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(54) Title: ADENOVIRUS POLYNUCLEOTIDES AND POLYPEPTIDES

(57) Abstract: The present invention relates to isolated polynucleotide and polypeptide sequences derived from novel chimpanzee adenovirus ChAd157, as well as to recombinant polynucleotides, vectors, adenoviruses, cells and compositions comprising said polynucleotide and polypeptide sequences.



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## **ADENOVIRUS POLYNUCLEOTIDES AND POLYPEPTIDES**

### **FIELD OF THE INVENTION**

5 The present invention relates to isolated polynucleotide and polypeptide sequences derived from novel chimpanzee adenovirus ChAd157, as well as to recombinant polynucleotides, vectors, adenoviruses, cells and compositions comprising said polynucleotide and polypeptide sequences.

### **10 BACKGROUND OF THE INVENTION**

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. Conventionally, E1 genes of adenovirus are deleted and replaced with a transgene cassette  
15 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.

Recombinant adenoviruses are useful in gene therapy and as vaccines. Viral vectors based on chimpanzee adenovirus represent an alternative to the use of human derived adenovirus  
20 vectors for the development of genetic vaccines. Adenoviruses isolated from chimpanzees are closely related to adenoviruses isolated from humans as demonstrated by their efficient propagation in cells of human origin. However, since human and chimpanzee adenoviruses are close relatives, serologic cross reactivity between the two virus species is possible.

25 There is a demand for vectors which effectively deliver molecules to a target and minimize the effect of pre-existing immunity to selected adenovirus serotypes in the population. One aspect of pre-existing immunity that is observed in humans is humoral immunity, which can result in the production and persistence of antibodies that are specific for adenoviral proteins. The humoral response elicited by adenovirus is mainly directed against the three major structural  
30 capsid proteins: fiber, penton and hexon.

### **SUMMARY OF THE INVENTION**

There is provided an isolated polynucleotide, wherein the polynucleotide encodes a  
35 polypeptide selected from the group consisting of:

- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1; and
- (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID  
40 NO: 1.

Also provided is a recombinant polynucleotide comprising a polynucleotide selected from the group consisting of:

- (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1; and
- (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

Also provided is a recombinant vector comprising a polynucleotide selected from the group consisting of:

- (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1; and
- (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

Also provided is a recombinant adenovirus comprising at least one polynucleotide or polypeptide selected from the group consisting of:

- (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1;
- (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1;
- (c) a polypeptide having the amino acid sequence according to SEQ ID NO: 1; and
- (d) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

Also provided is a composition comprising at least one of the following:

- (a) an isolated polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1;
- (b) an isolated polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1;
- (c) an isolated polypeptide having the amino acid sequence according to SEQ ID NO: 1;
- (d) an isolated functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1;

- (e) a vector comprising a polynucleotide as described in (a) or (b) above; and
- (f) a recombinant adenovirus comprising a polynucleotide as described in (a) or (b) above,

and a pharmaceutically acceptable excipient.

5

Also provided is a cell comprising at least one of the following:

- (a) an isolated polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,
- 10 (b) an isolated polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1;
- (c) a vector comprising a polynucleotide as described in (a) or (b) above, and
- 15 (d) a recombinant adenovirus comprising a polynucleotide as described in (a) or (b) above.

Also provided is an isolated adenoviral polypeptide selected from the group consisting of:

- 20 (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1; and
- (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

## DESCRIPTION OF THE FIGURES

25

Figure 1A-1D - Alignment of fiber protein sequences from the indicated simian adenoviruses.

- ChAd157 (SEQ ID NO:1)
- ChAd3 (SEQ ID NO:27)
- PanAd3 (SEQ ID NO:28)
- 30 ChAd17 (SEQ ID NO:29)
- ChAd19 (SEQ ID NO:30)
- ChAd24 (SEQ ID NO:31)
- ChAd155 (SEQ ID NO:7)
- ChAd11 (SEQ ID NO:32)
- 35 ChAd20 (SEQ ID NO:33)
- ChAd31 (SEQ ID NO:34)
- PanAd1 (SEQ ID NO:35)
- PanAd2 (SEQ ID NO:36)

- Figure 2 - Subgroup C BAC Shuttle schematic representation
- 40 Figure 3 - Subgroup C Plasmid Shuttle schematic representation
- Figure 4 - pChAd157  $\Delta$ E1/TetO hCMV GAG vector schematic representation
- Figure 5 - pARS SpeciesC Ad5orf6-2 shuttle schematic representation
- Figure 6 - plasmid carrying the ChAd157 RG schematic representation

- Figure 7 - Transgene Expression by ChAd157/GAG, ChAd19/GAG and ChAd155/GAG  
 Figure 8 - Western Blot analysis of lysates of Hela cells infected with ChAd155/RG and ChAd157/RG  
 Figure 9 - Immunological potency of ChAd157/GAG, ChAd155/GAG and ChAd19 GAG in  
 5 BALB/c mice  
 Figure 10 - Immunological potency of ChAd157/RG and ChAd155/RG in BALB/c mice  
 Figure 11 - Neutralization titers following preimmunization of mice with different ChAd vectors  
 Figure 12 - IFN- $\gamma$  ELISpot following vaccination of mice with ChAd157/GAG after various  
 10 preimmunization regimes

### DESCRIPTION OF THE SEQUENCES

- SEQ ID NO: 1 - Polypeptide sequence of ChAd157 fiber  
 15 SEQ ID NO: 2 - Polynucleotide sequence encoding ChAd157 fiber  
 SEQ ID NO: 3 - Polypeptide sequence of ChAd157 penton  
 SEQ ID NO: 4 - Polynucleotide sequence encoding ChAd157 penton  
 SEQ ID NO: 5 - Polypeptide sequence of ChAd157 hexon  
 SEQ ID NO: 6 - Polynucleotide sequence encoding ChAd157 hexon  
 20 SEQ ID NO: 7 - Polypeptide sequence of ChAd155 fiber  
 SEQ ID NO: 8 - Polynucleotide sequence encoding ChAd155 fiber  
 SEQ ID NO: 9 - Polypeptide sequence of ChAd155 penton  
 SEQ ID NO: 10 - Polynucleotide sequence encoding ChAd155 penton  
 SEQ ID NO: 11 - Polypeptide sequence of ChAd155 hexon  
 25 SEQ ID NO: 12 - Polynucleotide sequence encoding ChAd155 hexon  
 SEQ ID NO: 13 - Polynucleotide sequence encoding wide type ChAd155  
 SEQ ID NO: 14 - Polynucleotide sequence of Subgroup C BAC Shuttle (#1365)  
 SEQ ID NO: 15 - Polynucleotide sequence of pChAd157 $\Delta$ E1 TetO hCMV RpsL-Kana#1551  
 30 SEQ ID NO: 16 - HIV Gag polynucleotide sequence  
 SEQ ID NO: 17 - Polynucleotide sequence of pChAd157  $\Delta$ E1/TetO hCMV GAG#1557  
 SEQ ID NO: 18 - Ad5orf6 primer 1 polynucleotide sequence  
 SEQ ID NO: 19 - Ad5orf6 primer 2 polynucleotide sequence  
 SEQ ID NO: 20 - Fiber-E4 polyA primer 1 polynucleotide sequence  
 35 SEQ ID NO: 21 - Fiber-E4 polyA primer 2 polynucleotide sequence  
 SEQ ID NO: 22 - Polynucleotide sequence of ChAd157  $\Delta$ E1E4\_Ad5E4orf6/TetO hCMV RpsL-Kana#1594  
 SEQ ID NO: 23 - Rabies Glycoprotein polynucleotide sequence  
 SEQ ID NO: 24 - Polynucleotide sequence of pChAd157  $\Delta$ E1E4\_Ad5E4orf6/TetO hCMV  
 40 RG#1559  
 SEQ ID NO: 25 - CMVfor primer polynucleotide sequence  
 SEQ ID NO: 26 - CMVrev primer polynucleotide sequence  
 SEQ ID NO: 27 - Amino acid sequence for the fiber protein of ChAd3

	SEQ ID NO: 28 -	Amino acid sequence for the fiber protein of PanAd3
	SEQ ID NO: 29 -	Amino acid sequence for the fiber protein of ChAd17
	SEQ ID NO: 30 -	Amino acid sequence for the fiber protein of ChAd19
	SEQ ID NO: 31 -	Amino acid sequence for the fiber protein of ChAd24
5	SEQ ID NO: 32 -	Amino acid sequence for the fiber protein of ChAd11
	SEQ ID NO: 33 -	Amino acid sequence for the fiber protein of ChAd20
	SEQ ID NO: 34 -	Amino acid sequence for the fiber protein of ChAd31
	SEQ ID NO: 35 -	Amino acid sequence for the fiber protein of PanAd1
	SEQ ID NO: 36 -	Amino acid sequence for the fiber protein of PanAd2
10	SEQ ID NO: 37 -	Polynucleotide sequence of hCMV(tetO)
	SEQ ID NO: 38 -	Polynucleotide sequence of Subgroup C Plasmid Shuttle#1376
	SEQ ID NO: 39 -	Polynucleotide sequence of BGH polyA
	SEQ ID NO: 40 -	Polynucleotide sequence of pARS SpeciesC Ad5orf6-2
	SEQ ID NO: 41 -	Polynucleotide sequence of CMVFAM-TAMRA probe
15	SEQ ID NO: 42 -	Polynucleotide sequence encoding the enhanced hCMV promoter

## DETAILED DESCRIPTION OF THE INVENTION

20 Vectors, compositions and methods of the present invention may have one or more following improved characteristics over the prior art, including but not limited to higher productivity, improved immunogenicity, increased transgene expression or a distinct serologic cross reactivity profile.

25 Vectors, compositions and methods of the present invention may demonstrate a combination of properties, such as productivity, immunogenicity, transgene expression and/or serologic cross reactivity which mean they provide are a valuable alternative to known approaches.

### Adenovirus

30 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 virus genome is a linear, double-stranded DNA. The virus DNA is intimately associated with the highly basic protein VII and a small peptide pX (formerly termed mu). Another protein, V, is packaged with this DNA-protein  
35 complex and provides a structural link to the capsid via protein VI. The virus also contains a virus-encoded protease, which is necessary for processing of some of the structural proteins to produce mature infectious virus.

40 The adenoviral genome is well characterized. 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 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.

Adenoviruses are species-specific and different serotypes, i.e., types of viruses that are not cross-neutralized by antibodies, have been isolated from a variety of mammalian species. For example, more than 50 serotypes have been isolated from humans which are divided into six subgroups (A-F; B is subdivided into B1 and B2) based on sequence homology and on their ability to agglutinate red blood cells (Tatsis and Ertl *Molecular Therapy* (2004) 10:616-629). Numerous adenoviruses have been isolated from nonhuman simians such as chimpanzees, bonobos, rhesus macaques and gorillas, and they are classified into the same human groups based on phylogenetic relationships based on hexon or fiber sequences (Colloca *et al.* (2012) *Science Translational Medicine* 4:1-9; Roy *et al.* (2004) *Virology* 324: 361-372; Roy *et al.* (2010) *Journal of Gene Medicine* 13:17-25).

WO2005071093 discloses chimpanzee adenoviruses including ChAd19. WO2016198621 (PCT/EP2016/063329) discloses the chimpanzee adenoviruses ChAd155, which is incorporated herein by reference for the purpose of defining ChAd155 derived vectors.

### **Adenovirus Capsid Proteins Including the Fiber Protein and Polynucleotides Encoding These Proteins**

As outlined above, the adenoviral capsid comprises three major proteins, hexon, penton and fiber. 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. A remarkable difference in the surface of adenovirus capsids compared to that of most other icosahedral viruses is the presence of the long, thin fiber protein. The primary role of the fiber protein is the tethering of the viral capsid to the cell surface via its interaction with a cellular receptor.

The fiber proteins of many adenovirus serotypes share a common architecture: an N-terminal tail, a central shaft made of repeating sequences, and a C-terminal globular knob domain (or “head”). The central shaft domain consists of a variable number of beta-repeats. The beta-repeats connect to form an elongated structure of three intertwined spiralling strands that is highly rigid and stable. The shaft connects the N-terminal tail with the globular knob structure, which is responsible for interaction with the target cellular receptor. The globular nature of the adenovirus knob domain presents large surfaces for binding the receptor laterally and apically. The effect of this architecture is to project the receptor-binding site far from the virus capsid, thus freeing the virus from steric constraints presented by the relatively flat capsid surface.

Although fibers of many adenovirus serotypes have the same overall architecture, they have variable amino acid sequences that influence their function as well as structure. For example, a number of exposed regions on the surface of the fiber knob present an easily adaptable receptor binding site. The globular shape of the fiber knob allows receptors to bind at the sides of the knob or on top of the fiber knob. These binding sites typically lie on surface-exposed loops connecting beta-strands that are poorly conserved among human adenoviruses. The exposed side chains on these loops give the knob a variety of surface features while preserving the tertiary and quaternary structure. For example, the electrostatic potential and charge distributions at the knob surfaces can vary due to the wide range of isoelectric points in the fiber knob sequences, from pI approximately 9 for Ad 8, Ad 19, and Ad 37 to approximately 5 for subgroup B adenoviruses. As a structurally complex virus ligand, the fiber protein allows the presentation of a variety of binding surfaces (knob) in a number of orientations and distances (shaft) from the viral capsid.

One of the most obvious variations between some serotypes is fiber length. Studies have shown that the length of the fiber shaft strongly influences the interaction of the knob and the virus with its target receptors. Further, fiber proteins between serotypes can also vary in their ability to bend. Although beta-repeats in the shaft form a highly stable and regular structure, electron microscopy (EM) studies have shown distinct hinges in the fiber. Analysis of the protein sequence from several adenovirus serotype fibers pinpoints a disruption in the repeating sequences of the shaft at the third beta-repeat from the N-terminal tail, which correlates strongly with one of the hinges in the shaft, as seen by EM. The hinges in the fiber allow the knob to adopt a variety of orientations relative to the virus capsid, which may circumvent steric hindrances to receptor engagement requiring the correct presentation of the receptor binding site on the knob. For example, the rigid fibers of subgroup D Ads thus require a flexible receptor or one prepositioned for virus attachment, as they are unable to bend themselves. (Nicklin et al *Molecular Therapy* 2005 12:384–393)

The identification of specific cell receptors for different Ad serotypes and the knowledge of how they contribute to tissue tropism have been achieved through the use of fiber pseudotyping technology. Although Ads of some subgroups use CAR as a primary receptor, it is becoming clear that many Ads use alternate primary receptors, leading to vastly different tropism *in vitro* and *in vivo*. The fibers of these serotypes show clear differences in their primary and tertiary



- structures, such as fiber shaft rigidity, the length of the fiber shaft, and the lack of a CAR binding site and/or the putative HSPG binding motif, together with the differences in net charge within the fiber knob. Pseudotyping Ad 5 particles with an alternate fiber shaft and knob therefore provides an opportunity to remove important cell binding domains and, in addition, may allow more efficient (and potentially more cell-selective) transgene delivery to defined cell types compared to that achieved with Ad 5. Neutralization of fiber-pseudotyped Ad particles may also be reduced if the fibers used are from Ads with lower seroprevalence in humans or experimental models, a situation that favours successful administration of the vector (Nicklin et al. *Molecular Therapy* (2005) 12:384–393). Furthermore, full length fiber as well as isolated fiber knob regions, but not hexon or penton alone, are capable of inducing dendritic cell maturation and are associated with induction of a potent CD8+ T cell response (Molinier-Frenkel et al. *J. Biol. Chem.* (2003) 278:37175-37182). Taken together, adenoviral fiber plays an important role in at least receptor-binding and immunogenicity of adenoviral vectors.
- Illustrating the differences between the fiber proteins of Group C simian adenoviruses is the alignment provided in Figure 1. A striking feature is that the fiber sequences of these adenoviruses can be broadly grouped into having a short fiber, such as ChAd157, or long fiber, such as ChAd155. This length differential is due to a 36 amino acid deletion at approximately position 321 in the short fiber relative to the long fiber. In addition, there are a number of amino acid substitutions that differ between the short versus long fiber subgroup yet are consistent within each subgroup. While the exact function of these differences have not yet been elucidated, given the function and immunogenicity of fiber, they are likely to be significant. It has been shown that one of the determinants of viral tropism is the length of the fiber shaft. It has been demonstrated that an Ad5 vector with a shorter shaft has a lower efficiency of binding to CAR receptor and a lower infectivity (Ambriović-Ristov A. et al.: *Virology*. (2003) 312(2):425-33): It has been speculated that this impairment is the result of an increased rigidity of the shorter fiber leading to a less efficient attachment to the cell receptor (Wu, E et al.: *J Virol.* (2003) 77(13): 7225–7235).
- In one aspect of the invention there is provided an isolated fiber polypeptide of chimpanzee adenovirus ChAd157 and isolated polynucleotides encoding the fiber polypeptide of chimpanzee adenovirus ChAd157.
- The fiber protein is expected to contribute to low seroprevalence and can, thus, be used independently from the hexon and penton polypeptides from ChAd157 or in combination (with one or both of the hexon and penton) to suppress the affinity of an adenovirus to preexisting neutralizing antibodies, e.g. to manufacture a recombinant adenovirus with a reduced seroprevalence. Such a recombinant adenovirus may be a chimeric adenovirus with capsid proteins from different serotypes with at least a fiber protein from ChAd157.
- The ChAd157 fiber polypeptide sequence is provided in SEQ ID NO: 1.  
The ChAd157 penton polypeptide sequence is provided in SEQ ID NO: 3.  
The ChAd157 hexon polypeptide sequence is provided in SEQ ID NO: 5.

