M72/AS01E (admixture or co-administration) prime-boost vaccination strategies.

Figure 9: Percentage of M72-specific CD4 T cell response from lung tissue of CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 14PII.

Figure 10: Percentage of M72-specific CD8 T cell response from lung tissue of CB6F1 mice expressing IFN-gamma and/or IL-2 and/or TNF-alpha cytokines at 14PII.

Figure 11: Cytokine profile of the M72-specific CD4 T cells response in WBLO at 14PI in immunised CB6F1 mice.

Figure 12: Table showing the data values of the cytokine profile of the M72-specific CD4 T cells response in WBLO at 14PI in immunised CB6F1 mice.

Figure 13: Cytokine profile of the M72-specific CD4 T cells response in WBLO at 14PII in immunised CB6F1 mice.

Figure 14: Table showing the data values of the cytokine profile of the M72-specific CD4 T cells response in WBLO at 14PII in immunised CB6F1 mice.

Figure 15: Cytokine profile of the M72-specific CD4 T cells response in lung at 14PII in immunised CB6F1 mice.

Figure 16: Table showing the data values of the cytokine profile of the M72-specific CD4 T cells response in lung at 14PII in immunised CB6F1 mice.

Figure 17: Cytokine profile of the M72-specific CD8 T cells response in WBLO at 14PI in immunised CB6F1 mice.

Figure 18: Table showing the data values of the cytokine profile of the M72-specific CD8 T cells response in WBLO at 14PI in immunised CB6F1 mice.

Figure 19: Cytokine profile of the M72-specific CD8 T cells response in WBLO at 14PII in immunised CB6F1 mice.

Figure 20: Table showing the data values of the cytokine profile of the M72-specific CD8 T cells response in WBLO at 14PII in immunised CB6F1 mice.

Figure 21: Cytokine profile of the M72-specific CD8 T cells response in lung at 14PII in immunised CB6F1 mice.

Figure 22: Table showing the data values of the cytokine profile of the M72-specific CD8 T cells response in lung at 14PII in immunised CB6F1 mice.

Figure 23: Anti-M72 Ig tot serology at 13dPII.

Figure 24: Diagrammatic representation of M72-ChAd3 construct arrangement

Figure 25: Diagrammatic representation of M72-ChAd63 construct arrangement

## BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS

| | |
|---|---|
| SEQ ID No: 1 | *Mycobacterium tuberculosis* H37Rv Rv1196 polypeptide sequence |
| SEQ ID No: 2 | *Mycobacterium tuberculosis* F11 Rv1196 polypeptide sequence |
| SEQ ID No: 3 | *Mycobacterium tuberculosis* H37Rv Rv0125 polypeptide sequence (mature sequence) |
| SEQ ID No: 4 | M72 2-his polypeptide sequence |
| SEQ ID No: 5 | M72 2-his polynucleotide |
| SEQ ID No: 6 | M72 No his polypeptide sequence |
| SEQ ID No: 7 | M72 No his polynucleotide |
| SEQ ID No: 8 | M72 No his human optimised polynucleotide |
| SEQ ID No: 9 | ChAd3 polynucleotide |
| SEQ ID No: 10 | ChAd3 penton polypeptide sequence |
| SEQ ID No: 11 | ChAd3 hexon polypeptide sequence |
| SEQ ID No: 12 | ChAd3 fibre polypeptide sequence |
| SEQ ID No: 13 | M72-ChAd3 construct DNA |
| SEQ ID No: 14 | ChAd63 polynucleotide |
| SEQ ID No: 15 | ChAd63 penton polypeptide sequence |
| SEQ ID No: 16 | ChAd63 hexon polypeptide sequence |
| SEQ ID No: 17 | ChAd63 fibre polypeptide sequence |
| SEQ ID No: 18 | M72-ChAd63 construct DNA |
| SEQ ID No: 19 | ChAd155 polynucleotide |
| SEQ ID No: 20 | ChAd155 penton polypeptide sequence |
| SEQ ID No: 21 | ChAd155 hexon polypeptide sequence |
| SEQ ID No: 22 | ChAd155 fibre polypeptide sequence |

## DETAILED DESCRIPTION

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. About one third of the world's population are believed to be latently infected with TB bacilli, with about 9 million new cases of active TB and 1.5 million deaths each year. Around 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. (World Health Organisation *Tuberculosis Facts* 2014)

*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.

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, 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 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 (Cardona P-J *Inflammation & Allergy – Drug Targets* 2006 6:27-39; Cardona 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 (which typically lasts 6 months or more) 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. An estimated 480,000 people developed MDR-TB in 2013. MDR-TB is treatable by using second-line drugs. However, second-line treatment options are limited and recommended medicines are not always available. The extensive chemotherapy required (up to two years of treatment) is costly and can produce severe adverse drug reactions in patients.

Extensively drug-resistant TB (XDR-TB) occurs when resistance to second line medications develops on top of resistance to first line medications. It is estimated that about 9.0% of MDR-TB cases had XDR-TB (World Health Organisation *Tuberculosis Facts* 2014).

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. Consequently, accurate and early diagnosis of the disease are of utmost importance.

Currently, vaccination with attenuated 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. It is administrated at birth in TB endemic regions. However, the safety and efficacy of BCG is a source of controversy - while protecting against severe disease manifestation in children, the efficacy of BCG against disease in adults is variable. Additionally, some countries, such as the United States, do not vaccinate the general public with this agent.

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

Subunit vaccines based on late stage antigens could also be utilised in combination with early stage antigens to provide a multiphase vaccine. Alternatively, early and/or 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).

Mtb72f and M72 are fusion protein antigens of potential benefit for the treatment or prevention of tuberculosis. Mtb72f and M72 are derived from the *Mycobacterium tuberculosis* proteins Rv1196 and Rv0125, both genes are present in both virulent and avirulent strains of the *Mycobacterium tuberculosis* complex, and in BCG.

Rv1196 (described, for example, by the name Mtb39a in Dillon et al *Infection and Immunity* 1999 67(6): 2941-2950) is highly conserved, with 100% sequence identity across H37Rv, C, Haarlem, CDC1551, 94-M4241A, 98-R604INH-RIF-EM, KZN605, KZN1435, KZN4207, KZNR506 strains, the F11 strain having a single point mutation Q30K (most other clinical isolates have in excess of 90% identity to H37Rv). An adenovirus encoding an Rv1196 related antigen is described in Lewinsohn et al *Am J Respir Crit Care* Med 2002 116:843-848.

Rv0125 (described, for example, by the name Mtb32a in Skeiky et al *Infection and Immunity* 1999 67(8): 3998-4007) is also highly conserved, with 100% sequence identity across many strains. An adenovirus (human Ad5) encoding an Rv0125 related antigen is described in Zhang et al *Human Vaccines & Therapeutics* 2015 11(7):1803-1813 doi:

10.1080/21645515.2015.1042193. Full length Rv0125 includes an N-terminal signal sequence which is cleaved to provide the mature protein.

Mtb72f has been shown to provide protection in a number of animal models (see, for example: Brandt et al *Infect. Immun.* 2004 72(11):6622-6632; Skeiky et al *J. Immunol.* 2004 172:7618-7628; Tsenova et al *Infect. Immun.* 2006 74(4):2392-2401). Mtb72f has also been the subject of clinical investigations (Von Eschen et al 2009 *Human Vaccines* 5(7):475-482). M72 is an improved antigen which incorporates a single serine to alanine mutation relative to Mtb72f, resulting in improved stability characteristics. M72 related antigens have also been shown to be of value in a latent TB model (international patent application WO2006/117240, incorporated herein by reference). Previous pre-clinical and clinical investigations have led to M72 being administered in humans in conjunction with the immunostimulants 3-O-deacylated monophosphoryl lipid A (3D-MPL) and QS21 in a liposomal formulation and in a 0,1 month schedule using 10 ug M72 polypeptide, 25 ug 3D-MPL and 25 ug QS21 (see, for example, Leroux-Roels et al *Vaccine* 2013 31 2196-2206, Montoya et al *J. Clin. Immunol.* 2013 33(8): 1360-1375; Thacher EG et al *AIDS* 2014 28(12):1769-1781; Idoko OT et al *Tuberculosis (Edinb)* 2014 94(6):564-578; Penn-Nicholson A, et al *Vaccine* 2015 33(32):4025-4034 doi:10.1016/j.vaccine.2015.05.088).

A candidate vaccine utilising the antigen M72 is currently in a Phase IIB trial (ClinicalTrials.gov Identifier: NCT01755598) to evaluate the protective efficacy of two doses doses of adjuvanted protein against pulmonary TB, as compared to placebo, in adults aged 18 - 50 living in TB endemic countries. Nevertheless, a need for improved vaccination approaches remains.

In a first aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a polypeptide Rv1196 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv1196 related antigen.

In a second aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a non-human simian adenovirus encoding a Rv1196 related antigen to the subject, followed by administration of a polypeptide Rv1196 related antigen.

In a third aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a polypeptide Rv0125 related antigen to the subject, followed by administration of an immunogenic composition comprising a non-human simian adenovirus encoding a Rv0125 related antigen.

In a fourth aspect of the invention, there is provided a method for inducing an immune response in a subject comprising administration of a non-human simian adenovirus encoding a

Rv0125 related antigen, followed by administration of a polypeptide Rv0125 related antigen to the subject.

As used herein, administration of a first composition "followed by" administration of a second composition indicates that a time interval has elapsed between administration of the first composition and administration of the second composition. Suitably the time interval between administrations is one week to two years, in particular two weeks to eighteen months, typically three weeks to fifteen months, such as three weeks to six months, for example three weeks to two months, especially three weeks to six weeks such as around four weeks.

Also provided is a polypeptide Rv1196 related antigen, for use in inducing an immune response in a subject wherein the polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv1196 related antigen.

Similarly, there is provided a non-human simian adenovirus encoding a Rv1196 related antigen, for use in inducing an immune response in a subject wherein a polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv1196 related antigen.

Further, there is provided the use of a polypeptide Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv1196 related antigen.

Additionally, there is provided the use of a non-human simian adenovirus encoding a Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv1196 related antigen.

Also provided is a polypeptide Rv1196 related antigen, for use in inducing an immune response in a subject wherein a non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of the polypeptide Rv1196 related antigen.

Similarly, there is provided a non-human simian adenovirus encoding a Rv1196 related antigen, for use in inducing an immune response in a subject wherein the non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of a polypeptide Rv1196 related antigen.

Further, there is provided the use of a polypeptide Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of the polypeptide Rv1196 related antigen.

Also provided is the use of a non-human simian adenovirus encoding a Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of a polypeptide Rv1196 related antigen.

Also provided is a polypeptide Rv0125 related antigen, for use in inducing an immune response in a subject wherein the polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv0125 related antigen.

Similarly, there is provided a non-human simian adenovirus encoding a Rv0125 related antigen, for use in inducing an immune response in a subject wherein a polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv0125 related antigen.

Further, there is provided the use of a polypeptide Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv0125 related antigen.

Additionally, there is provided the use of a non-human simian adenovirus encoding a Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv0125 related antigen.

Also provided is a polypeptide Rv0125 related antigen, for use in inducing an immune response in a subject wherein a non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of the polypeptide Rv0125 related antigen.

Similarly, there is provided a non-human simian adenovirus encoding a Rv0125 related antigen, for use in inducing an immune response in a subject wherein the non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of a polypeptide Rv0125 related antigen.

Further, there is provided the use of a polypeptide Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of the polypeptide Rv0125 related antigen.

Also provided is the use of a non-human simian adenovirus encoding a Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of a polypeptide Rv0125 related antigen.

Suitably the polypeptide Rv1196 related antigen is provided in a composition which also comprises an adjuvant. Optionally, the adjuvant comprises a TLR agonist and/or an immunologically active saponin. The TLR agonist is suitably a TLR4 agonist.

Suitably the polypeptide Rv0125 related antigen is provided in a composition which also comprises an adjuvant. Optionally, the adjuvant comprises a TLR agonist and/or an immunologically active saponin. The TLR agonist is suitably a TLR4 agonist.

Suitably the polypeptide Rv1196 related antigen is provided in a composition which is substantially free of a non-human simian adenovirus encoding a Rv1196 related antigen, such as it does not comprise a non-human simian adenovirus encoding a Rv1196 related antigen. For example, it is substantially free of or does not comprise a non-human simian adenovirus encoding a mycobacterial antigen (such as it is substantially free of or does not comprise any non-human simian adenovirus) in particular it is substantially free of or does not comprise any adenovirus encoding a mycobacterial antigen (such as it is substantially free of or does not comprise any adenovirus). In some embodiments the polypeptide Rv1196 related antigen is provided in a composition which is substantially free of or does not comprise any adenovirus encoding a mycobacterial antigen.

Furthermore, the polypeptide Rv1196 related antigen is suitably not administered within a period of one day (such as two, three or six days) of a non-human simian adenovirus encoding a Rv1196 related antigen, such a non-human simian adenovirus encoding a Rv1196 related antigen. For example, a non-human simian adenovirus encoding a mycobacterial antigen (such as any non-human simian adenovirus) in particular any adenovirus encoding a mycobacterial antigen (such as any adenovirus). The polypeptide Rv1196 related antigen is suitably not administered within a period of one day (such as two, three or six days) of any adenovirus encoding a mycobacterial antigen

Suitably the non-human simian adenovirus encoding a Rv1196 related antigen is provided in a composition which is substantially free of or does not comprise a polypeptide Rv1196 related antigen. For example, it is substantially free of or does not comprise a polypeptide mycobacterial antigen (such as is substantially free of or it does not comprise any other antigens). In some embodiments the non-human simian adenovirus encoding a Rv1196 related antigen is provided in a composition which is substantially free of or does not comprise a polypeptide mycobacterial antigen.

Furthermore, the non-human simian adenovirus encoding a Rv1196 related antigen is suitably not administered within a period of one day (such as two, three or six days) of a polypeptide Rv1196 related antigen. For example, a polypeptide mycobacterial antigen (such as any other antigens). The non-human simian adenovirus encoding a Rv1196 related antigen is suitably not administered within a period of one day (such as two, three or six days) of a polypeptide mycobacterial antigen.

Suitably the polypeptide Rv0125 related antigen is provided in a composition which is substantially free of a non-human simian adenovirus encoding a Rv0125 related antigen, such as it does not comprise a non-human simian adenovirus encoding a Rv0125 related antigen. For example, it is substantially free of or does not comprise a non-human simian adenovirus encoding a mycobacterial antigen (such as it is substantially free of or does not comprise any non-human simian adenovirus) in particular it is substantially free of or does not comprise any adenovirus encoding a mycobacterial antigen (such as it is substantially free of or does not comprise any adenovirus). In some embodiments the polypeptide Rv0125 related antigen is provided in a composition which is substantially free of or does not comprise any adenovirus encoding a mycobacterial antigen.

Furthermore, the polypeptide Rv1196 related antigen is suitably not administered within a period of one day (such as two, three or six days) of a non-human simian adenovirus encoding a Rv0125 related antigen, such a non-human simian adenovirus encoding a Rv1196 related antigen. For example, a non-human simian adenovirus encoding a mycobacterial antigen (such as any non-human simian adenovirus) in particular any adenovirus encoding a mycobacterial antigen (such as any adenovirus). The polypeptide Rv0125 related antigen is suitably not administered within a period of one day (such as two, three or six days) of any adenovirus encoding a mycobacterial antigen

Suitably the non-human simian adenovirus encoding a Rv0125 related antigen is provided in a composition which is substantially free of or does not comprise a polypeptide Rv0125 related antigen. For example, it is substantially free of or does not comprise a polypeptide mycobacterial antigen (such as is substantially free of or it does not comprise any other antigens). In some embodiments the non-human simian adenovirus encoding a Rv0125 related antigen is provided in a composition which is substantially free of or does not comprise a polypeptide mycobacterial antigen.

Furthermore, the non-human simian adenovirus encoding a Rv0125 related antigen is suitably not administered within a period of one day (such as two, three or six days) of a polypeptide Rv1196 related antigen. For example, a polypeptide mycobacterial antigen (such as any other antigens). The non-human simian adenovirus encoding a Rv0125 related antigen is suitably not administered within a period of one day (such as two, three or six days) of a polypeptide mycobacterial antigen.

Suitably, the subject is a mammal, such as a bovine or human. In particular, the subject is a human.

By substantially free of, in the context of adenovirus, typically means comprising less than $10^4$, such as less than $10^3$, in particular less than $10^2$ or less than $10^1$ viral particles of the relevant type per dose. Suitable methods for determining the number of viral particles include Quantitative PCR Analysis, analytical HLPC or spectrophotometric methods based on $A_{260}$ nm.

By substantially free of, in the context of polypeptide antigen, typically means comprising less than 1 ug, such as less than 0.1 ug, in particular less than 0.01 ug of the relevant antigen or antigens per dose. Suitable methods for determining the amount of peptide antigen are known to the skilled person and depending on the composition, may combine purification methods to assist in facilitating an appropriate quantification method (such as analytical HLPC or spectrophotometric methods).

Typically, the aim of the method of the invention is to induce a protective immune response, i.e. immunise or vaccinate the subject against a related pathogen. The invention may therefore be applied for the prophylaxis, treatment or amelioration of infection by mycobacteria, such as infection by *Mycobacterium bovis or Mycobacterium tuberculosis,* in particular *Mycobacterium tuberculosis*.

The invention may be provided for the purpose of:

- prophylaxis of active tuberculosis due to infection (i.e. primary tuberculosis) or reactivation (i.e. secondary tuberculosis), such as by administering to a subject who is uninfected, or alternatively a subject who has a latent infection;
- prophylaxis of latent tuberculosis, such as by administering to a subject who is uninfected;
- treating latent tuberculosis;
- preventing or delaying reactivation of tuberculosis, especially the delay of reactivation, for example by a period of months, years or indefinitely; or
- treating active tuberculosis (such as to reduce the need for chemotherapeutic treatment: such as reduced term of chemotherapeutic treatment, complexity of drug regimen or dosage of chemotherapeutic treatment; alternatively, to reduce the risk of a later relapse following chemotherapeutic treatment).

The elicited immune response may be an antigen specific T cell response (which may be a systemic and/or a local response). Systemic responses may be detected, for example, from a sample of whole blood. Local responses (for example, the local response in the lung) may be detected from an appropriate sample of tissue (for example, lung tissue) or other locally focused samply method (e.g. bronchoalveolar lavage). The antigen specific T cell response may comprise a CD4+ T cell response, such as a response involving CD4+ T cells expressing a plurality of cytokines (e.g. IFNgamma, TNFalpha or IL2, especially IFNgamma, TNFalpha and IL2). Alternatively, or additionally, the antigen specific T cell response comprises a CD8+ T cell response, such as a response involving CD8+ T cells expressing a plurality of cytokines (e.g. IFNgamma, TNFalpha or IL2, especially IFNgamma, TNFalpha and IL2).

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

The terms “inactive infection”, “dormant infection” or “latent infection” or “latent tuberculosis” 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 which tests positive for infection, e.g. by Tuberculin skin test (TST) or Interferon–Gamma Release Assays (IGRAs), 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 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. by Tuberculin skin test (TST) or Interferon–Gamma Release Assays (IGRAs)) 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.

Suitability the methods are applied to a subject who is uninfected or who has a latent infection by mycobacteria, such as infection by *Mycobacterium tuberculosis*. In one embodiment the methods are applied to a subject who does not have an infection by *Mycobacterium tuberculosis* (in the context of human subjects) or *Mycobacterium bovis* (in the context of bovine subjects). In another embodiment the methods are applied to a subject who has a latent infection by mycobacteria, such as *Mycobacterium tuberculosis* (in the context of human subjects) or *Mycobacterium bovis* (in the context of bovine subjects).

In some embodiments, the subject has previously been vaccinated with BCG. The approaches of the present invention may, for example, be utilised for a subject at least one year after BCG vaccination, for example at least two years after BCG vaccination such as at least at least five years after BCG vaccination.

In some embodiments, the subject has previously been infected with *M. tuberculosis*.

Antigens of use in the invention.

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 known to the person skilled in the art (see, for example,

Paul, *Fundamental Immunology*, 3rd ed., 243-247 (1993); Beiβbarth et al *Bioinformatics* 2005 21(Suppl. 1):i29-i37). 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 scale of immune response, an immunogenic derivative of a reference sequence is desirably one which contains the majority (or suitably all) T cell epitopes intact. Mortier *et al BMC Immunology* 2015 16:63 undertake sequence conservation analysis and *in silico* human leukocyte antigen-peptide binding predictions for Mtb72f and M72 tuberculosis candidate vaccine antigens.

The skilled person will recognise that individual substitutions, deletions or additions to a protein which alters, adds or deletes a single amino acid or a small percentage of amino acids is an "immunogenic derivative" 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 immunogenic function.

Conservative substitution tables providing functionally similar amino acids are well known in the art. 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).

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.

Immunogenic derivatives 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. 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.

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

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

The terms "identical" or percentage "identity," in the context of two or more polypeptide sequences, refer to two or more sequences or sub-sequences that are the same or have a specified percentage of amino acid residues 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 window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition also refers to the compliment of a test sequence. Optionally, the identity exists over a region that is at least 200 amino acids in length, such as at least 300 amino acids or at least 400 amino acids. Suitably, the comparison is performed over a window corresponding to the entire length of the reference sequence (as opposed to the derivative sequence).

For sequence comparison, one sequence acts as the reference sequence, to which the test sequences are compared. When using a sequence comparison algorithm, test and reference 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 percentage sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, refers 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 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 computerised 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 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 dendogram showing the clustering 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 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 coordinates for 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.* 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 neighbourhood word score threshold (Altschul *et al., supra*). These initial neighbourhood 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, immunogenic derivatives of a polypeptide sequence will usually have 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, whole blood, lung tissue or bronchoalveolar lavage 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, TNF-alpha, IFN-gamma, IL-17, CD40L, CD69 etc) followed by analysis with a flow cytometer. 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.

In one embodiment the polypeptide antigen and the encoded antigen are Rv1196 related antigens. The term 'Rv1196 related antigen' refers to the Rv1196 protein provided in SEQ ID No: 1 or an immunogenic derivative thereof. As used herein the term "derivative" refers to an antigen that is modified relative to the reference sequence. Immunogenic derivatives are sufficiently similar to the reference sequence to substantially retain the immunogenic properties of the reference sequence and remain capable of allowing an immune response to be raised against the reference sequence. An immunogenic derivative may, for example, comprise a modified version of the reference sequence or alternatively may consist of a modified version of the reference sequence.

The Rv1196 related antigen may for example contain 2500 amino acid residues or fewer, such 1500 amino acid residues or fewer, in particular 1200 amino acid residues or fewer, especially 1000 amino acid residues or fewer, typically 800 amino acid residues or fewer.

Suitably the Rv1196 related antigen will comprise, such as consist of, a sequence having at least 70% identity to SEQ ID No: 1, such as at least 80%, in particular at least 90%, especially at least 95%, for example at least 98%, such as at least 99%.

A specific example of an Rv1196 related antigen is Rv1196 from *Mycobacterium tuberculosis* strain H37Rv, as provided in SEQ ID No: 1. Consequently, in one embodiment of the invention the Rv1196 related antigen is a protein comprising SEQ ID No: 1. In a second embodiment of the invention the Rv1196 related antigen is a protein consisting of SEQ ID No: 1.

A further example of an Rv1196 related antigen is Rv1196 from *Mycobacterium tuberculosis* strain F11. In one embodiment of the invention the Rv1196 related antigen is a protein comprising SEQ ID No: 2. In a second embodiment of the invention the Rv1196 related antigen is a protein consisting of SEQ ID No: 2.

Typical Rv1196 related antigens will comprise (such as consist of) an immunogenic derivative of SEQ ID No: 1 having a small number of deletions, insertions and/or substitutions. Examples are those having deletions of up to 5 residues at 0-5 locations, insertions of up to 5 residues at 0-5 five locations and substitution of up to 20 residues.

Other immunogenic derivatives of Rv1196 are those comprising (such as consisting of) a fragment of SEQ ID No: 1 which is at least 200 amino acids in length, such as at least 250 amino acids in length, in particular at least 300 amino acids in length, especially at least 350 amino acids in length.

Additional immunogenic derivatives of Rv1196 are those comprising, such as consisting of, a fragment of SEQ ID No: 2 which is at least 200 amino acids in length, such as at least 250 amino acids in length, in particular at least 300 amino acids in length, especially at least 350 amino acids in length.

Rv1196 related antigens may be prepared by methods previously described (e.g. Dillon et al *Infection and Immunity* 1999 67(6): 2941-2950; WO2006/117240), those provided in the Examples, or methods analogous thereto.

In one embodiment the polypeptide antigen and the encoded antigen are Rv0125 related antigens. The term 'Rv0125 related antigen' refers to the Rv0125 protein provided in SEQ ID No: 3 or an immunogenic derivative thereof. As used herein the term "derivative" refers to an antigen that is modified relative to the reference sequence. Immunogenic derivatives are sufficiently similar to the reference sequence to substantially retain the immunogenic properties of the reference sequence and remain capable of allowing an immune response to be raised against the reference sequence. An immunogenic derivative may, for example, comprise a modified version of the reference sequence or alternatively may consist of a modified version of the reference sequence.

The Rv0125 related antigen may for example contain 2500 amino acid residues or fewer, such 1500 amino acid residues or fewer, in particular 1200 amino acid residues or fewer, especially 1000 amino acid residues or fewer, typically 800 amino acid residues or fewer.

Suitably the Rv0125 related antigen will comprise, such as consist of, a sequence having at least 70% identity to SEQ ID No: 3, such as at least 80%, in particular at least 90%, especially at least 95%, for example at least 98%, such as at least 99%.

A specific example of an Rv0125 related antigen is Rv0125 from *Mycobacterium tuberculosis* strain H37Rv, as provided in SEQ ID No: 3. Consequently, in one embodiment of the invention the Rv0125 related antigen is a protein comprising SEQ ID No: 3. In a second embodiment of the invention the Rv0125 related antigen is a protein consisting of SEQ ID No: 3.

Typical Rv0125 related antigens will comprise (such as consist of) an immunogenic derivative of SEQ ID No: 3 having a small number of deletions, insertions and/or substitutions. Examples are those having deletions of up to 5 residues at 0-5 locations, insertions of up to 5 residues at 0-5 five locations and substitution of up to 20 residues.

Other immunogenic derivatives of Rv0125 are those comprising (such as consisting of) a fragment of SEQ ID No: 3 which is at least 150 amino acids in length, such as at least 200 amino acids in length, in particular at least 250 amino acids in length, especially at least 300 amino acids in length. Particular immunogenic derivatives of Rv0125 are those comprising (such as consisting of) the fragment of SEQ ID No: 3 corresponding to residues 1-195 of SEQ ID No: 3. Further immunogenic derivatives of Rv0125 are those comprising (such as consisting of) the fragment of SEQ ID No: 3 corresponding to residues 192-323 of SEQ ID No: 3.

Particularly preferred Rv0125 related antigens are derivatives of SEQ ID No: 3 wherein at least one (for example one, two or even all three) of the catalytic triad have been substituted or deleted, such that the protease activity has been reduced and the protein more easily produced – the catalytic serine residue may be deleted or substituted (e.g. substituted with alanine) and/or the catalytic histidine residue may be deleted or substituted and/or substituted the catalytic aspartic acid residue may be deleted or substituted. Especially of interest are derivatives of SEQ ID No: 3 wherein the catalytic serine residue has been substituted (e.g. substituted with alanine). Also of interest are Rv0125 related antigens which comprise, such as consist of, a sequence having at least 70% identity to SEQ ID No: 3, such as at least 80%, in particular at least 90%, especially at least 95%, for example at least 98%, such as at least 99% and wherein at least one of the catalytic triad have been substituted or deleted or those comprising, such as consisting of, a fragment of SEQ ID No: 3 which is at least 150 amino acids in length, such as at least 200 amino acids in length, in particular at least 250 amino acids in length, especially at least 300 amino acids in length and wherein at least one of the catalytic triad have been substituted or deleted. Further immunogenic derivatives of Rv0125 are those comprising (such as consisting of) the fragment of SEQ ID No: 3 corresponding to residues 192-

323 of SEQ ID No: 3 wherein at least one (for example one, two or even all three) of the catalytic triad have been substituted or deleted. Particular immunogenic derivatives of Rv0125 are those comprising (such as consisting of) the fragment of SEQ ID No: 3 corresponding to residues 1-195 of SEQ ID No: 3 wherein the catalytic serine residue (position 176 of SEQ ID No: 3) has been substituted (e.g. substituted with alanine).

In certain embodiments the polypeptide antigen and the encoded antigen are Rv1196 and Rv0125 related antigens, such as M72 related antigens. Particular derivatives of the M72 protein include those with additional His residues at the N-terminus (e.g. two His residues, as provided in SEQ ID No: 4; or a polyhistidine tag of five or particularly six His residues, which may be used for nickel affinity purification). Mtb72f which contains the original serine residue that has been mutated in M72, is a further derivative of M72, as are Mtb72f proteins with additional His residues at the N-terminus (e.g. two His residues; or a polyhistidine tag of five or particularly six His residues, which may be used for nickel affinity purification).

Nevertheless, the skilled person recognises that in some embodiments two distinct polypeptides, one being a Rv1196 related antigens and one being a Rv0125 related antigen may be provided within a composition. In such cases it will be recognised that the previously stated exclusions in respect of adenoviruses encoding a Rv1196 related antigen and adenoviruses encoding a Rv0125 related antigen may both be applied to the composition *mutatis mutandis*. Equally, the previously stated exclusions in respect of contemporaneous administration of adenoviruses encoding a Rv1196 related antigen and adenoviruses encoding a Rv0125 related antigen may both be applied *mutatis mutandis*.

Also in some embodiments a single adenovirus may encode two distinct polypeptides, one being a Rv1196 related antigen and one being a Rv0125 related antigen. In such cases it will be recognised that the previously stated exclusions in respect of a polypeptide Rv1196 related antigen and a polypeptide Rv0125 related antigen may both be applied to the composition *mutatis mutandis*. Equally, the previously stated exclusions in respect of contemporaneous administration of a polypeptide Rv1196 related antigen and a polypeptide Rv0125 related antigen may both be applied *mutatis mutandis*.