Polypeptides, Recombinant Adenoviruses, Compositions or Cells Comprising Polypeptide Sequences of ChAd157 Fiber or a Functional Derivative Thereof

- 5 Suitably the isolated polypeptide, recombinant adenovirus, composition or cell of the invention comprises a polypeptide having the amino acid sequence according to SEQ ID NO: 1.

The polypeptide, recombinant adenovirus, composition or cell of the invention may comprise a polypeptide which is a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

15 Alternatively the functional derivative has no more than one addition, deletion or substitution compared to SEQ ID NO: 1, such as one substitution compared to SEQ ID NO: 1.

Suitably the polypeptide, recombinant adenovirus, composition or cell according to the invention further comprises:

- 20 (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3; or  
(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,

and/or

- 25 (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5; or  
(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

30 Suitably, the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3 has an amino acid sequence which is at least 70% identical over its entire length to the amino acid sequence of SEQ ID NO: 3, such as at least 80%, especially at least 90%, for example at least 95% or at least 98%.

35 Suitably, the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5 has an amino acid sequence which is at least 70% identical over its entire length to the amino acid sequence of SEQ ID NO: 5, such as at least 80%, especially at least 90%, for example at least 95% or at least 98%.

40 In particular, the polypeptide, recombinant adenovirus, composition or cell according to the invention further comprises:

- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;

and/or

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 5.

5 Isolated Polynucleotides, Vectors, Recombinant Adenoviruses, Compositions or Cells  
comprising Polynucleotides Encoding ChAd157 Fiber or a Functional Derivative Thereof

Suitably the isolated polynucleotide, vector, recombinant adenovirus, composition or cell of the invention comprises a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1. Suitably the polynucleotide has a sequence according to SEQ ID NO: 2.

When the isolated polynucleotide, vector, recombinant adenovirus, composition or cell of the invention comprises a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1, suitably the polynucleotide has a sequence according to SEQ ID NO: 2 wherein one codon has been added, deleted or altered to encode a different amino acid.

20 Suitably the polynucleotide, vector, recombinant adenovirus, composition or cell of the invention further comprises a polynucleotide encoding:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3; or

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,

and/or

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5; or

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

Suitably, the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3 has an amino acid sequence which is at least 70% identical over its entire length to the amino acid sequence of SEQ ID NO: 3, such as at least 80%, especially at least 90%, for example at least 95% or at least 98%.

Suitably, the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5 has an amino acid sequence which is at least 70% identical over its entire length to the amino acid sequence of SEQ ID NO: 5, such as at least 80%, especially at least 90%, for example at least 95% or at least 98%.

In particular, the polynucleotide, vector, recombinant adenovirus, composition or cell of the invention further comprises a polynucleotide encoding:

- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;  
and/or
- 5 (b) a polypeptide having the amino acid sequence according to SEQ ID NO: 5.

The polynucleotide, vector, recombinant adenovirus, composition or cell of the invention may further comprise:

- (a) a polynucleotide according to SEQ ID NO: 4;  
10 and/or
- (b) a polynucleotide according to SEQ ID NO: 6.

### ChAd157 Backbones

- 15 The invention provides isolated polynucleotide sequences of chimpanzee adenovirus ChAd157, including that of wild type, unmodified ChAd157 and modified backbone constructs of ChAd157. These modified backbone constructs include those exemplified herein, such as pChAd157ΔE1 TetO hCMV RpsL-Kana#1551 (SEQ ID NO: 15) and ChAd157 ΔE1E4\_Ad5E4orf6/TetO hCMV RpsL-Kana#1594 (SEQ ID NO: 22). ChAd157 backbones  
20 may be used in the construction of recombinant replication-competent or replication-incompetent adenoviruses for example for the delivery of transgenes.

Annotation of the pChAd157 ΔE1/TetO hCMV GAG (SEQ ID NO: 17) sequence is provided below.

25 Annotations ChAd157DE1\_TetOhCMV\_GAG  
IX 3187..3651  
IVa2 Complement (3710..5045,5325..5337)  
Pol Complement(4816..8397, 13762..13770)  
30 VA RNAI 10230..10391  
pTP Complement(8196..10199,13762..13770)  
48K 10652..11914  
pIIIa 11938..13714  
III 13807..15588  
35 pVII 15603..16199  
V 16275..17390  
pX 17415..17660  
pVI 17750..18508  
Hexon 18623..21499  
40 Protease 21529..22158  
DBP Complement(22274..23926)  
92K 23976..26447  
22K 26164..26739  
33K Join(26164..26473,26679..27061)  
45 E2e promoter Complement(27027..27274)  
pVIII 27136..27819  
E3 12K 27820..28137  
E3 CR1-alphap0 28635..28835  
E3 gp18K 28838..29329

E3A 11K 30776..31072  
 E3 RID alpha 31084..31356  
 E3 RID beta 31359..31757  
 E3 15K 31750..32136  
 5 U exon Complement(32167..32331)  
 fibre 32342..33973  
 E4 ORF6/7 Complement(34181..34456,35168..35341)  
 E4 ORF6 Complement(34457..35341)  
 E4 ORF4 Complement(35241..35606)  
 10 E4 ORF3 Complement(35622..35969)  
 E4 ORF2 Complement(35966..36358)  
 E4 ORF1 Complement(36411..36797)

In one embodiment, fragments of the sequences of SEQ ID NO: 15, 22 and their  
 15 complementary strands, cDNA and RNA complementary thereto are provided. Suitably,  
 fragments are at least 15 nucleotides in length, more suitably 30 nucleotides in length, more  
 suitably 60 nucleotides in length, more suitably 120 nucleotides in length, more suitably 240,  
 more suitably 480 nucleotides in length and encompass functional fragments, i.e., fragments  
 20 which are of biological interest. For example, a functional fragment can express a desired  
 adenoviral product or may be useful in production of recombinant viral vectors. Such  
 fragments include the gene sequences listed above. In certain embodiments isolated  
 sequences of SEQ ID NO: 15, 22 and their complementary strands, cDNA and RNA  
 complementary thereto are provided.

25 Gene products of the ChAd157 adenovirus, such as proteins, enzymes, and fragments thereof,  
 which are encoded by the adenoviral nucleic acids, and the aforementioned fragments thereof,  
 described herein are provided. Such proteins include those encoded by the open reading  
 frames identified above and the proteins encoded by the polynucleotides provided in the  
 Sequence Listing.

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### Further ChAd157 Polynucleotides and Polypeptides

In some embodiments the polynucleotide of the invention comprises a polynucleotide encoding  
 a fiber polypeptide; a hexon polypeptide and fiber polypeptide; penton polypeptide and fiber  
 35 polypeptide; or hexon polypeptide, penton polypeptide and fiber polypeptide of the invention;  
 and may further comprise additional adenoviral polynucleotides, suitably ChAd157  
 polynucleotides. Thus, suitably the polynucleotide according to the invention comprises one or  
 more of the following:

- (a) an adenoviral 5'-inverted terminal repeat (ITR);
- 40 (b) an adenoviral E1A region, or a fragment thereof selected from among the  
 E1A\_280R and E1A\_243R regions;
- (c) an adenoviral E1B or IX region, or a fragment thereof selected from among the  
 group consisting of the E1B\_19K, E1B\_55K and IX regions;
- (d) an adenoviral E2B region; or a fragment thereof selected from among the group  
 45 consisting of the E2B\_pTP, E2B\_polymerase and E2B\_IVa2 regions;

- (e) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1\_13.6K, L1\_52K and L1\_pIIIa protein;
- 5 (f) an adenoviral L2 region or a L2 region comprising a polynucleotide encoding the penton protein of the invention, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2\_penton protein, the L2\_pVII protein, the L2\_V protein and the L2\_pX protein;
- (g) an adenoviral L3 region or a L3 region comprising a polynucleotide encoding the hexon protein of the invention, or a fragment thereof, said fragment encoding an
- 10 adenoviral protein selected from the group consisting of the L3\_pVI protein, the L3\_hexon protein and the L3\_protease protein;
- (h) an adenoviral E2A region;
- (i) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4\_100k protein, the L4\_33K protein,
- 15 the L4\_22K protein and protein L4\_VIII;
- (j) an adenoviral E3 region, or a fragment thereof selected from the group consisting of E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, and E3 ORF9;
- (k) an adenoviral L5 region or a L5 region comprising a polynucleotide encoding the
- 20 L5\_fiber fiber polypeptide of the invention
- (l) an adenoviral (such as Ad5) E4 region, or a fragment thereof selected from the group consisting of E4 ORF7, E4 ORF6, E4 ORF4, E4 ORF3, E4 ORF2, and E4 ORF1; in particular ORF6 of said E4 region;
- (m) an adenoviral 3'-ITR; and/or
- 25 (n) an adenoviral VAI or VAII RNA region, preferably an adenoviral VAI or VAII RNA region from an adenovirus other than ChAd157, more preferably from Ad5.

### Definitions

30 Suitably the polynucleotides or polypeptides of the invention are isolated. An "isolated" polynucleotide is one that is removed from its original environment. For example, a naturally-occurring polynucleotide is isolated if it is separated from some or all of the coexisting materials in the natural system. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of its natural environment or if it is comprised within

35 cDNA.

Suitably the polynucleotides of the invention are recombinant. Recombinant means that the polynucleotide is the product of at least one of cloning, restriction or ligation steps, or other procedures that result in a polynucleotide that is distinct from a polynucleotide found in nature.

40 A recombinant adenovirus is an adenovirus comprising a recombinant polynucleotide. A recombinant vector is a vector comprising a recombinant polynucleotide. 'A recombinant virus' includes progeny of the original recombinant virus. 'A recombinant vector' includes replicates

of the original recombinant vector. 'A recombinant polynucleotide' includes replicates of the original recombinant polynucleotide.

5 Suitably, the polypeptide sequence of the present invention contains at least one alteration with respect to a native sequence. Suitably, the polynucleotide sequences of the present invention contain at least one alteration with respect to a native sequence. For example, a polynucleotide introduced by genetic engineering techniques into a plasmid or vector derived from a different species (and often a different genus, subfamily or family) is a heterologous polynucleotide. A promoter removed from its native coding sequence and operatively linked to a coding sequence with which it is not naturally found linked is a heterologous promoter. A specific recombination site that has been cloned into a genome of a virus or viral vector, wherein the genome of the virus does not naturally contain it, is a heterologous recombination site. A heterologous nucleic acid sequence also includes a sequence naturally found in an adenoviral genome, but located at a non-native position within the adenoviral vector.

15 Typically, "heterologous" means derived from a genotypically distinct entity from that of the rest of the entity to which it is being compared. A heterologous nucleic acid sequence refers to any nucleic acid sequence that is not isolated from, derived from, or based upon a naturally occurring nucleic acid sequence of the adenoviral vector. A heterologous protein sequence refers to any protein sequence that is not isolated from, derived from, or based upon a naturally occurring protein sequence of the adenoviral vector "Naturally occurring" means a sequence found in nature and not synthetically prepared or modified. A sequence is "derived" from a source when it is isolated from a source but modified (e.g., by deletion, substitution (mutation), insertion, or other modification), suitably so as not to disrupt the normal function of the source gene.

20 A "functional derivative" of a polypeptide suitably refers to a modified version of a polypeptide, e.g. wherein one or more amino acids of the polypeptide may be deleted, inserted, modified and/or substituted. A derivative of an unmodified adenoviral capsid protein is considered functional if, for example:

- 25 (a) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a lower seroprevalence compared to an adenovirus comprising the unmodified capsid protein and/or
- 35 (b) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a higher host cell infectivity compared to an adenovirus comprising the unmodified capsid protein and/or
- (c) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a higher immunogenicity compared to an adenovirus comprising the unmodified capsid protein and/or
- 40 (d) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a higher level of transgene productivity compared to an adenovirus comprising the unmodified capsid protein.

Properties (a)-(d) above may suitably be measured using the methods described in the Examples section below.

5 Suitably, the polypeptide, vector or recombinant adenovirus has a low seroprevalence in a human population. "Low seroprevalence" may mean having a reduced pre-existing neutralizing antibody level as compared to human adenovirus 5 (Ad5). Similarly or alternatively, "low seroprevalence" may mean less than about 20% seroprevalence, less than about 15% seroprevalence, less than about 10% seroprevalence, less than about 5% seroprevalence, 10 less than about 4% seroprevalence, less than about 3% seroprevalence, less than about 2% seroprevalence, less than about 1% seroprevalence or no detectable seroprevalence. Seroprevalence can be measured as the percentage of individuals having a clinically relevant neutralizing titre (defined as a 50% neutralisation titer >200) using methods as described in Aste-Amézaga *et al.*, *Hum. Gene Ther.* (2004) 15(3):293-304.

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The terms polypeptide, peptide and protein are used interchangeably herein.

The term "simian" is typically meant to encompass nonhuman primates, for example Old World monkeys, New World monkeys, apes and gibbons. In particular, simian may refer to 20 nonhuman apes such as chimpanzees (*Pan troglodyte*), bonobos (*Pan paniscus*) and gorillas (genus *Gorilla*). Non-ape simians may include rhesus macaques (*Macaca mulatta*).

### Sequence Comparison

25 For the purposes of comparing two closely-related polynucleotide or polypeptide sequences, the "% identity" between a first sequence and a second sequence may be calculated using an alignment program, such as BLAST® (available at [blast.ncbi.nlm.nih.gov](http://blast.ncbi.nlm.nih.gov), last accessed 09 March 2015) using standard settings. The % identity is the number of identical residues divided by the number of residues in the reference sequence, multiplied by 100. The % 30 identity figures referred to above and in the claims are percentages calculated by this methodology. An alternative definition of % identity is the number of identical residues divided by the number of aligned residues, multiplied by 100. Alternative methods include using a gapped method in which gaps in the alignment, for example deletions in one sequence relative to the other sequence, are accounted for in a gap score or a gap cost in the scoring parameter. 35 For more information, see the BLAST® fact sheet available at [ftp.ncbi.nlm.nih.gov/pub/factsheets/HowTo\\_BLASTGuide.pdf](http://ftp.ncbi.nlm.nih.gov/pub/factsheets/HowTo_BLASTGuide.pdf), last accessed on 09 March 2015.

40 Sequences that preserve the functionality of the polynucleotide or a polypeptide encoded thereby are likely to be more closely identical. Polypeptide or polynucleotide sequences are said to be the same as or identical to other polypeptide or polynucleotide sequences, if they share 100% sequence identity over their entire length.



A "difference" between sequences refers to an insertion, deletion or substitution of a single amino acid residue in a position of the second sequence, compared to the first sequence. Two polypeptide sequences can contain one, two or more such amino acid differences. Insertions, deletions or substitutions in a second sequence which is otherwise identical (100% sequence identity) to a first sequence result in reduced percent sequence identity. For example, if the identical sequences are 9 amino acid residues long, one substitution in the second sequence results in a sequence identity of 88.9%. If the identical sequences are 17 amino acid residues long, two substitutions in the second sequence results in a sequence identity of 88.2%. If the identical sequences are 7 amino acid residues long, three substitutions in the second sequence results in a sequence identity of 57.1%. If first and second polypeptide sequences are 9 amino acid residues long and share 6 identical residues, the first and second polypeptide sequences share greater than 66% identity (the first and second polypeptide sequences share 66.7% identity). If first and second polypeptide sequences are 17 amino acid residues long and share 16 identical residues, the first and second polypeptide sequences share greater than 94% identity (the first and second polypeptide sequences share 94.1% identity). If first and second polypeptide sequences are 7 amino acid residues long and share 3 identical residues, the first and second polypeptide sequences share greater than 42% identity (the first and second polypeptide sequences share 42.9% identity).

Alternatively, for the purposes of comparing a first, reference polypeptide sequence to a second, comparison polypeptide sequence, the number of additions, substitutions and/or deletions made to the first sequence to produce the second sequence may be ascertained. An addition is the addition of one amino acid residue into the sequence of the first polypeptide (including addition at either terminus of the first polypeptide). A substitution is the substitution of one amino acid residue in the sequence of the first polypeptide with one different amino acid residue. A deletion is the deletion of one amino acid residue from the sequence of the first polypeptide (including deletion at either terminus of the first polypeptide).

For the purposes of comparing a first, reference polynucleotide sequence to a second, comparison polynucleotide sequence, the number of additions, substitutions and/or deletions made to the first sequence to produce the second sequence may be ascertained. An addition is the addition of one nucleotide residue into the sequence of the first polynucleotide (including addition at either terminus of the first polynucleotide). A substitution is the substitution of one nucleotide residue in the sequence of the first polynucleotide with one different nucleotide residue. A deletion is the deletion of one nucleotide residue from the sequence of the first polynucleotide (including deletion at either terminus of the first polynucleotide).

Suitably substitutions in the sequences of the present invention may be conservative substitutions. A conservative substitution comprises the substitution of an amino acid with another amino acid having a chemical property similar to the amino acid that is substituted (see, for example, Stryer et al, *Biochemistry*, 5<sup>th</sup> Edition 2002, pages 44-49). Preferably, the conservative substitution is a substitution selected from the group consisting of: (i) a substitution of a basic amino acid with another, different basic amino acid; (ii) a substitution of

an acidic amino acid with another, different acidic amino acid; (iii) a substitution of an aromatic amino acid with another, different aromatic amino acid; (iv) a substitution of a non-polar, aliphatic amino acid with another, different non-polar, aliphatic amino acid; and (v) a substitution of a polar, uncharged amino acid with another, different polar, uncharged amino acid. A basic amino acid is preferably selected from the group consisting of arginine, histidine, and lysine. An acidic amino acid is preferably aspartate or glutamate. An aromatic amino acid is preferably selected from the group consisting of phenylalanine, tyrosine and tryptophane. A non-polar, aliphatic amino acid is preferably selected from the group consisting of glycine, alanine, valine, leucine, methionine and isoleucine. A polar, uncharged amino acid is preferably selected from the group consisting of serine, threonine, cysteine, proline, asparagine and glutamine. In contrast to a conservative amino acid substitution, a non-conservative amino acid substitution is the exchange of one amino acid with any amino acid that does not fall under the above-outlined conservative substitutions (i) through (v).