Alternatively, two distinct adenovirus constructs may be provided, one encoding an Rv1196 related antigen and one encoding an Rv0125 related antigen. In such cases it will be recognised that the previously stated exclusions in respect of a polypeptide Rv1196 related antigen and a polypeptide Rv0125 related antigen may both be applied to the composition *mutatis mutandis*. Equally, the previously stated exclusions in respect of contemporaneous administration of a polypeptide Rv1196 related antigen and a polypeptide Rv0125 related antigen may both be applied *mutatis mutandis*.

Suitably an M72 related antigen will comprise, such as consist of, a sequence having at least 70% identity to SEQ ID No. 6, such as at least 80%, in particular at least 90%, especially at least 95%, such as at least 98%, for example at least 99%.

Typical M72 related antigens will comprise, such as consist of, a derivative of SEQ ID No: 6 having a small number of deletions, insertions and/or substitutions. Examples are those having deletions of up to 5 residues at 0-5 locations, insertions of up to 5 residues at 0-5 five locations and substitution of up to 20 residues.

Other derivatives of M72 are those comprising, such as consisting of, a fragment of SEQ ID No: 6 which is at least 450 amino acids in length, such as at least 500 amino acids in length, such as at least 550 amino acids in length, such as at least 600 amino acids in length, such as at least 650 amino acids in length or at least 700 amino acids in length. As M72 is a fusion protein derived from two individual antigens, any fragment of at least 450 residues will comprise a plurality of epitopes from the full length sequence (Skeiky et al *J. Immunol.* 2004 172:7618-7628; Skeiky *Infect. Immun.* 1999 67(8):3998-4007; Dillon *Infect. Immun.* 1999 67(6):2941-2950; ).

In particular embodiments the M72 related antigen will comprise residues 2-723 of SEQ ID No. 6, for example comprise (or consist of) SEQ ID No. 6.

In one embodiment, the polypeptide antigen corresponds to SEQ ID No. 4 and the encoded antigen to SEQ ID No. 6.

M72 related antigens may be prepared by methods previously described (WO2006/117240) or methods analogous thereto.

The polypeptide antigen may be the same as or may be similar to the encoded antigen. In one embodiment the polypeptide antigen is the same as the encoded antigen.

Suitably the polypeptide antigen is similar to the encoded antigen. For example, the encoded antigen may have 70% identity, such as at least 80 % identity, suitably at least 90% identity, in particular at least 95% identity to the polypeptide antigen. Alternatively, the encoded antigen may comprise a fragment of at least 100 amino acid residues, such as at least 200 amino acids residues, suitably at least 300 amino acid residues of the polypeptide antigen. In some cases, the encoded antigen comprises a fragment of at least 400 amino acid residues, in particular 500 amino acid residues, such as at least 600 and suitably at least 700 residues of the polypeptide mycobacterial antigen.

The polypeptide antigen and the adenovirus may be provided in the form of immunogenic compositions which comprise one or more further antigenic components.

Additional antigenic components may be intended to strengthen or complement the immune responses solicited in the field of tuberculosis prevention and therapy or additional antigens could be associated with other pathogens and are intended for co-administration for reasons of convenience. Where a number of antigenic components are present within a

composition, these may be provided in the form of individual polypeptides or fusion proteins. In some circumstances additional antigenic components may be provided as a polynucleotide (or polynucleotides) encoding one or more polypeptides.

Typically for administration to humans compositions containing a polypeptide Rv1196 related antigen will comprise between 1 ug and 100 ug of Rv1196 related antigen, such as between 1 ug and 50 ug per dose. Suitably between 1 ug and 50 ug of Rv1196 related antigen (such as between 5 ug and 50 ug), especially between 1 ug and 20 ug (such as between 5 ug and 20 ug) and in particular around or exactly 10 ug is provided.

Typically for administration to humans compositions containing a polypeptide Rv0125 related antigen will comprise between 1 ug and 100 ug of Rv0125 related antigen, such as between 1 ug and 50 ug per dose. Suitably between 1 ug and 50 ug of Rv0125 related antigen (such as between 5 ug and 50 ug), especially between 1 ug and 20 ug (such as between 5 ug and 20 ug) and in particular around or exactly 10 ug is provided.

Typically for administration to humans compositions containing a polypeptide M72 related antigen will comprise between 1 ug and 100 ug of M72 related antigen, such as between 1 ug and 50 ug per dose. Suitably between 1 ug and 50 ug of M72 related antigen (such as between 5 ug and 50 ug), especially between 1 ug and 20 ug (such as between 5 ug and 20 ug) and in particular around or exactly 10 ug is provided.

Generally, a polypeptide of use in the invention (if found in nature) will be an isolated polypeptide (i.e. separated from those components with which it may usually be found). For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

Adjuvants of use in the invention

As described above, in one aspect of the invention, polypeptide antigen is provided in an immunogenic composition which comprises an adjuvant. Suitably the adjuvant comprises a TLR agonist and/or an immunologically active saponin.

In some embodiments the adjuvant may comprise aluminium hydroxide or aluminium phosphate.

Thus, in one embodiment, the adjuvant comprises a TLR agonist. In another embodiment, the adjuvant comprises an immunologically active saponin. In yet another embodiment, the adjuvant comprises a TLR agonist and an immunologically active saponin.

The adjuvant may comprise a TLR agonist and a saponin in a liposomal formulation. The ratio of TLR agonist to saponin may be between 5:1 and 1:5 (w/w), suitably between 2:1 and 1:2, typically around 1:1.

The use of TLR agonists in adjuvants is well-known in the art and has been reviewed e.g. by Lahiri et al. (2008) Vaccine 26:6777. TLRs that can be stimulated to achieve an adjuvant effect include TLR2, TLR4, TLR5, TLR7, TLR8 and TLR9. TLR2, TLR4, TLR7 and TLR8 agonists, particularly TLR4 agonists are preferred.

Suitable TLR4 agonists include lipopolysaccharides, such as monophosphoryl lipid A (MPL) and 3-O-deacylated monophosphoryl lipid A (3D-MPL). US patent 4,436,727 discloses MPL and its manufacture. US patent 4,912,094 and reexamination certificate B1 4,912,094 discloses 3D-MPL and a method for its manufacture. Another TLR4 agonist is glucopyranosyl lipid adjuvant (GLA), a synthetic lipid A-like molecule (see, e.g. Fox et al. (2012) Clin. Vaccine Immunol 19:1633). In a further embodiment, the TLR4 agonist may be a synthetic TLR4 agonist such as a synthetic disaccharide molecule, similar in structure to MPL and 3D-MPL or may be synthetic monosaccharide molecules, such as the aminoalkyl glucosaminide phosphate (AGP) compounds disclosed in, for example, WO9850399, WO0134617, WO0212258, W03065806, WO04062599, WO06016997, WO0612425, WO03066065, and WO0190129. Such molecules have also been described in the scientific and patent literature as lipid A mimetics. Lipid A mimetics suitably share some functional and/or structural activity with lipid A, and in one aspect are recognised by TLR4 receptors. AGPs as described herein are sometimes referred to as lipid A mimetics in the art. In a preferred embodiment, the TLR4 agonist is 3D-MPL. TLR4 agonists, such as 3-O-deacylated monophosphoryl lipid A (3D-MPL), and their use as adjuvants in vaccines has e.g. been described in WO 96/33739 and WO2007/068907 and reviewed in Alving et al. (2012) *Curr Opin Immunol* 24:310.

The adjuvant may comprise an immunologically active saponin, such as an immunologically active saponin fraction, such as QS21.

Adjuvants comprising saponins have been described in the art. Saponins are described in: Lacaille-Dubois and Wagner (1996) A review of the biological and pharmacological activities of saponins. Phytomedicine vol 2:363. Saponins are known as adjuvants in vaccines. For example, Quil A (derived from the bark of the South American tree Quillaja Saponaria Molina), was described by Dalsgaard et al. in 1974 ("Saponin adjuvants", Archiv. fur die gesamte Virusforschung, Vol. 44, Springer Verlag, Berlin, 243) to have adjuvant activity. Purified fractions of Quil A have been isolated by HPLC which retain adjuvant activity without the toxicity associated with Quil A (Kensil et al. (1991) J. Immunol. 146: 431. Quil A fractions are also described in US 5,057,540 and "Saponins as vaccine adjuvants", Kensil, C. R., Crit Rev Ther Drug Carrier Syst, 1996, 12 (1-2):1-55.

Two such fractions, suitable for use in the present invention, are QS7 and QS21 (also known as QA-7 and QA-21). QS21 is a preferred immunologically active saponin fraction for use in the present invention. QS21 has been reviewed in Kensil (2000) In O'Hagan: Vaccine Adjuvants: preparation methods and research protocols. Homana Press, Totowa, New Jersey,

Chapter 15. Particulate adjuvant systems comprising fractions of Quil A, such as QS21 and QS7, are e.g. described in WO 96/33739, WO 96/11711 and WO2007/068907.

In addition to the other components, the adjuvant preferably comprises a sterol. The presence of a sterol may further reduce reactogenicity of compositions comprising saponins, see e.g. EP0822831. Suitable sterols include beta-sitosterol, stigmasterol, ergosterol, ergocalciferol and cholesterol. Cholesterol is particularly suitable. Suitably, the immunologically active saponin fraction is QS21 and the ratio of QS21:sterol is from 1:100 to 1:1 w/w, such as from 1:10 to 1:1 w/w, e.g. from 1:5 to 1:1 w/w.

In a preferred embodiment of the methods of the invention, the TLR4 agonist is 3D-MPL and the immunologically active saponin is QS21.

In some embodiments, the adjuvant is presented in the form of an oil-in-water emulsion, e.g. comprising squalene, alpha-tocopherol and a surfactant (see e.g. W095/17210) or in the form of a liposome. A liposomal presentation is preferred.

The term “liposome” when used herein refers to uni- or multilamellar (particularly 2, 3, 4, 5, 6, 7, 8, 9, or 10 lamellar depending on the number of lipid membranes formed) lipid structures enclosing an aqueous interior. Liposomes and liposome formulations are well known in the art. Liposomal presentations are e.g. described in WO96/33739 and WO2007/068907. Lipids which are capable of forming liposomes include all substances having fatty or fat-like properties. Lipids which can make up the lipids in the liposomes may be selected from the group comprising glycerides, glycerophospholipides, glycerophosphinolipids, glycerophosphonolipids, sulfolipids, sphingolipids, phospholipids, isoprenolides, steroids, stearines, sterols, archeolipids, synthetic cationic lipids and carbohydrate containing lipids. In a particular embodiment of the invention the liposomes comprise a phospholipid. Suitable phospholipids include (but are not limited to): phosphocholine (PC) which is an intermediate in the synthesis of phosphatidylcholine; natural phospholipid derivates: egg phosphocholine, egg phosphocholine, soy phosphocholine, hydrogenated soy phosphocholine, sphingomyelin as natural phospholipids; and synthetic phospholipid derivates: phosphocholine (didecanoyl-L-a-phosphatidylcholine [DDPC], dilauroylphosphatidylcholine [DLPC], dimyristoylphosphatidylcholine [DMPC], dipalmitoyl phosphatidylcholine [DPPC], Distearoyl phosphatidylcholine [DSPC], Dioleoyl phosphatidylcholine, [DOPC], 1-palmitoyl, 2-oleoylphosphatidylcholine [POPC], Dielaidoyl phosphatidylcholine [DEPC]), phosphoglycerol (1,2-Dimyristoyl-sn-glycero-3-phosphoglycerol [DMPG], 1,2-dipalmitoyl-sn-glycero-3-phosphoglycerol [DPPG], 1,2-distearoyl-sn-glycero-3-phosphoglycerol [DSPG], 1-palmitoyl-2-oleoyl-sn- glycero-3-phosphoglycerol [POPG]), phosphatidic acid (1,2-dimyristoyl-sn-glycero-3-phosphatidic acid [DMPA], dipalmitoyl phosphatidic acid [DPPA], distearoyl-phosphatidic acid [DSPA]), phosphoethanolamine (1,2-dimyristoyl-sn-glycero-3-phosphoethanolamine [DMPE], 1,2-Dipalmitoyl-sn-glycero-3-phosphoethanolamine [DPPE], 1,2-distearoyl-sn-glycero-3-phosphoethanolamine [DSPE], 1,2-

Dioleoyl-sn-Glycero-3-Phosphoethanolamine [DOPE]), phoshoserine, polyethylene glycol [PEG] phospholipid.

Liposome size may vary from 30 nm to several um depending on the phospholipid composition and the method used for their preparation. In particular embodiments of the invention, the liposome size will be in the range of 50 nm to 500 nm and in further embodiments 50 nm to 200 nm. Dynamic laser light scattering is a method used to measure the size of liposomes well known to those skilled in the art.

In a particularly suitable embodiment, liposomes used in the invention comprise DOPC and a sterol, in particular cholesterol. Thus, in a particular embodiment, compositions of the invention comprise QS21 in any amount described herein in the form of a liposome, wherein said liposome comprises DOPC and a sterol, in particular cholesterol.

Preferably, the adjuvant comprises 3D-MPL and QS21 in a liposomal formulation.

The adjuvant may comprise 1 to 100 micrograms of TLR4 agonist per dose.

The adjuvant may comprise 1 to 100 micrograms of immunologically active saponin per dose.

In one embodiment for human use, the adjuvant comprises between 12.5 and 75 micrograms of 3D-MPL and between 12.5 and 75 micrograms of QS21 per dose in a liposomal formulation.

In another embodiment, the adjuvant comprises between 12.5 and 37.5, such as between 20 and 30 micrograms (for example about or exactly 25 micrograms), of 3D-MPL and between 12.5 and 37.5, such as between 20 and 30 micrograms (for example about or exactly 25 micrograms) of QS21 in a liposomal formulation per dose. Suitably the amount of 3D-MPL is the same as the amount of QS21.

The polypeptide or adenovirus should be presented in a pharmaceutically acceptable form, appropriate to the intended delivery route. Solutions should have a pharmaceutically acceptable osmolality to avoid cell distortion or lysis. A pharmaceutically acceptable osmolality will generally mean that solutions will have an osmolality which is approximately isotonic or mildly hypertonic. Suitably the immunogenic compositions of the present invention will have an osmolality in the range of 250 to 750 mOsm/kg, for example, the osmolality may be in the range of 250 to 550 mOsm/kg, such as in the range of 280 to 500 mOsm/kg. Osmolality may be measured according to techniques known in the art, such as by the use of a commercially available osmometer, for example the Advanced® Model 2020 available from Advanced Instruments Inc. (USA). An "isotonicity agent" is a compound that is physiologically tolerated and imparts a suitable tonicity to a formulation (*e.g.* immunogenic compositions of the invention) to prevent the net flow of water across cell membranes that are in contact with the formulation. Aqueous adjuvant compositions are known which contain 100 mM sodium chloride or more, for

example adjuvant system A (ASA) in WO 2005/112991 and WO2008/142133 or the liposomal adjuvants disclosed in WO2007/068907.

In some embodiments, the isotonicity agent used for the composition is a salt. In other embodiments, however, the composition comprises a non-ionic isotonicity agent and the concentration of sodium chloride or the ionic strength in the composition is less than 100 mM, such as less than 80 mM, e.g. less than 30 mM, such as less 10 mM or less than 5 mM. The composition may comprise a non-ionic isotonicity agent and conductivity of the composition is less than 5 mS/cm, such as less than 4 mS/cm. In a preferred embodiment, the non-ionic isotonicity agent is a polyol, such as sorbitol. The concentration of sorbitol may e.g. between about 3% and about 15% (w/v), such as between about 4% and about 10% (w/v). Adjuvants comprising an immunologically active saponin fraction and a TLR4 agonist wherein the isotonicity agent is salt or a polyol have been described in WO2012/080369 and WO2012/080370 which are incorporated herein by reference.

The pH of the immunogenic compositions should be suitable for administration. Typically the pH will be in the range 6.0 to 9.0, such as 7.0 to 9.0, especially 7.25 to 8.75, such as 7.5 to 8.5, in particular pH 7.75 to 8.25. A pH of about 8.0 is of particular interest.

For liquid compositions administered parenterally, the volume of the composition will typically be in the region of 50ul to 2ml (depending on the specific route). A volume of 400-600ul, such as around 500ul is typically used, in particular for administration by the intramuscular route.

The compositions will generally be sterile.

Adenoviral vectors

Adenovirus has been widely used for gene transfer applications due to its ability to achieve highly efficient gene transfer in a variety of target tissues and large transgene capacity. Adenoviral vectors of use in the present invention may be derived from a range of mammalian hosts. Over 100 distinct serotypes of adenovirus have been isolated which infect various mammalian species. These adenoviral serotypes have been categorised into six subgenera (A–F; B is subdivided into B1 and B2) according to sequence homology and on their ability to agglutinate red blood cells (Tatsis and Ertl *Molecular Therapy* (2004) 10:616–629).

Examples of human-derived adenoviruses are Ad1, Ad2, Ad4, Ad5, Ad6, Ad11, Ad 24, Ad34 and Ad35. Although Ad5-based vectors have been used extensively in a number of gene therapy trials, there may be limitations on the use of Ad5 and other human group C adenoviral vectors due to preexisting immunity in the general population due to natural infection. Ad5 and other human group C members tend to be among the most seroprevalent serotypes. Additionally, immunity to existing vectors may develop as a result of exposure to the vector during treatment. These types of preexisting or developed immunity to seroprevalent vectors may limit the effectiveness of gene therapy or vaccination efforts. Alternative adenovirus

serotypes, thus constitute very important targets in the pursuit of gene delivery systems capable of evading the host immune response.

The adenoviral vector of use in the present invention is derived from a non-human simian adenovirus. Numerous adenoviruses have been isolated from non-human simians such as chimpanzees, bonobos, rhesus macaques and gorillas, and vectors derived from these adenoviruses induce strong immune responses to transgenes encoded by these vectors (Colloca et al. (2012) Sci. Transl. Med. 4:1-9; Roy et al. (2004) Virol. 324: 361-372; Roy et al. (2010) J. of Gene Med. 13:17-25). Certain advantages of vectors based on non-human simian adenoviruses include the relative lack of cross-neutralising antibodies to these adenoviruses in the target population. For example, cross-reaction of certain chimpanzee adenoviruses with pre-existing neutralizing antibody responses is only present in 2% of the target population compared with 35% in the case of certain candidate human adenovirus vectors.

Specifically, the adenoviral vector is derived from a non-human simian adenovirus, in particular a chimpanzee adenovirus such as ChAd3, ChAd63, ChAd83, ChAd155, Pan 5, Pan 6, Pan 7 (also referred to as C7) or Pan 9. Examples of such strains are described in WO03/000283, WO2005/071093, WO2010/086189 and GB1510357.5 and are also available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, and other sources. Alternatively, adenoviral vectors may be derived from non-human simian adenoviruses isolated from bonobos, such as PanAd1, PanAd2 or PanAd3. Examples of such vectors described herein can be found for example in WO2005/071093 and WO2010/086189. Adenoviral vectors may also be derived from adenoviruses isolated from gorillas as described in WO2013/52799, WO2013/52811 and WO2013/52832.

Certain adenoviral vectors may demonstrate one or more following improved characteristics over other vectors: higher productivity, improved immunogenicity and increased transgene expression.

In one embodiment the adenoviral vector is a non-human simian adenovirus containing at least a penton selected from SEQ ID No: 10 or SEQ ID No: 20, a hexon selected from SEQ ID No: 11 or SEQ ID No: 21 or a fibre selected from SEQ ID No: 12 or SEQ ID No: 22, in particular a penton and hexon, penton and fibre, or hexon and fibre, such as a penton, hexon and fibre. In certain examples the adenoviral vector is a non-human simian adenovirus containing at least the penton of SEQ ID No: 10, the hexon of SEQ ID No: 11 or the fibre of SEQ ID No: 12, in particular a penton and hexon, penton and fibre, or hexon and fibre. In other examples the adenoviral vector is a non-human simian adenovirus containing at least the penton of SEQ ID No: 20, the hexon of SEQ ID No: 21 or the fibre of SEQ ID No: 22, in particular a penton and hexon, penton and fibre, or hexon and fibre.

In an embodiment the adenoviral vector is derived from as ChAd3 and contains at least a penton (SEQ ID No: 10), hexon (SEQ ID No: 11) and fibre (SEQ ID No: 12) therefrom.

In one embodiment the adenoviral vector is derived from as ChAd155 and contains a penton (SEQ ID No: 20), hexon (SEQ ID No: 21) and fibre (SEQ ID No: 22) therefrom.

In one embodiment the adenoviral vector is a non-human simian adenovirus containing at least the penton of SEQ ID No: 15, the hexon of SEQ ID No: 16 or the fibre of SEQ ID No: 17, in particular a penton and hexon, penton and fibre, or hexon and fibre. In some examples the adenoviral vector is derived from as ChAd63 containing at least the penton of SEQ ID No: 15, the hexon of SEQ ID No: 16 and the fibre of SEQ ID No: 17.

*Adenoviral vector structure*

Adenoviruses have a characteristic morphology with an icosahedral capsid comprising three major proteins, hexon (II), penton base (III) and a knobbed fiber (IV), along with a number of other minor proteins, VI, VIII, IX, IIIa and IVa2. The hexon accounts for the majority of the structural components of the capsid, which consists of 240 trimeric hexon capsomeres and 12 penton bases. The hexon has three conserved double barrels, while the top has three towers, each tower containing a loop from each subunit that forms most of the capsid. The base of hexon is highly conserved between adenoviral serotypes, while the surface loops are variable (Tatsis and Ertl *Molecular Therapy* (2004) 10:616–629). Penton is another adenoviral capsid protein that forms a pentameric base to which fiber attaches. The trimeric fiber protein protrudes from the penton base at each of the 12 vertices of the capsid and is a knobbed rod-like structure. The primary role of the fibre protein is the tethering of the viral capsid to the cell surface via the interaction of the knob region with a cellular receptor, and variations in the flexible shaft as well as knob regions of fiber are characteristic of the different serotypes (Nicklin et al Molecular Therapy 2005 12:384–393).

The adenoviral genome is well characterised. The linear, double-stranded DNA is associated with the highly basic protein VII and a small peptide pX (also termed mu). Another protein, V, is packaged with this DNA-protein complex and provides a structural link to the capsid via protein VI. There is general conservation in the overall organization of the adenoviral genome with respect to specific open reading frames being similarly positioned, e.g. the location of the E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4 and L5 genes of each virus. Each extremity of the adenoviral genome comprises a sequence known as an inverted terminal repeat (ITR), which is necessary for viral replication. The 5' end of the adenoviral genome contains the 5 ' cis-elements necessary for packaging and replication; i.e., the 5' ITR sequences (which function as origins of replication) and the native 5 ' packaging enhancer domains (that contain sequences necessary for packaging linear Ad genomes and enhancer elements for the E1 promoter). The 3' end of the adenoviral genome includes the 3 ' cis-elements (including the ITRs) necessary for packaging and encapsidation. The virus also comprises a virus-encoded protease, which is necessary for processing some of the structural proteins required to produce infectious virions. The structure of the adenoviral genome is described on the basis of the order

in which the viral genes are expressed following host cell transduction. More specifically, the viral genes are referred to as early (E) or late (L) genes according to whether transcription occurs prior to or after onset of DNA replication. In the early phase of transduction, the E1A, E1B, E2A, E2B, E3 and E4 genes of adenovirus are expressed to prepare the host cell for viral replication. During the late phase of infection, expression of the late genes L1-L5, which encode the structural components of the virus particles, is activated.

Annotation of the ChAd3 wild type sequence (SEQ ID NO: 9) sequence is provided below.

CDS (38 total)

E1A 30.8K
Start: 589 End: 1544
Original Location Description:
join(589..1129,1243..1544)

E1A 25.5K
Start: 589 End: 1544
Original Location Description:
join(589..991,1243..1544)

E1B 22K
Start: 1716 End: 2279
Original Location Description:
1716..2279

E1B 57K
Start: 2021 End: 3544
Original Location Description:
2021..3544

IX
Start: 3640 End: 4104
Original Location Description:
3640..4104

IVa2
Start: 4163 End: 5790 (Complementary)
Original Location Description:
complement(4163..5499,5778..5790)

pol
Start: 5269 End: 14236 (Complementary)
Original Location Description:
complement(5269..8865,14228..14236)

pTP
Start: 8664 End: 14236 (Complementary)
Original Location Description:
complement(8664..10667,14228..14236)

48K
Start: 11120 End: 12379
Original Location Description:
11120..12379

pIIIa
Start: 12403 End: 14181
Original Location Description:

12403..14181

III
Start: 14273 End: 16054
Penton
Original Location Description:
14273..16054

pVII
Start: 16069 End: 16665
Original Location Description:
16069..16665

V
Start: 16738 End: 17853
Original Location Description:
16738..17853

pX
Start: 17878 End: 18123
Original Location Description:
17878..18123

pVI
Start: 18219 End: 18974
Original Location Description:
18219..18974

hexon
Start: 19086 End: 21968
Original Location Description:
19086..21968

protease
Start: 21998 End: 22627
Original Location Description:
21998..22627

DBP
Start: 22743 End: 24395 (Complementary)
Original Location Description:
complement(22743..24395)

92K
Start: 24445 End: 26940
Original Location Description:
24445..26940

22K
Start: 26630 End: 27229
Original Location Description:
26630..27229

33K
Start: 26630 End: 27551
Original Location Description:
join(26630..26966,27169..27551)

pVIII
Start: 27626 End: 28309
Original Location Description:
27626..28309

E3 12K

Start: 28310 End: 28627
Original Location Description:
28310..28627

E3 CR1-alphap0
Start: 29125 End: 29325
Original Location Description:
29125..29325

E3 gp18K
Start: 29328 End: 29819
Original Location Description:
29328..29819

E3 33K
Start: 29848 End: 30738
Original Location Description:
29848..30738

E3A 11 K
Start: 31293 End: 31589
Original Location Description:
31293..31589

E3 RID alpha
Start: 31601 End: 31873
Original Location Description:
31601..31873

E3 RID beta
Start: 31876 End: 32274
Original Location Description:
31876..32274

E3 15K
Start: 32267 End: 32653
Original Location Description:
32267..32653

U exon
Start: 32684 End: 32848 (Complementary)
Original Location Description:
complement(32684..32848)

fiber
Start: 32859 End: 34490
Original Location Description:
32859..34490

E4ORF6/7
Start: 34698 End: 35858 (Complementary)
Original Location Description:
complement(34698..34973,35685..35858)

E4 ORF6
Start: 34974 End: 35858 (Complementary)
Original Location Description:
complement(34974..35858)

E4 ORF4
Start: 35758 End: 36123 (Complementary)
Original Location Description:
complement(35758..36123)

E4 ORF3
Start: 36139 End: 36486 (Complementary)
Original Location Description:
complement(36139..36486)

E4 ORF2
Start: 36483 End: 36875 (Complementary)
Original Location Description:
complement(36483..36875)

E4 ORF1
Start: 36928 End: 37314 (Complementary)
Original Location Description:
complement(36928..37314)

Misc. Feature (3 total)

VA RNA I
Start: 10693 End: 10860
Original Location Description:
10693..10860

VA II
Start: 10927 End: 11102
Original Location Description:
10927..11102

E3 deletion - 5'
Start: 28642 End: 28647
Original Location Description:
28642..28647

Annotation of the ChAd63 wild type sequence (SEQ ID NO: 14) sequence is provided below.

```
LOCUS       ChAd63                35994 bp    DNA     linear       27-JUL-2015
DEFINITION  Chimp adenovirus 163, complete genome.
COMMENT     Annotation according to alignment of ChAd63 against the human
            Adenovirus 4 reference strain NC_003266
FEATURES             Location/Qualifiers
     source          1..35994
                     /organism="Chimpanzee adenovirus 63"
                     /mol_type="genomic DNA"
                     /acronym="ChAd63"
     repeat_region   1..129
                     /standard_name="ITR"
                     /rpt_type=inverted
     gene            479..1501
                     /gene="E1A"
     regulatory      479..484
                     /regulatory_class="TATA_box"
                     /gene="E1A"
     CDS             join(576..1143,1229..1437)
                     /gene="E1A"
                     /product="control protein E1A"
                     /translation="MRHLRDLPGNVFLATGNEILELVVDAMMGDDPPEPPTPFEAPSL
                     YDLYDLEVDVPENDPNEEAVNDLFSDAALLAAEQANTDSGSDSDSSLHTPRPGRGEKK
                     IPELKGEELDLRCYEECLPPSDDEEDEEAIRAAASEGVKVAGESFSLDCPTLPGHGCK
                     SCEFHRMNTGDKNVMCALCYMRAYNHCVYSPVSDVDETPTSECISSPPEIGEEPPEDI
                     IHRPVAVRVTGRRAAVESLDDLLQGGDEPLDLCTRKRPRH"
     intron          1144..1228
                     /gene="E1A"
     regulatory      1495..1501
                     /regulatory_class="polyA_signal_sequence"
```

```
                    /gene="E1A"
     gene           1555..3953
                    /gene="E1B"
     regulatory     1555..1664
                    /regulatory_class="TATA_box"
                    /gene="E1B"
     CDS            1601..2179
                    /gene="E1B"
                    /codon_start=1
                    /product="control protein E1B 19K"
                    /translation="MEIWTVLEDFHQTRQLLENSSAEVSYLWRFCFGGPLAKLVYRAK
                    QDYKDQFEDILRECPGIFDSLNLGHQSHFNQSILRALDFSTPGRTTAAVAFFAFILDK
                    WSQETHFSRDYRLDCLAVALWRTWRCQRLNAISGYLPVQPVDTLRILSLQSPQEHQRR
                    QQPQQEQQQEEEEDREENLRAGLDPPVAEEEE"
     CDS            1906..3420
                    /gene="E1B"
                    /codon_start=1
                    /product="control protein E1B 55K"
                    /translation="MESRNPFQQGLPSGLLSSSFVENMEVPAPECNLRLLASTAGRHA
                    EDPESPVTPGTPTPPAAAAGAAARGGGGPRREPESRSGPSGGGGGGVADLFPELRRVL
                    TRSSSGRERGIKRERHEETSHRTELTVSLMSRRRPESVWWHEVQSQGIDEVSVMHEKY
                    SLEQVKTCWLEPEDDWEVAIRNYAKLALKPDKKYKITKLINIRNSCYISGNGAEVEIS
                    TQERAAFRCCMMNMYPGVVGMEGVTFMNTRFRGDGYNGVVFMANTKLTVHGCSFFGFN
                    NMCIEAWGSVSVRGCSFSANWMGVVGRTKSVVSVKKCLFERCHLGVMSEGEAKVKHCA
                    STETGCFVLIKGNAKVKHNMICGASDERGYQMLTCAGGNSHMLATVHVASHPRKTWPE
                    FEHNVMTRCNVHLGSRRGMFMPYQCNMQFVKVLLEPDAMSRVSLTGVFDMNVELWKIL
                    RYDESKTRCRACECGGKHARLQPVCVEVTEDLRPDHLVLSCNGTEFGSSGEESD"
     gene           3454..3953
                    /gene="IX"
     regulatory     3454..3459
                    /regulatory_class="TATA_box"
                    /gene="IX"
     CDS            3505..3933
                    /gene="IX"
                    /product="capsid protein IX"
                    /translation="MSGSASFEGGVFSPYLTGRLPSWAGVRQNVMGSTVDGRPVQPAN
                    SSTLTYATLSSSSVDAAAAAAAASAASAVRGMALGAGYYSSLVANSSSTNNPASLNEE
                    KLLLLMAQLEALTQRLGELTQQVAQLQAETRAAVATVKTK"
     regulatory     3929..3934
                    /regulatory_class="polyA_signal_sequence"
                    /note="E1B, IX"
     regulatory     3944..3949
                    /regulatory_class="polyA_signal_sequence"
                    /note="E1B, IX"
     regulatory     3948..3953
                    /regulatory_class="polyA_signal_sequence"
                    /note="E1B, IX"
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| | DRCITLEKSTQTVQGPRSAACGLFCCMFLHAFVHWPDRPMDKNPTMNLLTGVPNGMLQ |
| | SPQVEPTLRRNQEALYRFLNAHSAYFRSHRARIEKATAFDRMNQDM" |
| regulatory | 21834..21839 |
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| | /gene="L3" |
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| | /note="E2A, E2A-L" |
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| | /product="single-stranded DNA-binding protein" |
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| | LTTMMGRFLQGFVHSHSQIAHKNWECTGCALWLHGCTEAEGKLRCLHGTVMIQKEHTI |
| | EMDVASENGQRALKENPDRAKITQNRWGRSVVQLANNDARCCVHDAGCATNQFSSKSC |
| | GVFFTEGGKAQQAFRQLEAFMKAMYPGMSSEQAQMMLIPLHCDCNHKPGCVPSMGRQT |
| | CKMTPFGMANAEDLDVEGITDATVLASVKHPALMVFQCCNPVYRNSRAQNAGPNCDFK |
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| | PNPRLNFYPVFAVPEALATYHLFFKNQRIPVSCRANRTRADALLNLGPGARLPDITSL |
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| | PALNLPPKVMSAVMDQVLIKRASPLSEEEMQDPESSDEGKPVVSDEQLARWLGASSTP |
| | QSLEERRKLMMAVVLVTVELECLRRFFADAETLRKVEENLHYLFRHGFVRQACKISNV |
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| | Q" |
| intron | complement(24157..26296) |
| | /note="E2A, E2B" |

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Annotation of the ChAd155 wild type sequence (SEQ ID NO: 19) sequence is provided below.

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DEFINITION  Chimp adenovirus 155, complete genome.
COMMENT     Annotation according to alignment of ChAd155 against the human
            Adenovirus 2 reference strain NC_001405
            Two putative ORFs in the E3 region added manually
FEATURES             Location/Qualifiers
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*Transgenes*

Adenoviral vectors may be used to deliver desired RNA or protein sequences, for example heterologous sequences, for *in vivo* expression. A vector may include any genetic element including naked DNA, a phage, transposon, cosmid, episome, plasmid, or a virus. By "expression cassette" (or "minigene") is meant the combination of a selected heterologous gene (transgene) and the other regulatory elements necessary to drive translation, transcription and/or expression of the gene product in a host cell.

Typically, an adenoviral vector is designed such that the expression cassette is located in a nucleic acid molecule which contains other adenoviral sequences in the region native to a selected adenoviral gene. The expression cassette may be inserted into an existing gene region to disrupt the function of that region, if desired. Alternatively, the expression cassette may be inserted into the site of a partially or fully deleted adenoviral gene. For example, the expression cassette may be located in the site of a mutation, insertion or deletion which renders non-

functional at least one gene of a genomic region selected from the group consisting of E1A, E1B, E2A, E2B, E3 and E4. The term "renders non-functional" means that a sufficient amount of the gene region is removed or otherwise disrupted, so that the gene region is no longer capable of producing functional products of gene expression. If desired, the entire gene region may be removed (and suitably replaced with the expression cassette). Suitably, E1 genes of adenovirus are deleted and replaced with an expression cassette consisting of the promoter of choice, cDNA sequence of the gene of interest and a poly A signal, resulting in a replication defective recombinant virus.

A transgene sequence may also include a reporter sequence, which upon expression produces a detectable signal. Such reporter sequences include, without limitation, DNA sequences encoding β-lactamase, β-galactosidase (LacZ), alkaline phosphatase, thymidine kinase, green fluorescent protein (GFP), chloramphenicol acetyltransferase (CAT), luciferase, membrane bound proteins including, for example, CD2, CD4, CD8, the influenza hemagglutinin protein, and others well known in the art, to which high affinity antibodies directed thereto exist or can be produced by conventional means, and fusion proteins comprising a membrane bound protein appropriately fused to an antigen tag domain from, among others, hemagglutinin or Myc. These coding sequences, when associated with regulatory elements which drive their expression, provide signals detectable by conventional means, including enzymatic, radiographic, colorimetric, fluorescence or other spectrographic assays, fluorescent activating cell sorting assays and immunological assays, including enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and immunohistochemistry.

In addition to the transgene the expression cassette also includes conventional control elements which are operably linked to the transgene in a manner that permits its transcription, translation and/or expression in a cell transfected with the adenoviral vector. As used herein, "operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in trans or at a distance to control the gene of interest.

Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (poly A) signals including rabbit beta-globin polyA; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (e.g., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. Among other sequences, chimeric introns may be used.

A "promoter" is a nucleotide sequence that permits binding of RNA polymerase and directs the transcription of a gene. Typically, a promoter is located in the 5 ' non-coding region of a gene, proximal to the transcriptional start site of the gene. Sequence elements within

promoters that function in the initiation of transcription are often characterized by consensus nucleotide sequences. Examples of promoters include, but are not limited to, promoters from bacteria, yeast, plants, viruses, and mammals (including humans). A great number of expression control sequences, including promoters which are internal, native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

Examples of constitutive promoters include, without limitation, the TBG promoter, the retroviral Rous sarcoma virus LTR promoter (optionally with the enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer, see, e.g., Boshart et al, Cell, 41:521-530 (1985)), the CASI promoter (WO2012/115980), the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1a promoter (Invitrogen).

Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, e.g., acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech and Ariad. Many other systems have been described and can be readily selected by one of skill in the art. For example, inducible promoters include the zinc-inducible sheep metallothionine (MT) promoter and the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter. Other inducible systems include the T7 polymerase promoter system (WO 98/10088); the ecdysone insect promoter (No et al, Proc. Natl. Acad. Sci. USA, 93:3346-3351 (1996)), the tetracycline-repressible system (Gossen et al, Proc. Natl. Acad. Sci. USA, 89:5547-5551 (1992)), the tetracycline-inducible system (Gossen et al, Science, 378:1766-1769 (1995), see also Harvey et al, Curr. Opin. Chem. Biol, 2:512-518 (1998)). Other systems include the FK506 dimer, VP16 or p65 using castradiol, diphenol murislerone, the RU486-inducible system (Wang et al, Nat. Biotech., 15:239-243 (1997) and Wang et al, Gene Ther., 4:432-441 (1997)) and the rapamycin-inducible system (Magari et al, J. Clin. Invest., 100:2865-2872 (1997)). The effectiveness of some inducible promoters increases over time. In such cases one can enhance the effectiveness of such systems by inserting multiple repressors in tandem, e.g., TetR linked to a TetR by an IRES.

The transgene may be operably linked to a tissue-specific promoter. For instance, if expression in skeletal muscle is desired, a promoter active in muscle should be used. These include the promoters from genes encoding skeletal β-actin, myosin light chain 2A, dystrophin, muscle creatine kinase, as well as synthetic muscle promoters with activities higher than naturally occurring promoters (see Li et al, Nat. Biotech., 17:241-245 (1999)). Examples of promoters that are tissue-specific are known for liver (albumin, Miyatake et al, J. Virol, 71:5124-32 (1997); hepatitis B virus core promoter, Sandig et al, Gene Ther., 3:1002-9 (1996); alpha-

fetoprotein (AFP), Arbuthnot et al., Hum. Gene Ther., 7: 1503-14 (1996)), bone osteocalcin (Stein et al, Mol. Biol. Rep., 24:185-96 (1997)); bone sialoprotein (Chen et al., J. Bone Miner. Res., 11:654-64 (1996)), lymphocytes (CD2, Hansal et al, J. Immunol, 161:1063-8 (1998); immunoglobulin heavy chain; T cell receptor chain), neuronal such as neuron-specific enolase (NSE) promoter (Andersen et al, Cell. Mol. Neurobiol, 13:503-15 (1993)), neurofilament light-chain gene (Piccioli et al, Proc. Natl. Acad. Sci. USA, 88:5611-5 (1991)), and the neuron-specific vgf gene (Piccioli et al, Neuron, 15:373-84 (1995)), among others.

In some embodiments, the Woodchuck Hepatitis Virus Posttranscriptional Regulatory Element (WPRE) (Zuffrey et al. (1999) J Virol; 73(4):2886-9) may be operably linked to the transgene.

*Adenoviral vector construction*

Adenoviral vectors are generated by the modification of the wild type adenovirus to express heterologous genes and/or delete or inactivate undesirable adenoviral sequences. Adenoviral vectors may also have altered replication competency. For example the vector may be replication defective or have limited replication such that it has a reduced ability to replicate in non-complementing cells, compared to the wild type virus. This may be brought about by mutating the virus e.g. by functionally inactivating or deleting a gene involved in replication, for example E1a, E1b, E2, E3 or E4 .

The adenoviral vectors in accordance with the present invention may comprise a functionally inactivated or deleted E1. Thus the adenoviral vectors according to the invention may be replication defective due to the absence of the ability to express adenoviral E1a and/or E1b. The recombinant adenoviruses may also bear functional inactivations in other genes (see WO 03/000283) for example, deletions in E3 or E4 genes. The adenovirus delayed early gene E3 may be eliminated from the adenovirus sequence which forms part of the recombinant virus. The function of E3 is not necessary to the production of the recombinant adenovirus particle. Thus, it is unnecessary to replace the function of this gene product in order to package a recombinant adenovirus useful in the invention. In one particular embodiment the recombinant adenoviruses have functionally deleted E1 and E3 genes. The construction of such vectors is described in Roy et al., Human Gene Therapy 15:519-530, 2004.

Recombinant adenoviruses may also be constructed having a functional deletion of the E4 gene. In a particular embodiment, the recombinant adenoviruses have functionally deleted E1 and E4 genes as described in Colloca et al. (2012) Sci. Transl. Med. 4:1-9; Roy et al. (2004) Virol.324: 361-372. In some embodiments it may be desirable to retain the E4 ORF6 function. In one embodiment, the native E4 ORF6 region may be replaced by a heterologous E4 ORF6, such as from Ad5. Thus, in one particular embodiment, the adenoviral vector may be functionally deleted in E1 and have the E4 ORF6 region from Ad5.

Adenovirus vectors according to the invention may also contain a functional deletion in the delayed early gene E2a. Deletions may also be made in any of the late genes L1 through to L5 of the adenovirus genome. Similarly deletions in the intermediate genes IX and IVa may be useful.

Other deletions may be made in the other structural or non-structural adenovirus genes. The above deletions may be used individually, e.g. an adenovirus sequence for use in the present invention may contain deletions of E1 only. Alternatively, deletions of entire genes or portions thereof effective to destroy their biological activity may be used in any combination. For example in one exemplary vector, the adenovirus sequences may have deletions of the E1 genes and the E4 gene, or of the E1, E2a and E3 genes, or of the E1 and E3 genes (such as functional deletions in E1a and E1b, and a deletion of at least part of E3), or of the E1, E2a and E4 genes, with or without deletion of E3 and so on. Such deletions may be partial or full deletions of these genes and may be used in combination with other mutations, such as temperature sensitive mutations to achieve a desired result.

These vectors are generated using techniques known to those of skill in the art. Such techniques include conventional cloning techniques of cDNA such as those described in texts, use of overlapping oligonucleotide sequences of the adenovirus genomes, polymerase chain reaction, and any suitable method which provides the desired nucleotide sequence. Particularly suitable methods include standard homologous recombination methods such as those provided in Colloca et al. (2012) Sci. Transl. Med. 4:1-9; Roy et al. (2004) Virol.324: 361-372; Roy et al. (2010) J. of Gene Med. 13:17-25; and WO2010/085984 or recombineering methods as described in Warming et al. Nuc. Acids Res. (2005) 33:e36.

Suitably, an adenovirus sequence for use in the present invention will contain functional inactivation (such as deletion) of at least the E1 and E4 genes, optionally with E3 functional inactivation (such as deletion), in conjunction with Ad5E4orf6 gene substitution.

In one embodiment the adenovirus comprises functional inactivation (such as deletion) of the E1 and E4 genes, with incorporation of E4orf6 from Ad5. In such embodiments adenovirus is suitably derived from ChAd155, ChAd3 or ChAd63, particularly ChAd3.

In a second embodiment the adenovirus comprises functional inactivation (such as deletion) of the E1, E3 and E4 genes, with incorporation of E4orf6 from Ad5. In such embodiments adenovirus is suitably derived from ChAd155, ChAd3 or ChAd63, particularly ChAd63.

*Adenoviral vector production*

The adenoviral vectors can be produced using any suitable cell line in which the virus is capable of replication. In particular, complementing cell lines which provide the factors missing from the viral vector that result in its impaired replication characteristics (such as E1) can be used. Without limitation, such a cell line may be HeLa (ATCC Accession No. CCL 2), A549

(ATCC Accession No. CCL 185), HEK 293, KB (CCL 17), Detroit (*e.g.*, Detroit 510, CCL 72) and WI-38 (CCL 75) cells, among others. These cell lines are all available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209. Other suitable parent cell lines may be obtained from other sources, such as PER.C6™ cells, as represented by the cells deposited under ECACC no. 96022940 at the European Collection of Animal Cell Cultures (ECACC) at the Centre for Applied Microbiology and Research (CAMR, UK) or Her 96 cells (Crucell).