#### 15 **Vectors and Recombinant Adenovirus**

The ChAd157 sequences of the invention are useful as therapeutic agents and in construction of a variety of vector systems, recombinant adenovirus and host cells. Suitably the term "vector" refers to a nucleic acid that has been substantially altered (e.g., a gene or functional region that has been deleted and/or inactivated) relative to a wild type sequence and/or incorporates a heterologous sequence, *i.e.*, nucleic acid obtained from a different source (also called an "insert"), and replicating and/or expressing the inserted polynucleotide sequence, when introduced into a cell (e.g., a host cell). For example, the insert may be all or part of the ChAd157 sequences described herein. In addition or alternatively, a ChAd157 vector may be a ChAd157 adenovirus comprising one or more deletions or inactivations of viral genes, such as E1 or other viral gene or functional region described herein. Such a ChAd157, which may or may not comprise a heterologous sequence, is often called a "backbone" and may be used as is or as a starting point for additional modifications to the vector.

A vector may be any suitable nucleic acid molecule including naked DNA, a plasmid, a virus, a cosmid, phage vector such as lambda vector, an artificial chromosome such as a BAC (bacterial artificial chromosome), or an episome. Alternatively, a vector may be a transcription and/or expression unit for cell-free *in vitro* transcription or expression, such as a T7-compatible system. The vectors may be used alone or in combination with other adenoviral sequences or fragments, or in combination with elements from non-adenoviral sequences. The ChAd157 sequences are also useful in antisense delivery vectors, gene therapy vectors, or vaccine vectors. Thus, further provided are gene delivery vectors, and host cells which contain the ChAd157 sequences.

The term "replication-competent" adenovirus refers to an adenovirus which can replicate in a host cell in the absence of any recombinant helper proteins comprised in the cell. Suitably, a "replication-competent" adenovirus comprises the following intact or functional essential early

genes: E1A, E1B, E2A, E2B, E3 and E4. Wild type adenoviruses isolated from a particular animal will be replication competent in that animal.

5 The term "replication-incompetent" or "replication-defective" adenovirus refers to an adenovirus which is incapable of replication because it has been engineered to comprise at least a functional deletion (or "loss-of-function" mutation), i.e. a deletion or mutation which impairs the function of a gene without removing it entirely, e.g. introduction of artificial stop codons, deletion or mutation of active sites or interaction domains, mutation or deletion of a regulatory sequence of a gene etc, or a complete removal of a gene encoding a gene product that is  
10 essential for viral replication, such as one or more of the adenoviral genes selected from E1A, E1B, E2A, E2B, E3 and E4 (such as E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, E3 ORF9, E4 ORF7, E4 ORF6, E4 ORF4, E4 ORF3, E4 ORF2 and/or E4 ORF1). Particularly suitably E1 and optionally E3 and/or E4 are deleted. If deleted, the aforementioned deleted gene region will suitably not be considered in the alignment when  
15 determining % identity with respect to another sequence.

The present invention provides vectors such as recombinant adenovirus that deliver a protein, suitably a heterologous protein, to cells, either for therapeutic or vaccine purposes. A vector  
20 may include any genetic element including naked DNA, a phage, transposon, cosmid, episome, plasmid, or a virus. Such vectors contain DNA of ChAd157 as disclosed herein and a minigene. By "minigene" (or "expression cassette") 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.

25 Typically, a ChAd157-derived adenoviral vector is designed such that the minigene is located in a nucleic acid molecule which contains other adenoviral sequences in the region native to a selected adenoviral gene. The minigene may be inserted into an existing gene region to disrupt the function of that region, if desired. Alternatively, the minigene may be inserted into the site of a partially or fully deleted adenoviral gene. For example, the minigene may be  
30 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  
35 (and suitably replaced with the minigene).

For example, for a production vector useful for generation of a recombinant virus, the vector may contain the minigene and either the 5' end of the adenoviral genome or the 3' end of the adenoviral genome, or both the 5' and 3' ends of the adenoviral genome. The 5' end of the  
40 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. Suitably, a recombinant adenovirus contains both 5' and 3' adenoviral cis-elements and the minigene (suitably containing a transgene) is located between the 5' and 3' adenoviral sequences. A ChAd157-based adenoviral vector may also contain additional adenoviral sequences.

5

Suitably, ChAd157-based vectors contain one or more adenoviral elements derived from the adenoviral ChAd157 genome of the invention. In one embodiment, the vectors contain adenoviral ITRs from ChAd157 and additional adenoviral sequences from the same adenoviral serotype. In another embodiment, the vectors contain adenoviral sequences that are derived from a different adenoviral serotype than that which provides the ITRs.

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As defined herein, a pseudotyped adenovirus refers to an adenovirus in which the capsid proteins of the adenovirus are from a different adenovirus than the adenovirus which provides the ITRs.

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Further, chimeric or hybrid adenoviruses may be constructed using the adenoviruses described herein using techniques known to those of skill in the art (e.g., US 7,291,498).

ITRs and any other adenoviral sequences present in the vector of the present invention may be obtained from many sources. A variety of adenovirus strains are available from the American Type Culture Collection, Manassas, Virginia, or available by request from a variety of commercial and institutional sources. Further, the sequences of many such strains are available from a variety of databases including, e.g., PubMed and GenBank. Homologous adenovirus vectors prepared from other chimpanzee or from human adenoviruses are described in the published literature (for example, US 5,240,846). The DNA sequences of a number of adenovirus types are available from GenBank, including type Ad5 (GenBank Accession Number M73370). The adenovirus sequences may be obtained from any known adenovirus serotype, such as serotypes 2, 3, 4, 7, 12 and 40, and further including any of the presently identified human types. Similarly adenoviruses known to infect nonhuman animals (e.g., simians) may also be employed in the vector constructs of this invention (e.g., US 6,083,716). The viral sequences, helper viruses (if needed), and recombinant viral particles, and other vector components and sequences employed in the construction of the vectors described herein may be obtained as described below.

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### 35 **Sequence, Vector and Adenovirus Production**

The sequences of the invention may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Suitable production techniques are well known to those of skill in the art. Alternatively, peptides can also be synthesized by well-known solid phase peptide synthesis methods.

40

The adenoviral plasmids (or other vectors) may be used to produce adenoviral vectors. In one embodiment, the adenoviral vectors are adenoviral particles which are replication-incompetent.

In one embodiment, the adenoviral particles are rendered replication-incompetent by deletions in the E1A and/or E1B genes, in particular the E1A and E1B. Alternatively, the adenoviruses are rendered replication-incompetent by another means, optionally while retaining the E1A and/or E1B genes. Similarly, in some embodiments, reduction of an immune response to the  
5 vector may be accomplished by deletions in the E2B and/or DNA polymerase genes. The adenoviral vectors can also contain other mutations to the adenoviral genome, e.g., temperature-sensitive mutations or deletions in other genes. In other embodiments, it is desirable to retain an intact E1A and/or E1B region in the adenoviral vectors. Such an intact E1 region may be located in its native location in the adenoviral genome or placed in the site of  
10 a deletion in the native adenoviral genome (e.g., in the E3 region).

In the construction of adenovirus vectors for delivery of a gene to a mammalian (such as human) cell, a range of modified adenovirus nucleic acid sequences can be employed in the vectors. For example, all or a portion of the adenovirus delayed early gene E3 may be  
15 eliminated from the adenovirus sequence which forms a part of the recombinant virus. The function of E3 is believed to be irrelevant to the function and production of the recombinant virus particle. Adenovirus vectors may also be constructed having a deletion of at least the ORF6 region of the E4 gene, and more desirably because of the redundancy in the function of this region, the entire E4 region. Still another vector of the invention contains a deletion in the  
20 delayed early gene E2A. Deletions may also be made in any of the late genes L1 to L5 of the adenovirus genome. Similarly, deletions in the intermediate genes IX and IVa2 may be useful for some purposes. Other deletions may be made in the other structural or non-structural adenovirus genes. The above discussed deletions may be used individually, i.e., an adenovirus sequence for use as described herein may contain deletions in only a single  
25 region. 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 sequence 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, or of E1, E2A and E4 genes, with or without deletion of E3, and so on. Any one or more of the E genes may suitably be replaced with an E  
30 gene (or one or more E gene open reading frames) sourced from a different strain of adenovirus. Particularly suitably the ChAd157 E1 and E3 genes are deleted and the ChAd157E4 gene is replaced with E4Ad5orf6. As discussed above, such deletions and/or substitutions may be used in combination with other mutations, such as temperature-sensitive mutations, to achieve a desired result.

35 An adenoviral vector lacking one or more essential adenoviral sequences (e.g., E1A, E1B, E2A, E2B, E4 ORF6, L1, L2, L3, L4 and L5) may be cultured in the presence of the missing adenoviral gene products which are required for viral infectivity and propagation of an adenoviral particle. These helper functions may be provided by culturing the adenoviral vector  
40 in the presence of one or more helper constructs (e.g., a plasmid or virus) or a packaging host cell.

#### Complementation of Replication-Incompetent Vectors

To generate recombinant adenoviruses deleted in any of the genes described above, the function of the deleted gene region, if essential to the replication and infectivity of the virus, must be supplied to the recombinant virus by a helper virus or cell line, i.e., a complementation or packaging cell line.

#### *Helper Viruses*

Depending upon the adenovirus gene content of the viral vectors employed to carry the minigene, a helper adenovirus or non-replicating virus fragment may be used to provide sufficient adenovirus gene sequences necessary to produce an infective recombinant viral particle containing the minigene. Useful helper viruses contain selected adenovirus gene sequences not present in the adenovirus vector construct and/or not expressed by the packaging cell line in which the vector is transfected. In one embodiment, the helper virus is replication-defective and contains adenovirus genes in addition, suitably, to one or more of the sequences described herein. Such a helper virus is suitably used in combination with an E1 expressing (and optionally additionally E3 expressing) cell line.

A helper virus may optionally contain a reporter gene. A number of such reporter genes are known to the art as well as described herein. The presence of a reporter gene on the helper virus which is different from the transgene on the adenovirus vector allows both the adenoviral vector and the helper virus to be independently monitored. This reporter is used to enable separation between the resulting recombinant virus and the helper virus upon purification.

#### *Complementation Cell Lines*

In many circumstances, a cell line expressing the one or more missing genes which are essential to the replication and infectivity of the virus, such as human E1, can be used to transcomplement a chimpanzee adenoviral vector. This is particularly advantageous because, due to the diversity between the chimpanzee adenovirus sequences of the invention and the human adenovirus sequences found in currently available packaging cells, the use of the current human E1-containing cells prevents the generation of replication-competent adenoviruses during the replication and production process.

Alternatively, if desired, one may utilize the sequences provided herein to generate a packaging cell or cell line that expresses, at a minimum, the E1 gene from ChAd157 or from another adenovirus (such as human adenovirus, e.g. hAd5 E1, or another ChAd E1) under the transcriptional control of a promoter for expression in a selected parent cell line. Inducible or constitutive promoters may be employed for this purpose. Examples of such promoters are described in detail elsewhere in this document. A parent cell is selected for the generation of a novel cell line expressing any desired ChAd157 gene. Without limitation, such a parent 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.

5 Such E1-expressing cell lines are useful in the generation of recombinant adenovirus E1 deleted vectors. Additionally, or alternatively, cell lines that express one or more adenoviral gene products, e.g., E1A, E1B, E2A, E3 and/or E4, can be constructed using essentially the same procedures as used in the generation of recombinant viral vectors. Such cell lines can be utilised to transcomplement adenovirus vectors deleted in the essential genes that encode those products, or to provide helper functions necessary for packaging of a helper-dependent virus (e.g., adeno-associated virus). The preparation of a host cell involves techniques such as assembly of selected DNA sequences.

15 In another alternative, the essential adenoviral gene products are provided in trans by the adenoviral vector and/or helper virus. In such an instance, a suitable host cell can be selected from any biological organism, including prokaryotic (e.g., bacterial) cells, and eukaryotic cells, including, insect cells, yeast cells and mammalian cells.

20 Host cells may be selected from among any mammalian species, including, without limitation, cells such as A549, WEHI, 3T3, 10T1/2, HEK 293 cells or Per.C6 (both of which express functional adenoviral E1) [Fallaux, FJ et al, (1998), Hum Gene Ther, 9:1909-1917], Saos, C2C12, L cells, HT1080, HepG2 and primary fibroblast, hepatocyte and myoblast cells derived from mammals including human, monkey, mouse, rat, rabbit, and hamster.

25 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 useful for producing adenoviral vectors expressing toxic proteins ([www.okairos.com/e/inners.php?m=00084](http://www.okairos.com/e/inners.php?m=00084), last accessed 13 April 2015).

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#### Assembly of a Viral Particle and Transfection of a Cell Line

35 Generally, when delivering the vector comprising the minigene by transfection, the vector is delivered in an amount from about 5 µg to about 100 µg DNA, and preferably about 10 to about 50 µg DNA to about  $1 \times 10^4$  cells to about  $1 \times 10^{13}$  cells, and preferably about  $10^5$  cells. However, the relative amounts of vector DNA to host cells may be adjusted, taking into consideration such factors as the selected vector, the delivery method and the host cells selected.

40 Introduction into the host cell of the vector may be achieved by any means known in the art, including transfection, and infection. One or more of the adenoviral genes may be stably integrated into the genome of the host cell, stably expressed as episomes, or expressed transiently. The gene products may all be expressed transiently, on an episome or stably

integrated, or some of the gene products may be expressed stably while others are expressed transiently.

5 Introduction of vectors into the host cell may also be accomplished using techniques known to the skilled person. Suitably, standard transfection techniques are used, e.g., CaPC transfection or electroporation.

10 Assembly of the selected DNA sequences of the adenovirus (as well as the transgene and other vector elements) into various intermediate plasmids, and the use of the plasmids and vectors to produce a recombinant viral particle are all achieved using conventional techniques. Such techniques include conventional cloning techniques of cDNA, use of overlapping oligonucleotide sequences of the adenovirus genomes, polymerase chain reaction, and any suitable method which provides the desired nucleotide sequence. Standard transfection and co-transfection techniques are employed, e.g., CaPC precipitation techniques. Other  
15 conventional methods employed include homologous recombination of the viral genomes, plaquing of viruses in agar overlay, methods of measuring signal generation, and the like.

For example, following the construction and assembly of the desired minigene-containing viral vector, the vector is transfected in vitro in the presence of a helper virus into the packaging cell  
20 line. Homologous recombination occurs between the helper and the vector sequences, which permits the adenovirus-transgene sequences in the vector to be replicated and packaged into virion capsids, resulting in the recombinant viral vector particles. The resulting recombinant adenoviruses are useful in transferring a selected transgene to a selected cell. In in vivo experiments with the recombinant virus grown in the packaging cell lines, the E1-deleted  
25 recombinant adenoviral vectors of the invention demonstrate utility in transferring a transgene to a non-simian mammal, preferably a human, cell.

### Transgenes

30 The transgene is a nucleic acid sequence, heterologous to the vector sequences flanking the transgene, which encodes a protein of interest. The nucleic acid coding sequence is operatively linked to regulatory components in a manner which permits transgene transcription, translation, and/or expression in a host cell.

35 The composition of the transgene sequence will depend upon the use to which the resulting vector will be put. For example, the transgene may be a therapeutic transgene or an immunogenic transgene. Alternatively, a transgene sequence may include a reporter sequence, which upon expression produces a detectable signal. Such reporter sequences include, without limitation, DNA sequences encoding  $\beta$ -lactamase,  $\beta$ -galactosidase (LacZ),  
40 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 one embodiment, the transgene is a non-marker sequence encoding a product which is useful in biology and medicine, such as a therapeutic transgene or an immunogenic transgene such as proteins, RNA, enzymes, or catalytic RNAs. Desirable RNA molecules include tRNA, dsRNA, ribosomal RNA, catalytic RNAs, and antisense RNAs. One example of a useful RNA sequence is a sequence which extinguishes expression of a targeted nucleic acid sequence in the treated animal.

The transgene may be used for treatment, e.g., of genetic deficiencies, as a cancer therapeutic or vaccine, for induction of an immune response, and/or for prophylactic vaccine purposes. As used herein, induction of an immune response refers to the ability of a protein to induce a T cell and/or a humoral immune response to the protein.

The term prophylaxis means the provision of a medicament in advance, this may be in advance of exposure to a pathogen (pre-exposure prophylaxis) or in advance of the development of disease symptoms (post-exposure prophylaxis). The terms treatment and therapy are used interchangeably herein and mean the administration of medicament during disease.

By the term disease is meant a disorder of structure or function in a subject, especially one that produces specific symptoms or that affects a specific location and is not simply a direct result of physical injury.

### 30 Regulatory Elements

In addition to the transgene the vector 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 plasmid vector or infected with the virus produced by the invention. 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.

5 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. An exemplary WPRE is provided in SEQ ID NO: 26.

10 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  
15 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)),  
20 the CASI promoter, the SV40 promoter, the dihydrofolate reductase promoter, the  $\beta$ -actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1a promoter (Invitrogen).