A particularly suitable complementation cell line is the Procell92 cell line. The Procell92 cell line is based on HEK 293 cells which express adenoviral E1 genes, transfected with the Tet repressor under control of the human phosphoglycerate kinase-1 (PGK) promoter, and the G418-resistance gene (Vitelli et al. PLOS One (2013) 8(e55435):1-9). Procell92.S is adapted for growth in suspension conditions and is also useful for producing adenoviral vectors expressing toxic proteins (www.okairos.com/e/inners.php?m=00084, last accessed 13 April 2015).

*Adenoviral delivery methods and dosage*

The adenoviral vectors may be as administered in immunogenic compositions. An immunogenic composition as described herein is a composition comprising one or more recombinant vectors capable of inducing an immune response, for example a humoral (e.g., antibody) and/or cell-mediated (e.g., a cytotoxic T cell) response, against the transgene product delivered by the vector following delivery to a mammal, suitably a human. A recombinant adenovirus may comprise (suitably in any of its gene deletions) a gene encoding the desired immunogen and may therefore be used in a vaccine.

Such vaccine or other immunogenic compositions may be formulated in a suitable delivery vehicle. Generally, doses for the immunogenic compositions are in the range defined below under 'Delivery Methods and Dosage'.

Optionally, a vaccine or immunogenic composition of the invention may be formulated to contain other components, including, e.g., adjuvants, stabilizers, pH adjusters, preservatives and the like. An adjuvant can be administered with a priming DNA vaccine encoding an antigen to enhance the antigen-specific immune response compared with the immune response generated upon priming with a DNA vaccine encoding the antigen only.

The adenoviral vector may be prepared for administration by being suspended or dissolved in a pharmaceutically or physiologically acceptable carrier such as isotonic saline; isotonic salts solution or other formulations that will be apparent to those skilled in the art. The appropriate carrier will be evident to those skilled in the art and will depend in large part upon the route of administration. The compositions described herein may be administered to a mammal in a sustained release formulation using a biodegradable biocompatible polymer, or by on-site delivery using micelles, gels and liposomes.

In some embodiments, the recombinant adenovirus of the invention is administered to a subject by intramuscular injection, intravaginal injection, intravenous injection, intraperitoneal injection, subcutaneous injection, epicutaneous administration, intradermal administration, nasal administration or oral administration. Delivery to the lung may also be desirable. Intramuscular delivery may be a typical route, for reasons of simplicity and convenience.

If the therapeutic regimen involves co-administration of one or more adenoviral vectors and a further component, each formulated in different compositions, they are favourably administered co-locationally at or near the same site. For example, the components can be administered (e.g. via an administration route selected from intramuscular, transdermal, intradermal, sub-cutaneous) to the same side or extremity ("co-lateral" administration) or to opposite sides or extremities ("contra-lateral" administration).

Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective adult human or veterinary dosage of the viral vector generally contains $1x10^5$ to $1x10^{15}$ viral particles, such as from $1x10^8$ to $1x10^{12}$ (e.g., $1x10^8$, $5x10^8$, $1x10^9$, $5x10^9$, $1x10^{10}$, $2.5x10^{10}$, $5x10^{10}$, $1x10^{11}$ $5x10^{11}$, $1x10^{12}$ particles). Alternatively, a viral vector can be administered at a dose that is typically from $1x10^5$ to $1x10^{10}$ plaque forming units (PFU), such as $1x10^5$ PFU, $5x10^5$ PFU, $1x10^6$ PFU, $5x10^6$ PFU, $1x10^7$ PFU, $5x10^7$ PFU, $1x10^8$ PFU, $5x10^8$ PFU, $1x10^9$ PFU, $5x10^9$ PFU, or $1x10^{10}$ PFU. Dosages will vary depending upon the size of the animal and the route of administration. For example, a suitable human or veterinary dosage (for about an 80 kg animal) for intramuscular injection is in the range of about $1 \times 10^9$ to about $5 \times 10^{12}$ particles per mL, for a single site. Optionally, multiple sites of administration may be used. In another example, a suitable human or veterinary dosage may be in the range of about $1 \times 10^{11}$ to about $1 \times 10^{15}$ particles for an oral formulation.

The adenoviral vector can be quantified by Quantitative PCR Analysis (Q-PCR), for example with primers and probe designed on CMV promoter region using as standard curve serial dilution of plasmid DNA containing the vector genome with expression cassette including HCMV promoter. The copy number in the test sample is determined by the parallel line analysis method. Alternative methods for vector particle quantification can be analytical HPLC or spectrophotometric method based on $A_{260}$ nm.

Generally a human dose will be in a volume of between 0.5ml and 2 ml. Thus the composition described herein can be formulated in a volume of, for example 0.5, 1.0, 1.5 or 2.0 ml human dose per individual or combined immunogenic components. A volume of 400-600ul, such as around 500ul is typically used, in particular for administration by the intramuscular route.

One of skill in the art may adjust these doses, depending on the route of administration and the therapeutic or vaccine application for which the recombinant vector is employed. The

levels of expression of the transgene, or for an adjuvant, the level of circulating antibody, can be monitored to determine the frequency of dosage administration.

The therapeutic levels of, or level of immune response against, the protein encoded by the selected transgene can be monitored to determine the need, if any, for boosters. Following an assessment of CD8+ T cell response, or optionally, antibody titers, in the serum, optional booster immunizations may be desired. Optionally, the adenoviral vector may be delivered in a single administration or in various combination regimens, e.g., in combination with a regimen or course of treatment involving other active ingredients or in a prime-boost regimen.

M72 Transgene

A further aspect of the present invention relates to a novel polynucleotide encoding an M72 antigen which has been optimised for use in the present invention but will also have utility in other contexts. Consequently, the invention also provides a polynucleotide comprising SEQ ID No: 8 or a degenerate variant thereof having at least 95% identity to SEQ ID No: 8 (such as at least 98% identity, suitably at least 99% identity, in particular at least 99.5% identity and especially 100% identity). Also provided is a polynucleotide consisting of SEQ ID No: 8 or a degenerate variant thereof having at least 95% identity to SEQ ID No: 8 (such as at least 98% identity, in suitably at least 99% identity, particular at least 99.5% identity and especially 100% identity). By the term degenerate variant is meant a variant of the polynucleotide which encodes the same polypeptide.

The optimised polynucleotide helps ensure the benefits of the present invention are fully achieved through efficient transgene expression in human cells.

Adenoviral constructs

A further aspect of the present invention relates to novel adenoviral constructs of use in the present invention but also having utility in other contexts. Consequently, the invention also provides a non-human simian adenovirus comprising a transgene encoding a Rv1196 or Rv0125 related antigen. Suitably the non-human simian adenovirus comprises a penton of SEQ ID No: 10, a hexon of SEQ ID No: 11 or a fibre of SEQ ID No: 12, in particular a penton of SEQ ID No: 10, a hexon of SEQ ID No: 11 and a fibre of SEQ ID No: 12. Alternatively, the non-human simian adenovirus comprises a penton of SEQ ID No: 15, a hexon of SEQ ID No: 16 or a fibre of SEQ ID No: 17, in particular a penton of SEQ ID No: 15, a hexon of SEQ ID No: 16 and a fibre of SEQ ID No: 17. Also, the non-human simian adenovirus may comprise a penton of SEQ ID No: 20, a hexon of SEQ ID No: 21 or a fibre of SEQ ID No: 22, in particular a penton of SEQ ID No: 21, a hexon of SEQ ID No: 22 and a fibre of SEQ ID No: 23.

The transgene encoding a Rv1196 related antigen may be a sequence encoding a polypeptide comprising, such as consisting of, a sequence having at least 90% identity to SEQ ID No: 1, especially at least 95%, for example at least 98%, such as at least 99% to SEQ ID No: 1, such as SEQ ID No: 1.

The transgene encoding a Rv0125 related antigen may be a sequence encoding a polypeptide comprising, such as consisting of, a sequence having at least 90% identity to SEQ ID No: 3, especially at least 95%, for example at least 98%, such as at least 99% to SEQ ID No: 3, such as SEQ ID No: 3.

Suitably the transgene will encode an antigen comprising (such as consisting of) a sequence having at least 90% identity to SEQ ID No. 6. Alternatively, the transgene will encode an antigen comprising (such as consisting of) a fragment of SEQ ID No: 6 which is at least 450 amino acids in length. In some embodiments the transgene will encode an antigen comprising (such as consisting of) amino acids 2-723 of SEQ ID No. 6. Suitably the transgene comprises SEQ ID No: 8 or a degenerate variant thereof having at least 95% identity to SEQ ID No: 8. In some embodiments the transgene comprises SEQ ID No: 8.

Suitably the adenovirus is replication deficient. For example, the adenovirus comprises functional inactivation (such as deletion) of the E1 gene. The adenovirus may comprise functional inactivation (such as deletion) of the E4 gene. The adenovirus may also comprise functional inactivation (such as deletion) of the E3 gene. The adenovirus may also comprise an Ad5E4orf6 gene substitution.

Exemplary adenovirus constructs according to the invention are those having the polynucleotide sequence of SEQ ID No: 13 or 18.

An additional aspect of the invention is a polynucleotide sequence comprising SEQ ID No: 13 or 18, such as a polynucleotide sequence consisting of SEQ ID No: 13 or 18.

Immunisation regimes, target populations and modes of administration

In one embodiment the subject receives a single dose of the polypeptide antigen and a single dose of the associated adenovirus. In other embodiments the subject receives two doses of the polypeptide antigen and a single dose of the associated adenovirus (the additional dose of polypeptide antigen may be given prior to initiation of the standard protein/adeno or adeno/protein methods or following completion of the standard methods). In other embodiments the subject receives one dose of the polypeptide antigen and two doses of associated adenovirus (the additional dose of the associated adenovirus may be given prior to initiation of the standard protein/adeno or adeno/protein methods or following completion of the standard methods). When two doses of adenovirus encoding antigen are provided, they may or may not make use of the same adenovirus strain and insert.

When the subject receives two doses of polypeptide antigen, suitably the additional dose is one week to three months, in particular two weeks to two months, typically three weeks to six weeks, such as three weeks to five weeks, for example around four weeks prior to initiation or following completion of the standard method.

When the subject receives two doses of associated adenovirus, suitably the additional dose is one week to three months, in particular two weeks to two months, typically three weeks to six weeks, such as three weeks to five weeks, for example around four weeks prior to initiation or following completion of the standard method.

The subject to be treated using the method of the invention may be of any age. In one aspect of the invention, the subject is human.

In one embodiment the subject is an adult human (typically aged 18-60).

The polypeptide and adenovirus compositions may be administered via various suitable routes, including parenteral, such as intramuscular or subcutaneous administration.

In one particular embodiment, the one or more of the compositions is administered intradermally. The term intradermally as used herein is intended to refer to the application of antigens into the dermis and/or epidermis of human skin. Intradermal application of an immunogenic composition may be performed by using any cutaneous method known to the skilled person including, but not limited to, delivery using a short needle device (a device comprising a microneedle that is between about 0.2 and about 0.6 mm in length) or delivery using a skin patch. Suitable devices for use with the cutaneous vaccines described herein include short needle devices such as those described in US 4,886,499, US5,190,521, US 5,328,483, US 5,527,288, US 4,270,537, US 5,015,235, US 5,141,496, US 5,417,662 and EP1092444. Cutaneous vaccines may also be administered by devices which limit the effective penetration length of a needle into the skin, such as those described in WO99/34850. Also suitable are jet injection devices which deliver liquid vaccines to the dermis via a liquid jet injector or via a needle. Also suitable are ballistic powder/particle delivery devices which use compressed gas to accelerate vaccine in powder form through the outer layers of the skin to the dermis. Skin patches will generally comprise a backing plate which includes a solid substrate. Patches deliver the antigen and adjuvant used in the invention to the dermis or epidermis. In particular embodiment, the patches useful in the present invention comprise a plurality of microprojections. The microprojections may be of any shape suitable for piercing the stratum corneum, epidermis and/or dermis and delivery and antigen and adjuvant to the epidermis or dermis. In a particular embodiment, microprojections are biodegradable and comprise a biodegradable polymer.

In an alternative approach, the polypeptide may be administered intramuscularly and the adenovirus administered intranasally or via aerosol to the lungs.

Suitably, both compositions are administered intramuscularly.

Immunogenic compositions used in the invention may be made by admixing the antigen(s) and the adjuvant. The antigen(s) may be provided in a lyophilized form or in a liquid formulation. A kit may be provided comprising a first container comprising the antigen and a second container comprising the adjuvant.

Suitably, the compositions according to the present invention have a human dose volume of between 0.05 ml and 1 ml, such as between 0.1 and 0.5 ml, in particular a dose volume of about 0.5 ml, or 0.7 ml. The volume of the second immunogenic composition may be reduced, and e.g. be between 0.05 ml and 0.5 ml, such as between 0.1 and 0.2 ml. The volumes of the compositions used may depend on the delivery route with smaller doses being given by the intradermal route.

Additional embodiments of the invention include:

(a) A non-human simian adenovirus comprising a transgene encoding a Rv1196 or Rv0125 related antigen, said adenovirus having at least the penton of SEQ ID No: 20, the hexon of SEQ ID No: 21 or the fibre of SEQ ID No: 22.

(b) The non-human simian adenovirus according to (a), comprising the penton (SEQ ID No: 20), hexon (SEQ ID No: 21) and fibre (SEQ ID No: 22) protein from ChAd155.

(c) The non-human simian adenovirus according to either (a) or (b) wherein the encoded antigen comprises a sequence having at least 90% identity to SEQ ID No. 6.

(d) The non-human simian adenovirus according to any one of (a), (b) or (c) wherein the encoded antigen comprises a fragment of SEQ ID No: 6 which is at least 450 amino acids in length, such as 2-723 of SEQ ID No. 6.

(e) The non-human simian adenovirus according to any one of (a) to (d), which is a replication deficient adenovirus.

(f) The non-human simian adenovirus according to any one of (a) to (e), wherein the adenovirus comprises functional inactivation (such as deletion) of the E1 gene.

(g) The non-human simian adenovirus according to any one of (a) to (f), wherein the adenovirus comprises functional inactivation (such as deletion) of the E4 gene.

(h) The non-human simian adenovirus according to any one of (a) to (g), wherein the adenovirus comprises functional inactivation (such as deletion) of the E3 gene.

(i) The non-human simian adenovirus according to any one of (a) to (e), wherein the adenovirus comprises an Ad5E4orf6 gene substitution.

The teaching of all references in the present application, including patent applications and granted patents, are herein fully incorporated by reference. A composition or method or process defined as “comprising” certain elements is understood to encompass a composition, method or process (respectively) consisting of those elements. The invention will be further described by reference to the following, non-limiting, example:

## EXAMPLES

## Example 1 – Generation of ChAd3 and ChAd63 vectors encoding M72 protein

### Making constructs

An M72 DNA sequence was optimized by GeneArt® (Life Technologies Corporation) for human expression (SEQ ID No: 8). According to standard methods, the optimised DNA sequence was synthesized and cloned by GeneWiz® under control of HCMV promoterTetO system and BGH polyA sequences into the shuttle plasmid PVJ using the EcoRV-NotI restriction sites. This plasmid was cleaved with SpeI and SgfI restriction enzymes and recombined into either ChAd3 (with E1 and E4 deletions) or ChAd63 (with E1, E3 and E4 deletions) vectors by homologous recombination in *E. coli* BJ5183.

Briefly, the construction of ChAd3 vectors proceeded through the steps provided below.

The pChAd3 vector is derived from the wild type chimp adenovirus 3 genome. The wild type chimp adenovirus type 3 was isolated from a healthy young chimpanzee housed at the New Iberia Research Center facility (New Iberia Research Center; The University of Louisiana at Lafayette) using standard procedures. The viral genome was then cloned in a plasmid vector and subsequently modified to carry the following modifications in different regions of ChAd3 viral genome:

1) deletion of the E1 region (from bp 460 to bp 3543) of the viral genome;

2) deletion of the entire ChAd3 E4 coding region (spanning from nucleotide 34634-37349 of ChAd3 wild type sequence) and substitution with Ad5E4orf6 gene. The deleted region all of the E4 region with the exception of E4 native promoter and polyadenylation signal.

The construction of ChAd 63 vectors proceeded through the steps provided below.

The wild type chimp adenovirus type 63 was isolated from a healthy group of Chimpanzee housed by the New Iberia facility using standard procedures. The viral genome was then cloned in a plasmid vector and subsequently modified to carry the following modifications in different regions of ChAd3 viral genome:

1) deletion of the E1 region (from bp 456 to bp 3421) of the viral genome;

2) deletion of the E3 region (from 27208 bp to 31786 bp) of the viral genome;

3) deletion of the entire ChAd63 E4 coding region (spanning from nucleotide 33825 to 36216 of ChAd63 wt sequence) and substitution with Ad5E4orf6 gene. The deleted region contained all E4 region with the exception of E4 native promoter and polyadenylation signal.

### Confirmatory testing

Rescues and viruses amplification (from passage 1 to passage 4) were generated in procell-92.S cell line according to standard procedures and the genetic structure of the viral DNAs was checked at passage 3 (M72-ChAd63) or passage 4 (M72-ChAd3) by two different restriction patterns. Each recombinant virus was purified from 1 litre scale culture through a CsCl gradient

method. Purified viruses were titred by quantitative PCR and the infectivity measured by a hexon immunostaining method.

Good M72 expression was confirmed by Western Blot, after HeLa cell line infection with purified viruses. Genomic stability was evaluated until passage 10 and the DNA sequence of complete expression cassette were confirmed by sequencing.

## Example 2 – Adenovirus Dose Investigation in Mice

**Test Groups**

The aim of this study was to assess and compare the immunogenicity of 2 chimpanzee adenoviruses encoding for the tuberculosis M72 antigen: M72-ChAd3 and M72-ChAd63. The adenoviruses were produced according to Example 1.

Female 6 week old CB6F1/OlaHsd mice, 12 mice per group, were injected by the intramuscular route with 50ul at day 0 (ChAd 3 solution: pH 7.4, 10mM TRIS, 10 mM histidine, 5% sucrose, 75 mM NaCl, 1 mM $MgCl_2$, 0.02% polysorbate 80, 0.1 mM EDTA, 0.5% (v/v) ethanol; ChAd63 solution: pH 6.6, 10 mM histidine, 7.5% sucrose, 35 mM NaCl, 1 mM $MgCl_2$, 0.1% polysorbate 80, 0.1 mM EDTA, 0.5% (v/v) ethanol):

| Group | Adenovirus | Number of Viral Particles |
|---|---|---|
| 1 | M72-ChAd3 | 10^10 |
| 2 | M72-ChAd3 | 10^9 |
| 3 | M72-ChAd3 | 10^8 |
| 4 | M72-ChAd3 | 10^7 |
| 5 | M72-ChAd63 | 10^10 |
| 6 | M72-ChAd63 | 10^9 |
| 7 | M72-ChAd63 | 10^8 |
| 8 | M72-ChAd63 | 10^7 |

In order to have sufficient volume, the whole blood of 4 pools of 3 mice for groups was collected at days 7, 14, and 21.

**Measurement of cellular immune response - Intracellular cytokine staining (ICS)**

Leukocyte isolation from whole blood

At each time point, blood was collected from each mouse and subsequently pooled (4 pools of 3 mice). Blood was collected in tubes containing, RPMI/additives (RPMI 1640, supplemented with glutamine, penicillin/streptomycin, sodium pyruvate, non-essential amino-acids and 2-mercaptoethanol) containing heparin 5000 unit/ml (Heparin Leo). Ten volumes of Lysing buffer were added to the whole blood and tubes were incubated at room temperature (RT) for 10 min. After centrifugation (335g, 10 min at RT), the pellet was harvested in RPMI/additives and filtered (Cell strainer 100um). Cells were pelleted again (335g, 10 min at RT) and re-suspended in Complete

Medium (RPMI 1640, supplemented with glutamine, penicillin/streptomycin, sodium pyruvate, non-essential amino-acids and 2-mercaptoethanol, and 5% heat inactivated fetal calf serum).

*In vitro* stimulation of fresh leukocytes

Leukocytes were plated in round bottom 96-well plates at approximately 1 million cells per well. Leukocytes were then stimulated for 6 hours (37°C, 5% $CO_2$) with anti-CD28 (clone 37.51) and anti-CD49d (clone 9C10) at 1ug/ml, with or without 1ug/ml of peptides covering the M72 sequence (mixture of 15-mer peptides overlapping by 11 amino acid residues). After a 2 hour stimulation period, BD GolgiPlug™ containing brefeldin A diluted in complete medium (final dilution 1/1000) was added for 4 additional hours. Plates were then transferred at 4°C, overnight.

ICS IFNg, IL-2, TNF-a

Cells were stained and analysed using a 5-colour ICS assay.

Cells were transferred to V-bottom 96-well plates, centrifuged at 189g for 5 min at 4 °C after wash with 200ul Flow Buffer (PBS 1X, 1% FCS), re-suspended the cells in 50ul Flow Buffer containing anti- CD16/32 (clone 2.4G2) diluted 1/50, for 10 min at 4 °C. Then, 50 ul Flow Buffer containing anti-CD4-V450 (clone RM4-5, diluted 1/50) and anti-CD8-PerCp-Cy5.5 (clone 53-6.7, diluted 1/50) antibodies and LIVE/DEAD® Pacific Orange (Life Technologies, diluted 1/500) was added for 30 min at 4 °C. Cells were centrifuged (189g for 5 min at 4 °C) and washed with 200ul Flow Buffer.

Leukocytes were fixed and permeabilised by adding 200ul of Cytofix/Cytoperm solution (Becton Dickinson commercial buffer) for 20 min at 4 °C. Cells were centrifuged (189g for 5 min at 4 °C) and washed with 200ul Perm/Wash buffer (Becton Dickinson commercial buffer diluted 1:10 in distilled water). After an additional centrifugation step, cells were stained in 50ul Perm/Wash buffer with anti-IL2-FITC (clone JES6-5H4, diluted 1/400), anti- IFNg-APC (clone XMG1.2, diluted 1/200) and anti-TNFa-PE (clone MP6-XT22, diluted 1/700) antibodies, for 1 hour at 4 °C. Cells were washed twice with the Perm/Wash buffer re-suspended in 220ul PBS. Stained cells were analysed by flow cytometry using a LSRII and the FlowJo software.

**Results**

As seen in Figures 1 and 2 (CD4 T cell response for M72-ChAd3 and M72-ChAd63 constructs respectively) and Figures 3 and 4 (CD8 T cell response for M72-ChAd3 and M72-ChAd63 constructs respectively) a dose of $1x10^8$ viral particles per mouse induced the highest level M72 specific response at timepoint 14PI for both the M72-ChAd3 and M72-ChAd63 constructs.

## Example 3 – Investigation of the impact of adenovirus and adjuvant coformulation on infectivity

The impact of the co-formulation was evaluated with recombinant eGFP-ChAd3 or eGFP-ChAd63. These ChAd3 and ChAd 63 are controls constructed to express the green fluorescent protein instead of the M72 transgene in the respective ChAdenovirus backbones (E1-E4 deleted

ChAd3 and E1-E3-E4 deleted ChAd63). Co-formulation with the AS01E (a liposomal formulation of the TLR4 agonist 3D-MPL and the saponin QS21) was evaluated via an infectivity assay based on HeLa cells.

**Materials and Methods**

Infectivity Test

HeLa cells were grown in an exponential growth and seeded for 24 h before infection. HeLa cells were used between passage P45 and P65 (Molbiol; GSK Rix).

*DAY 0: Cell harvest*

The medium was removed from the flask and the cells rinsed carefully with DPBS to remove residual cell medium. 5ml of Trypsin-EDTA was added onto the cells followed by observing the cells under an inverted microscope until the cell layer detached and dispersed (2 to 4 minutes). The cell suspension was gently pipetted up and down and transferred into the Falcon tube and centrifuged at 1200rpm for 5 to 10 minutes at room temperature. The cell pellet was re-suspended in an appropriate volume and counted. The cells were seeded in a 96 well- plate at 1.5 $x10^4$ cells/ well (HeLa cells are expected to be at 3 x $10^4$ cells /well at the day of infection

*DAY 1: Infection Day*

The HeLa cells were observed and were between 50% to 80% confluent. The entire medium was removed from the cells. The recombinant eGFP-ChAd3 and eGFP-ChAd63 stocks were diluted down to a final titre of $5x10^7$vp/ml in 80ul of complete dulbecco modified eagle medium (DMEM). This volume is for 1 well. 80ul of each sample was added in each well to infect (this is done in duplicate). A negative control of uninfected HeLa cells with a formulation with buffers alone in complete DMEM was used to measure any negative impact on the adeno-infectivity due to the adjuvant buffer. A positive infection control of HeLa cells infected with eGFP-ChAd3 (same condition of infection) was processed in identical conditions. After 3 hours at 37 °C, 5% $CO_2$, 120ul of complete DMEM was added and then cultured at 37 °C, 5% $CO_2$ for approximately 24 hours.

*Day 2: Harvest and FACS read out*

The cell supernatants were harvested in a 96 well-plate. Hela cells were rinsed with 40µl of trypsin/ EDTA and then incubated with an additional 40µl of the trypsin/ EDTA mix. Once the cells were detaching from the plate, each well was then gently flushed to recover all the cells. The 96-well plate was then centrifuged at 1200rpm for 10 minutes. The supernatants were discarded. The cells were suspended in 200ul of DPBS and kept at 4 °C until FACS acquisition was done on them (LSRII Beckman Dickinson).

**Results**

| Test Group | Description | %GFP | | | %viability (average) |
|---|---|---|---|---|---|
| | | A | B | Average | |

| | | | | | |
|---|---|---|---|---|---|
| 1 | DMEM control | 0 | 0 | 0 | 89.14 |
| 2 | AS01E | 0 | 0 | 0 | 91.20 |
| 3 | AS01E + eGFP-ChAd3 | 81.9 | 84.79 | 83.35 | 89.01 |
| 4 | AS01E + eGFP-ChAd63 | 70.43 | 73.28 | 71.86 | 88.95 |
| 5 | AS buffer + eGFP-ChAd3 | 86.4 | 86.93 | 86.67 | 88.57 |
| 6 | AS buffer + eGFP-ChAd63 | 69.59 | 71.38 | 70.49 | 87.49 |
| 7 | eGFP-ChAd3 | 78.78 | 81.29 | 80.04 | 90.96 |
| 8 | eGFP-ChAd63 | 51.43 | 53.46 | 52.45 | 90.41 |

AS buffer pH 8.0, 10mM $PO_4$, 5mM NaCl, 4.7% sorbitol

ChAd3 buffer: pH 7.4, 10mM TRIS, 10 mM histidine, 5% sucrose, 75 mM NaCl, 1 mM $MgCl_2$, 0.02% polysorbate 80, 0.1 mM EDTA, 0.5% (v/v) ethanol

ChAd63 buffer: pH 6.6, 10 mM histidine, 7.5% sucrose, 35 mM NaCl, 1 mM $MgCl_2$, 0.1% polysorbate 80, 0.1 mM EDTA, 0.5% (v/v) ethanol

The data are expressed as the percentage of cells expressing GFP correlating with the number of cells infected by the ChAd-GFP virus. For all conditions, cell viability has been recorded. This was done to assess any possible cell toxicity which could mislead the conclusion. Fortunately, this was not the case as the cell viability through all the conditions was acceptable and comparable.

According to the data, no negative impact of the AS on either ChAd3- or ChAd63- GFP is observed. The ChAd3-GFP vector co-formulated with AS01E kept its infectivity potential, which was comparable to the ChAd3-GFP alone.

Same observation was made for ChAd63-GFP. In the latter case, an increase of infectivity was even observed which may be due to the buffers used in which the adenovirus was diluted.

## Example 4 – Investigation of the impact of adenovirus and adjuvant coformulation on QS21 quenching

The aim of the study was to check the detoxification of QS21.

*Characterisations*

| Group | Description | Visual aspect | H (sticks) | Osmo (mosm/kg) |
|---|---|---|---|---|
| 1 | AS01E | Opalescent | 5.5-6 | 291 |
| 2 | eGFP-ChAd3 at $2.10x10^9$ in AS01E | Slightly Opalescent | 5-5.5 | 289 |
| 3 | eGFP-ChAd63 at $2.10x10^9$ in AS01E | Slightly Opalescent | 5-5.5 | 297 |
| 4 | eGFP-ChAd3 at $2.10x10^9$ in AS01E buffer | Clear | 5-5.5 | 292 |
| 5 | eGFP-ChAd63 at $2.10x10^9$ in AS01E buffer | Clear | 5-5.5 | 304 |
| 6 | eGFP-ChAd3 at $2.10x10^9$ | Clear | 7 | 425 |

| | | | | |
|---|---|---|---|---|
| 7 | eGFP-ChAd63 at $2.10x10^9$ | Clear | 6-6.5 | 408 |

The formulated samples containing the adjuvant or the adjuvant buffer have an osmolality ≥ 285 mOsm/kg. The pH was taken on indicator stick.

*Washing of red blood cells*

The red blood cells (10ml) were centrifuged for 10 minutes at 1600rpm (550g) at 4 °C and the supernatant removed. The red blood cells were re-suspended gently with a volume of buffer DPBS equivalent to the original volume (± 10ml). The operation was repeated (min 2-3 times) until the supernatant was clear (reddish staining disappeared, but the supernatant never becomes completely translucent) and then eliminated the last supernatant after washing. The pellet was stored at 4 °C for 3 to 4 days maximum if not used directly (and washed again the day it is used) or was diluted around 10 times in buffer if used the same day.

*Pre dilutions of red blood cells*

Different pre dilutions of the red blood cells were performed. The pre dilution for which one a 100% of lysis is reached with an OD value (540 nm) between 1.5 and 2 was selected.

The following dilutions were prepared in haemolysis tubes:

| Dilution | Red blood cells | dPBS |
|---|---|---|
| 1/10 | 100 ul | 900 ul |
| 1/12.5 | 100 ul | 1150 ul |
| 1/15 | 100 ul | 1400 ul |

The red blood cells were centrifuged (10ml) for 10 minutes at 1600rpm (550g) at 4 °C. 100ul of the predilution was removed, mixed with 900ul of WFI and centrifuged for 5 minutes at 2000 rpm (900g). The supernatant was transferred in a cuvette for spectroscopy and measured the OD at 540 nm. The dilution chosen gave a OD between 1.5 and 2.

*QS21 standard curve preparation*

The standard curve of QS21 was made from a QS21 working solution (at 2mg/ml) diluted extemporaneously to 20ug/ml in $PO_4$/Sorbitol buffer.

Determination of lytic activity was carried out by a limit test.

1. Limit of detection (LOD) was defined as the lowest concentration of QS21 leading to an OD:

- Higher than the base level (OD>0.1)
- Around three times higher than OD's buffer (the "0 ug" QS21)
- In the ascendant part of the curve
- Determined for each test.

2. QS21 lytic activity was held to be positive in the adjuvant samples if the OD for the adjuvant sample was greater than the $OD_{LOD}$.

Example QS21 curve

| Samples | QS21 (ug) | O.D. Sample | O.D. Buffer | Delta (O.D. sample – O.D. buffer ) | *Pass/fail |
|---|---|---|---|---|---|
| AS01E | 45 | 0.151 | 0.122 | 0.029 | PASS |
| ChAd3 in AS01E | 45 | 0.148 | 0.122 | 0.026 | PASS |
| ChAd63 in AS01E | 45 | 0.143 | 0.122 | 0.021 | PASS |

*Pass: if Delta (O.D. sample- O.D. buffer) < LOD (O.D.) test of the day

*Fail: if Delta (O.D. sample- O.D. buffer) > LOD (O.D.) test of the day

Conclusion

When formulating eGFP-ChAd3 and eGFP-ChAd63 separately with AS01E, the adjuvant size remains unchanged after formulation. Furthermore, there is no free QS21 after formulation, as seen by the red blood cell lysis test.

## Example 5 – M72 dosage regimes

Evaluating the application of non-replicative chimp adeno vectors expressing M72 in the context of a tuberculosis vaccine, by assessing both homologous (ChAd/ChAd) and heterologous (Prot/ChAd or ChAd/Prot) prime-boost vaccination strategies as well as in combination with M72/AS01E given as admixed or in co-administration.

**Materials and Methods**

Animal model

Female mouse CB6F1/OlaHsd - 6 weeks old – 12 mice per group – were injected by intramuscular route with 50ul at days 0-28 as indicated in table below.

| Gr. | Admin D0 | | | Admin D28 | | |
|---|---|---|---|---|---|---|
| | Antigen | Dose | Solution | Antigen | Dose | Solution |
| Benchmark | | | | | | |
| 1 | M72/AS01E | 1ug | AS buffer | M72/AS01E | 1ug | AS buffer |

| | | | | | | |
|---|---|---|---|---|---|---|
| Priming: Adeno/Boost: Protein | | | | | | |
| 2 | M72-ChAd3 | 10^8vp | ChAd3 buffer | M72/AS01E | 1ug | AS buffer |
| 3 | M72-ChAd63 | 10^8vp | ChAd63 buffer | | | |
| 4 | eGFP-ChAd3 | 10^8vp | ChAd3 buffer | | | |
| Priming: Protein/Boost: Adeno | | | | | | |
| 5 | M72/AS01E | 1ug | AS buffer | M72-ChAd3 | 10^8vp | ChAd3 buffer |
| 6 | | 1ug | AS buffer | M72-ChAd63 | 10^8vp | ChAd63 buffer |
| Priming: Adeno + AS/ Boost: Adeno+ AS | | | | | | |
| 7 | M72-ChAd3 /AS01E | 10^8vp | AS buffer | M72-ChAd3 /AS01E | 10^8vp | AS buffer |
| Priming: Adeno/Boost: Adeno | | | | | | |
| 8 | M72-ChAd3 | 10^8vp | ChAd3 buffer | M72-ChAd3 | 10^8vp | ChAd3 buffer |
| 9 | M72-ChAd3 | 10^8vp | ChAd3 buffer | M72-ChAd63 | 10^8vp | ChAd63 buffer |
| 10 | M72-ChAd63 | 10^8vp | ChAd63 buffer | M72-ChAd3 | 10^8vp | ChAd3 buffer |
| Combo Priming and Boost; Adeno + Protein | | | | | | |
| 11 | M72/AS01E M72-ChAd3 Combo | 1ug 10^8vp | AS buffer | M72/AS01E M72-ChAd3 Combo | 1ug 10^8vp | AS buffer |
| 12 | M72/AS01E Co-Ad M72-ChAd3 | 1ug 10^8vp | AS buffer (adjuvanted protein) and ChAd3 buffer (adeno) | M72/AS01E Co-Ad M72-ChAd3 | 1ug 10^8vp | AS buffer (adjuvanted protein) and ChAd3 buffer (adeno) |
| 13 | M72/AS01E eGFPChAd3 Combo | 1ug 10^8vp | AS buffer | M72/AS01E eGFPChAd3 Combo | 1ug 10^8vp | AS buffer |

AS buffer: approx pH 8.0, 10mM $PO_4$, 5mM NaCl, 4.7% sorbitol

ChAd3 buffer: pH 7.4, 10mM TRIS, 10 mM histidine, 5% sucrose, 75 mM NaCl, 1 mM $MgCl_2$, 0.02% polysorbate 80, 0.1 mM EDTA, 0.5% (v/v) ethanol

ChAd63 buffer: pH 6.6, 10 mM histidine, 7.5% sucrose, 35 mM NaCl, 1 mM $MgCl_2$, 0.1% polysorbate 80, 0.1 mM EDTA, 0.5% (v/v) ethanol

| Fluid | Test | Time point of collection | Comment |
|---|---|---|---|
| Whole Blood | ICS | D14(14PI) | Evaluation of peripheral whole blood responses of TB antigen-specific CD4 and CD8 cells, as determined by the simultaneous measurement of IFNg, IL-2, TNF-a , after restimulation with overlapping 15-mer peptide pools |
| Whole Blood/ Lung | ICS | D42(14PII)* | Evaluation of peripheral whole blood and lung responses of TB antigen-specific CD4 and CD8 cells, as determined by the simultaneous measurement of IFNg, IL-2, TNF-a , IL-17 after restimulation with overlapping 15-mer peptide pools |
| Serum | Serology anti-M72 IgTot | D41(13PII)** | |

*Limitations of +/- 36 lung collection per day, therefore the study was performed in several replicates

**Due to practical constraints, serum samples were taken 1 day prior to whole blood

In order to have sufficient volume, the whole blood of 4 pools of 3 mice for groups was collected at days 14, and 42. At day 42, the same process was applied for lungs.

Due to limitations of collection per day, one pool of each group was treated per day- during 4 days in order to have 4 pools per groups. Individual sera were collected at day 41.

The mice were identified in order to do the link between PI and PII for the both read-outs ICS and serology.

*Cellular immune response-Intracellular cytokine staining (ICS)*

Leukocyte isolation from Whole Blood

At each time point, blood was collected from each mouse and subsequently pooled (4 pools of 3 mice). Blood was collected in tubes containing, RPMI/additives (RPMI 1640, supplemented with Glutamine, Penicillin/streptomycin, Sodium Pyruvate, non-essential amino-acids and 2-mercaptoethanol) containing heparin (1/10). Ten volumes of Lysing buffer were added to the whole blood and tubes were incubated at room temperature (RT) for 10 min. After centrifugation (335g, 10 min at RT), the pellet was harvested in RPMI/additives and filtered (Cell strainer 100µm). Cells were pelleted again (335g, 10 min at RT) and re-suspended in Complete Medium (RPMI 1640,

supplemented with Glutamine, Penicillin/streptomycin, Sodium Pyruvate, non-essential amino-acids and 2-mercaptoethanol, and 5% Heat inactivated Fetal Calf Serum).

Leukocyte isolation from Lung