In some embodiments, the promoter is a CASI promoter (see, for example, WO2012/115980). The CASI promoter is a synthetic promoter which contains a portion of the CMV enhancer, a  
25 portion of the chicken beta-actin promoter, and a portion of the UBC enhancer. In some embodiments, the CASI promoter can include a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more, sequence identity to SEQ ID NO: 12. In some embodiments, the promoter comprises or consists of a nucleic acid sequence of SEQ ID NO: 12.  
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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  
35 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  
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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  
5 enhance the effectiveness of such systems by inserting multiple repressors in tandem, e.g., TetR linked to a TetR by an IRES.

In some embodiments the promoter is an enhanced hCMV promoter, such as provided in SEQ  
10 ID NO: 42.

In another embodiment, the native promoter for the transgene will be used. The native promoter may be preferred when it is desired that expression of the transgene should mimic the native expression. The native promoter may be used when expression of the transgene must be regulated temporally or developmentally, or in a tissue-specific manner, or in  
15 response to specific transcriptional stimuli. In a further embodiment, other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

The transgene may be operably linked to a tissue-specific promoter. For instance, if  
20 expression in skeletal muscle is desired, a promoter active in muscle should be used. These include the promoters from genes encoding skeletal  $\beta$ -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  
25 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.

Optionally, vectors carrying transgenes encoding therapeutically useful or immunogenic  
35 products may also include selectable markers or reporter genes which may include sequences encoding geneticin, hygromycin or puromycin resistance, among others. Such selectable reporters or marker genes (preferably located outside the viral genome to be packaged into a viral particle) can be used to signal the presence of the plasmids in bacterial cells, such as ampicillin resistance. Other components of the vector may include an origin of replication.  
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These vectors are generated using the techniques and sequences provided herein, in conjunction with 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.

### **Therapeutics and Prophylaxis**

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The recombinant ChAd157-based vectors are useful for gene transfer to a human or non-simian mammal in vitro, ex vivo, and in vivo.

10 The recombinant adenovirus vectors described herein can be used as expression vectors for the production of the products encoded by the heterologous transgenes in vitro. For example, the recombinant replication-incompetent adenovirus containing a transgene may be transfected into a complementation cell line as described above.

15 A ChAd157-derived recombinant adenoviral vector provides an efficient gene transfer vehicle that can deliver a selected transgene to a selected host cell in vivo or ex vivo even where the organism has neutralizing antibodies to one or more adenovirus serotypes. In one embodiment, the vector and the cells are mixed ex vivo; the infected cells are cultured using conventional methodologies; and the transduced cells are re-infused into the patient. These techniques are particularly well suited to gene delivery for therapeutic purposes and for  
20 immunisation, including inducing protective immunity.

### Immunogenic Transgenes

25 The recombinant ChAd157 vectors may also be administered in immunogenic compositions. An immunogenic composition as described herein is a composition comprising one or more recombinant ChAd157 vector 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 a 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  
30 encoding a desired immunogen and may therefore be used in a vaccine. The recombinant adenoviruses can be used as prophylactic or therapeutic vaccines against any pathogen for which the antigen(s) crucial for induction of an immune response and able to limit the spread of the pathogen has been identified and for which the cDNA is available.

35 By the term immunogen is meant a polypeptide which is capable of eliciting an immune response. Suitably the immunogen is an antigen which comprises at least one B or T cell epitope. The elicited immune response may be an antigen specific B cell response, which produces neutralizing antibodies. The elicited immune response may be an antigen specific T cell response, which may be a systemic and/or a local response. The antigen specific T cell  
40 response may comprise a CD4+ T cell response, such as a response involving CD4+ T cells expressing a plurality of cytokines, e.g. IFN $\gamma$ , TNF $\alpha$  and/or 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., IFN $\gamma$ , TNF $\alpha$  and/or IL2.

5 The term immunise therefore means the administration of an immunogen (or polynucleotide encoding the immunogen as appropriate to the context), to elicit an immune response.

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'. The levels of immunity of the selected gene can be  
10 monitored to determine the need, if any, for boosters. Following an assessment of antibody titers in the serum, optional booster immunizations may be desired.

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. Examples of suitable adjuvants are provided below under 'Adjuvants'. Such an  
15 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. Alternatively, such an adjuvant can be administered with a polypeptide antigen which is administered in an administration regimen  
20 involving the ChAd157 vectors of the invention (as described below under 'Administration Regimens').

The recombinant adenoviruses are administered in an immunogenic amount, that is, an amount of recombinant adenovirus that is effective in a route of administration to transfect the  
25 desired target cells and provide sufficient levels of expression of the selected gene to induce an immune response. Where protective immunity is provided, the recombinant adenoviruses are considered to be vaccine compositions useful in preventing infection and/or recurrent disease.

30 The recombinant vectors described herein are expected to be highly efficacious at inducing cytolytic T cells and antibodies directed to the inserted heterologous antigenic protein expressed by the vector.

Immunogens expressed by the inventive vectors which are useful to immunize a human or  
35 non-human animal against other pathogens include, e.g., bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or from a cancer cell or tumor cell. For example, immunogens may be selected from a variety of viral families. Examples of viral families against which an immune response would be desirable include Lyssaviruses such as rabies viruses, respiratory viruses such as respiratory  
40 syncytial virus (RSV) and other paramyxoviruses such as human metapneumovirus, hMPV and parainfluenza viruses (PIV).

Suitable rabies antigens which are useful as immunogens to immunize a human or non-human animal can be selected from the rabies viral glycoprotein (G), RNA polymerase (L), matrix protein (M), nucleoprotein (N) and phosphoprotein (P). The term "G protein" or "glycoprotein" or "G protein polypeptide" or "glycoprotein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of a rabies glycoprotein polypeptide. The term "L protein" or "RNA polymerase protein" or "L protein polypeptide" or "RNA polymerase protein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of a rabies RNA polymerase protein polypeptide. The term "M protein" or "matrix protein" or "M protein polypeptide" or "matrix protein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of a rabies matrix protein polypeptide. The term "N protein" or "nucleoprotein" or "N protein polypeptide" or "nucleoprotein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of a rabies nucleoprotein polypeptide. The term "P protein" or "phosphoprotein" or "P protein polypeptide" or "phosphoprotein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of a rabies phosphoprotein polypeptide.

Suitable antigens of RSV which are useful as immunogens to immunize a human or non-human animal can be selected from: the fusion protein (F), the attachment protein (G), the matrix protein (M2) and the nucleoprotein (N). The term "F protein" or "fusion protein" or "F protein polypeptide" or "fusion protein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of an RSV Fusion protein polypeptide. Similarly, the term "G protein" or "G protein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of an RSV Attachment protein polypeptide. The term "M protein" or "matrix protein" or "M protein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of an RSV Matrix protein and may include either or both of the M2-1 (which may be written herein as M2.1) and M2-2 gene products. Likewise, the term "N protein" or "Nucleocapsid protein" or "N protein polypeptide" refers to a polypeptide or protein having all or part of an amino acid sequence of an RSV Nucleoprotein.

Two groups of human RSV strains have been described, the A and B groups, based mainly on differences in the antigenicity of the G glycoprotein. Numerous strains of RSV have been isolated to date, any of which are suitable in the context of the antigens of the immunogenic combinations disclosed herein. Exemplary strains indicated by GenBank and/or EMBL Accession number can be found in US published application number 2010/0203071 (WO2008114149), which is incorporated herein by reference for the purpose of disclosing the nucleic acid and polypeptide sequences of RSV F and G proteins suitable for use in present invention. In an embodiment, the RSV F protein can be an ectodomain of an RSV F Protein (F $\Delta$ TM).

Exemplary M and N protein nucleic acids and protein sequences can be found, e.g., in US published application number 2014/0141042 (WO2012/089833), which are incorporated herein for purpose of disclosing the nucleic acid and polypeptide sequences of RSV M and N proteins suitable for use in present invention.

Suitably, for use with in present invention, a nucleic acid encodes an RSV F antigen and RSV, M and N antigens. More specifically, the nucleic acid encodes an RSV F $\Delta$ TM antigen and RSV M2-1 and N antigens, wherein a self-cleavage site is included between the RSV F $\Delta$ TM antigen and the RSV M2-1 and a flexible linker is included between the RSV M2-1 and N antigens. In one embodiment a suitable nucleic acid encodes the polypeptide represented by SEQ ID NO:37

In one embodiment, the immunogen may be from a retrovirus, for example a lentivirus such as the Human Immunodeficiency Virus (HIV). In such an embodiment, immunogens may be derived from HIV-1 or HIV-2.

The HIV genome encodes a number of different proteins, each of which can be immunogenic in its entirety or as a fragment when expressed by vectors of the present invention. Envelope proteins include gp120, gp41 and Env precursor gp160, for example. Non-envelope proteins of HIV include for example internal structural proteins such as the products of the gag and pol genes and other non-structural proteins such as Rev, Nef, Vif and Tat. In an embodiment the vector of the invention encodes one or more polypeptides comprising HIV Gag.

The Gag gene is translated as a precursor polyprotein that is cleaved by protease to yield products that include the matrix protein (p17), the capsid (p24), the nucleocapsid (p9), p6 and two space peptides, p2 and p1, all of which are examples of fragments of Gag.

The Gag gene gives rise to the 55-kilodalton (kD) Gag precursor protein, also called p55, which is expressed from the unspliced viral mRNA. During translation, the N terminus of p55 is myristoylated, triggering its association with the cytoplasmic aspect of cell membranes. The membrane-associated Gag polyprotein recruits two copies of the viral genomic RNA along with other viral and cellular proteins that triggers the budding of the viral particle from the surface of an infected cell. After budding, p55 is cleaved by the virally encoded protease (a product of the pol gene) during the process of viral maturation into four smaller proteins designated MA (matrix [p17]), CA (capsid [p24]), NC (nucleocapsid [p9]), and p6, all of which are examples of fragments of Gag. In one embodiment, the vectors of the present invention comprise a Gag polypeptide of SEQ ID NO: 16.

### 35 Adjuvants

An "adjuvant" as used herein refers to a composition that enhances the immune response to an immunogen. Examples of such adjuvants include but are not limited to inorganic adjuvants (e.g. inorganic metal salts such as aluminium phosphate or aluminium hydroxide), organic adjuvants (e.g. saponins, such as QS21, or squalene), oil-based adjuvants (e.g. Freund's complete adjuvant and Freund's incomplete adjuvant), cytokines (e.g. IL-1 $\beta$ , IL-2, IL-7, IL-12, IL-18, GM-CSF, and INF- $\gamma$ ) particulate adjuvants (e.g. immuno-stimulatory complexes (ISCOMS), liposomes, or biodegradable microspheres), virosomes, bacterial adjuvants (e.g.

monophosphoryl lipid A, such as 3-de-O-acylated monophosphoryl lipid A (3D-MPL), or muramyl peptides), synthetic adjuvants (e.g. non-ionic block copolymers, muramyl peptide analogues, or synthetic lipid A), synthetic polynucleotides adjuvants (e.g. polyarginine or polylysine) and immunostimulatory oligonucleotides containing unmethylated CpG dinucleotides ("CpG").

One suitable adjuvant is monophosphoryl lipid A (MPL), in particular 3-de-O-acylated monophosphoryl lipid A (3D-MPL). Chemically it is often supplied as a mixture of 3-de-O-acylated monophosphoryl lipid A with either 4, 5, or 6 acylated chains. It can be purified and prepared by the methods taught in GB 2122204B, which reference also discloses the preparation of diphosphoryl lipid A, and 3-O-deacylated variants thereof. Other purified and synthetic lipopolysaccharides have been described (U.S. Pat. No. 6,005,099 and EP 0 729 473 B1; Hilgers et al., 1986, *Int.Arch.Allergy.Immunol.*, 79(4):392-6; Hilgers et al., 1987, *Immunology*, 60(1):141-6; and EP 0 549 074 B1).

Saponins are also suitable adjuvants (see Lacaille-Dubois, M and Wagner H, A review of the biological and pharmacological activities of saponins. *Phytomedicine* vol 2 pp 363-386 (1996)). For example, the saponin Quil A (derived from the bark of the South American tree *Quillaja Saponaria* Molina), and fractions thereof, are described in U.S. Pat. No. 5,057,540 and Kensil, *Crit. Rev. Ther. Drug Carrier Syst.*, 1996, 12:1-55; and EP 0 362 279 B1. Purified fractions of Quil A are also known as immunostimulants, such as QS21 and QS17; methods of their production is disclosed in U.S. Pat. No. 5,057,540 and EP 0 362 279 B1. Also described in these references is QS7 (a non-haemolytic fraction of Quil-A). Use of QS21 is further described in Kensil et al. (1991, *J. Immunology*, 146: 431-437). Combinations of QS21 and polysorbate or cyclodextrin are also known (WO 99/10008). Particulate adjuvant systems comprising fractions of QuilA, such as QS21 and QS7 are described in WO 96/33739 and WO 96/11711.

Another adjuvant is an immunostimulatory oligonucleotide containing unmethylated CpG dinucleotides ("CpG") (Krieg, *Nature* 374:546 (1995)). CpG is an abbreviation for cytosine-guanosine dinucleotide motifs present in DNA. CpG is known as an adjuvant when administered by both systemic and mucosal routes (WO 96/02555, EP 468520, Davis et al, *J.Immunol.*, 1998, 160:870-876; McCluskie and Davis, *J.Immunol.*, 1998, 161:4463-6). CpG, when formulated into vaccines, may be administered in free solution together with free antigen (WO 96/02555) or covalently conjugated to an antigen (WO 98/16247), or formulated with a carrier such as aluminium hydroxide (Brazolot-Millan et al., *Proc. Natl. Acad. Sci., USA*, 1998, 95:15553-8).

Adjuvants such as those described above may be formulated together with carriers, such as liposomes, oil in water emulsions, and/or metallic salts (including aluminum salts such as aluminum hydroxide). For example, 3D-MPL may be formulated with aluminum hydroxide (EP 0 689 454) or oil in water emulsions (WO 95/17210); QS21 may be formulated with cholesterol containing liposomes (WO 96/33739), oil in water emulsions (WO 95/17210) or alum (WO



98/15287); CpG may be formulated with alum (Brazolot-Millan, supra) or with other cationic carriers.

5 Combinations of adjuvants may be utilized in the present invention, in particular a combination of a monophosphoryl lipid A and a saponin derivative (see, e.g., WO 94/00153; WO 95/17210; WO 96/33739; WO 98/56414; WO 99/12565; WO 99/11241), more particularly the combination of QS21 and 3D-MPL as disclosed in WO 94/00153, or a composition where the QS21 is quenched in cholesterol-containing liposomes (DQ) as disclosed in WO 96/33739. Alternatively, a combination of CpG plus a saponin such as QS21 is an adjuvant suitable for use in the present invention. A potent adjuvant formulation involving QS21, 3D-MPL & 10 tocopherol in an oil in water emulsion is described in WO 95/17210 and is another formulation for use in the present invention. Saponin adjuvants may be formulated in a liposome and combined with an immunostimulatory oligonucleotide. Thus, suitable adjuvant systems include, for example, a combination of monophosphoryl lipid A, preferably 3D-MPL, together with an aluminium salt (e.g. as described in WO00/23105). A further exemplary adjuvant 15 comprises QS21 and/or MPL and/or CpG. QS21 may be quenched in cholesterol-containing liposomes as disclosed in WO 96/33739.

20 Other suitable adjuvants include alkyl Glucosaminide phosphates (AGPs) such as those disclosed in WO9850399 or U.S. Pat. No. 6,303,347 (processes for preparation of AGPs are also disclosed), or pharmaceutically acceptable salts of AGPs as disclosed in U.S. Pat. No. 6,764,840. Some AGPs are TLR4 agonists, and some are TLR4 antagonists. Both are thought to be useful as adjuvants.

25 It has been found (WO 2007/062656, which published as US 2011/0293704 and is incorporated by reference for the purpose of disclosing invariant chain sequences) that the fusion of the invariant chain to an antigen which is comprised by an expression system used for vaccination increases the immune response against said antigen, if it is administered with an adenovirus. Accordingly, in one embodiment of the invention, the immunogenic transgene 30 may be co-expressed with invariant chain in a recombinant ChAd157 viral vector.

In another embodiment, the invention provides the use of the capsid of ChAd157 (optionally an intact or recombinant viral particle or an empty capsid is used) to induce an immunomodulatory effect response, or to enhance or adjuvant a cytotoxic T cell response to another active agent 35 by delivering a ChAd157 capsid to a subject. The ChAd157 capsid can be delivered alone or in a combination regimen with an active agent to enhance the immune response thereto. Advantageously, the desired effect can be accomplished without infecting the host with an adenovirus.

#### 40 Administration Regimens

Commonly, the ChAd157 recombinant adenoviral vectors will be utilized for delivery of therapeutic or immunogenic molecules (such as proteins). It will be readily understood for both

applications, that the recombinant adenoviral vectors of the invention are particularly well suited for use in regimens involving repeat delivery of recombinant adenoviral vectors. Such regimens typically involve delivery of a series of viral vectors in which the viral capsids are alternated. The viral capsids may be changed for each subsequent administration, or after a  
5 pre-selected number of administrations of a particular serotype capsid (e.g. one, two, three, four or more). Thus, a regimen may involve delivery of a recombinant adenovirus with a first capsid, delivery with a recombinant adenovirus with a second capsid, and delivery with a recombinant adenovirus with a third capsid. A variety of other regimens which use the  
10 adenovirus capsids of the invention alone, in combination with one another, or in combination with other adenoviruses (which are preferably immunologically non-cross reactive) will be apparent to those of skill in the art. Optionally, such a regimen may involve administration of recombinant adenovirus with capsids of other non-human primate adenoviruses, human adenoviruses, or artificial sequences such as are described herein.