Lung was collected in tubes containing, RPMI/additives (RPMI 1640, supplemented with Glutamine, Penicillin/streptomycin, Sodium Pyruvate, non-essential amino-acids and 2-mercaptoethanol). The sample was transferred in to a Petri dish and the specimen cut in to small pieces (approximately 5x5mm). The specimens were re-suspended in a gentleMACS C tube (violet) containing 10ml of pre-warmed complete medium containing Liberase (0.0625UI/ml = 50ul) + DNase (25ug = 25ul). The C tube was attached upside down into the sleeve of the gentle MACS Dissociator and the Program mouse-lung 02 (40sec) ran. At the end of the program, the C tube was detached and the C tube incubated for 30min at 37 °C in a shaking incubator. After the incubation the sample was transferred on to a cell strainer (100um) placed on a 50ml falcon tube. The cell strainer was rinsed twice with 5ml Complete Medium (RPMI 1640, supplemented with Glutamine, Penicillin/streptomycin, Sodium Pyruvate, non-essential amino-acids and 2-mercaptoethanol, and 5% Heat inactivated Fetal Calf Serum). Complete Medium was added until 45 ml. The cells were centrifuged (400g for 10min – 4 °C), aspirated the supernatant and then re-suspended cells in 10ml Complete Medium. This step of washing was repeated. After the second wash, the cells were re-suspended in 3ml Percoll P30. The Percoll P30 layer containing the cells was placed on top of the Percoll P40/P75 layers gradient. The cells were centrifuged for 20mins 754g at RT. The cells considered were at the interphase between P40 and P75 at the end of centrifugation (lower interphase). The P30 layer was aspirated and cells collected at interphase P40-P75. The cells were collected in 15ml tube and Complete Medium added to a final volume of 15ml. The cells were centrifuged (900g for 10min – 4 °C). The supernatant was aspirated and the cells washed with 15ml Complete Medium twice. The pellet was re-suspended with Complete Medium to a volume final of 250ul. The cells were counted with Macsquant method including viability with PI.

In vitro stimulation of fresh leukocytes

Leukocytes were plated in round bottom 96-well plates at approximately 1 million cells per well. Leukocytes were then stimulated for 6 hours (37 °C, 5% $CO_2$) with anti-CD28 (clone 37.51) and anti-CD49d (clone 9C10) at 1ug/ml, with or without 1ug/ml of peptides covering the M72 sequence. After a 2 hour- stimulation, BD GolgiPlug™ containing brefeldin A diluted in complete medium (final dilution 1/1000) was added for 4 additional hours. Plates were then transferred at 4 °C, overnight.

ICS IFNg, IL-2, TNF-a -at 14PI - WBLO

Cells were stained and analyzed using a 5-colour ICS assay.

Cells were transferred to V-bottom 96-well plates, centrifuged at 189g for 5 min at 4 °C after wash with 200ul Flow Buffer (PBS 1X, 1% FCS), re-suspended the cells in 50ul Flow Buffer

containing anti- CD16/32 (clone 2.4G2) diluted 1/50, for 10min at 4 °C. Then, 50 ul Flow Buffer containing anti-CD4-V450 (clone RM4-5, diluted 1/50) and anti-CD8-PerCp-Cy5.5 (clone 53-6.7, diluted 1/50) antibodies and Live&Dead PO (diluted 1/500) was added for 30 min at 4 °C. Cells were centrifuged (189g for 5 min at 4 °C) and washed with 200ul Flow Buffer.

Leukocytes were fixed and permeabilized by adding 200ul of Cytofix/Cytoperm solution (Becton Dickinson commercial buffer) for 20 min at 4 °C. Cells were centrifuged (189g for 5 min at 4 °C) and washed with 200ul Perm/Wash buffer (Becton Dickinson commercial buffer diluted 1:10 in distilled water). After an additional centrifugation step, cells were stained in 50ul Perm/Wash buffer with anti-IL2-FITC (clone JES6-5H4, diluted 1/400), anti- IFNg-APC (clone XMG1.2, diluted 1/200) and anti-TNFa-PE (clone MP6-XT22, diluted 1/700) antibodies, for 1 hour at 4 °C. Cells were washed twice with the Perm/Wash buffer re-suspended in 220ul PBS. Stained cells were analyzed by flow cytometry using a LSRII and the FlowJo software.

ICS IFNg, IL-2, TNF-a and IL-17 at 14PII – WBLO & Lung

The same protocol was used except for the step cytokine; Cells were stained in 50ul Perm/Wash buffer with anti-IL2-FITC (clone JES6-5H4, diluted 1/400), anti- IFNg-APC (clone XMG1.2, diluted 1/200) and anti-TNFa-PE (clone MP6-XT22, diluted 1/700), anti-IL17 BV786 (clone TC11-18H10, diluted 1/50) antibodies, for 1 hour at 4 °C.

*Humoral response- Anti-M72 Ig tot Serology by Elisa*

96-well Elisa plates were coated with the recombinant antigen M72 at 0.25ug/ml in PBS and incubated overnight at 4 °C. Sera from vaccinated mice at Post II were diluted at 1/5000 or 1/40000 for repeat, in PBS (0.2%)-BSA and then a 2 fold serial dilution is performed from well 1 to 12 and incubated. Serial dilutions of the standard and control material were used to calculate the anti-M72 antibody standard titres of tested sera and to ensure validity of the test. Plates were washed with PBS 0.1% tween20 buffer after each incubation step. A biotinylated goat antibody specific for mice Ig is then added and the antigen-antibody complex is revealed by incubation with a streptavidin-peroxidase complex and a peroxidase substrate ortho-phenylenediamine dihydrochlorid/$H_2O_2$. The Optical densities (O.D.) were recorded at 490-620 nm. The anti-M72 antibody titre of each individual mouse serum is determined from the standard curve of the ELISA using a regression model and expressed in ELISA unit (EU)/ml. Geometric Mean Titres (GMT) are then calculated for each group of mice.

**Results**

T cell responses

*A. M72-specific CD4 T & CD8 T cells responses*

To evaluate the application of non-replicative chimp adeno vectors expressing M72 in the context of a tuberculosis vaccine, both homologous (ChAd/ChAd) and heterologous (Prot/ChAd or

ChAd/Prot) prime-boost vaccination strategies were assessed as well as in combination with M72/AS01E4 given as admixed or in co-administration. The prime/boost and combo strategies were evaluated in a D0-D28 schedule. Whole blood was collected at 14PI and 14PII to assess the systemic induction of M72 specific CD4 and CD8 T cells.

Across all groups, a specific CD4 T cell response was observed in whole blood with the peak response being below 3% (Figures 5 and 6). The highest levels of M72 specific CD4 T cells in whole blood were seen with the heterologous (Prot/ChAd or ChAd/Prot) vaccine strategies (Figure 5). Priming the mice with M72-ChAd vectors and boosting with M72/AS01E induced higher level of M72 specific CD4 T cells than the opposite and in both cases the M72-ChAd3 was more potent than the M72-ChAd63 (Figure 5). Prime-boost vaccination with M72-ChAd vectors, either homologous (M72-ChAd3 / M72-ChAd3) +/- AS01E, or heterologous (M72-ChAd3/M72-ChAd63 or M72-ChAd63/M72-ChAd3), did not provide an added value in terms of the magnitude of the CD4 T cell response as compared to the M72/AS01E benchmark (Figure 6). Combining both M72-ChAd3 and M72/AS01E slightly induced higher level of M72 specific CD4 T cells as compared to the M72/AS01E benchmark, but lower than heterologous (Prot/ChAd or ChAd/Prot) prime-boost vaccination. Co-administration induced similar M72 specific CD4 T cells levels than the combinations suggesting that physical proximity is not required (Figure 6).

The level of M72 specific CD8 T cell was found to be highly increased in mice receiving a M72-ChAd vector either as a prime, boost or both. When the M72-ChAd vector was included during the priming, the level of M72 specific CD8 T cell did not further increase after boosting except when mice where primed with M72-ChAd63 and boosted with M72-ChAd3 (Figures 7 and 8). This also suggests that the M72-ChAd3 is more potent than M72-ChAd63. Boosting the M72/AS01E priming with M72-ChAd3 induced higher levels of CD8 T cells (Median=30%) than with M72-ChAd63 (Median = 17%). The addition of M72-ChAd3 to the adjuvanted M72 protein in a combo also highly increased the level of M72 specific CD8 T cells (Median = 13%) as compared to the current benchmark (Median=0.2%).

The same general pattern of response was observed in the lung (Figure 9) as compared to the whole blood (Figures 5 and 6) except for the admixed combination vaccine strategy. In the lungs, combination strategy induced a lower level of response than whole blood, whereby a comparable level of M72 specific CD4 T cells could be observed with the combination vaccine and with heterologous (Prot/ChAd or ChAd/Prot) prime-boost vaccination, all of which showed an increased CD4 T cell level as compared to the current benchmark.

The general pattern of the M72 specific CD8 T cell response in the lungs (Figure 10) also reflected what was observed in the whole blood (Figures 7 and 8). Very low levels of specific CD8 T cell response was observed when mice received the benchmark M72/AS01E (Figure 10) and addition of M72-ChAd vector highly improved the level of CD8 T cells. The highest level of M72 specific CD8 T cell was seen when mice where primed with M72/AS01E and boosted with M72-ChAd3 (Median=36%-Figure 10).

*B. Cytokine profile of the M72-specific CD4 & CD8 T cells responses*

In groups that were primed with M72/AS01E, the M72-specific CD4+T cell response mostly included double (IL-2/TNFa) secreting cells in the whole blood at 14PI (Figures 11 and 12). In contrast, priming with a M72-ChAd vector induced a polyfunctional M72 specific CD4 T cell response with a majority of triple positive (IL2/IFNg/TNFa), and to a lower extend, double (IFNg/TNFa) and single (IFNg only) producing CD4 T cells (Figures 11 and 12). Combining both the protein and the ChAd vector induced low levels of triple (IL2/IFNg/TNFa), and double (IFNg/TNFa) producing CD4 T cells (Figures 11 and 12).

A similar CD4+ T cell cytokine expression profiles was observed at 14PII in whole blood (Figures 13 and 14) and in the lungs (Figures 15 and 16) across all groups where vaccination strategy included a M72-ChAd vector. The M72-specific CD4+T cell response included predominantly triple (IL2/IFNg/TNFa) and double (IFNg/TNFa) positive cells. In comparison to the benchmark, a reduced level of IL2/TNFa and increased level of IFNg/TNFa secreting cells were observed in the presence of a M72-ChAd vector. The IL-17 secretion was also assessed at 14dPII both in whole blood and in the lungs. However, the detected levels were extremely low across all conditions.

Similar M72-specific CD8 T cell cytokine profiles were observed across all positive groups in whole blood at 14PI (Figures 17 and 18), at 14PII (Figures 19 and 20) as well as in the lungs at 14PII (Figures 21 and 22). The M72-specific CD8 T cell responses were mostly composed of double (IFNg/TNFa) and single (IFNg only) producing CD8 T cells. Low levels of IL2/INFg/TNFa and very low levels of TNFa producing CD8+T cell were also detected.

Taken together, the vaccination strategy did not notably impact the cytokine profile of M72 specific CD8 T cell.

<u>Antibody responses</u>

*A. Anti-M72 Ig tot serology*

As shown in Figure 23, the anti-M72 Ig Tot serology was highly variable across all groups and non-responders were observed with all vaccination strategies except in the combined approach given in co-administration. As for the T cell response, the M72-ChAd3 seems more potent than the M72-ChAd63 at inducing an immune response as the number of non-responding animals is increased when M72-ChAd63 is used.

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.

All documents referred to herein, including patents and patent applications, are incorporated by reference in their entirety.

5

CLAIMS

1. A method for inducing an immune response in a subject comprising:
(i) administration of a polypeptide Rv1196 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv1196 related antigen; or
(ii) administration of a polypeptide Rv0125 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv0125 related antigen.

2. A method for inducing an immune response in a subject comprising:
(i) administration of a non-human simian adenovirus encoding a Rv1196 related antigen, followed by administration of a polypeptide Rv1196 related antigen to the subject; or
(ii) administration of a non-human simian adenovirus encoding a Rv0125 related antigen, followed by administration of a polypeptide Rv0125 related antigen to the subject.

3. The method according to claim 1 or 2 comprising:
(i) administration of a polypeptide Rv1196 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv1196 related antigen; or
(ii) administration of a non-human simian adenovirus encoding a Rv1196 related antigen, followed by administration of a polypeptide Rv1196 related antigen to the subject.

4. The method according to claim 1 or 2 comprising:
(i) administration of a polypeptide Rv0125 related antigen to the subject, followed by administration of a non-human simian adenovirus encoding a Rv0125 related antigen; or
(ii) administration of a non-human simian adenovirus encoding a Rv0125 related antigen, followed by administration of a polypeptide Rv0125 related antigen to the subject.

5. A polypeptide Rv1196 related antigen, for use in inducing an immune response in a subject wherein:
(i) the polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv1196 related antigen; or
(ii) a non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of the polypeptide Rv1196 related antigen.

6. A non-human simian adenovirus encoding a Rv1196 related antigen, for use in inducing an immune response in a subject wherein:
(i) a polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv1196 related antigen; or
(ii) the non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of a polypeptide Rv1196 related antigen.

7. Use of a polypeptide Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv1196 related antigen.

8. Use of a non-human simian adenovirus encoding a Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a polypeptide Rv1196 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv1196 related antigen.

9. Use of a polypeptide Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of the polypeptide Rv1196 related antigen.

10. Use of a non-human simian adenovirus encoding a Rv1196 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the non-human simian adenovirus encoding a Rv1196 related antigen is administered to the subject, followed by the administration of a polypeptide Rv1196 related antigen.

11. A polypeptide Rv0125 related antigen, for use in inducing an immune response in a subject wherein:
(i) the polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv0125 related antigen; or
(ii) a non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of the polypeptide Rv0125 related antigen.

12. A non-human simian adenovirus encoding a Rv0125 related antigen, for use in inducing an immune response in a subject wherein:
(i) a polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv0125 related antigen; or
(ii) the non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of a polypeptide Rv0125 related antigen.

13. Use of a polypeptide Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of a non-human simian adenovirus encoding a Rv0125 related antigen.

14. Use of a non-human simian adenovirus encoding a Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a polypeptide Rv0125 related antigen is administered to the subject, followed by the administration of the non-human simian adenovirus encoding a Rv0125 related antigen.

15. Use of a polypeptide Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein a non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of the polypeptide Rv0125 related antigen.

16. Use of a non-human simian adenovirus encoding a Rv0125 related antigen, in the manufacture of a medicament for inducing an immune response in a subject wherein the non-human simian adenovirus encoding a Rv0125 related antigen is administered to the subject, followed by the administration of a polypeptide Rv0125 related antigen.

17. The method, use, polypeptide or adenovirus of any of claims 1 to 3 or 5 to 10 wherein the polypeptide Rv1196 related antigen comprises a sequence having at least 90% identity to SEQ ID No: 1.

18. The method, use, polypeptide or adenovirus of any of claims 1 to 3 or 5 to 10 wherein the polypeptide Rv1196 related antigen comprises a fragment of SEQ ID No: 1 which is at least 200 amino acids in length.

19. The method, use, polypeptide or adenovirus of any of claims 1 to 3 or 5 to 10, 17 or 18 wherein the encoded Rv1196 related antigen comprises a sequence having at least 90% identity to SEQ ID No: 1.

20. The method, use, polypeptide or adenovirus of any of claims 1 to 3 or 5 to 10, 17 or 18 wherein the encoded Rv1196 related antigen comprises a fragment of SEQ ID No: 1 which is at least 200 amino acids in length.

21. The method, use, polypeptide or adenovirus of any of claims 1, 2, 4 or 11 to 16 wherein the polypeptide Rv0125 related antigen comprises a sequence having at least 90% identity to SEQ ID No: 3.

22. The method, use, polypeptide or adenovirus of any of claims 1, 2, 4 or 11 to 16 wherein the polypeptide Rv0125 related antigen comprises a fragment of SEQ ID No: 3 which is at least 150 amino acids in length.

23. The method, use, polypeptide or adenovirus of any of claims 1, 2, 4 or 11 to 16, 21 or 22 wherein the encoded Rv0125 related antigen comprises a sequence having at least 90% identity to SEQ ID No: 3.

24. The method, use, polypeptide or adenovirus of any of claims 1 to 3 or 5 to 10, 21 or 22 wherein the encoded Rv0125 related antigen comprises a fragment of SEQ ID No: 3 which is at least 150 amino acids in length.

25. The method, use, polypeptide or adenovirus of any of claims 1 to 24 wherein the polypeptide antigen contains 1500 amino acid residues or fewer.

26. The method, use, polypeptide or adenovirus of any of claims 1 to 25 wherein the encoded antigen contains 1500 amino acid residues or fewer.

27. The method, use, polypeptide or adenovirus of any of claims 1 to 26 wherein a polypeptide antigen comprising an Rv1196 related antigen and a polypeptide antigen comprising an Rv0125 related antigen are provided.

28. The method, use, polypeptide or adenovirus of any of claims 1 to 27 wherein an adenovirus encoding an Rv1196 related antigen and an adenovirus encoding an Rv0125 related antigen are provided.

29. The method, use, polypeptide or adenovirus of any of claims 1 to 27 wherein the adenovirus encodes an Rv1196 related antigen and an Rv0125 related antigen.

30. The method, use, polypeptide or adenovirus of any of claims 1 to 29 wherein the polypeptide antigen comprises a sequence having at least 90% identity to SEQ ID No. 6.

31. The method, use, polypeptide or adenovirus of any of claims 1 to 29 wherein the polypeptide antigen comprises a fragment of SEQ ID No: 6 which is at least 450 amino acids in length, such as amino acids 2-723 of SEQ ID No. 6.

32. The method, use, polypeptide or adenovirus of any of claims 1 to 30 wherein the encoded antigen comprises a sequence having at least 90% identity to SEQ ID No. 6.

33. The method, use, polypeptide or adenovirus of any of claims 1 to 30 wherein the encoded antigen comprises a fragment of SEQ ID No: 6 which is at least 450 amino acids in length, such as amino acids 2-723 of SEQ ID No. 6.

34. The method, use, polypeptide or adenovirus of any one of claims 1 to 33, wherein the subject is a human.

35. The method, use, polypeptide or adenovirus of any one of claims 1 to 34, wherein the polypeptide and the adenovirus are administered intramuscularly.

36. The method, use, polypeptide or adenovirus of any one of claims 1 to 35, wherein the polypeptide and the adenovirus are administered in a dose range of 400-600ul inclusive.

37. The method, use, polypeptide or adenovirus of any one of claims 1 to 36, wherein the dose range of the polypeptide is 1 to 100 ug inclusive.

38. The method, use, polypeptide or adenovirus of any one of claims 1 to 37, wherein the dose range of the adenovirus is $1x10^5$ to $1x10^{15}$ viral particles inclusive.

39. The method, use, polypeptide or adenovirus of any of claims 1 to 38 wherein the polypeptide antigen is provided in a composition which also comprises an adjuvant.

40. The method, use, polypeptide or adenovirus of claim 39, wherein the adjuvant comprises a TLR agonist and/or an immunologically active saponin.

41. The method, use, polypeptide or adenovirus of claim 40, wherein the adjuvant comprises 3D-MPL.

42. The method, use, polypeptide or adenovirus of either claim 40 or 41, wherein the adjuvant comprises QS21.

43. The method, use, polypeptide or adenovirus of claim 42, wherein the adjuvant comprises 3D-MPL and QS21 in a liposomal formulation.

44. The method, use, polypeptide or adenovirus of either claim 42 or 43, wherein the polypeptide antigen is provided in a composition which comprises between 12.5 and 75 micrograms of 3D-MPL inclusive and between 12.5 and 75 micrograms of QS21 inclusive.

45. The method, use, polypeptide or adenovirus of any of claims 1 to 44 wherein the time interval between administrations is in the range from one week to three months inclusive.

46. The method, use, polypeptide or adenovirus of any of claims 1 to 45, for the prophylaxis, treatment or amelioration of infection by mycobacteria, such as *Mycobacterium tuberculosis*.

47. The method, use, polypeptide or adenovirus of claim 46, for the prophylaxis of infection by mycobacteria, such as *Mycobacterium tuberculosis*.

48. The method, use, polypeptide or adenovirus of claim 46, for the treatment of infection by mycobacteria, such as *Mycobacterium tuberculosis*.

49. The method, use, polypeptide or adenovirus of any of claims 1 to 47, wherein the subject is not infected.

50. The method, use, polypeptide or adenovirus of any of claims 1 to 46 or 48, wherein the subject has a latent infection.

51. The method, use, polypeptide or adenovirus of any of claims 1 to 46 or 48, wherein the subject has an active infection.

52. The method, use, polypeptide or adenovirus of any one of claims 1 to 49, wherein the subject has previously been vaccinated with BCG.

53. The method, use, polypeptide or adenovirus of any one of claims 1 to 49, wherein the immune response comprises CD4 T cells expressing IFN-gamma, TNF-alpha and IL-2.

54. The method, use, polypeptide or adenovirus of any one of claims 1 to 53, wherein the adenovirus is a chimpanzee adenovirus.

55. The method, use, polypeptide or adenovirus of claim 54, wherein the adenovirus is replication defective.

56. The method, use, polypeptide or adenovirus of either claim 54 or 55, wherein the adenovirus is a ChAd3.

57. The method, use, polypeptide or adenovirus of either claim 54 or 55, wherein the adenovirus is a ChAd63.

58. The method, use, polypeptide or adenovirus of any one of claims 54 to 57, wherein the adenovirus comprises functional inactivation (such as deletion) of at least the E1 and E4 genes, optionally with E3 functional inactivation (such as deletion), in conjunction with Ad5E4orf6 gene substitution.

59. The method, use, polypeptide or adenovirus of any one of claims 1 to 58 wherein the polypeptide Rv1196 related antigen is provided in a composition which is substantially free of a non-human simian adenovirus encoding a Rv1196 related antigen, such as substantially free of a non-human simian adenovirus encoding a mycobacterial antigen, in particular substantially free of any non-human simian adenovirus, especially substantially free of any adenovirus encoding a mycobacterial antigen (such as substantially free of any adenovirus).

60. The method, use, polypeptide or adenovirus of any one of claims 1 to 58 wherein the polypeptide Rv0125 related antigen is provided in a composition which is substantially free of non-human simian adenovirus encoding a Rv0125 related antigen, such as

substantially free of a non-human simian adenovirus encoding a mycobacterial antigen, in particular substantially free of any non-human simian adenovirus, especially substantially free of any adenovirus encoding a mycobacterial antigen (such as substantially free of any adenovirus).

61. The method, use, polypeptide or adenovirus of any one of claims 1 to 58 wherein the polypeptide Rv1196 related antigen is provided in a composition which does not comprise a non-human simian adenovirus encoding a Rv1196 related antigen, such as it does not comprise a non-human simian adenovirus encoding a mycobacterial antigen, in particular it does not comprise any non-human simian adenovirus, especially it does not comprise any adenovirus encoding a mycobacterial antigen (such as it does not comprise any adenovirus).

62. The method, use, polypeptide or adenovirus of any one of claims 1 to 58 wherein the polypeptide Rv0125 related antigen is provided in a composition which does not comprise a non-human simian adenovirus encoding a Rv0125 related antigen, such as it does not comprise a non-human simian adenovirus encoding a mycobacterial antigen, in particular it does not comprise any non-human simian adenovirus, especially it does not comprise any adenovirus encoding a mycobacterial antigen (such as it does not comprise any adenovirus).

63. The method, use, polypeptide or adenovirus of any one of claims 1 to 62 wherein the non-human simian adenovirus encoding a Rv1196 related antigen is provided in a composition which is substantially free of a polypeptide Rv1196 related antigen, such as substantially free of a polypeptide mycobacterial antigen, in particular substantially free of any other antigens.

64. The method, use, polypeptide or adenovirus of any one of claims 1 to 62 wherein the non-human simian adenovirus encoding a Rv0125 related antigen is provided in a composition which is substantially free of a polypeptide Rv0125 related antigen, such as substantially free of a polypeptide mycobacterial antigen, in particular substantially free of any other antigens.

65. The method, use, polypeptide or adenovirus of any one of claims 1 to 62 wherein the non-human simian adenovirus encoding a Rv1196 related antigen is provided in a composition which does not comprise a polypeptide Rv1196 related antigen, such as it

does not comprise a polypeptide mycobacterial antigen, in particular it does not comprise any other antigens.

66. The method, use, polypeptide or adenovirus of any one of claims 1 to 62 wherein the non-human simian adenovirus encoding a Rv0125 related antigen is provided in a composition which does not comprise a polypeptide Rv0125 related antigen, such as it does not comprise a polypeptide mycobacterial antigen, in particular it does not comprise any other antigens.

67. The method, use, polypeptide or adenovirus of any one of claims 1 to 66 wherein the polypeptide Rv1196 related antigen is not administered within a period of one day (such as two, three or six days) of a non-human simian adenovirus encoding a Rv1196 related antigen, such a non-human simian adenovirus encoding a Rv1196 related antigen, for example, a non-human simian adenovirus encoding a mycobacterial antigen (such as any non-human simian adenovirus) in particular any adenovirus encoding a mycobacterial antigen (such as any adenovirus).

68. The method, use, polypeptide or adenovirus of any one of claims 1 to 66 wherein the polypeptide Rv0125 related antigen is not administered within a period of one day (such as two, three or six days) of a non-human simian adenovirus encoding a Rv0125 related antigen, such a non-human simian adenovirus encoding a Rv0125 related antigen, for example, a non-human simian adenovirus encoding a mycobacterial antigen (such as any non-human simian adenovirus) in particular any adenovirus encoding a mycobacterial antigen (such as any adenovirus).

69. The method, use, polypeptide or adenovirus of any one of claims 1 to 68 wherein the non-human simian adenovirus encoding a Rv1196 related antigen is not administered within a period of one day (such as two, three or six days) of a polypeptide Rv1196 related antigen, for example, any polypeptide mycobacterial antigen (such as any other antigens).

70. The method, use, polypeptide or adenovirus of any one of claims 1 to 68 wherein the non-human simian adenovirus encoding a Rv0125 related antigen is not administered within a period of one day (such as two, three or six days) of a polypeptide Rv0125 related antigen, for example, any polypeptide mycobacterial antigen (such as any other antigens).

71. A non-human simian adenovirus comprising a transgene encoding a Rv1196 or Rv0125 related antigen.

72. The non-human simian adenovirus according to claim 71, containing at least the penton of SEQ ID No: 10, the hexon of SEQ ID No: 11 or the fibre of SEQ ID No: 12.

73. The non-human simian adenovirus according to claim 72, comprising the penton (SEQ ID No: 10), hexon (SEQ ID No: 11) and fibre (SEQ ID No: 12) protein from ChAd3.

74. The non-human simian adenovirus according to claim 71, comprising at least the penton of SEQ ID No: 15, the hexon of SEQ ID No: 16 or the fibre of SEQ ID No: 17.

75. The non-human simian adenovirus according to claim 74, comprising a penton (SEQ ID No: 16), hexon (SEQ ID No: 17) and fibre (SEQ ID No: 18) protein from ChAd63.

76. The non-human simian adenovirus according to any one of claims 71 to 75 wherein the encoded antigen comprises a sequence having at least 90% identity to SEQ ID No. 6.

77. The non-human simian adenovirus according to any one of claims 71 to 76 wherein the encoded antigen comprises a fragment of SEQ ID No: 6 which is at least 450 amino acids in length, such as 2-723 of SEQ ID No. 6.

78. The non-human simian adenovirus according to any one of claims 71 to 77, which is a replication deficient adenovirus.

79. The non-human simian adenovirus according to any one of claims 71 to 78, wherein the adenovirus comprises functional inactivation (such as deletion) of the E1 gene.

80. The non-human simian adenovirus according to any one of claims 71 to 79, wherein the adenovirus comprises functional inactivation (such as deletion) of the E4 gene.

81. The non-human simian adenovirus according to any one of claims 71 to 80, wherein the adenovirus comprises functional inactivation (such as deletion) of the E3 gene.

82. The non-human simian adenovirus according to any one of claims 71 to 81, wherein the adenovirus comprises an Ad5E4orf6 gene substitution.

83. The non-human simian adenovirus according to claim 71, consisting of the sequence of SEQ ID No: 13.

84. The non-human simian adenovirus according to claim 71, consisting of the sequence of SEQ ID No: 18.

85. A polynucleotide comprising SEQ ID No: 8 or comprising a degenerate variant thereof having at least 95% identity to SEQ ID No: 8.

86. The polynucleotide of claim 85, comprising SEQ ID No: 8 or comprising a degenerate variant having at least 98% identity to SEQ ID No: 8.

87. The polynucleotide of claim 85, consisting of SEQ ID No: 8 or consisting of a degenerate variant having at least 95% identity to SEQ ID No: 8.

88. The polynucleotide of claim 85, consisting of SEQ ID No. 8 or consisting of a degenerate variant having at least 98% identity to SEQ ID No: 8.

89. The polynucleotide of claim 85, comprising SEQ ID No: 8.

90. The polynucleotide of claim 89, consisting of SEQ ID No: 8.

Figure **1**

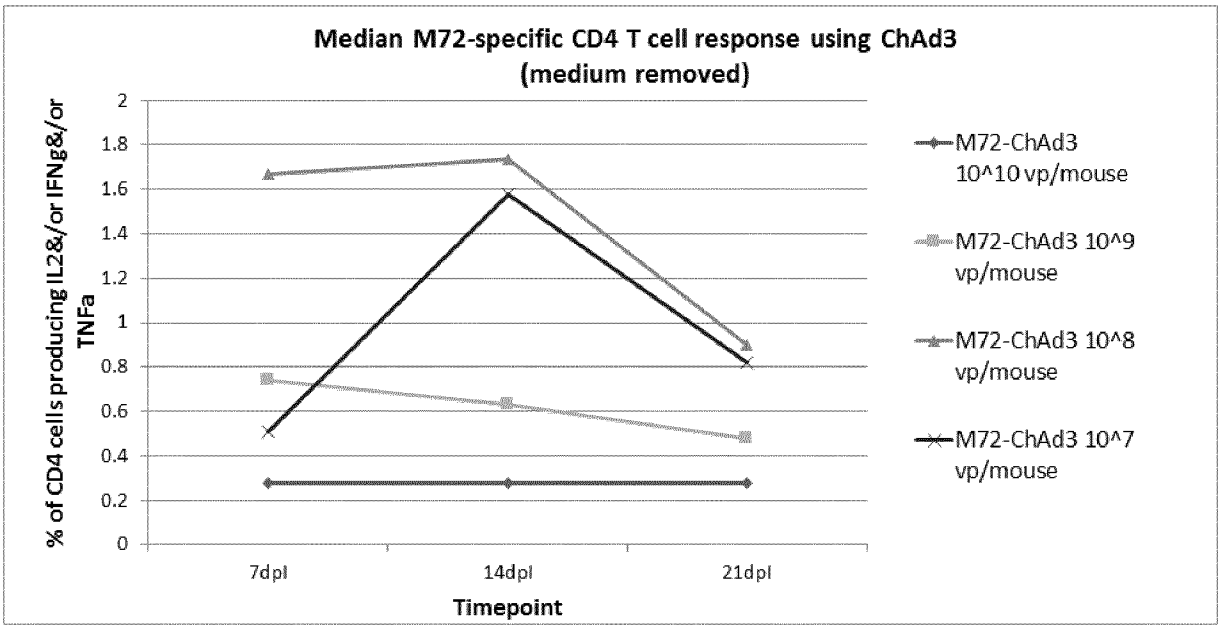


Figure **2**

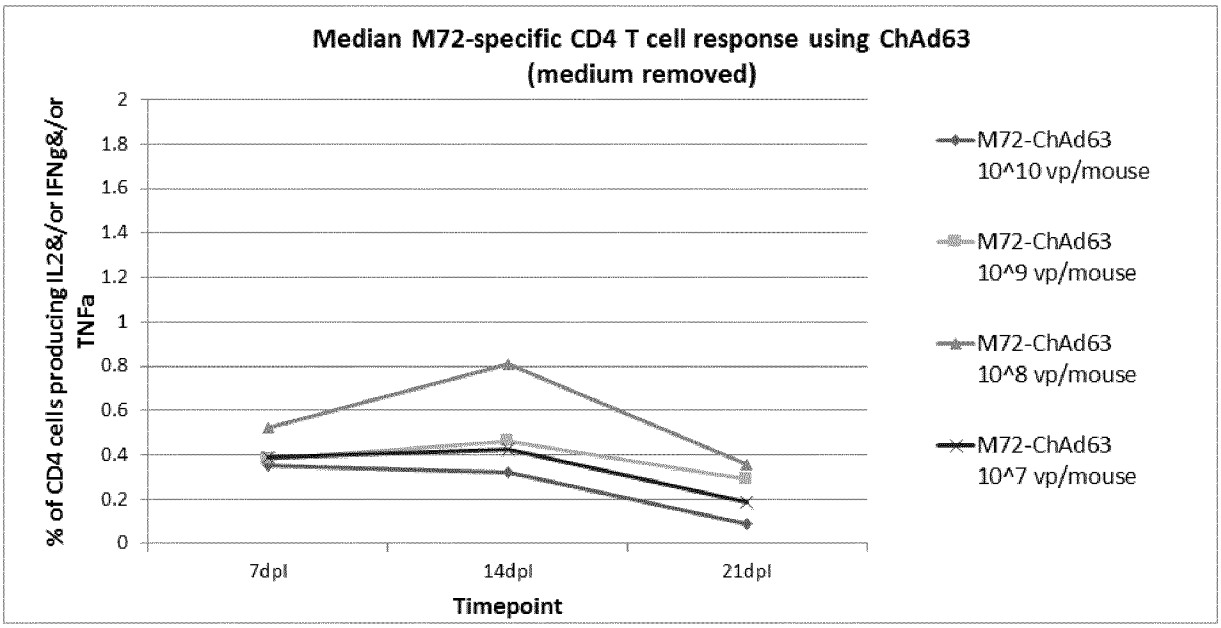

Figure **3**

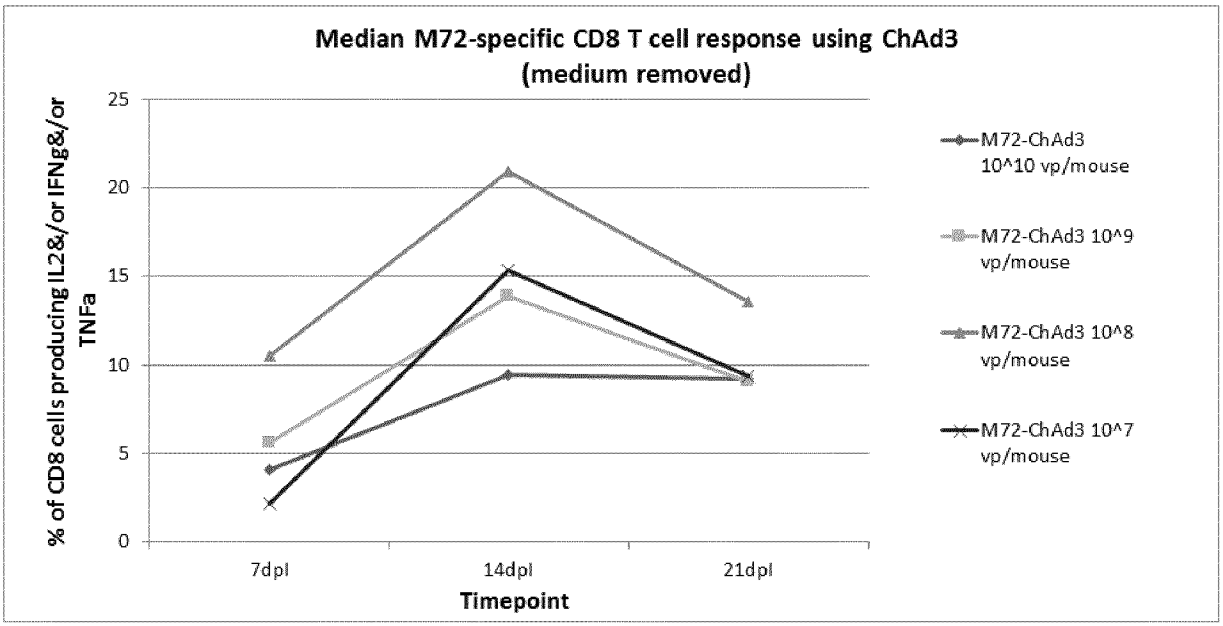


Figure **4**

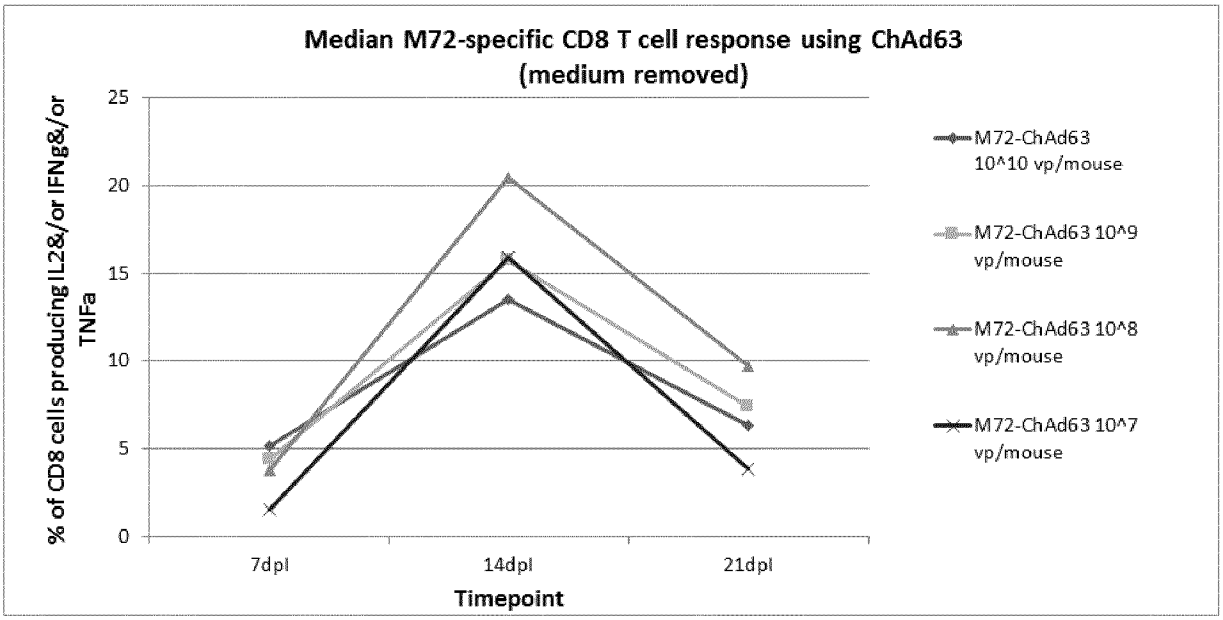

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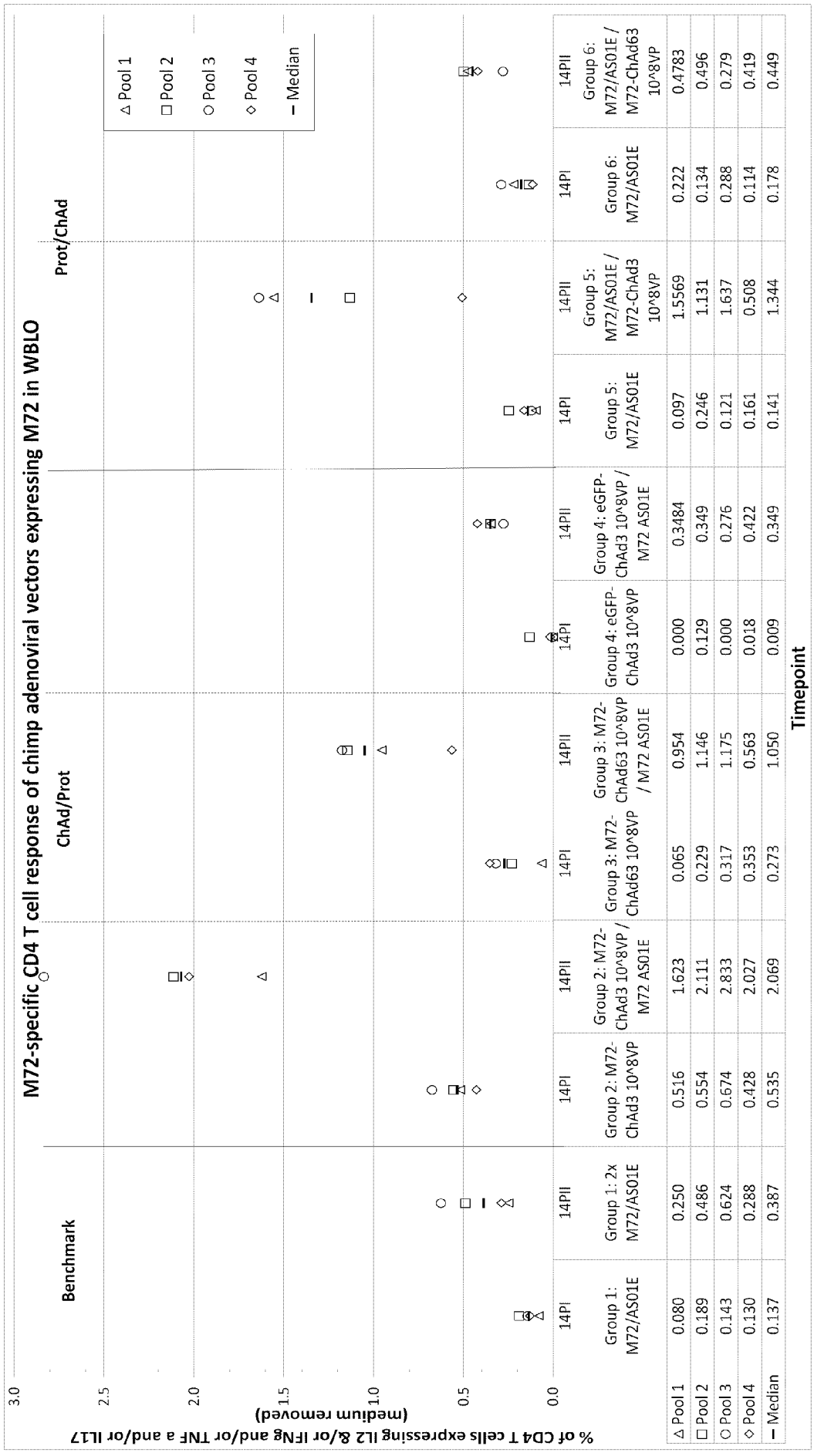
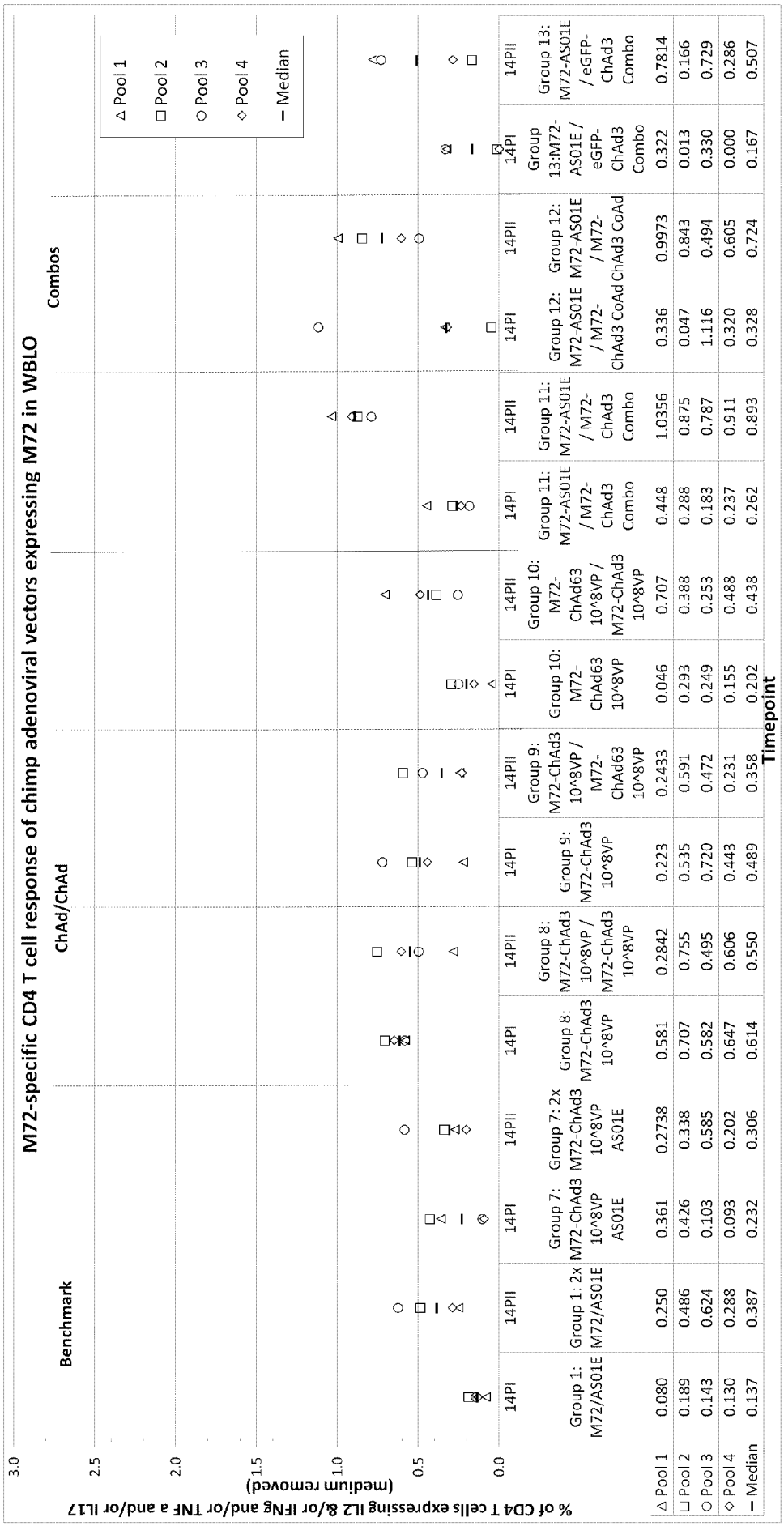
Figure 5



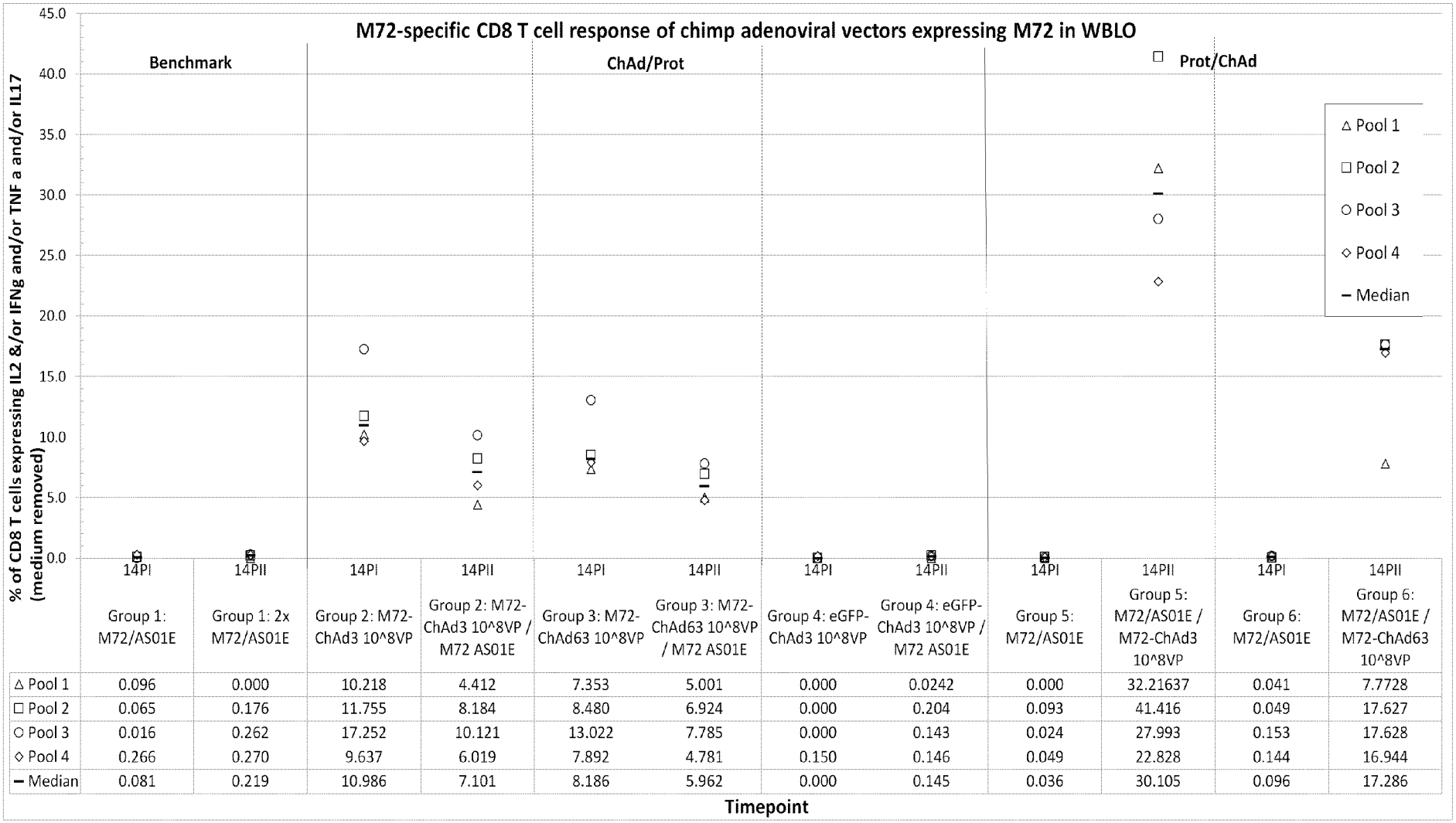

| | Group 1: M72/AS01E | | Group 1: 2x M72/AS01E | | Group 2: M72-ChAd3 10^8VP | Group 2: M72-ChAd3 10^8VP / M72 AS01E | Group 3: M72-ChAd63 10^8VP | Group 3: M72-ChAd63 10^8VP / M72 AS01E | Group 4: eGFP-ChAd3 10^8VP | Group 4: eGFP-ChAd3 10^8VP / M72 AS01E | Group 5: M72/AS01E | Group 5: M72/AS01E / M72-ChAd3 10^8VP | Group 6: M72/AS01E | Group 6: M72/AS01E / M72-ChAd63 10^8VP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 14PI | 14PII | 14PI | 14PII | 14PI | 14PII | 14PI | 14PII | 14PI | 14PII | 14PI | 14PII | 14PI | 14PII |
| △ Pool 1 | 0.080 | 0.250 | 0.516 | 1.623 | 0.065 | 0.954 | 0.000 | 0.3484 | 0.097 | 1.5569 | 0.222 | 0.4783 | | |
| □ Pool 2 | 0.189 | 0.486 | 0.554 | 2.111 | 0.229 | 1.146 | 0.129 | 0.349 | 0.246 | 1.131 | 0.134 | 0.496 | | |
| ○ Pool 3 | 0.143 | 0.624 | 0.674 | 2.833 | 0.317 | 1.175 | 0.000 | 0.276 | 0.121 | 1.637 | 0.288 | 0.279 | | |
| ◇ Pool 4 | 0.130 | 0.288 | 0.428 | 2.027 | 0.353 | 0.563 | 0.018 | 0.422 | 0.161 | 0.508 | 0.114 | 0.419 | | |
| – Median | 0.137 | 0.387 | 0.535 | 2.069 | 0.273 | 1.050 | 0.009 | 0.349 | 0.141 | 1.344 | 0.178 | 0.449 | | |

Figure 6




| | Group 1: M72/AS01E 14PI | Group 1: 2x M72/AS01E 14PII | Group 7: M72-ChAd3 10^8VP AS01E 14PI | Group 7: 2x M72-ChAd3 10^8VP AS01E 14PII | Group 8: M72-ChAd3 10^8VP 14PI | Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP 14PII | Group 9: M72-ChAd3 10^8VP 14PI | Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP 14PII | Group 10: M72-ChAd63 10^8VP 14PI | Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP 14PII | Group 11: M72-AS01E / M72-ChAd3 Combo 14PI | Group 11: M72-AS01E / M72-ChAd3 Combo 14PII | Group 12: M72-AS01E / M72-ChAd3 CoAd 14PI | Group 12: M72-AS01E / M72-ChAd3 CoAd 14PII | Group 13:M72-AS01E / eGFP-ChAd3 Combo 14PI | Group 13: M72-AS01E / eGFP-ChAd3 Combo 14PII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| △ Pool 1 | 0.080 | 0.250 | 0.361 | 0.2738 | 0.581 | 0.2842 | 0.223 | 0.2433 | 0.046 | 0.707 | 0.448 | 1.0356 | 0.336 | 0.9973 | 0.322 | 0.7814 |
| □ Pool 2 | 0.189 | 0.486 | 0.426 | 0.338 | 0.707 | 0.755 | 0.535 | 0.591 | 0.293 | 0.388 | 0.288 | 0.875 | 0.047 | 0.843 | 0.013 | 0.166 |
| ○ Pool 3 | 0.143 | 0.624 | 0.103 | 0.585 | 0.582 | 0.495 | 0.720 | 0.472 | 0.249 | 0.253 | 0.183 | 0.787 | 1.116 | 0.494 | 0.330 | 0.729 |
| ◇ Pool 4 | 0.130 | 0.288 | 0.093 | 0.202 | 0.647 | 0.606 | 0.443 | 0.231 | 0.155 | 0.488 | 0.237 | 0.911 | 0.320 | 0.605 | 0.000 | 0.286 |
| – Median | 0.137 | 0.387 | 0.232 | 0.306 | 0.614 | 0.550 | 0.489 | 0.358 | 0.202 | 0.438 | 0.262 | 0.893 | 0.328 | 0.724 | 0.167 | 0.507 |

Figure 7




| | 14PI Group 1: M72/AS01E | 14PII Group 1: 2x M72/AS01E | 14PI Group 2: M72-ChAd3 10^8VP | 14PII Group 2: M72-ChAd3 10^8VP / M72 AS01E | 14PI Group 3: M72-ChAd63 10^8VP | 14PII Group 3: M72-ChAd63 10^8VP / M72 AS01E | 14PI Group 4: eGFP-ChAd3 10^8VP | 14PII Group 4: eGFP-ChAd3 10^8VP / M72 AS01E | 14PI Group 5: M72/AS01E | 14PII Group 5: M72/AS01E / M72-ChAd3 10^8VP | 14PI Group 6: M72/AS01E | 14PII Group 6: M72/AS01E / M72-ChAd63 10^8VP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| △ Pool 1 | 0.096 | 0.000 | 10.218 | 4.412 | 7.353 | 5.001 | 0.000 | 0.0242 | 0.000 | 32.21637 | 0.041 | 7.7728 |
| □ Pool 2 | 0.065 | 0.176 | 11.755 | 8.184 | 8.480 | 6.924 | 0.000 | 0.204 | 0.093 | 41.416 | 0.049 | 17.627 |
| ○ Pool 3 | 0.016 | 0.262 | 17.252 | 10.121 | 13.022 | 7.785 | 0.000 | 0.143 | 0.024 | 27.993 | 0.153 | 17.628 |
| ◇ Pool 4 | 0.266 | 0.270 | 9.637 | 6.019 | 7.892 | 4.781 | 0.150 | 0.146 | 0.049 | 22.828 | 0.144 | 16.944 |
| – Median | 0.081 | 0.219 | 10.986 | 7.101 | 8.186 | 5.962 | 0.000 | 0.145 | 0.036 | 30.105 | 0.096 | 17.286 |

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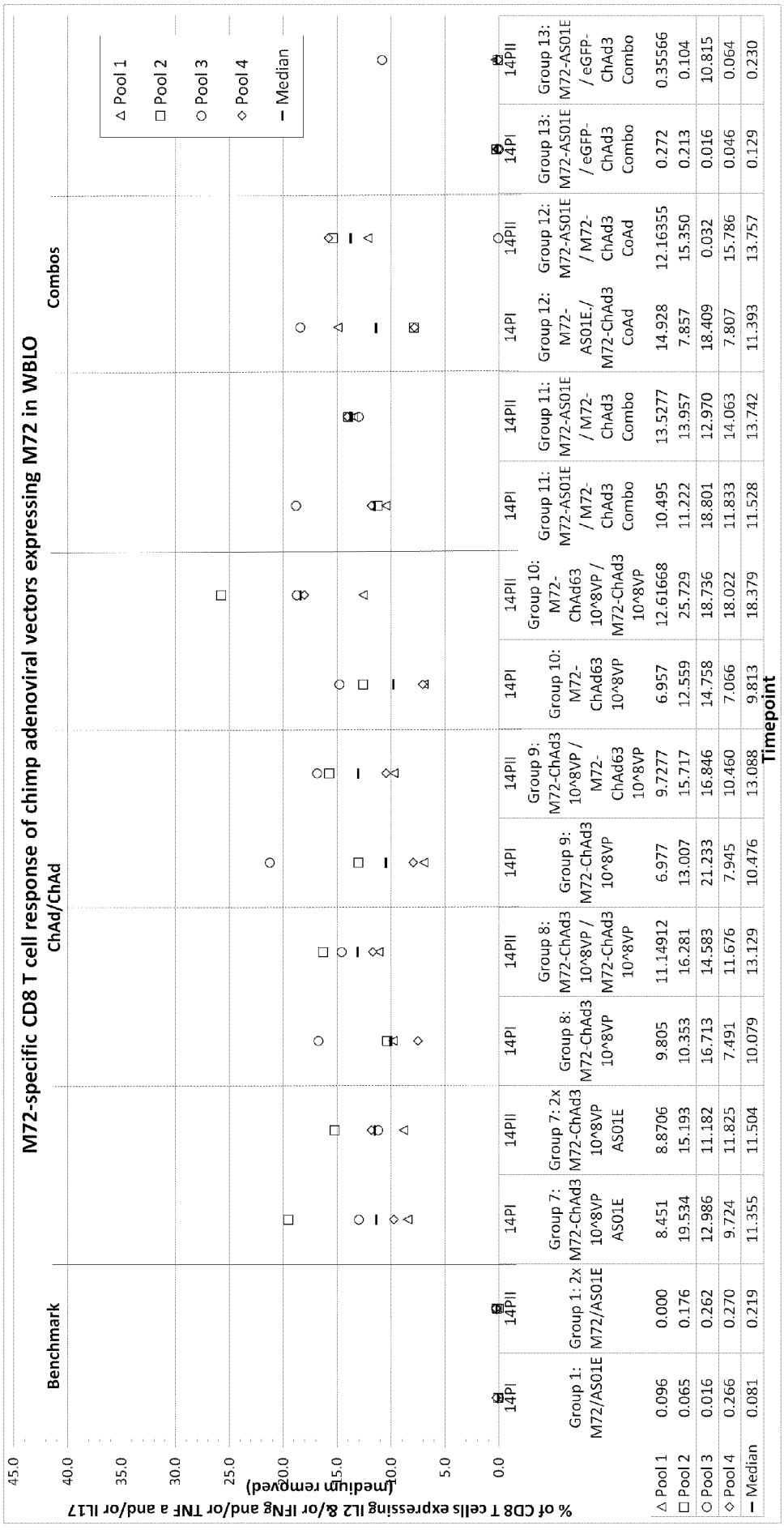
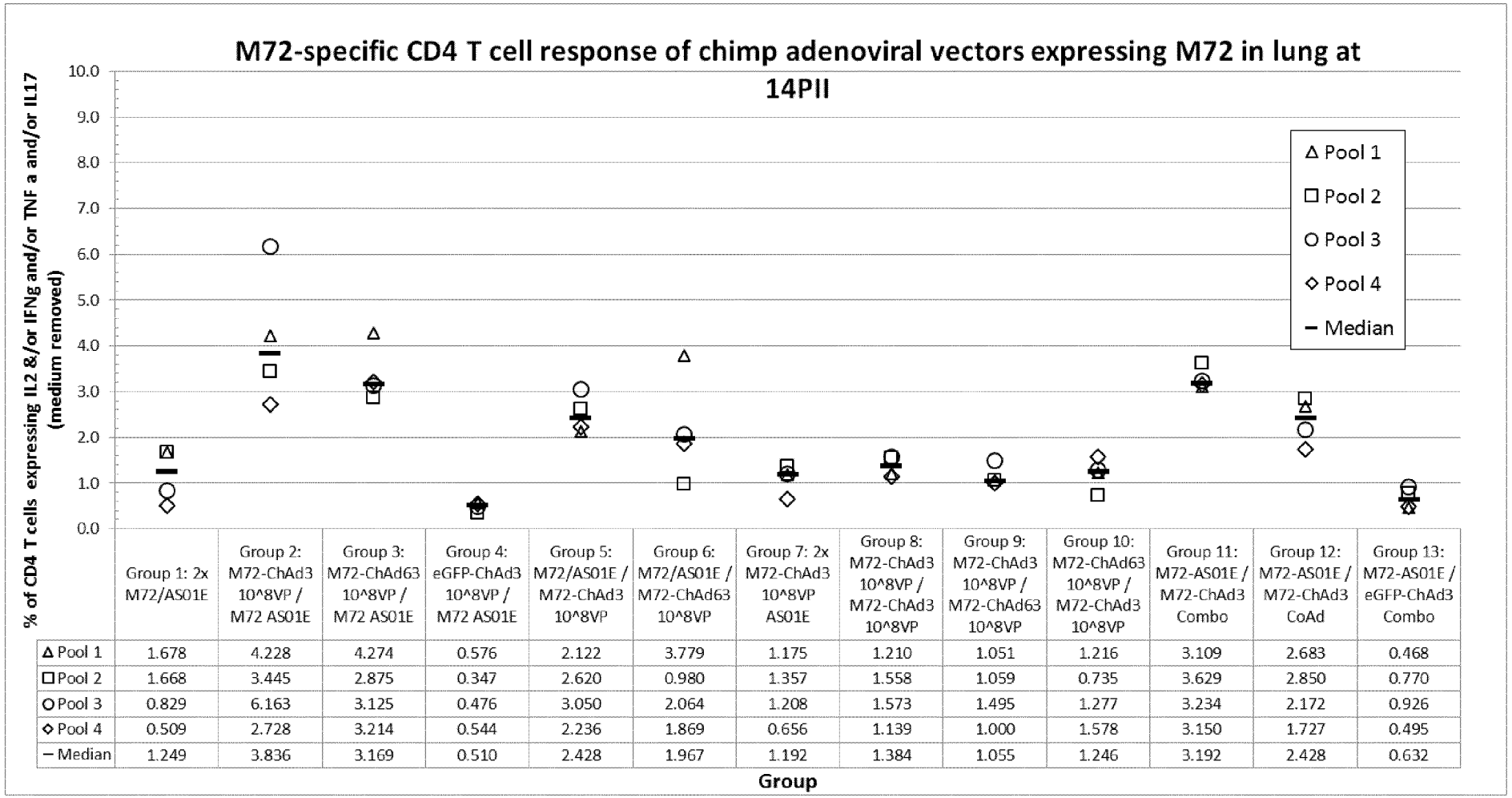
Figure 8




| | Group 1: M72/AS01E | 14PI | 14PII | Group 1: 2x M72/AS01E | 14PI | 14PII | Group 7: 2x M72-ChAd3 10^8VP AS01E | 14PI | 14PII | Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP | 14PI | 14PII | Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP | 14PI | 14PII | Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP | 14PI | 14PII | Group 11: M72-AS01E / M72-ChAd3 Combo | 14PI | 14PII | Group 12: M72-AS01E./ M72-ChAd3 CoAd | 14PI | 14PII | Group 12: M72-AS01E / M72-ChAd3 CoAd | 14PI | 14PII | Group 13: M72-AS01E / eGFP-ChAd3 Combo | 14PI | 14PII | Group 13: M72-AS01E / eGFP-ChAd3 Combo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| △ Pool 1 | 0.096 | 0.000 | | | 8.451 | | 8.8706 | 9.805 | | 11.14912 | 6.977 | | 9.7277 | 6.957 | | 12.61668 | 10.495 | | 13.5277 | 14.928 | | 12.16355 | 0.272 | | 0.35566 | | | | | | |
| □ Pool 2 | 0.065 | 0.176 | | | 19.534 | | 15.193 | 10.353 | | 16.281 | 13.007 | | 15.717 | 12.559 | | 25.729 | 11.222 | | 13.957 | 7.857 | | 15.350 | 0.213 | | 0.104 | | | | | | |
| ○ Pool 3 | 0.016 | 0.262 | | | 12.986 | | 11.182 | 16.713 | | 14.583 | 21.233 | | 16.846 | 14.758 | | 18.736 | 18.801 | | 12.970 | 18.409 | | 0.032 | 0.016 | | 10.815 | | | | | | |
| ◇ Pool 4 | 0.266 | 0.270 | | | 9.724 | | 11.825 | 7.491 | | 11.676 | 7.945 | | 10.460 | 7.066 | | 18.022 | 11.833 | | 14.063 | 7.807 | | 15.786 | 0.046 | | 0.064 | | | | | | |
| – Median | 0.081 | 0.219 | | | 11.355 | | 11.504 | 10.079 | | 13.129 | 10.476 | | 13.088 | 9.813 | | 18.379 | 11.528 | | 13.742 | 11.393 | | 13.757 | 0.129 | | 0.230 | | | | | | |

Figure **9**




| | Group 1: 2x M72/AS01E | Group 2: M72-ChAd3 10^8VP / M72 AS01E | Group 3: M72-ChAd63 10^8VP / M72 AS01E | Group 4: eGFP-ChAd3 10^8VP / M72 AS01E | Group 5: M72/AS01E / M72-ChAd3 10^8VP | Group 6: M72/AS01E / M72-ChAd63 10^8VP | Group 7: 2x M72-ChAd3 10^8VP AS01E | Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP | Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP | Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP | Group 11: M72-AS01E / M72-ChAd3 Combo | Group 12: M72-AS01E / M72-ChAd3 CoAd | Group 13: M72-AS01E / eGFP-ChAd3 Combo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| △ Pool 1 | 1.678 | 4.228 | 4.274 | 0.576 | 2.122 | 3.779 | 1.175 | 1.210 | 1.051 | 1.216 | 3.109 | 2.683 | 0.468 |
| □ Pool 2 | 1.668 | 3.445 | 2.875 | 0.347 | 2.620 | 0.980 | 1.357 | 1.558 | 1.059 | 0.735 | 3.629 | 2.850 | 0.770 |
| ○ Pool 3 | 0.829 | 6.163 | 3.125 | 0.476 | 3.050 | 2.064 | 1.208 | 1.573 | 1.495 | 1.277 | 3.234 | 2.172 | 0.926 |
| ◇ Pool 4 | 0.509 | 2.728 | 3.214 | 0.544 | 2.236 | 1.869 | 0.656 | 1.139 | 1.000 | 1.578 | 3.150 | 1.727 | 0.495 |
| – Median | 1.249 | 3.836 | 3.169 | 0.510 | 2.428 | 1.967 | 1.192 | 1.384 | 1.055 | 1.246 | 3.192 | 2.428 | 0.632 |

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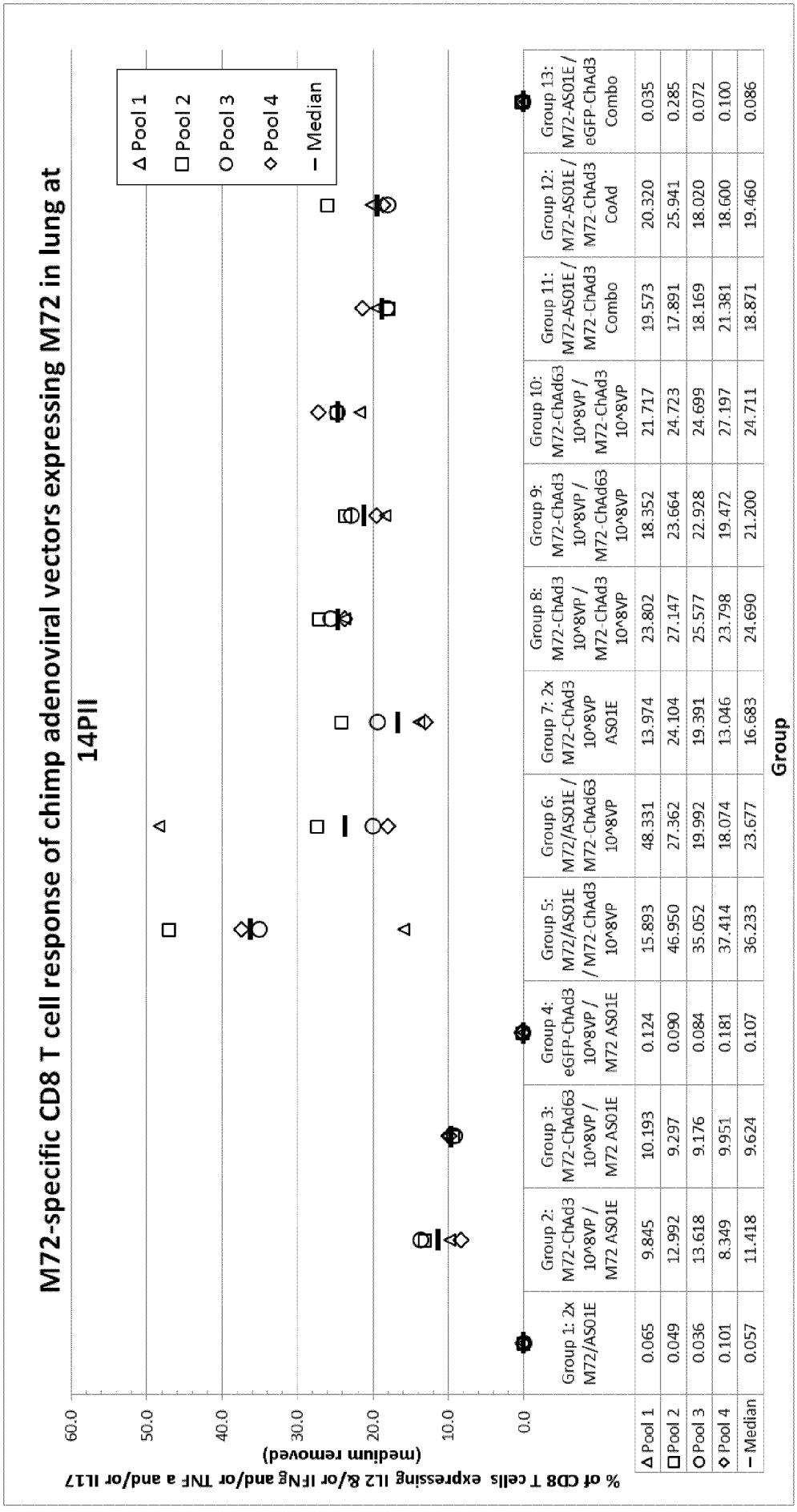
Figure 10