15 The adenoviral vectors of the invention are particularly well suited for therapeutic regimens in which multiple adenoviral-mediated deliveries of transgenes are desired, e.g., in regimens involving redelivery of the same transgene or in combination regimens involving delivery of other transgenes. Such regimens may involve administration of a ChAd157 adenoviral vector, followed by re-administration with a vector from the same serotype adenovirus. Particularly  
20 desirable regimens involve administration of a ChAd157 adenoviral vector, in which the source of the adenoviral capsid sequences of the vector delivered in the first administration differs from the source of adenoviral capsid sequences of the viral vector utilized in one or more of the subsequent administrations. For example, a therapeutic regimen involves administration of a ChAd157 vector and repeat administration with one or more adenoviral vectors of the same  
25 or different serotypes.

In another example, a therapeutic regimen involves administration of an adenoviral vector followed by repeat administration with a ChAd157 vector which has a capsid which differs from the source of the capsid in the first delivered adenoviral vector, and optionally further  
30 administration with another vector which is the same or, preferably, differs from the source of the adenoviral capsid of the vector in the prior administration steps. These regimens are not limited to delivery of adenoviral vectors constructed using the ChAd157 sequences. Rather, these regimens can readily utilize other adenoviral sequences, including, without limitation, other adenoviral sequences including other non-human primate adenoviral sequences, or  
35 human adenoviral sequences, in combination with the ChAd157 vectors.

In a further example, a therapeutic regimen may involve either simultaneous (such as co-administration) or sequential (such as a prime-boost) delivery of (i) one or more ChAd157 adenoviral vectors and (ii) a further component such as non-adenoviral vectors, non-viral  
40 vectors, and/or a variety of other therapeutically useful compounds or molecules such as antigenic proteins optionally simultaneously administered with adjuvant. Examples of co-administration include homo-lateral co-administration and contra-lateral co-administration (further described below under 'Delivery Methods and Dosage').

Suitable non-adenoviral vectors for use in simultaneous or particularly in sequential delivery (such as prime-boost) with one or more ChAd157 adenoviral vectors include one or more poxviral vectors. Suitably, the poxviral vector belongs to the subfamily chordopoxvirinae, more  
5 suitably to a genus in said subfamily selected from the group consisting of orthopox, parapox, yatapox, avipox (suitably canarypox (ALVAC) or fowlpox (FPV)) and molluscipox. Even more suitably, the poxviral vector belongs to the orthopox and is selected from the group consisting of vaccinia virus, NYVAC (derived from the Copenhagen strain of vaccinia), Modified Vaccinia Ankara (MVA), cowpoxvirus and monkeypox virus. Most suitably, the poxviral vector is MVA.

10 "Simultaneous" administration suitably refers to the same ongoing immune response. Preferably both components are administered at the same time (such as simultaneous administration of both DNA and protein), however, one component could be administered within a few minutes (for example, at the same medical appointment or doctor's visit), within a  
15 few hours. Such administration is also referred to as co-administration. In some embodiments, co-administration may refer to the administration of an adenoviral vector, an adjuvant and a protein component. In other embodiments, co-administration refers to the administration of an adenoviral vector and another viral vector, for example a second adenoviral vector or a poxvirus such as MVA. In other embodiments, co-administration refers to the administration of  
20 an adenoviral vector and a protein component, which is optionally adjuvanted.

A prime-boost regimen may be used. Prime-boost refers to two separate immune responses: (i) an initial priming of the immune system followed by (ii) a secondary or boosting of the immune system many weeks or months after the primary immune response has been  
25 established.

Such a regimen may involve the administration of a recombinant ChAd157 vector to prime the immune system to second, booster, administration with a traditional antigen, such as a protein (optionally co-administered with adjuvant), or a recombinant virus carrying the sequences  
30 encoding such an antigen (e.g., WO 00/11140). Alternatively, an immunization regimen may involve the administration of a recombinant ChAd157 vector to boost the immune response to a vector (either viral or DNA-based) encoding an antigen. In another alternative, an immunization regimen involves administration of a protein followed by booster with a recombinant ChAd157 vector encoding the antigen. In one example, the prime-boost regimen  
35 can provide a protective immune response to the virus, bacteria or other organism from which the antigen is derived. In another embodiment, the prime-boost regimen provides a therapeutic effect that can be measured using conventional assays for detection of the presence of the condition for which therapy is being administered.

40 Preferably, a boosting composition is administered about 2 to about 27 weeks after administering the priming composition to the subject. The administration of the boosting composition is accomplished using an effective amount of a boosting composition containing or capable of delivering the same antigen or a different antigen as administered by the priming

vaccine. The boosting composition may be composed of a recombinant viral vector derived from the same viral source or from another source. Alternatively, the boosting composition can be a composition containing the same antigen as encoded in the priming vaccine, but in the form of a protein, which composition induces an immune response in the host. The primary requirements of the boosting composition are that the antigen of the composition is the same antigen, or a cross-reactive antigen, as that encoded by the priming composition.

A low cross-reactivity between neutralizing antibodies for ChAd157 and certain other adenoviral vectors, such as ChAd155, is beneficial in contexts where multiple vector administrations are required. Multiple administrations may be for the purpose of the separate delivery of different transgenes (e.g. encoding immunogens associated different medical indications) or delivery of the same or similar transgenes (e.g. in a prime-boost regime to increase the immune response for a particular medical indication).

Consequently, there is provided a recombinant adenoviral vector of the invention encoding a transgene, for administration to a subject which has previously been exposed to a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof, as described herein (e.g. does not comprise a ChAd157 fiber, hexon or penton as described herein, such as a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton, especially a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton). In particular, there is provided a recombinant adenoviral vector of the invention encoding a transgene for administration to a subject which has previously been administered a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof, as described herein (e.g. does not comprise a ChAd157 fiber, hexon or penton as described herein, such as a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton, especially a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton). Suitably the recombinant adenoviral vector which does not comprise a ChAd157 fiber is one which has low cross-reactivity with ChAd157. In one embodiment the recombinant adenoviral vector which does not comprise a ChAd157 fiber encodes a transgene directed at a different medical indication or indications as the recombinant adenoviral vector of the invention transgene. In another embodiment the recombinant adenoviral vector which does not comprise a ChAd157 fiber encodes a transgene directed at the same medical indication or indications as the recombinant adenoviral vector of the invention transgene (e.g. such as the same transgene).

Also provided is a recombinant adenoviral vector of the invention encoding a transgene for administration to a subject which may (i.e. it is intended or expected will) subsequently be exposed to a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof, as described herein (e.g. does not comprise a ChAd157 fiber, hexon or penton as described herein, such as a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton, especially a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton). In particular, there is provided a recombinant adenoviral vector of the invention encoding a transgene for administration to a subject which may

subsequently be administered a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof, as described herein (e.g. does not comprise a ChAd157 fiber, hexon or penton as described herein, such as a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton, especially a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton). Suitably the recombinant adenoviral vector which does not comprise a ChAd157 fiber is one which has low cross-reactivity with ChAd157. In one embodiment the recombinant adenoviral vector which does not comprise a ChAd157 fiber encodes a transgene directed at a different medical indication or indications as the recombinant adenoviral vector of the invention transgene. In another embodiment the recombinant adenoviral vector which does not comprise a ChAd157 fiber encodes a transgene directed at the same medical indication or indications as the recombinant adenoviral vector of the invention transgene (e.g. such as the same transgene).

The present invention therefore provides a method for eliciting an immune response in a subject, said method comprising:

- (a) administering to the subject a recombinant adenoviral vector of the invention encoding a first transgene; and
- (b) administering to the subject a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof as described herein, the vector encoding a second transgene;

wherein steps (a) and (b) may be undertaken in either order and the first and second transgenes may be the same or different.

The first and second transgenes will typically encode immunogens which are useful to immunize a human or non-human animal against a pathogen such as bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell. The first and second transgenes may encode the same or different immunogens. When encoding different immunogens, these may be directed to the same or different pathogen or cancer cell or tumor cell.

Consequently, there is also provided a method for the prophylaxis or treatment of a subject, said method comprising:

- (a) administering to the subject a recombinant adenoviral vector of the invention encoding a first transgene encoding an immunogen which is useful to immunize a human or non-human animal against a pathogen such as bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell; and
- (b) administering to the subject a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof as described herein, the vector encoding a second transgene encoding an immunogen which is useful to immunize a human or non-human animal against a different pathogen such as bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell;

wherein steps (a) and (b) may be undertaken in either order.

The recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof as described herein, suitably does not comprise a ChAd157 fiber, ChAd157  
5 hexon or ChAd157 fiber, such as does not comprise a ChAd157 fiber, ChAd157 hexon or ChAd157 fiber or functional derivatives thereof having at least 98% identity thereto.

The recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof as described herein may be a recombinant adenoviral vector comprising a  
10 ChAd155 fiber, hexon and/or penton, especially a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton.

As mentioned, a recombinant adenoviral vector of the invention may be used for delivery of therapeutic or immunogenic molecules in conjunction with a recombinant adenoviral vector  
15 comprising a ChAd155 fiber, hexon and/or penton. The recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton will comprise a fiber, penton and/or hexon according to SEQ ID NOs: 7, 9 and 11, in particular a fiber, penton and hexon according to SEQ ID NOs: 7, 9 and 11.

20 By the term low cross-reactivity is meant that immunisation with a first vector does not elicit a notable neutralising antibody response to a second vector, i.e. not significantly impacting the immunological potency of the second vector. Neutralising antibody responses can be determined with methods analogous to Example 7 herein. Desirably, immunisation with a first vector twice elicits a neutralising titer which is on average less than 50% of the level arising  
25 from immunisation with the second vector, such as less than 75%, suitably less than 90%.

By the term "subject" is meant any animal, suitably a mammal, and in particular a human.

#### Delivery Methods and Dosage

30 The 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  
35 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.

40 In some embodiments, the recombinant adenovirus of the invention is administered to a subject by intramuscular injection, intravaginal administration, intravenous injection, intraperitoneal injection, subcutaneous injection, epicutaneous administration, intradermal administration, nasal administration, rectal administration or oral administration. Sublingual administration may also be of interest.

If the therapeutic regimen involves co-administration of one or more ChAd157 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  $1 \times 10^5$  to  $1 \times 10^{15}$  viral particles, such as from  $1 \times 10^8$  to  $1 \times 10^{12}$  (e.g.,  $1 \times 10^8$ ,  $2.5 \times 10^8$ ,  $5 \times 10^8$ ,  $1 \times 10^9$ ,  $1.5 \times 10^9$ ,  $2.5 \times 10^9$ ,  $5 \times 10^9$ ,  $1 \times 10^{10}$ ,  $1.5 \times 10^{10}$ ,  $2.5 \times 10^{10}$ ,  $5 \times 10^{10}$ ,  $1 \times 10^{11}$ ,  $1.5 \times 10^{11}$ ,  $2.5 \times 10^{11}$ ,  $5 \times 10^{11}$ ,  $1 \times 10^{12}$  particles). Alternatively, a viral vector can be administered at a dose that is typically from  $1 \times 10^5$  to  $1 \times 10^{10}$  plaque forming units (PFU), such as  $1 \times 10^5$  PFU,  $2.5 \times 10^5$  PFU,  $5 \times 10^5$  PFU,  $1 \times 10^6$  PFU,  $2.5 \times 10^6$  PFU,  $5 \times 10^6$  PFU,  $1 \times 10^7$  PFU,  $2.5 \times 10^7$  PFU,  $5 \times 10^7$  PFU,  $1 \times 10^8$  PFU,  $2.5 \times 10^8$  PFU,  $5 \times 10^8$  PFU,  $1 \times 10^9$  PFU,  $2.5 \times 10^9$  PFU,  $5 \times 10^9$  PFU, or  $1 \times 10^{10}$  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 viral 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.

An immunologically effective amount of a nucleic acid may suitably be between 1 ng and 100 mg. For example, a suitable amount can be from 1  $\mu$ g to 100 mg. An appropriate amount of the particular nucleic acid (e.g., vector) can readily be determined by those of skill in the art. Exemplary effective amounts of a nucleic acid component can be between 1 ng and 100  $\mu$ g, such as between 1 ng and 1  $\mu$ g (e.g., 100 ng-1  $\mu$ g), or between 1  $\mu$ g and 100  $\mu$ g, such as 10 ng, 50 ng, 100 ng, 150 ng, 200 ng, 250 ng, 500 ng, 750 ng, or 1  $\mu$ g. Effective amounts of a nucleic acid can also include from 1  $\mu$ g to 500  $\mu$ g, such as between 1  $\mu$ g and 200  $\mu$ g, such as between 10 and 100  $\mu$ g, for example 1  $\mu$ g, 2  $\mu$ g, 5  $\mu$ g, 10  $\mu$ g, 20  $\mu$ g, 50  $\mu$ g, 75  $\mu$ g, 100  $\mu$ g, 150  $\mu$ g, or 200  $\mu$ g. Alternatively, an exemplary effective amount of a nucleic acid can be between 100  $\mu$ g and 1 mg, such as from 100  $\mu$ g to 500  $\mu$ g, for example, 100  $\mu$ g, 150  $\mu$ g, 200  $\mu$ g, 250  $\mu$ g, 300  $\mu$ g, 400  $\mu$ g, 500  $\mu$ g, 600  $\mu$ g, 700  $\mu$ g, 800  $\mu$ g, 900  $\mu$ g or 1 mg.

Generally a human dose will be in a volume of between 0.1ml and 2 ml. Thus the composition described herein can be formulated in a volume of, for example 0.1, 0.15, 0.2, 0.5, 1.0, 1.5 or 2.0 ml human dose per individual or combined immunogenic components.

- 5 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.
- 10 If one or more priming and/or boosting steps are used, this step may include a single dose that is administered hourly, daily, weekly or monthly, or yearly. As an example, mammals may receive one or two doses containing between about 10  $\mu$ g to about 50  $\mu$ g of plasmid in carrier. The amount or site of delivery is desirably selected based upon the identity and condition of the mammal.
- 15 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 recombinant ChAd157 vectors may be
- 20 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.
- The present invention will now be further described by means of the following non-limiting
- 25 examples.

## EXAMPLES

### Example 1: Isolation of ChAd157 and Vector Construction

30 29 different wild type chimpanzee adenoviruses were isolated from healthy young chimpanzees housed in different European facilities using standard procedures as described in Colloca *et al.* Sci Transl Med. 2012 Jan 4;4(115):115ra2 and WO2010/086189, which is hereby incorporated by reference for the purpose of describing adenoviral isolation and

35 characterization techniques.

The 29 wild type viruses were subsequently pooled; the viral genome of the pool was cloned by homologous recombination in *E. coli* BJ5183 cells using a BAC shuttle, to create a minilibrary of vectors carrying the deletion of E1 region. The minilibrary of  $\Delta$ E1 vectors was

40 transfected into the Procell 92 cell line; the rescued vectors were serially passaged for 16 passages of infection. At passage 16 the viral DNA was prepared from the amplified vector and cloned by homologous recombination in *E. coli* BJ5183 cells using a plasmid shuttle. The



prevalent vector species was identified as ChAd157 $\Delta$ E1 vector and subsequently modified to include the following additional modifications of the vector backbone:

- a) deletion of the E4 region (from bp 34413 to bp 37127) of the  $\Delta$ E1 virus;
- b) insertion of the E4orf6 derived from human Ad5.

5

#### 1.1: $\Delta$ E1 minilibrary generation

The pool of 29 wild type virus was used to obtain a pooled viral genome. The pooled viral genome was cloned into a BAC vector by homologous recombination in *E. coli* strain BJ5183 co-transformed with pooled viral DNA and Subgroup C BAC Shuttle (#1365) (SEQ ID NO: 14). As shown in the schematic of Figure 2, the Subgroup C Shuttle is a BAC vector dedicated to the cloning of ChAd belonging to species C and therefore contains the pIX gene and DNA fragments derived from right and left ends (including right and left ITRs) of species C ChAd viruses.

15

The Species C BAC Shuttle also contains a RpsL-Kana cassette inserted between left end and the pIX gene. In addition, an Amp-LacZ-SacB selection cassette, flanked by IScel restriction sites, is present between the pIX gene and right end of the viral genome. In particular, the BAC Shuttle comprised the following features: Left ITR: bp 27 to 139, hCMV(tetO) RpsL-Kana cassette: bp 493 to 3396, pIX gene: bp 3508 to 3972, IScel restriction sites: bp 3990 and 7481, Amp-LacZ-SacB selection cassette: bp 4000 to 7471, Right ITR: bp 7805 to 7917. hCMV(tetO) is provided in SEQ ID NO: 37.

BJ5183 cells were co-transformed by electroporation with the pool of purified viral DNAs and with Subgroup C BAC Shuttle vector digested with IScel restriction enzyme and then purified from gel. Homologous recombination occurring between pIX gene and right ITR sequences (present at the ends of Species C BAC Shuttle linearized DNA) and homologous sequences present in pooled viral DNA lead to the insertion of the different viral genomic DNA in the BAC shuttle vector. At the same time, the viral E1 regions were deleted and substituted by the RpsL-Kana cassette, generating BAC/Minilibrary $\Delta$ E1/TetO hCMV RpsL-Kana.

30

#### 1.2: $\Delta$ E1 minilibrary amplification in Procell 92 cell line and cloning of ChAd157 $\Delta$ E1 vector.

The  $\Delta$ E1 minilibrary was digested with PmeI and used to transfect Procell 92 packaging cell line, in order to rescue the library of different viruses in bulk. 10 days post transfection, the cells were harvested and the cell lysate was subjected to three cycle of freeze (-70°C) and thaw (+37°C), clarified by centrifugation at 2000 rpm and used to infect fresh cells. 16 serial passages of virus amplification were performed, in order to select the viral species for efficiency of propagation in Procell92 cells. The virus (-es) at passage 16 were purified by two CsCl gradient centrifugations and viral DNA was extracted and cloned by homologous recombination in *E. coli* BJ5183 cells using a plasmid shuttle. In detail, BJ5183 cells were co-transformed with purified viral DNA and Subgroup C Plasmid Shuttle (SEQ ID NO: 38). As shown in the diagram of Figure 3, the Subgroup C Plasmid Shuttle is a plasmid vector

40

dedicated to the cloning of ChAd belonging to species C and therefore contains the DNA fragments derived from right and left ends (including right and left ITRs) of species C ChAd viruses.

- 5 Homologous recombination between right and left ITR DNA sequences present at the ends of linearized Subgroup C Plasmid Shuttle (digested with PshAI/NdeI/XbaI) and viral genomic DNAs allowed its insertion in the plasmid vector. 30 different clones were amplified and analysed by Restriction analysis and 9 different species were identified. 19/30 clones showed the same restriction patterns and represented the predominant species; one of these clones  
10 was selected and identified as pChAd157 $\Delta$ E1 TetO hCMV RpsL-Kana#1551 (SEQ ID NO: 15).

### 1.3: Construction of ChAd157 $\Delta$ E1/TetO hCMV GAG#1557

- The GAG cassette (GAG polynucleotide sequence SEQ ID NO: 16) was cloned into a linearised pre-adeno acceptor vector via homologous recombination in *E. coli* by exploiting the  
15 homology existing between HCMV promoter and BGH polyA sequences (SEQ ID NO: 39).

The plasmid pARS CV32TetOhCMV GAG was cleaved with SpeI and SphI to excise the 2.44 Kb fragment containing HCMV promoter with tetO, HIV-GAG and BGH polyA sequence.

- 20 The HIV-GAG 2.44Kb fragment was cloned by homologous recombination into pChAd157  $\Delta$ E1 /TetO hCMV RpsL-Kana (#1551) acceptor vector (SnaBI digested) carrying the RpsL-Kana selection cassette under control of HCMV and BGHpA.. The resulting construct was pChAd157  $\Delta$ E1/TetO hCMV GAG#1557 vector (SEQ ID NO: 17).

- 25 The structure of the plasmid carrying the ChAd157 GAG is reported in Figure 4.

### 1.4: Construction of ChAd157 $\Delta$ E1E4 Ad5E4orf6/TetO hCMV RpsL-Kana#1594.

- ChAd157 $\Delta$ E1 vector was subsequently modified to carry the following modifications in the  
30 backbone:

- a) deletion of the E4 region (from bp 34413 to bp 37127) of the  $\Delta$ E1 virus;
- b) insertion of the E4orf6 derived from human Ad5.

- A deletion of E4 region spanning from nucleotide 34413 to 37127 ( $\Delta$ E1 vector sequence  
35 coordinates) was introduced in the vector backbone by replacing the native E4 region with Ad5 E4orf6 coding sequence by using a strategy involving several steps of cloning and homologous recombination in *E. coli*. E4 coding region was completely deleted while E4 native promoter and polyadenylation signal were conserved. To this end, a shuttle vector was constructed to allow the insertion of Ad5orf6 by replacing ChAd157 native E4 region by  
40 homologous recombination in *E. coli* BJ5183 as detailed below.

- Construction of pARS SpeciesC Ad5E4orf6-1:

Ad5orf6 containing DNA fragment was obtained by PCR using Ad5 DNA as template, with the oligonucleotides: 5'-ATACGGACTAGTGGAGAAGTACTCGCCTACATG-3' (SEQ ID NO: 18)

and 5'-ATACGGAAGATCTAAGACTTCAGGAAATATGACTAC-3' (SEQ ID NO: 19). The PCR fragment was digested with BglII and SpeI and cloned into pARS Species C RLD-EGFP shuttle digested with BglII and SpeI, generating the plasmid pARS Species C Ad5orf6-1.

- Construction of pARS SpeciesC Ad5E4orf6-2:

- 5 A 144 bp DNA fragment containing the Fiber-E4 polyA (from bp 34269 to bp 34412 of ChAd157ΔE1 vector) was amplified by PCR using as template the plasmid pChAd157 ΔE1 /TetO hCMV RpsL-Kana (#1551) with the following oligonucleotides: 5'-ATTCAAGTGTACAGGCGCGCCAAAGCATGACACTGATGTTTCATTTC-3' (SEQ ID NO: 20) and 5'-ACTAGGACTAGTTATAAGCTAGAATGGGGCTTTGC-3' (SEQ ID NO: 21). The PCR  
10 fragment was digested with BsrGI and SpeI and cloned into pARS SubGroupC Ad5orf6-1 digested with BsrGI and SpeI, generating the plasmid pARS SpeciesC Ad5orf6-2 (SEQ ID NO: 40).

- The resulting plasmid pARS SpeciesC Ad5orf6-2 was then used to replace the E4 with  
15 Ad5orf6 within ChAd157 backbone. To this end, the plasmid pChAd157ΔE1 TetO hCMV RpsL-Kana#1551 was digested with PacI and co-transformed into BJ5183 cells with the plasmid pARS SpeciesC Ad5orf6-2 BamHI/Ascl digested, to obtain the pChAd157 ΔE1E4\_Ad5E4orf6/TetO hCMV RpsL-Kana (#1594) preadeno plasmid (SEQ ID NO: 22).

#### 20 1.5: Construction of ChAd157 ΔE1E4 Ad5E4orf6/TetO hCMV RG#1559.

The Rabies viral Glycoprotein (RG) expression cassette (Rabies Glycoprotein polynucleotide sequence SEQ ID NO: 23) was cloned into a linearised pre-adeno acceptor vector via homologous recombination in *E. coli* by exploiting the homology existing between HCMV promoter and BGH polyA sequences.

- 25 The plasmid pvjTetOhCMV-bghpolyA\_RG was cleaved with SpeI and AsiSI to excise the 2.59 Kb fragment containing HCMV promoter with tetO, RG and BGHpolyA sequence.

- The resulting RG 2.59 Kb fragment was cloned by homologous recombination into pChAd157  
30 ΔE1E4\_Ad5E4orf6/TetO hCMV RpsL-Kana (#1594) acceptor vector carrying the RpsL-Kana selection cassette under control of HCMV and BGHpA. The acceptor preAd plasmid was linearized with the restriction endonuclease SnaBI. The resulting construct was pChAd157 ΔE1E4\_Ad5E4orf6/TetO hCMV RG#1559 vector (SEQ ID NO: 24).

- 35 The structure of the plasmid carrying the ChAd157 RG is reported in Figure 6.

### **Example 2: Vector production**

- The productivity of ChAd157 was evaluated in comparison to ChAd19 and ChAd155 in the  
40 Procell 92 cell line.

#### 2.1: Production of vectors comprising an HIV Gag transgene

ChAd157/GAG, ChAd19/GAG, ChAd155/GAG (ChAd157, ChAd19 and ChAd155 vectors expressing an HIV Gag transgene) were rescued and amplified in Procell 92; the lysates were used to infect 1 T25 flask of Procell 92 cultivated in monolayer with each vector. A multiplicity of infection (MOI) of 300 vp/cell was used and the infections were performed in presence of tetracycline because ChAd19/GAG lacked the transcriptional control mediated by the insertion of the TetO operator in the hCMV promoter. The infected cells were harvested when full cytopathic effect was evident (48 hours post-infection for ChAd157/GAG and ChAd155/GAG and 5 days post-infections for ChAd19/GAG); the viruses were released from the infected cells by 3 cycles of freeze/thaw (-70° to 37°C) then the lysate was clarified by centrifugation. The clarified lysates were quantified by Quantitative PCR Analysis with primers and probe complementary to the CMV promoter region. The oligonucleotide sequences are the following: CMVfor 5'-CATCTACGTATTAGTCATCGCTATTACCA-3' (SEQ ID NO: 25), CMVrev 5'-GACTTGGAATCCCCGTGAGT-3' (SEQ ID NO: 26), CMVFAM-TAMRA probe 5'-ACATCAATGGGCGTGGATAGCGGTT-3' (SEQ ID NO: 41) (QPCRs were run on ABI Prism 7900 Sequence detector – Applied Biosystem).

The resulting volumetric titers (vp/ml) measured on clarified lysates and the specific productivity expressed in virus particles per cell (vp/cell) are provided in Table 1 below.

20

Table 1: GAG vector productivity.

<b>Vector</b>	<b>Volumetric productivity (vp/ml)</b>	<b>Total vp</b>	<b>Cell specific productivity (vp/cell)</b>
<b>ChAd157/GAG</b>	4.61E+09	2.30E+10	7.68E+03
<b>ChAd155/GAG</b>	5.42E+09	2.71E+10	9.04E+03
<b>ChAd19/GAG</b>	4.80E+08	2.40E+09	8.00E+02

## 2.2: Production of vectors comprising an RG transgene

A different set of experiments were performed to evaluate the productivity of RG vaccine vectors in Procell 92 cultivated in suspension. The experiment compared ChAd157/RG and ChAd155/RG in parallel by infecting Procell 92 at a cell density of  $5 \times 10^5$  cells/ml. A multiplicity of infection (MOI) of 300 vp/cell was used. The infected cells were harvested 4 days post infection; the virus was released from the infected cells by 3 cycles of freeze/thaw and the lysate was clarified by centrifugation. The clarified lysates were then quantified by QPCR as reported above.

30

The volumetric productivity and the cell specific productivity are provided in Table 2 below.

Table 2: RG vector productivity.

Vector	Volumetric productivity (vp/ml)	Total vp	Cell specific productivity (vp/cell)
ChAd157/RG	9.39E+09	4.69E+11	1.88E+04
ChAd155/RG	1.41E+10	7.04E+11	2.81E+04

### Example 3: Transgene Expression Levels

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#### 3.1: Expression level of HIV Gag transgene

Expression levels were compared in parallel experiments by infecting HeLa cells with ChAd19, ChAd155 and ChAd157 vectors comprising an HIV Gag transgene.

10

HeLa cells were seeded in 35 mm dishes and infected with ChAd19/GAG, ChAd157/GAG and ChAd155/GAG purified viruses using a MOI=250 vp/cell. The supernatants of infected HeLa cells were harvested 48 hours post-infection, and the production of secreted HIV GAG protein was quantified by using a commercial ELISA Kit (HIV-1 p24 ELISA Kit, PerkinElmer Life Science). The quantification was performed according to the manufacturer's instruction by using an HIV-1 p24 antigen standard curve.

15

The results, expressed in pg/ml of GAG protein, are illustrated in Figure 7.

#### 3.2: Expression level of RG transgene

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A western blot analysis was also performed to evaluate the rabies glycoprotein expression provided by the ChAd157/RG vector in comparison to ChAd155/RG vector. To this end, HeLa cells were seeded in 35mm dishes and infected with ChAd157/RG and ChAd155/RG purified viruses using a MOI=250 vp/cell. Cell lysates were harvested 48hours post-infection and the transgene expression level was evaluated by reducing SDS-PAGE followed by Western Blot analysis.

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Equivalent quantities of proteins extracts were loaded on reducing SDS gel; after electrophoresis separation, the proteins were transferred to a nitrocellulose membrane to be probed with a Rabbit Polyclonal anti-GP (Cat. No. RBVGP11-S  $\alpha$ Diagnostic, diluted 1:1000). After the incubation with primary antibody, the membrane was washed and then incubated with anti-rabbit horseradish peroxidase (HRP) conjugate secondary antibody. Finally the assay was developed by chemiluminescence using enhanced chemiluminescence (ECL) detection reagents (W3252282 PIERCE). The Western Blot results are shown in Figure 8.

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A band of about 57 kD indicated by the arrow was revealed by polyclonal antibody anti-GP, which corresponds to the expected weight of rabies glycoprotein.

5 The result demonstrated that the expression level of ChAd157 vector appears comparable to that provided by ChAd155.

#### **Example 4: Evaluation of immunological potency by mouse immunization experiments**

##### 4.1: Immunogenicity of vectors comprising the HIV Gag transgene

10 The immunogenicity ChAd157/GAG vector was evaluated in parallel with ChAd155/GAG and ChAd19/GAG in BALB/c mice (6 per group). The experiment was performed by injecting  $10^7$  viral particles intramuscularly. T-cell response was measured 3 weeks after the immunization by ex vivo interferon- $\gamma$  (IFN- $\gamma$ ) enzyme-linked immunospot (ELISpot) using a GAG CD8+ T cell epitope mapped in BALB/c mice. The results obtained are reported in Figure 9, expressed as  
15 IFN $\gamma$  Spot Forming Cells (SFC) per million of splenocytes.

Each dot represents the response in a single mouse, and the line corresponds to the geomean for each dose group. Frequency of positive mice to the CD8 immunodominant peptide is shown on the x axis.

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##### 4.2 Immunogenicity of vectors comprising the RG transgene

The immunological potency of ChAd157/RG and ChAd155/RG vectors was evaluated in BALB/c mice. Both vectors were injected intramuscularly with  $10^7$  and  $10^6$  vp doses. The splenocytes of immunized mice were isolated seven weeks after vaccination and analysed by  
25 IFN $\gamma$  ELISpot (Figure 10), using peptide pools from RG as antigen.

The levels of immune response were reduced in line with decreasing dosage, as expected. Moreover, ChAd155RG vector induced higher T cell response than ChAd157 RG, although they were not significantly different (Figure 10).

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#### **Example 5: Evaluation of infectivity**

##### 5.1 Infectivity of vectors comprising the HIV Gag transgene

The infectivity of purified viruses was evaluated in adherent Procell 92 cells utilizing an  
35 antibody against adenovirus hexon protein to visualize infected cells by immunocytochemistry staining. The antibody against hexon protein recognizes all serotypes of adenoviruses. To this end, Procell92 cells were seeded in 24well plate at a cell density of  $2 \times 10^5$  viable cell/ml and infected in duplicate with ChAd157/GAG and ChAd155/GAG and ChAd19/GAG vectors using a MOI= 1 vp/cell, 0.5 vp/cell and 0.25 vp/cell. 48 hours post-infection, infected cells were fixed  
40 by cold methanol and then labelled with the anti-hexon antibody. Excess antibody is removed. The labelled cells are then incubated with a secondary antibody conjugated with horseradish peroxidase and the detection is performed by using a commercial kit VECTOR NOVARED Substrate Kit (SK-4800). Detection is accomplished when the horseradish peroxidase enzyme

label reacts with the DAB substrate resulting in a dark brown product. The labelled, dark brown cells were then quantified by light microscopy and the infectious titer calculated. The results are shown in the table below

<b>Virus</b>	<b>Vp/ml</b>	<b>Ifu/ml</b>	<b>R (vp/ifu)</b>
<b>ChAd155 GAG</b>	1.32E+11	1.58E+09	<b>84</b>
<b>ChAd157 GAG</b>	1.17E+11	1.23E+09	<b>95</b>
<b>ChAd19 GAG</b>	4.46E+10	3.86E+08	<b>116</b>

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The result demonstrated that the infectivity of ChAd155 and ChAd157 viruses are comparable and higher than ChAd19.

#### 5.2 Infectivity of vectors comprising the RG transgene

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The infectivity of ChAd157/RG and ChAd155/RG purified viruses was evaluated in adherent Procell 92 cells by Hexon Immunostaining as reported above. The results are shown in the table below

<b>Virus</b>	<b>Vp/ml</b>	<b>Ifu/ml</b>	<b>R (vp/ifu)</b>
<b>ChAd155/RG</b>	4.23E+11	4.06E+09	<b>104</b>
<b>ChAd157/RG</b>	1.97E+11	1.46E+09	<b>133</b>

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The result demonstrated that the infectivity of ChAd155 and ChAd157 viruses are comparable

#### **Example 6: Evaluation of Cross-neutralization between ChAd155 and ChAd157 vectors**

##### 6.1 Testing *in vivo* if ChAd155 and ChAd157 vectors are different serotypes

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The cross-neutralization between ChAd155 and ChAd157 vectors was assessed in BALB/c mice (6 per group). Mice were preimmunized twice at week 0 and week 3 with  $10^9$  vp of ChAd155 or ChAd157 expressing RG or were mock-vaccinated with saline buffer. Three weeks later, all mice were then immunized once with  $10^9$  vp of ChAd157 encoding HIV gag

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Groups	n	Pre-immunization 2x w0 and w3	dose (vp)	Immunization w6	dose (vp)
1	6	PBS	-	ChAd157-GAG	$10^9$
2	6	ChAd155-RG	$10^9$	ChAd157-GAG	$10^9$
3	6	ChAd157-RG	$10^9$	ChAd157-GAG	$10^9$

Neutralization titers to the preimmunizing vectors were measured in sera at week 5 (2 weeks post second injection) by in vitro neutralization assay (Figure 11). Finally, T cell response against gag was tested on splenocytes 3 weeks after immunization by IFN- $\gamma$  ELISpot, using a GAG CD8+ T cell epitope mapped in BALB/c mice (Figure 12). The doses of vectors used for preimmunization were able to elicit good neutralizing activities against the two Ad vectors, although with some variability. Anti ChAd155 neutralizing antibodies do not cross-react against ChAd157 and vice-versa (Figure 11). Moreover, ChAd157-Gag T-cell response was not affected by anti-ChAd155 preimmunity, confirming that cross-neutralization was not observed (Figure 12).

Taken together, these data suggest that ChAd155 and ChAd157 viruses are distinct adenovirus serotypes.