| | Group 1: 2x M72/AS01E | Group 2: M72-ChAd3 10^8VP / M72 AS01E | Group 3: M72-ChAd63 10^8VP / M72 AS01E | Group 4: eGFP-ChAd3 10^8VP / M72 AS01E | Group 5: M72/AS01E / M72-ChAd3 10^8VP | Group 6: M72/AS01E / M72-ChAd63 10^8VP | Group 7: 2x M72-ChAd3 10^8VP AS01E | Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP | Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP | Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP | Group 11: M72-AS01E / M72-ChAd3 Combo | Group 12: M72-AS01E / M72-ChAd3 CoAd | Group 13: M72-AS01E / eGFP-ChAd3 Combo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Δ Pool 1 | 0.065 | 9.845 | 10.193 | 0.124 | 15.893 | 48.331 | 13.974 | 23.802 | 18.352 | 21.717 | 19.573 | 20.320 | 0.035 |
| □ Pool 2 | 0.049 | 12.992 | 9.297 | 0.090 | 46.950 | 27.362 | 24.104 | 27.147 | 23.664 | 24.723 | 17.891 | 25.941 | 0.285 |
| ○ Pool 3 | 0.036 | 13.618 | 9.176 | 0.084 | 35.052 | 19.992 | 19.391 | 25.577 | 22.928 | 24.699 | 18.169 | 18.020 | 0.072 |
| ◇ Pool 4 | 0.101 | 8.349 | 9.951 | 0.181 | 37.414 | 18.074 | 13.046 | 23.798 | 19.472 | 27.197 | 21.381 | 18.600 | 0.100 |
| – Median | 0.057 | 11.418 | 9.624 | 0.107 | 36.233 | 23.677 | 16.683 | 24.690 | 21.200 | 24.711 | 18.871 | 19.460 | 0.086 |

Figure 11

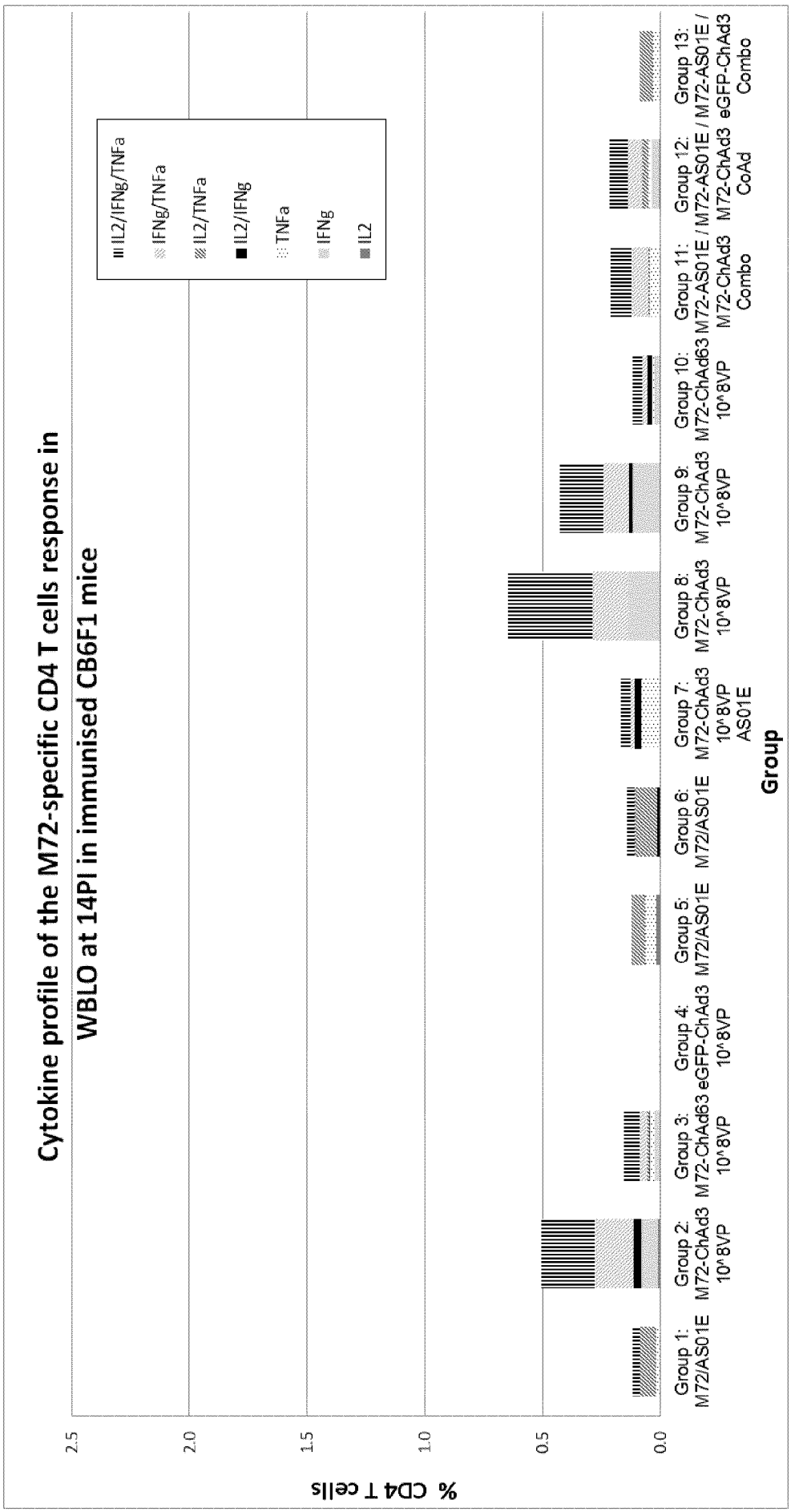

Cytokine profile of the M72-specific CD4 T cells response in WBLO at 14PI in immunised CB6F1 mice
IL2/IFNg/TNFa
IFNg/TNFa
IL2/TNFa
IL2/IFNg
TNFa
IFNg
IL2
% CD4 T cells
2.5
2.0
1.5
1.0
0.5
0.0
Group 1: M72/AS01E
Group 2: M72-ChAd3 10^8VP
Group 3: M72-ChAd63 10^8VP
Group 4: eGFP-ChAd3 10^8VP
Group 5: M72/AS01E
Group 6: M72/AS01E
Group 7: M72-ChAd3 10^8VP AS01E
Group 8: M72-ChAd3 10^8VP
Group 9: M72-ChAd3 10^8VP
Group 10: M72-ChAd63 10^8VP
Group 11: M72-AS01E / M72-ChAd3 Combo
Group 12: M72-AS01E / M72-ChAd3 CoAd
Group 13: M72-AS01E / eGFP-ChAd3 Combo
Group

Figure **12**

| | % CD4 T cells expressing cytokines (WBLO at 14PI) | | | | | | |
|---|---|---|---|---|---|---|---|
| | **IL2** | **IFNg** | **TNFa** | **IL2/IFNg** | **IL2/TNFa** | **IFNg/TNFa** | **IL2/IFNg/ TNFa** |
| **Group 1** | 0.000 | 0.000 | 0.018 | 0.000 | 0.072 | 0.000 | 0.029 |
| **Group 2** | 0.011 | 0.071 | 0.000 | 0.032 | 0.000 | 0.166 | 0.225 |
| **Group 3** | 0.000 | 0.025 | 0.017 | 0.006 | 0.006 | 0.035 | 0.064 |
| **Group 4** | 0.000 | 0.000 | 0.009 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 5** | 0.016 | 0.000 | 0.048 | 0.000 | 0.056 | 0.000 | 0.000 |
| **Group 6** | 0.000 | 0.000 | 0.000 | 0.013 | 0.095 | 0.000 | 0.034 |
| **Group 7** | 0.000 | 0.002 | 0.079 | 0.026 | 0.000 | 0.020 | 0.041 |
| **Group 8** | 0.000 | 0.137 | 0.002 | 0.000 | 0.000 | 0.148 | 0.362 |
| **Group 9** | 0.000 | 0.116 | 0.000 | 0.018 | 0.000 | 0.106 | 0.190 |
| **Group 10** | 0.000 | 0.027 | 0.007 | 0.023 | 0.000 | 0.018 | 0.042 |
| **Group 11** | 0.000 | 0.000 | 0.043 | 0.000 | 0.008 | 0.072 | 0.091 |
| **Group 12** | 0.006 | 0.032 | 0.012 | 0.000 | 0.027 | 0.060 | 0.081 |
| **Group 13** | 0.000 | 0.000 | 0.030 | 0.000 | 0.059 | 0.000 | 0.000 |

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Figure 13

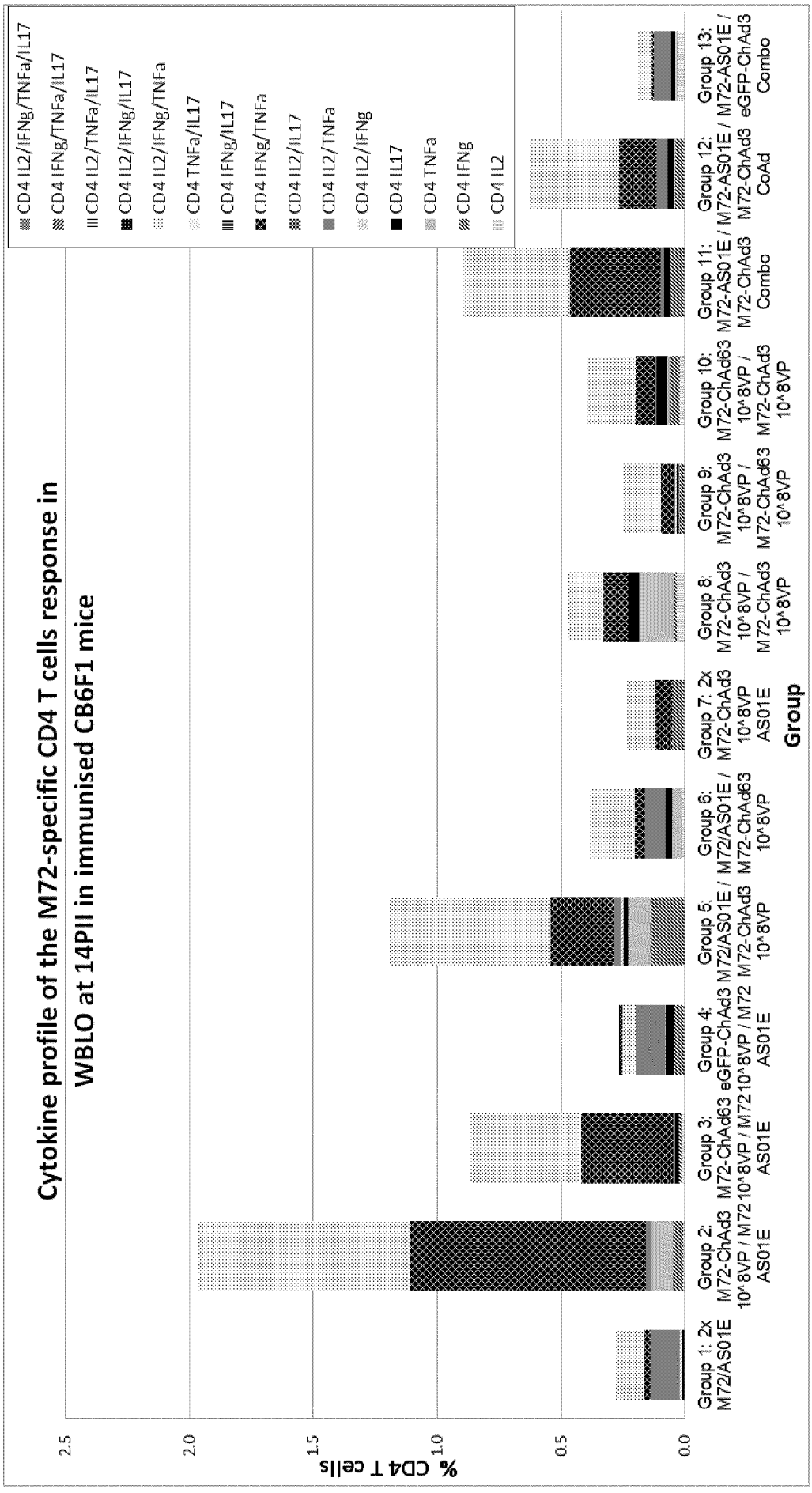
Cytokine profile of the M72-specific CD4 T cells response in
WBLO at 14PII in immunised CB6F1 mice
% CD4 T cells
2.5
2.0
1.5
1.0
0.5
0.0
CD4 IL2/IFNg/TNFa/IL17
CD4 IFNg/TNFa/IL17
CD4 IL2/TNFa/IL17
CD4 IL2/IFNg/IL17
CD4 IL2/IFNg/TNFa
CD4 TNFa/IL17
CD4 IFNg/IL17
CD4 IFNg/TNFa
CD4 IL2/IL17
CD4 IL2/TNFa
CD4 IL2/IFNg
CD4 IL17
CD4 TNFa
CD4 IFNg
CD4 IL2
Group 1: 2x M72/AS01E
Group 2: M72-ChAd3 10^8VP / M72 AS01E
Group 3: M72-ChAd63 10^8VP / M72 AS01E
Group 4: eGFP-ChAd3 10^8VP / M72 AS01E
Group 5: M72/AS01E / M72-ChAd3 10^8VP
Group 6: M72/AS01E / M72-ChAd63 10^8VP
Group 7: 2x M72-ChAd3 10^8VP AS01E
Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP
Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP
Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP
Group 11: M72-AS01E / M72-ChAd3 Combo
Group 12: M72-AS01E / M72-ChAd3 CoAd
Group 13: M72-AS01E / eGFP-ChAd3 Combo
Group

Figure **14**

| | % CD4 T cells expressing cytokines (WBLO at 14PI) | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **CD4 IL2** | **CD4 IFNg** | **CD4 TNFa** | **CD4 IL17** | **CD4 IL2/ IFNg** | **CD4 IL2/ TNFa** | **CD4 IL2/ IL17** | **CD4 IFNg/ TNFa** | **CD4 IFNg/ IL17** | **CD4 TNFa/ IL17** | **CD4 IL2/ IFNg/ TNFa** | **CD4 IL2/ IFNg/ IL17** | **CD4 IL2/ TNFa/ IL17** | **CD4 IFNg/ TNFa/ IL17** | **CD4 IL2/ IFNg/ TNFa/ IL17** |
| **Group 1** | 0.000 | 0.000 | 0.000 | 0.011 | 0.009 | 0.119 | 0.000 | 0.029 | 0.000 | 0.000 | 0.112 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 2** | 0.005 | 0.044 | 0.084 | 0.000 | 0.000 | 0.026 | 0.000 | 0.951 | 0.000 | 0.000 | 0.855 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 3** | 0.014 | 0.009 | 0.000 | 0.016 | 0.000 | 0.009 | 0.000 | 0.370 | 0.000 | 0.000 | 0.449 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 4** | 0.001 | 0.041 | 0.000 | 0.036 | 0.001 | 0.115 | 0.000 | 0.000 | 0.000 | 0.000 | 0.058 | 0.014 | 0.000 | 0.000 | 0.000 |
| **Group 5** | 0.000 | 0.140 | 0.090 | 0.018 | 0.011 | 0.028 | 0.000 | 0.255 | 0.000 | 0.000 | 0.649 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 6** | 0.009 | 0.002 | 0.041 | 0.027 | 0.000 | 0.085 | 0.000 | 0.040 | 0.000 | 0.000 | 0.177 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 7** | 0.000 | 0.051 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.068 | 0.000 | 0.000 | 0.119 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 8** | 0.033 | 0.008 | 0.142 | 0.047 | 0.000 | 0.000 | 0.000 | 0.098 | 0.000 | 0.000 | 0.142 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 9** | 0.000 | 0.019 | 0.007 | 0.007 | 0.008 | 0.002 | 0.000 | 0.052 | 0.000 | 0.000 | 0.157 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 10** | 0.022 | 0.041 | 0.009 | 0.043 | 0.000 | 0.008 | 0.000 | 0.073 | 0.000 | 0.000 | 0.204 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 11** | 0.000 | 0.063 | 0.000 | 0.019 | 0.000 | 0.016 | 0.000 | 0.365 | 0.000 | 0.000 | 0.436 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 12** | 0.000 | 0.039 | 0.004 | 0.027 | 0.000 | 0.045 | 0.000 | 0.150 | 0.000 | 0.000 | 0.365 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 13** | 0.028 | 0.000 | 0.013 | 0.013 | 0.000 | 0.071 | 0.000 | 0.009 | 0.000 | 0.000 | 0.059 | 0.000 | 0.000 | 0.000 | 0.000 |

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Figure 15

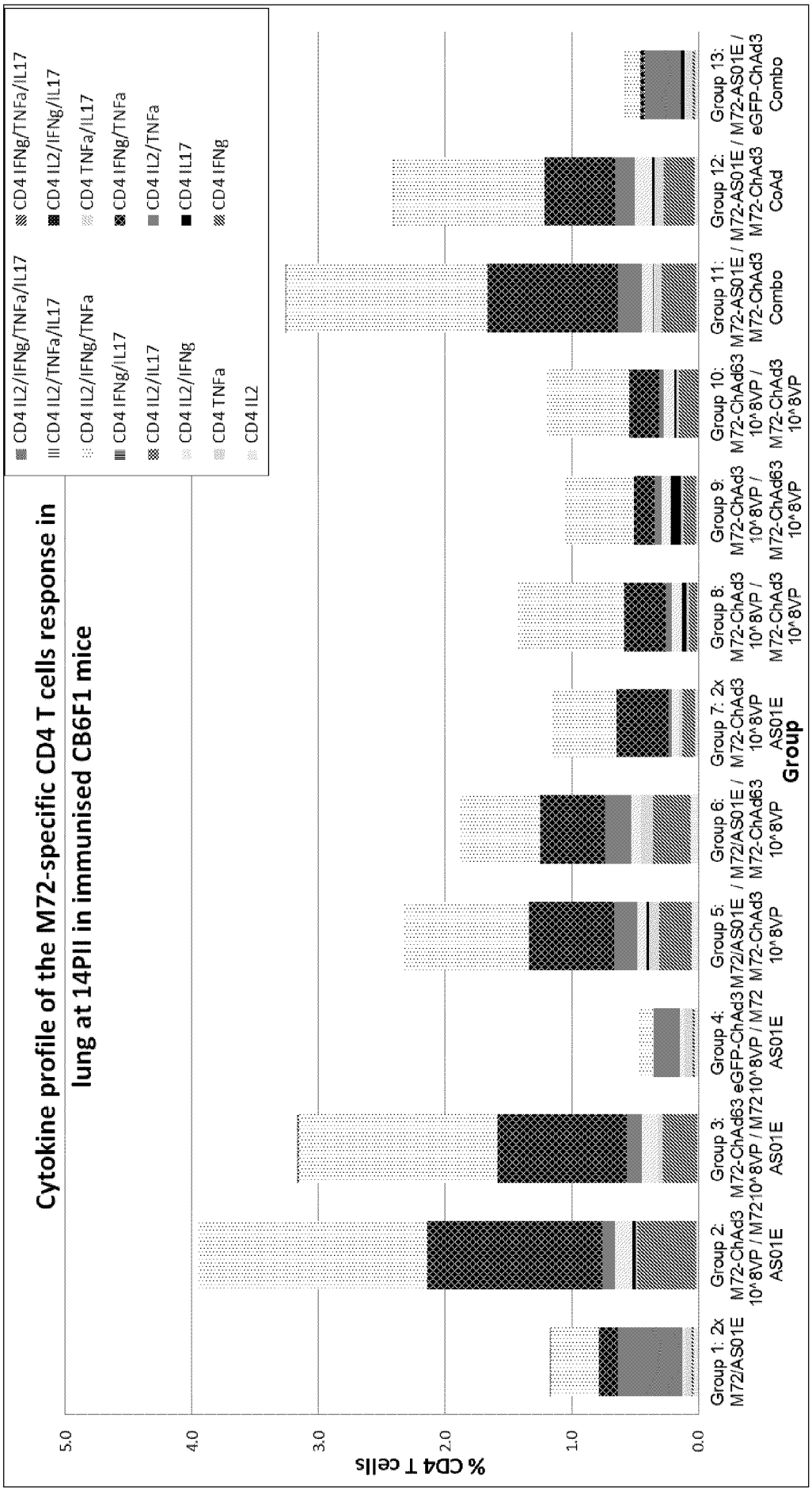
Cytokine profile of the M72-specific CD4 T cells response in lung at 14PII in immunised CB6F1 mice
% CD4 T cells
5.0
4.0
3.0
2.0
1.0
0.0
CD4 IL2/IFNg/TNFa/IL17
CD4 IL2/TNFa/IL17
CD4 IL2/IFNg/TNFa
CD4 IFNg/IL17
CD4 IL2/IL17
CD4 IL2/IFNg
CD4 TNFa
CD4 IL2
CD4 IFNg/TNFa/IL17
CD4 IL2/IFNg/IL17
CD4 TNFa/IL17
CD4 IFNg/TNFa
CD4 IL2/TNFa
CD4 IL17
CD4 IFNg
Group 1: 2x M72/AS01E
Group 2: M72-ChAd3 10^8VP / M72 AS01E
Group 3: M72-ChAd63 10^8VP / M72 AS01E
Group 4: eGFP-ChAd3 10^8VP / M72 AS01E
Group 5: M72/AS01E / M72-ChAd3 10^8VP
Group 6: M72/AS01E / M72-ChAd63 10^8VP
Group 7: 2x M72-ChAd3 10^8VP AS01E
Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP
Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP
Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP
Group 11: M72-AS01E / M72-ChAd3 Combo
Group 12: M72-AS01E / M72-ChAd3 CoAd
Group 13: M72-AS01E / eGFP-ChAd3 Combo
Group

Figure **16**

| | % CD4 T cells expressing cytokines (lung at 14PII) | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **CD4 IL2** | **CD4 IFNg** | **CD4 TNFa** | **CD4 IL17** | **CD4 IL2/ IFNg** | **CD4 IL2/ TNFa** | **CD4 IL2/ IL17** | **CD4 IFNg/ TNFa** | **CD4 IFNg/ IL17** | **CD4 TNFa/ IL17** | **CD4 IL2/ IFNg/ TNFa** | **CD4 IL2/ IFNg/ IL17** | **CD4 IL2/ TNFa/ IL17** | **CD4 IFNg/ TNFa/ IL17** | **CD4 IL2/ IFNg/ TNFa/ IL17** |
| **Group 1** | 0.000 | 0.000 | 0.000 | 0.011 | 0.009 | 0.119 | 0.000 | 0.029 | 0.000 | 0.000 | 0.112 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 2** | 0.005 | 0.044 | 0.084 | 0.000 | 0.000 | 0.026 | 0.000 | 0.951 | 0.000 | 0.000 | 0.855 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 3** | 0.014 | 0.009 | 0.000 | 0.016 | 0.000 | 0.009 | 0.000 | 0.370 | 0.000 | 0.000 | 0.449 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 4** | 0.001 | 0.041 | 0.000 | 0.036 | 0.001 | 0.115 | 0.000 | 0.000 | 0.000 | 0.000 | 0.058 | 0.014 | 0.000 | 0.000 | 0.000 |
| **Group 5** | 0.000 | 0.140 | 0.090 | 0.018 | 0.011 | 0.028 | 0.000 | 0.255 | 0.000 | 0.000 | 0.649 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 6** | 0.009 | 0.002 | 0.041 | 0.027 | 0.000 | 0.085 | 0.000 | 0.040 | 0.000 | 0.000 | 0.177 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 7** | 0.000 | 0.051 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.068 | 0.000 | 0.000 | 0.119 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 8** | 0.033 | 0.008 | 0.142 | 0.047 | 0.000 | 0.000 | 0.000 | 0.098 | 0.000 | 0.000 | 0.142 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 9** | 0.000 | 0.019 | 0.007 | 0.007 | 0.008 | 0.002 | 0.000 | 0.052 | 0.000 | 0.000 | 0.157 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 10** | 0.022 | 0.041 | 0.009 | 0.043 | 0.000 | 0.008 | 0.000 | 0.073 | 0.000 | 0.000 | 0.204 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 11** | 0.000 | 0.063 | 0.000 | 0.019 | 0.000 | 0.016 | 0.000 | 0.365 | 0.000 | 0.000 | 0.436 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 12** | 0.000 | 0.039 | 0.004 | 0.027 | 0.000 | 0.045 | 0.000 | 0.150 | 0.000 | 0.000 | 0.365 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 13** | 0.028 | 0.000 | 0.013 | 0.013 | 0.000 | 0.071 | 0.000 | 0.009 | 0.000 | 0.000 | 0.059 | 0.000 | 0.000 | 0.000 | 0.000 |

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Figure 17

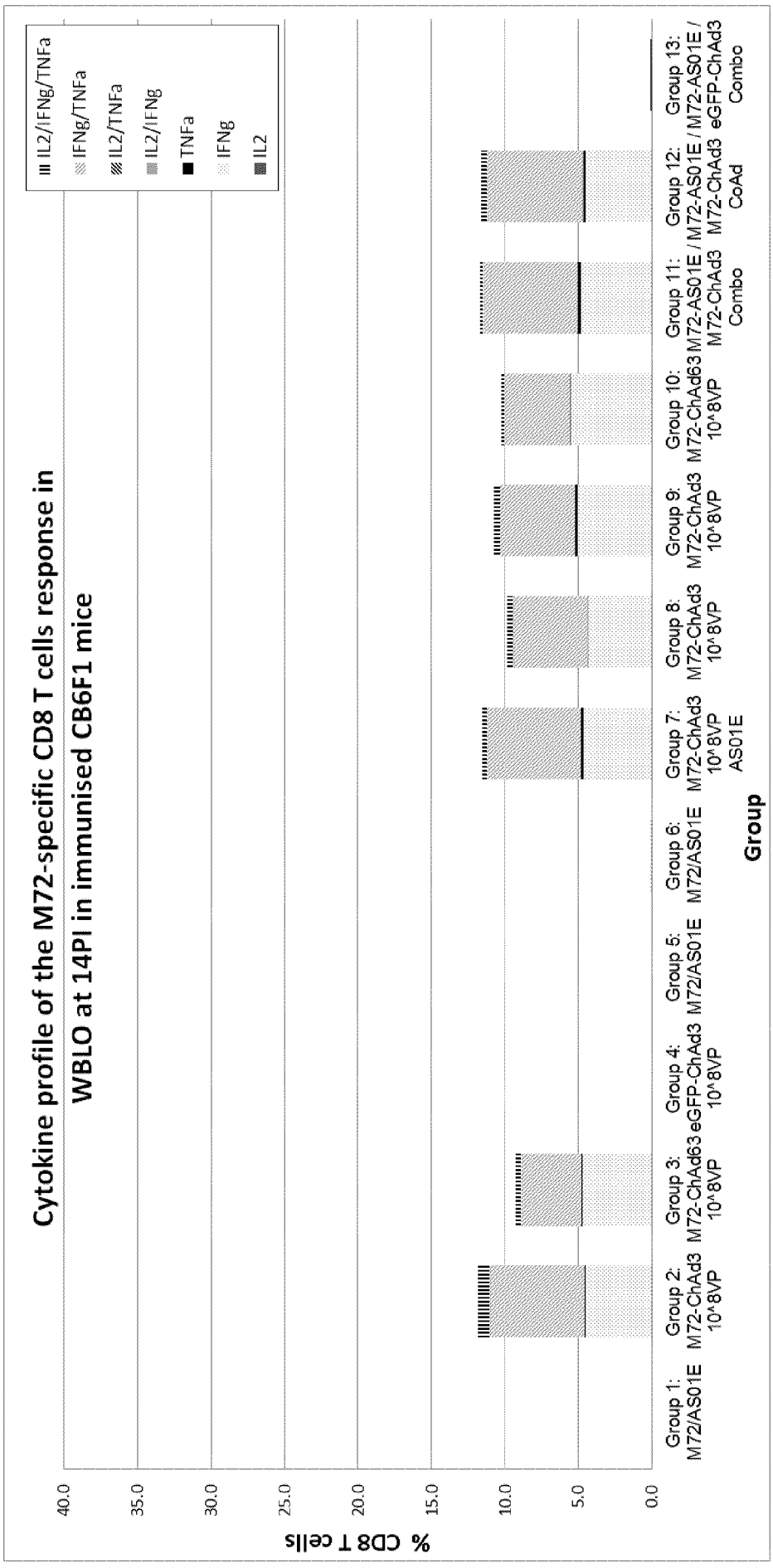
Cytokine profile of the M72-specific CD8 T cells response in
WBLO at 14PI in immunised CB6F1 mice
IL2/IFNg/TNFa
IFNg/TNFa
IL2/TNFa
IL2/IFNg
TNFa
IFNg
IL2
% CD8 T cells
40.0
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
Group 1: M72/AS01E
Group 2: M72-ChAd3 10^8VP
Group 3: M72-ChAd63 10^8VP
Group 4: eGFP-ChAd3 10^8VP
Group 5: M72/AS01E
Group 6: M72/AS01E
Group 7: M72-ChAd3 10^8VP AS01E
Group 8: M72-ChAd3 10^8VP
Group 9: M72-ChAd3 10^8VP
Group 10: M72-ChAd63 10^8VP
Group 11: M72-AS01E / M72-ChAd3 Combo
Group 12: M72-AS01E / M72-ChAd3 CoAd
Group 13: M72-AS01E / eGFP-ChAd3 Combo
Group

Figure **18**

| | % CD8 T cells expressing cytokines (whole blood at 14PI) | | | | | | |
|---|---|---|---|---|---|---|---|
| | IL2 | IFNg | TNFa | IL2/IFNg | IL2/TNFa | IFNg/TNFa | IL2/IFNg/ TNFa |
| Group 1 | 0.000 | 0.009 | 0.040 | 0.000 | 0.000 | 0.000 | 0.000 |
| Group 2 | 0.005 | 4.528 | 0.046 | 0.047 | 0.000 | 6.451 | 0.749 |
| Group 3 | 0.000 | 4.744 | 0.041 | 0.022 | 0.000 | 4.155 | 0.293 |
| Group 4 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Group 5 | 0.000 | 0.012 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Group 6 | 0.000 | 0.021 | 0.009 | 0.000 | 0.000 | 0.019 | 0.000 |
| Group 7 | 0.000 | 4.694 | 0.141 | 0.000 | 0.000 | 6.410 | 0.321 |
| Group 8 | 0.000 | 4.352 | 0.000 | 0.038 | 0.000 | 5.090 | 0.410 |
| Group 9 | 0.000 | 5.046 | 0.180 | 0.017 | 0.000 | 5.064 | 0.510 |
| Group 10 | 0.000 | 5.515 | 0.050 | 0.009 | 0.000 | 4.455 | 0.234 |
| Group 11 | 0.000 | 4.850 | 0.233 | 0.000 | 0.000 | 6.440 | 0.182 |
| Group 12 | 0.000 | 4.547 | 0.118 | 0.035 | 0.000 | 6.545 | 0.385 |
| Group 13 | 0.000 | 0.000 | 0.102 | 0.000 | 0.000 | 0.000 | 0.000 |

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Figure 19

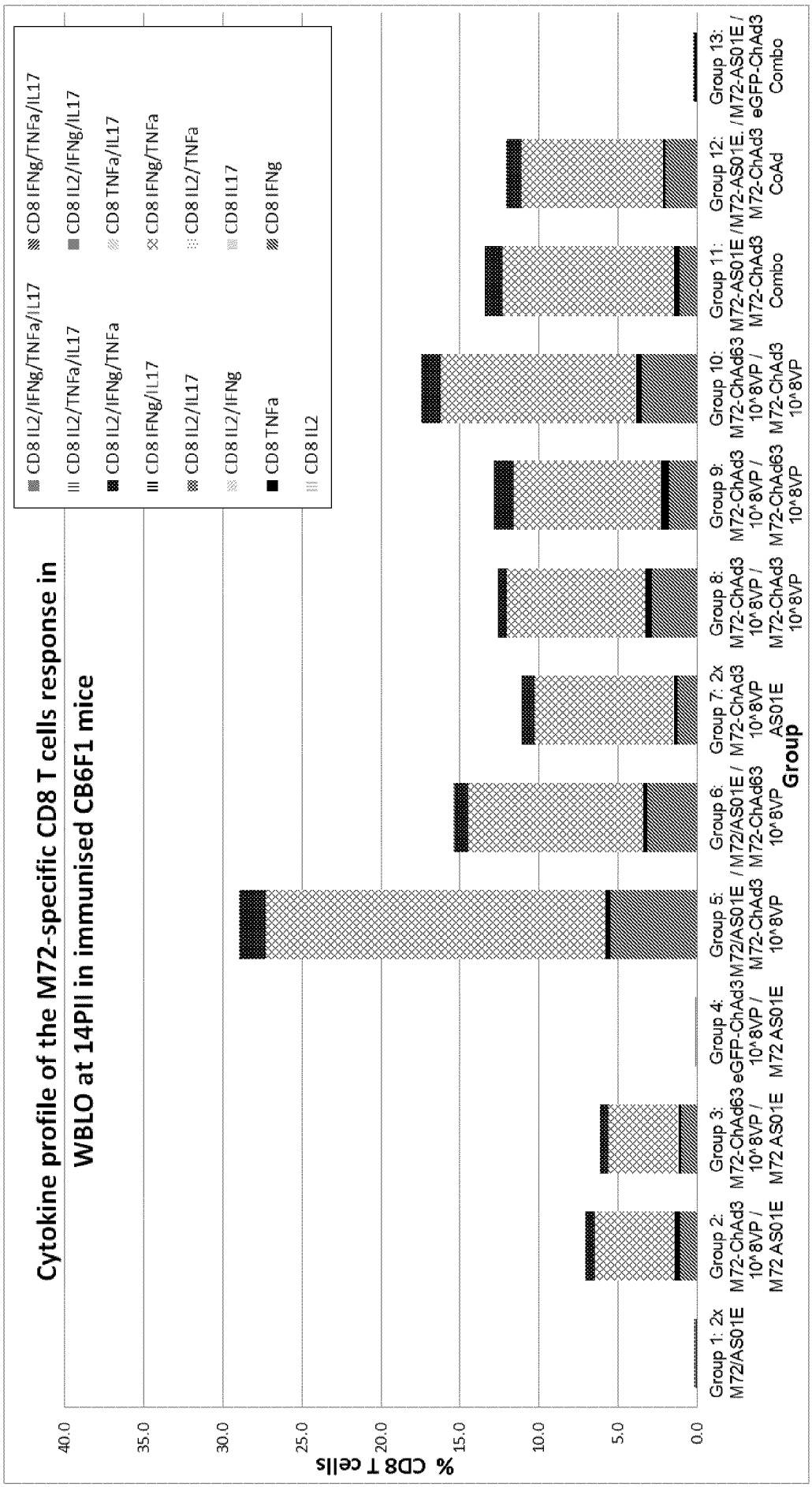
Cytokine profile of the M72-specific CD8 T cells response in WBLO at 14PII in immunised CB6F1 mice
% CD8 T cells
0.0
5.0
10.0
15.0
20.0
25.0
30.0
35.0
40.0
CD8 IL2/IFNg/TNFa/IL17
CD8 IL2/TNFa/IL17
CD8 IL2/IFNg/TNFa
CD8 IFNg/IL17
CD8 IL2/IL17
CD8 IL2/IFNg
CD8 TNFa
CD8 IL2
CD8 IFNg/TNFa/IL17
CD8 IL2/IFNg/IL17
CD8 TNFa/IL17
CD8 IFNg/TNFa
CD8 IL2/TNFa
CD8 IL17
CD8 IFNg
Group 1: 2x M72/AS01E
Group 2: M72-ChAd3 10^8VP / M72 AS01E
Group 3: M72-ChAd63 10^8VP / M72 AS01E
Group 4: eGFP-ChAd3 10^8VP / M72 AS01E
Group 5: M72/AS01E / M72-ChAd3 10^8VP
Group 6: M72/AS01E / M72-ChAd63 10^8VP
Group 7: 2x M72-ChAd3 10^8VP AS01E
Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP
Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP
Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP
Group 11: M72-AS01E / M72-ChAd3 Combo
Group 12: M72-AS01E. / M72-ChAd3 CoAd
Group 13: M72-AS01E / eGFP-ChAd3 Combo
Group

Figure **20**

| | % CD8 T cells expressing cytokines (whole blood at 14PII) | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | CD8 IL2 | CD8 IFNg | CD8 TNFa | CD8 IL17 | CD8 IL2/ IFNg | CD8 IL2/ TNFa | CD8 IL2/ IL17 | CD8 IFNg/ TNFa | CD8 IFNg/ IL17 | CD8 TNFa/ IL17 | CD8 IL2/ IFNg/ TNFa | CD8 IL2/ IFNg/ IL17 | CD8 IL2/ TNFa/ IL17 | CD8 IFNg/ TNFa/ IL17 | CD8 IL2/ IFNg/ TNFa/ IL17 |
| **Group 1** | 0.022 | 0.000 | 0.073 | 0.000 | 0.000 | 0.013 | 0.000 | 0.000 | 0.000 | 0.000 | 0.013 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 2** | 0.000 | 1.033 | 0.358 | 0.031 | 0.011 | 0.014 | 0.000 | 5.025 | 0.000 | 0.000 | 0.611 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 3** | 0.035 | 0.939 | 0.207 | 0.027 | 0.000 | 0.000 | 0.000 | 4.370 | 0.000 | 0.000 | 0.544 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 4** | 0.009 | 0.019 | 0.010 | 0.018 | 0.000 | 0.000 | 0.000 | 0.011 | 0.003 | 0.000 | 0.014 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 5** | 0.000 | 5.514 | 0.238 | 0.000 | 0.023 | 0.000 | 0.000 | 21.497 | 0.004 | 0.000 | 1.670 | 0.000 | 0.000 | 0.011 | 0.000 |
| **Group 6** | 0.009 | 3.145 | 0.208 | 0.001 | 0.000 | 0.000 | 0.000 | 11.115 | 0.009 | 0.000 | 0.837 | 0.000 | 0.000 | 0.011 | 0.000 |
| **Group 7** | 0.023 | 1.196 | 0.271 | 0.030 | 0.000 | 0.000 | 0.000 | 8.742 | 0.021 | 0.000 | 0.773 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 8** | 0.019 | 2.830 | 0.401 | 0.000 | 0.017 | 0.000 | 0.000 | 8.740 | 0.002 | 0.004 | 0.584 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 9** | 0.000 | 1.771 | 0.522 | 0.000 | 0.019 | 0.000 | 0.000 | 9.275 | 0.000 | 0.000 | 1.218 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 10** | 0.014 | 3.514 | 0.346 | 0.009 | 0.039 | 0.006 | 0.000 | 12.300 | 0.008 | 0.000 | 1.220 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 11** | 0.000 | 1.141 | 0.318 | 0.010 | 0.007 | 0.007 | 0.000 | 10.800 | 0.000 | 0.000 | 1.145 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 12** | 0.000 | 1.965 | 0.204 | 0.000 | 0.024 | 0.000 | 0.000 | 8.900 | 0.000 | 0.000 | 0.910 | 0.000 | 0.000 | 0.012 | 0.000 |
| **Group 13** | 0.000 | 0.019 | 0.148 | 0.018 | 0.000 | 0.006 | 0.000 | 0.011 | 0.013 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |

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Figure 21

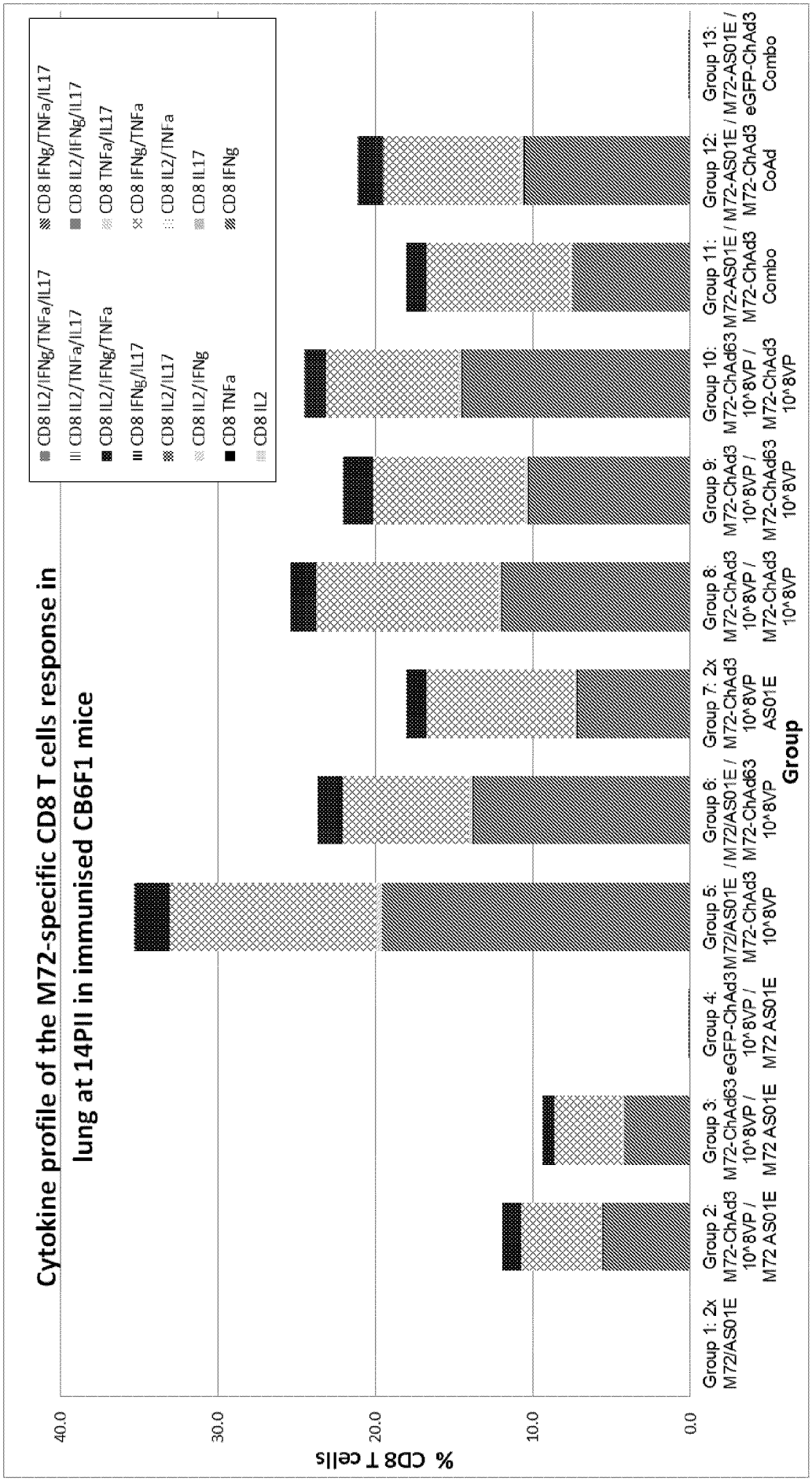
Cytokine profile of the M72-specific CD8 T cells response in lung at 14PII in immunised CB6F1 mice
% CD8 T cells
0.0
10.0
20.0
30.0
40.0
CD8 IL2/IFNg/TNFa/IL17
CD8 IL2/TNFa/IL17
CD8 IL2/IFNg/TNFa
CD8 IFNg/IL17
CD8 IL2/IL17
CD8 IL2/IFNg
CD8 TNFa
CD8 IL2
CD8 IFNg/TNFa/IL17
CD8 IL2/IFNg/IL17
CD8 TNFa/IL17
CD8 IFNg/TNFa
CD8 IL2/TNFa
CD8 IL17
CD8 IFNg
Group 1: 2x M72/AS01E
Group 2: M72-ChAd3 10^8VP / M72 AS01E
Group 3: M72-ChAd63 10^8VP / M72 AS01E
Group 4: eGFP-ChAd3 10^8VP / M72.AS01E
Group 5: M72/AS01E / M72-ChAd3 10^8VP
Group 6: M72/AS01E / M72-ChAd63 10^8VP
Group 7: 2x M72-ChAd3 10^8VP AS01E
Group 8: M72-ChAd3 10^8VP / M72-ChAd3 10^8VP
Group 9: M72-ChAd3 10^8VP / M72-ChAd63 10^8VP
Group 10: M72-ChAd63 10^8VP / M72-ChAd3 10^8VP
Group 11: M72-AS01E / M72-ChAd3 Combo
Group 12: M72-AS01E / M72-ChAd3 CoAd
Group 13: M72-AS01E / eGFP-ChAd3 Combo
Group

Figure **22**

| | % CD8 T cells expressing cytokines (lung at 14PII) | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | CD8 IL2 | CD8 IFNg | CD8 TNFa | CD8 IL17 | CD8 IL2/ IFNg | CD8 IL2/ TNFa | CD8 IL2/ IL17 | CD8 IFNg/ TNFa | CD8 IFNg/ IL17 | CD8 TNFa/ IL17 | CD8 IL2/ IFNg/ TNFa | CD8 IL2/ IFNg/ IL17 | CD8 IL2/ TNFa/ IL17 | CD8 IFNg/ TNFa/ IL17 | CD8 IL2/ IFNg/ TNFa/ IL17 |
| **Group 1** | 0.003 | 0.001 | 0.000 | 0.006 | 0.004 | 0.000 | 0.000 | 0.007 | 0.000 | 0.000 | 0.014 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 2** | 0.000 | 5.514 | 0.043 | 0.000 | 0.140 | 0.004 | 0.000 | 5.038 | 0.000 | 0.000 | 1.190 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 3** | 0.005 | 4.198 | 0.015 | 0.012 | 0.077 | 0.000 | 0.000 | 4.324 | 0.004 | 0.000 | 0.728 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 4** | 0.000 | 0.015 | 0.001 | 0.013 | 0.013 | 0.000 | 0.000 | 0.009 | 0.006 | 0.000 | 0.042 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 5** | 0.000 | 19.541 | 0.012 | 0.000 | 0.351 | 0.000 | 0.000 | 13.197 | 0.003 | 0.000 | 2.192 | 0.000 | 0.000 | 0.003 | 0.000 |
| **Group 6** | 0.004 | 13.756 | 0.078 | 0.000 | 0.233 | 0.000 | 0.000 | 8.007 | 0.000 | 0.000 | 1.550 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 7** | 0.003 | 7.149 | 0.077 | 0.008 | 0.125 | 0.000 | 0.000 | 9.360 | 0.003 | 0.000 | 1.253 | 0.000 | 0.000 | 0.003 | 0.000 |
| **Group 8** | 0.000 | 11.930 | 0.074 | 0.000 | 0.186 | 0.000 | 0.000 | 11.598 | 0.000 | 0.000 | 1.605 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 9** | 0.000 | 10.236 | 0.070 | 0.000 | 0.229 | 0.000 | 0.000 | 9.624 | 0.000 | 0.000 | 1.860 | 0.000 | 0.000 | 0.002 | 0.000 |
| **Group 10** | 0.007 | 14.468 | 0.033 | 0.000 | 0.209 | 0.000 | 0.000 | 8.383 | 0.006 | 0.000 | 1.357 | 0.000 | 0.000 | 0.006 | 0.000 |
| **Group 11** | 0.000 | 7.477 | 0.015 | 0.001 | 0.108 | 0.003 | 0.000 | 9.159 | 0.001 | 0.000 | 1.245 | 0.000 | 0.000 | 0.000 | 0.000 |
| **Group 12** | 0.008 | 10.488 | 0.095 | 0.000 | 0.248 | 0.002 | 0.000 | 8.624 | 0.012 | 0.000 | 1.595 | 0.000 | 0.000 | 0.002 | 0.000 |
| **Group 13** | 0.000 | 0.010 | 0.030 | 0.015 | 0.000 | 0.000 | 0.000 | 0.018 | 0.000 | 0.000 | 0.006 | 0.000 | 0.000 | 0.000 | 0.000 |

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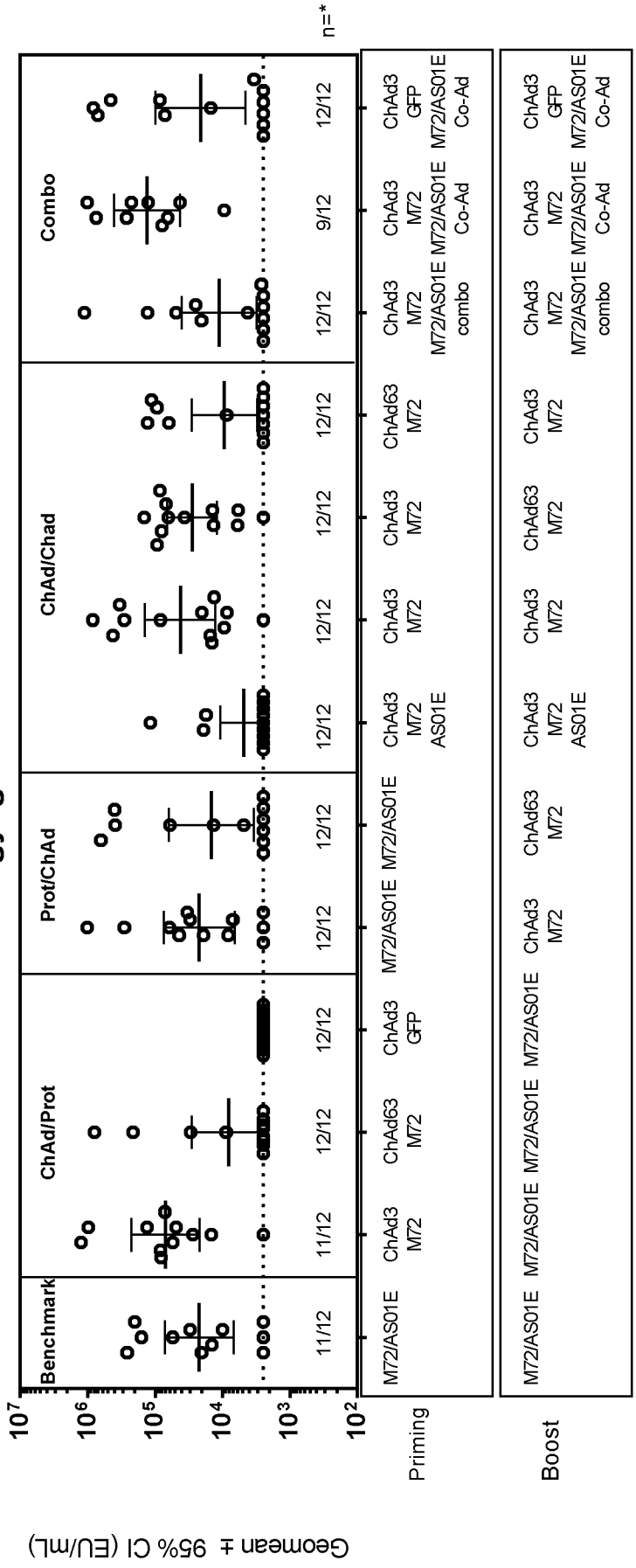
Figure 23




*Due to technical issue, the number of animal / gorup is between 9 to 12 as indicated

Figure 24

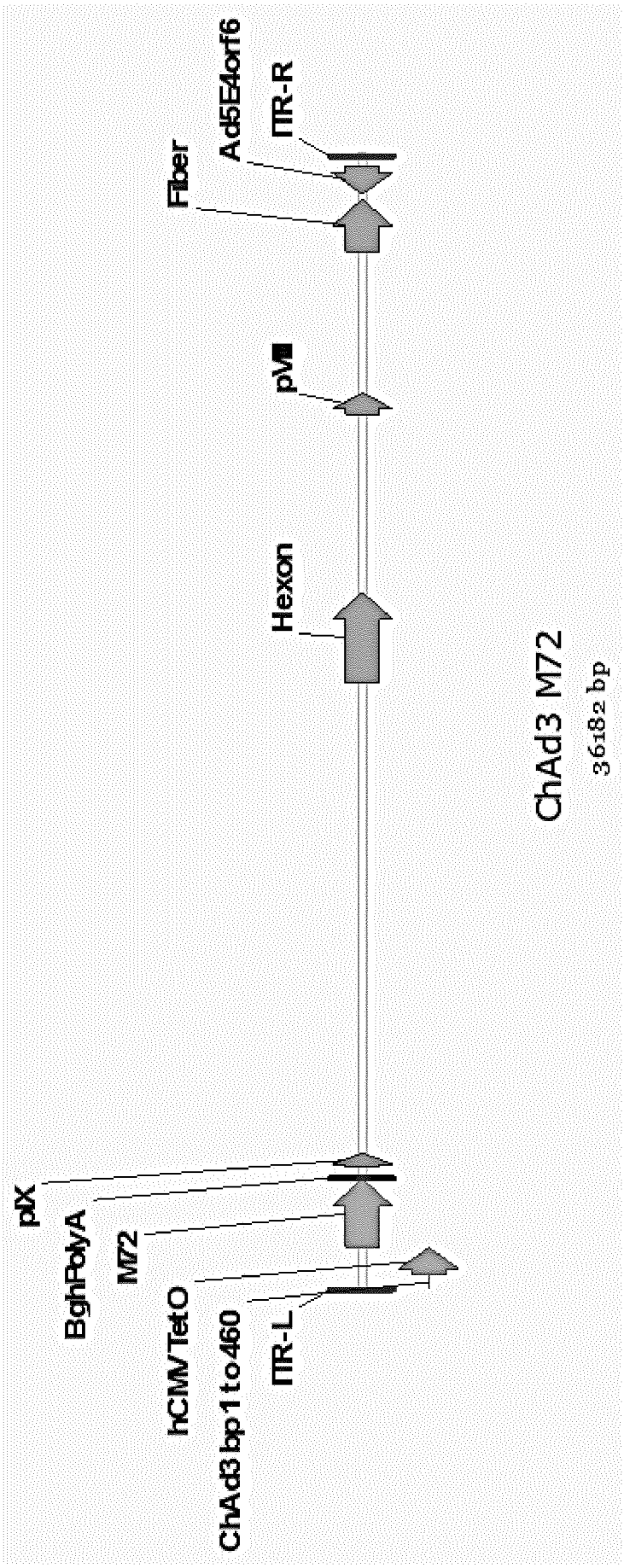
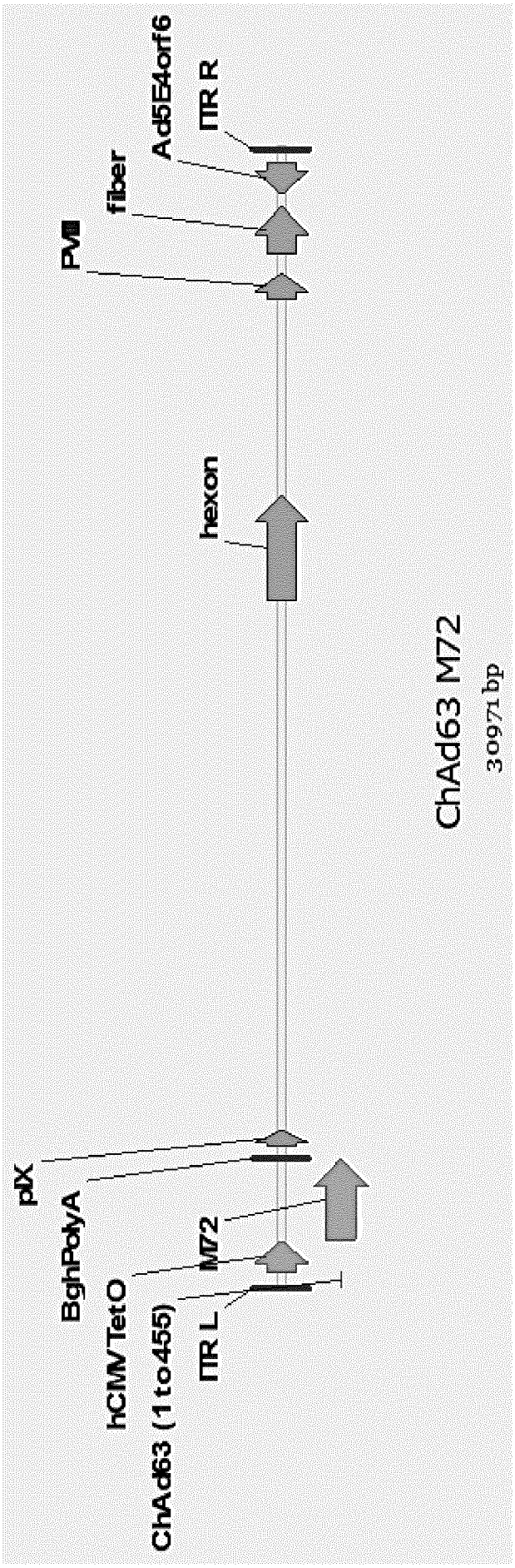

pIX
BghPolyA
M72
hCMVTetO
ChAd3 bp1 to 460
ITR-L
Hexon
pVI
Fiber
Ad5E4orf6
ITR-R
ChAd3 M72
36182 bp

Figure 25


ChAd63 (1 to 455)
hCMV TetO
BghPolyA
pIX
ITR L
M72
hexon
PVI
fiber
Ad5E4orf6
ITR R
ChAd63 M72
30971 bp

# INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/067622

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K39/04 C12N7/00 C12N15/861 C07K14/075
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, BIOSIS, Sequence Search, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

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"&" document member of the same patent family

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 25 October 2016 | 08/11/2016 |

| Name and mailing address of the ISA/ | Authorized officer |
|---|---|
| European Patent Office, P.B. 5818 Patentlaan 2<br>NL - 2280 HV Rijswijk<br>Tel. (+31-70) 340-2040,<br>Fax: (+31-70) 340-3016 | Renggli-Zulliger, N |

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