**CLAIMS**

1. An isolated polynucleotide, wherein the polynucleotide encodes a polypeptide selected from the group consisting of:
  - (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1, and
  - (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.
2. A recombinant polynucleotide comprising a polynucleotide selected from the group consisting of:
  - (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1, and
  - (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.
3. A recombinant vector comprising a polynucleotide selected from the group consisting of:
  - (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1, and
  - (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.
4. A recombinant adenovirus comprising at least one polynucleotide or polypeptide selected from the group consisting of:
  - (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,
  - (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,
  - (c) a polypeptide having the amino acid sequence according to SEQ ID NO: 1, and
  - (d) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

5. A composition comprising at least one of the following:
  - (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,
  - (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,
  - (c) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,
  - (d) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,
  - (e) a vector according to claim 3, and
  - (f) a recombinant adenovirus according to claim 4,and a pharmaceutically acceptable excipient.
6. A cell comprising at least one of the following:
  - (a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,
  - (b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,
  - (c) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,
  - (d) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,
  - (e) a vector according to claim 3, and
  - (f) a recombinant adenovirus according to claim 4.
7. An isolated adenoviral polypeptide selected from the group consisting of:
  - (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1, and
  - (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.
8. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 6, wherein the polynucleotide encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the

functional derivative has an amino acid sequence which is at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

9. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 6, wherein the polynucleotide encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1.
10. The polynucleotide, vector, adenovirus, composition or cell according to claim 9, wherein the polynucleotide has a sequence according to SEQ ID NO: 2.
11. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 10, further comprising a polynucleotide encoding:
  - (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;or
  - (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,or
  - (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5;or
  - (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.
12. The polynucleotide, vector, adenovirus, composition or cell according to claim 11, further comprising a polynucleotide encoding:
  - (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;or
  - (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 98% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,or
  - (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5;or
  - (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 98% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

13. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 10, further comprising a polynucleotide encoding:
- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;
- or
- (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 98% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,
- and
- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5;
- or
- (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 98% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.
14. The polynucleotide, vector, adenovirus, composition or cell according to claim 13, further comprising a polynucleotide encoding:
- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;
- or
- (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 98% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,
- and
- (a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5;
- or
- (b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 98% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.
15. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 11 to 14, wherein the polynucleotide comprises a sequence according to SEQ ID NO: 4.
16. The polynucleotide, vector, adenovirus, composition or cell according to claim any one of claims 11 to 15, wherein the polynucleotide comprises a sequence according to SEQ ID NO: 6.
17. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 16, wherein the polynucleotide comprises at least one of the following:
- (a) an adenoviral 5'-end, preferably an adenoviral 5' inverted terminal repeat;

- (b) an adenoviral E1A region, or a fragment thereof selected from among the E1A\_280R and E1A\_243R regions;
  - (c) an adenoviral E1B or IX region, or a fragment thereof selected from among the group consisting of the E1B\_19K, E1B\_55K or IX regions;
  - (d) an adenoviral E2b region; or a fragment thereof selected from among the group consisting of the E2B\_pTP, E2B\_Polymerase and E2B\_IVa2 regions;
  - (e) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1\_13.6k protein, L1\_52k and L1\_IIIa protein;
  - (f) an adenoviral L2 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2\_penton protein according to claim 3, L2\_pVII, L2\_V, and L2\_pX protein;
  - (g) an adenoviral L3 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L3\_pVI protein, L3\_hexon protein according to claim 2 and L3\_protease;
  - (h) an adenoviral E2A region;
  - (i) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4\_100k protein, the L4\_33k protein and protein L4\_VIII;
  - (j) an adenoviral E3 region, or a fragment thereof selected from the group consisting of E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, and E3 ORF9;
  - (k) an adenoviral L5 region, or a fragment thereof said fragment encoding the L5\_fiber fiber protein according to claim 1;
  - (l) an adenoviral E4 region, or a fragment thereof selected from the group consisting of E4 ORF7, E4 ORF6, E4 ORF4, E4 ORF3, E4 ORF2, and E4 ORF1;
  - (m) an adenoviral 3'-end, preferably an adenoviral 3' inverted terminal repeat; and/or
  - (n) an adenoviral VAI or VAII RNA region, preferably an adenoviral VAI or VAII RNA region from an adenovirus other than ChAd157, more preferably from Ad5.
18. The polynucleotide, vector, adenovirus, composition or cell according to claim 17, wherein the polynucleotide comprises at least one of the following:
- (a) an adenoviral 5'-end, preferably an adenoviral 5' inverted terminal repeat;
  - (e) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1\_13.6k protein, L1\_52k and L1\_IIIa protein;
  - (f) an adenoviral L2 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2\_penton protein according to claim 3, L2\_pVII, L2\_V, and L2\_pX protein;

- (g) an adenoviral L3 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L3\_pVI protein, L3\_hexon hexon protein according to claim 2 and L3\_protease;
  - (i) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4\_100k protein, the L4\_33k protein and protein L4\_VIII;
  - (k) an adenoviral L5 region, or a fragment thereof said fragment encoding the L5\_fiber fiber protein according to claim 1;
  - (m) an adenoviral 3'-end, preferably an adenoviral 3' inverted terminal repeat.
19. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 16, wherein the polynucleotide comprises an adenoviral VAI or VAII RNA region.
20. The polynucleotide, vector, adenovirus, composition or cell according to claim 19, wherein the VAI or VAII RNA region is from an adenovirus other than ChAd157.
21. The polynucleotide, vector, adenovirus, composition or cell according to claim 20, wherein the VAI or VAII RNA region is from Ad5.
22. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 16, wherein the polynucleotide comprises or consists of a polynucleotide which is at least 95% identical over its entire length to a reference sequence that consists essentially of SEQ ID NO: 15 or 22.
23. The polynucleotide, vector, adenovirus, composition or cell according to claim 22, wherein the polynucleotide comprises or consists of a polynucleotide which is at least 99% identical over its entire length to the reference sequence.
24. The polynucleotide, vector, adenovirus, composition or cell according to claim 23, wherein the polynucleotide comprises or consists of a polynucleotide which is at least 99.5% identical over its entire length to the reference sequence.
25. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 22 to 24, wherein the polynucleotide comprises or consists of a polynucleotide which is identical over its entire length to the reference sequence.
26. The polynucleotide, vector, adenovirus, composition or cell according to claim 25, wherein the reference sequence is SEQ ID NO: 15.
27. The polynucleotide, vector, adenovirus, composition or cell according to claim 25, wherein the reference sequence is SEQ ID NO: 22.

28. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 16, wherein the polynucleotide comprises a mutation 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.
29. The polynucleotide, vector, adenovirus, composition or cell according to claim 28, wherein the polynucleotide lacks at least one gene of a genomic region selected from the group consisting of E1A, E1B, E2A, E2B, E3 and/or E4.
30. The polynucleotide, vector, adenovirus, composition or cell according to either claim 28 or 29, wherein the genomic regions are E1A and/or E1B.
31. The polynucleotide, vector, adenovirus, composition or cell according to any one of claims 1 to 16, wherein the polynucleotide comprises a deletion of the E1 genomic region.
32. The adenovirus according to any one of claims 4 and 8 to 31, wherein the recombinant adenovirus is replication-competent.
33. The adenovirus according to any one of claims 4 and 8 to 32, wherein the recombinant adenovirus is replication-incompetent.
34. The adenovirus of any one of claims 4 and 8 to 33, wherein the recombinant adenovirus comprises a nucleic acid sequence encoding a protein, wherein the nucleic acid sequence is operatively linked to one or more sequences which direct expression of said protein in a host cell.
35. The adenovirus according to claim 34, wherein the protein is an antigenic protein or a fragment thereof.
36. The adenovirus according to claim 35 wherein the protein is a heterologous protein or fragment thereof.
37. The adenovirus of claim 36, wherein the protein is derived from a virus.
38. The adenovirus of any one of claims 34 to 37, wherein the one or more sequences which direct expression of said product in a host cell includes a sequence selected from one or more of the group consisting of: transcription initiation, transcription termination, promoter and enhancer sequences.
39. The adenovirus of claim 38, wherein the one or more sequences which direct expression of said product in a host cell includes a promoter sequence.

40. The adenovirus of claim 39, wherein the promoter sequence is selected from the group consisting of an internal promoter, a native promoter, RSV LTR promoter, CMV promoter, SV40 promoter, dihydrofolate reductase promoter,  $\beta$ -actin promoter, PGK promoter, EF1a promoter and CASI promoter.
41. The adenovirus of claim 39, wherein the promoter sequence is an enhanced hCMV promoter, such as provided in SEQ ID NO: 42.
42. The adenovirus according to any one of claims 4 and 8 to 41, wherein the adenovirus has a seroprevalence of less than 10% in human subjects and preferably no seroprevalence in human subjects.
43. The adenovirus according to any one of claims 4 and 8 to 42, wherein the adenovirus is capable of infecting a mammalian cell.
44. The composition according to any one of claims 5 and 8 to 43, comprising an adjuvant selected from the list consisting of: inorganic adjuvants (e.g. inorganic metal salts such as aluminium phosphate or aluminium hydroxide), organic adjuvants (e.g. saponins, such as QS21, or squalene), oil-based adjuvants (e.g. Freund's complete adjuvant and Freund's incomplete adjuvant), cytokines (e.g. IL-1 $\beta$ , IL-2, IL-7, IL-12, IL-18, GM-CSF, and INF- $\gamma$ ) particulate adjuvants (e.g. immuno-stimulatory complexes (ISCOMS), liposomes, or biodegradable microspheres), virosomes, bacterial adjuvants (e.g. monophosphoryl lipid A, such as 3-de-O-acylated monophosphoryl lipid A (3D-MPL), or muramyl peptides), synthetic adjuvants (e.g. non-ionic block copolymers, muramyl peptide analogues, or synthetic lipid A), synthetic polynucleotides adjuvants (e.g. polyarginine or polylysine) and immunostimulatory oligonucleotides containing unmethylated CpG dinucleotides ("CpG").
45. The composition according to claim 44, wherein the adjuvant is a 3D-MPL and/or QS21.
46. The cell according to any one of claims 6 and 8 to 31, wherein the cell is a host cell that expresses at least one adenoviral gene selected from the group consisting of E1A, E1B, E2A, E2B, E3 E4, L1, L2, L3, L4 and L5.
47. The cell according to claim 45 wherein the host cell is grown in suspension.
48. A polynucleotide, polypeptide, vector, adenovirus, composition or cell according to any one of claims 1 to 47, for use as a medicament.
49. A polynucleotide, polypeptide, vector, adenovirus, composition or cell according to claim 48, for use as a vaccine.



50. Use of the polynucleotide, polypeptide, vector, adenovirus, composition or cell according to any one of claims 1 to 47 for the therapy or prophylaxis of a disease.
51. A method of inducing an immune response in a subject comprising administering the polynucleotide, polypeptide, vector, adenovirus, composition or cell according to any one of claims 1 to 47 to the subject.
52. An isolated polynucleotide comprising or consisting of the sequence according to SEQ ID NO: 2.
53. A recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene for administration to a subject which has previously been exposed to a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof, as described herein.
54. The recombinant adenoviral vector according to claim 53, wherein the subject which has previously been exposed to a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton.
55. The recombinant adenoviral vector according to claim 54, wherein the subject which has previously been exposed to a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton.
56. The recombinant adenoviral vector according to claim 54 or 55, wherein the recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton encodes a transgene directed at a different medical indication or indications to the recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene.
57. The recombinant adenoviral vector according to claim 54 or 55, wherein the recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton encodes a transgene directed at the same medical indication or indications to the recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene.
58. The recombinant adenoviral vector according to claim 54 or 55, wherein the recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton encodes the same transgene as to the recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene.
59. The recombinant adenoviral vector according to any one of claims 53 to 58, wherein the transgenes encode an immunogen which are useful to immunize a human or non-human animal against a pathogen such as bacteria, fungi, parasitic microorganisms or

multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell.

60. A recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene for administration to a subject which may subsequently be exposed to a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof, as described herein.
61. The recombinant adenoviral vector according to claim 60, wherein the subject which may subsequently be exposed to a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton.
62. The recombinant adenoviral vector according to claim 61, wherein the subject which may subsequently be exposed to a recombinant adenoviral vector comprising a ChAd155 fiber, hexon and penton.
63. The recombinant adenoviral vector according to claim 61 or 62, wherein the recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton encodes a transgene directed at a different medical indication or indications to the recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene.
64. The recombinant adenoviral vector according to claim 61 or 62, wherein the recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton encodes a transgene directed at the same medical indication or indications to the recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene.
65. The recombinant adenoviral vector according to claim 61 or 62, wherein the recombinant adenoviral vector comprising a ChAd155 fiber, hexon and/or penton encodes the same transgene as the recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a transgene.
66. The recombinant adenoviral vector according to any one of claims 60 to 65, wherein the transgenes encode an immunogen which are useful to immunize a human or non-human animal against a pathogen such as bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell.
67. A method for eliciting an immune response in a subject, said method comprising:
  - (a) administering to the subject a recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a first transgene; and

- (b) administering to the subject a recombinant adenoviral vector which does not comprise a ChAd157 fiber, the vector encoding a second transgene;  
wherein steps (a) and (b) may be undertaken in either order and the first and second transgenes may be the same or different.
68. A method for the prophylaxis or treatment of a subject, said method comprising:  
(a) administering to the subject a recombinant adenoviral vector according to any one of claims 4 and 8 to 43 encoding a first transgene encoding an immunogen which is useful to immunize a human or non-human animal against a pathogen such as bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell; and  
(b) administering to the subject a recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof as described herein, the vector encoding second transgene encoding an immunogen which is useful to immunize a human or non-human animal against a different pathogen such as bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or against a cancer cell or tumor cell;  
wherein steps (a) and (b) may be undertaken in either order.
69. The recombinant adenoviral vector or method according to any one of claims 53 to 68, wherein the recombinant adenoviral vector which does not comprise a ChAd157 fiber, or functional derivative thereof as described herein has a low cross-reactivity with the recombinant adenoviral vector according to any one of claims 4 or 8 to 43.
70. The recombinant adenoviral vector or method according to claim 69, wherein immunisation with a first vector elicits a neutralising titer which is on average less than 50% of the level arising from immunisation with the second vector.
71. The recombinant adenoviral vector or method according to any one of claims 53 to 70, wherein the recombinant adenoviral vector which does not comprise a ChAd157 fiber does not comprise a ChAd157 fiber, ChAd157 hexon or ChAd157 fiber or functional derivatives thereof having at least 98% identity thereto.

Figure 1A

	10	20	30	40	50	60	70	80	
12_ChAd157	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
01_ChAd3	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
02_PanAd3	MKRKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
03_ChAd17	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
04_ChAd19	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
05_ChAd24	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
06_ChAd155	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
07_ChAd11	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
08_ChAd20	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
09_ChAd31	MKRTKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
10_PanAd1	MKRKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
11_PanAd2	MKRKTSDESNFVVPYDTE	GPPSVFFLTPPFVSPDGFQES	PPGVL	SNLAEPLVTS	HGMAL	KMGSGLS	LDDAGNLT	80	
12_ChAd157	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
01_ChAd3	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
02_PanAd3	QDITTA	PPPLKKT	KTNLSLETS	PLTVS	SGLTVA	AAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	159	
03_ChAd17	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
04_ChAd19	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
05_ChAd24	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
06_ChAd155	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
07_ChAd11	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
08_ChAd20	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
09_ChAd31	QDITTA	PPPLKKT	KTNLSLETS	PLTVSTSGALT	VAAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	LATKGPLTVSEGKLAL	160	
10_PanAd1	QDITTA	PPPLKKT	KTNLSLETS	PLTVS	SGLTVA	AAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	159	
11_PanAd2	QDITTA	PPPLKKT	KTNLSLETS	PLTVS	SGLTVA	AAAAPLAVAGTSL	TMQSEAPLTVQDAKLT	159	

Figure 1B

12_ChAd157	170	180	190	200	210	220	230	240	240
01_ChAd3	170	180	190	200	210	220	230	240	240
02_PanAd3	170	180	190	200	210	220	230	240	239
03_ChAd17	170	180	190	200	210	220	230	240	240
04_ChAd19	170	180	190	200	210	220	230	240	240
05_ChAd24	170	180	190	200	210	220	230	240	240
06_ChAd155	170	180	190	200	210	220	230	240	240
07_ChAd11	170	180	190	200	210	220	230	240	240
08_ChAd20	170	180	190	200	210	220	230	240	240
09_ChAd31	170	180	190	200	210	220	230	240	240
10_PanAd1	170	180	190	200	210	220	230	240	239
11_PanAd2	170	180	190	200	210	220	230	240	239
12_ChAd157	250	260	270	280	290	300	310	320	320
01_ChAd3	250	260	270	280	290	300	310	320	320
02_PanAd3	250	260	270	280	290	300	310	320	319
03_ChAd17	250	260	270	280	290	300	310	320	320
04_ChAd19	250	260	270	280	290	300	310	320	320
05_ChAd24	250	260	270	280	290	300	310	320	320
06_ChAd155	250	260	270	280	290	300	310	320	320
07_ChAd11	250	260	270	280	290	300	310	320	320
08_ChAd20	250	260	270	280	290	300	310	320	320
09_ChAd31	250	260	270	280	290	300	310	320	320
10_PanAd1	250	260	270	280	290	300	310	320	319
11_PanAd2	250	260	270	280	290	300	310	320	319

Figure 1C

12_ChAd157	KISSGLDYDNGAIIKLGTGLSFDNTGATVGN	364
01_ChAd3	KISSGLDYDNGAIIKLGTGLSFDNTGATVGN	364
02_PanAd3	KISSGLDYDNGAIIKLGTGLSFDNTGATVGN	363
03_ChAd17	KISSGLDYDNGAIIKLGTGLSFDNTGATVGN	364
04_ChAd19	KISSGLDYDNGAIIKLGTGLSFDNTGATVGN	364
05_ChAd24	KISSGLDYDNGAIIKLGTGLSFDNTGATVGN	364
06_ChAd155	KIKTAKGLIYBDDTAIAINAGBDCFDGSGDTPFKKIGLGDYDS	400
07_ChAd11	KIKTAKGLIYBDDTAIAINPEBDFEFGSGDTPFKKIGLGDYDS	400
08_ChAd20	KIKTAKGLIYBDDTAIAINASBQCPDSSSDTPFKKIGLGDYDS	400
09_ChAd31	KIKTAKGLIYBDDTAIAIASBQCFDSSSDTPFKKIGLGDYDS	400
10_PanAd1	KIKTAKGLIYBDDTAIAIAGBQCFDSSSDTPFKKIGLGDYDS	399
11_PanAd2	KIKTAKGLIYBDDTAIAIAGBQCFDSSSDTPFKKIGLGDYDS	399
12_ChAd157	TPDPSNCRISKDKKFTLVLTCKGSOILASV	444
01_ChAd3	TPDPSNCRISKDKKFTLVLTCKGSOILASV	444
02_PanAd3	TPDPSNCRISKDKKFTLVLTCKGSOILASV	442
03_ChAd17	TPDPSNCRISKDKKFTLVLTCKGSOILASV	444
04_ChAd19	TPDPSNCRISKDKKFTLVLTCKGSOILASV	444
05_ChAd24	TPDPSNCRISKDKKFTLVLTCKGSOILASV	444
06_ChAd155	TPDPSNCRISKDKAKFTLVLTCKGSOILASV	480
07_ChAd11	TPDPSNCRISKDKAKFTLVLTCKGSOILASV	480
08_ChAd20	TPDPSNCRISKDKAKFTLVLTCKGSOILASV	480
09_ChAd31	TPDPSNCRISKDKAKFTLVLTCKGSOILASV	480
10_PanAd1	TPDPSNCRISKDKAKFTLVLTCKGSOILASV	479
11_PanAd2	TPDPSNCRISKDKAKFTLVLTCKGSOILASV	479

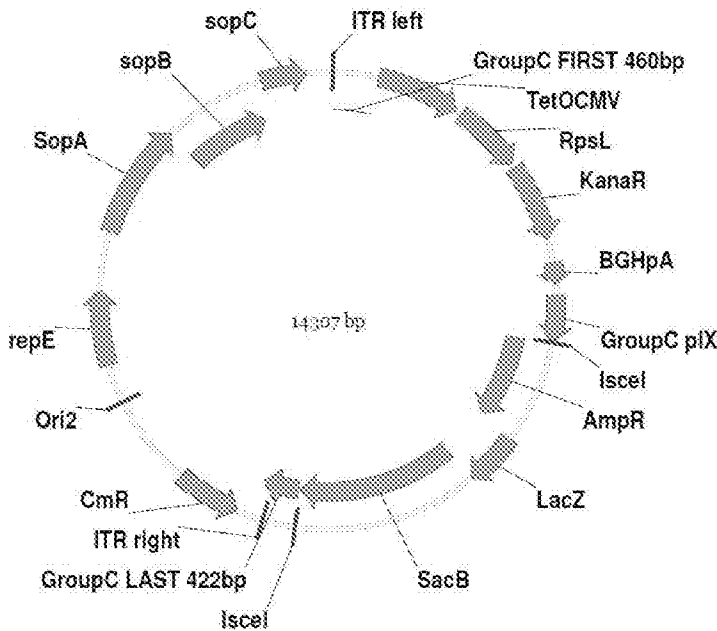
Figure 1D

12_ChAd157	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	560
01_ChAd3	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
02_PanAd3	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
03_ChAd17	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
04_ChAd19	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
05_ChAd24	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
06_ChAd155	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
07_ChAd11	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
08_ChAd20	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
09_ChAd31	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
10_PanAd1	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558
11_PanAd2	STNVAITNAVGFMPNLTAYPKTQSOTAKNIVSQVYLVNGDKSKPMTLTITLNGTNE	558

570

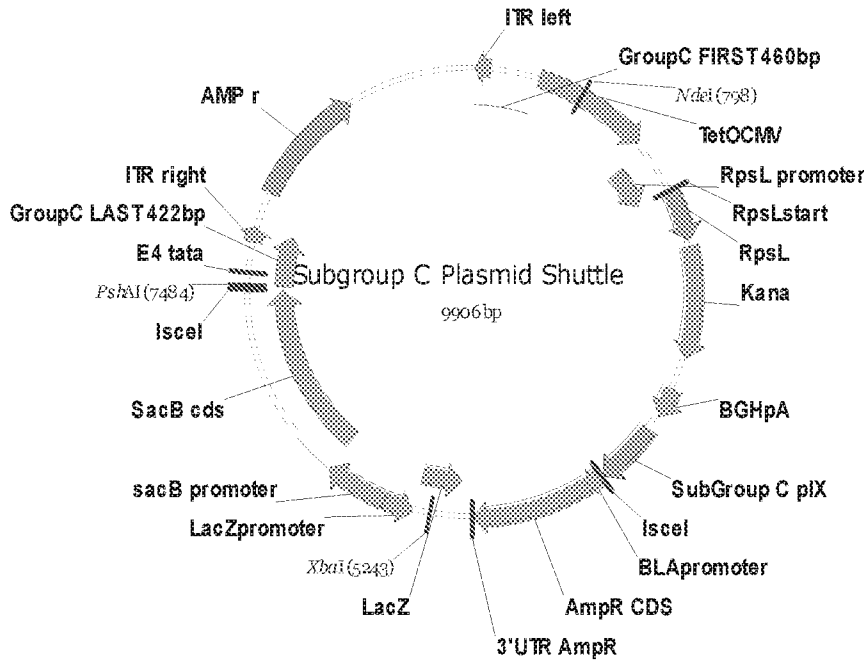
12_ChAd157	YETETINSFTFSYIA	543
01_ChAd3	YETETINSFTFSYIA	543
02_PanAd3	YETETINSFTFSYIA	541
03_ChAd17	YETETINSFTFSYIA	543
04_ChAd19	YETETINSFTFSYIA	543
05_ChAd24	YETETINSFTFSYIA	543
06_ChAd155	YETETINSFTFSYIA	578
07_ChAd11	YETETINSFTFSYIA	578
08_ChAd20	YETETINSFTFSYIA	578
09_ChAd31	YETETINSFTFSYIA	578
10_PanAd1	YETETINSFTFSYIA	577
11_PanAd2	YETETINSFTFSYIA	577

Figure 2



<b>ITR left:</b>
bp 27 to 139
<b>GroupC FIRST 460bp:</b>
bp 27 to 486
<b>hCMV(tetO) RpsL-Kana cassette:</b> bp 493 to 3396
<b>piX gene:</b> bp 3508 to 3972
<b>ISceI restriction sites:</b> bp 3990 and 7481
<b>Amp-LacZ-SacB selection cassette:</b> bp 4000 to 7471
<b>GroupC LAST 422bp:</b> bp 7496 to 7917
<b>ITR right:</b> bp 7805 to 7917

Figure 3



<b>ITR left:</b>
bp 9 to 121
<b>GroupC FIRST 460bp:</b>
bp 9 to 468
<b>hCMV(tetO) RpsL-Kana cassette:</b> bp 475 to 3378
<b>piX gene:</b> bp 3490 to 3951
<b>ISceI restriction sites:</b> bp 3964 and bp 7454
<b>Amp-LacZ-SacB selection cassette:</b> bp 3982 to 7453
<b>GroupC LAST 422bp:</b> bp 7478 to 7899
<b>ITR right:</b> bp 7787 to 7899



Figure 4

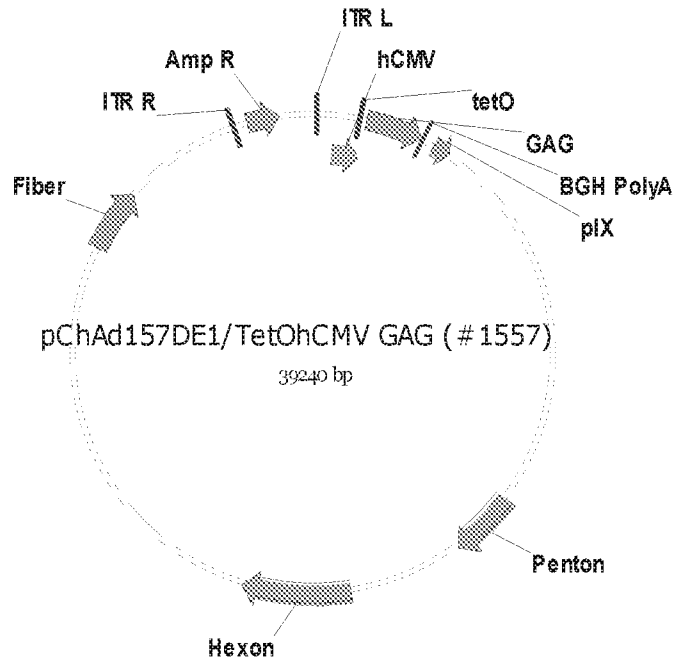


Figure 5

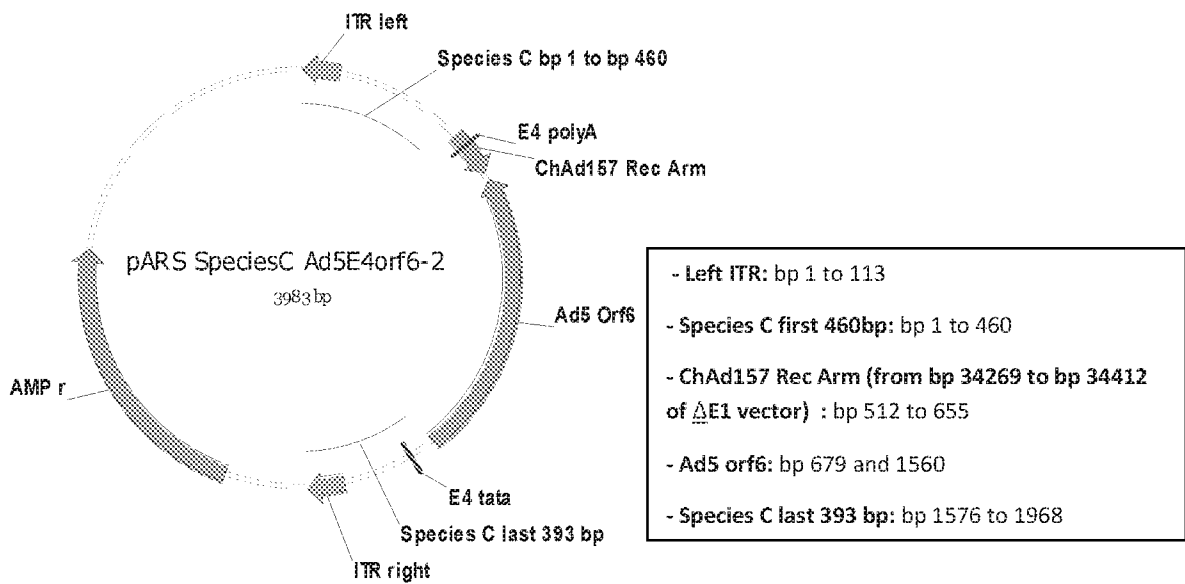


Figure 6

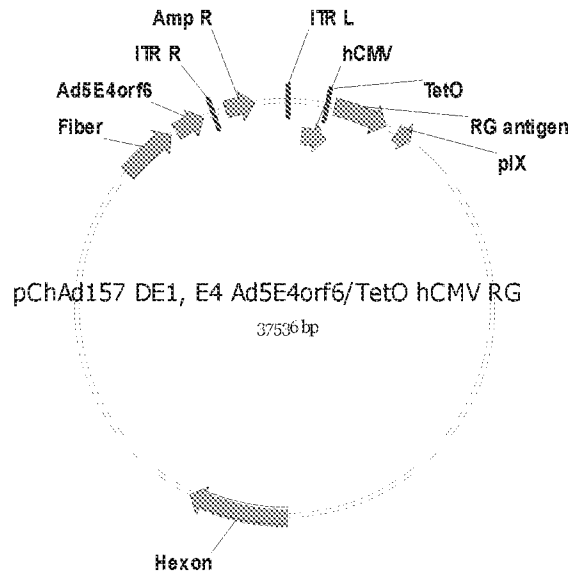


Figure 7

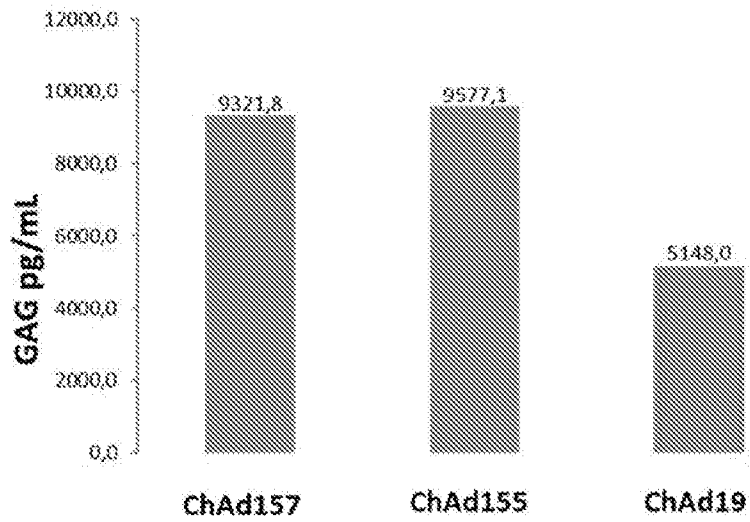


Figure 8

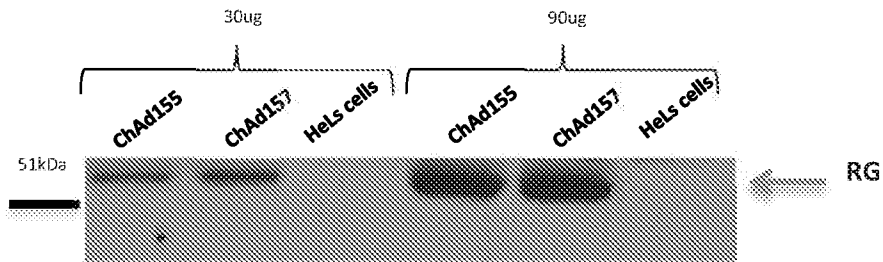


Figure 9

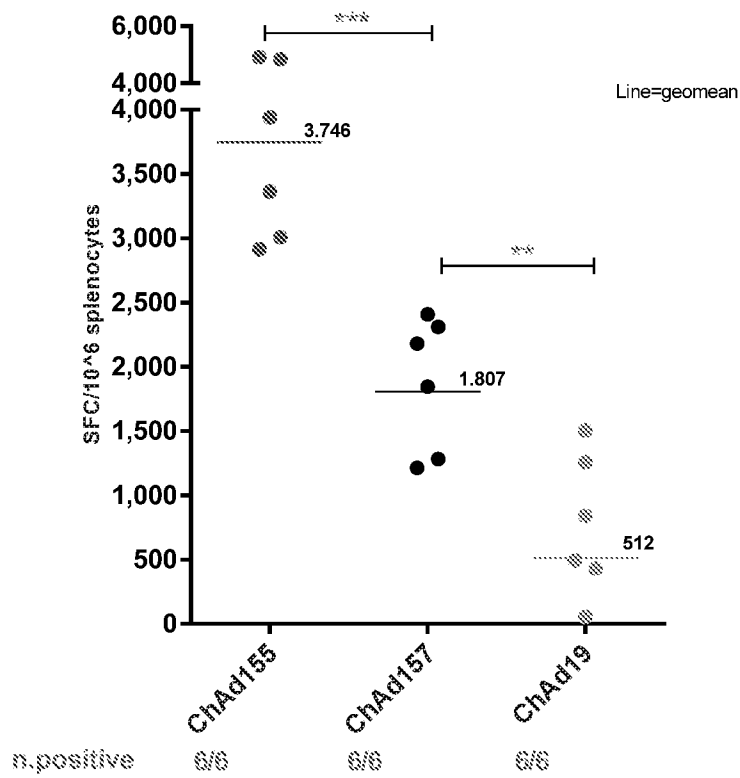


Figure 10

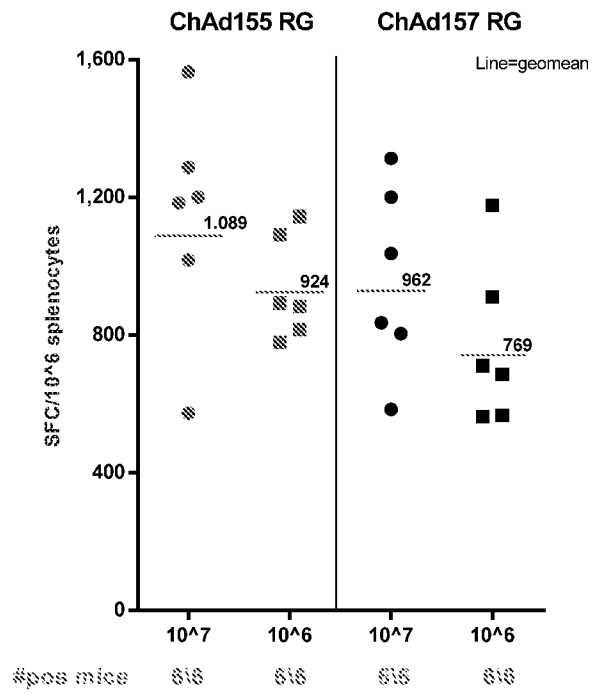


Figure 11

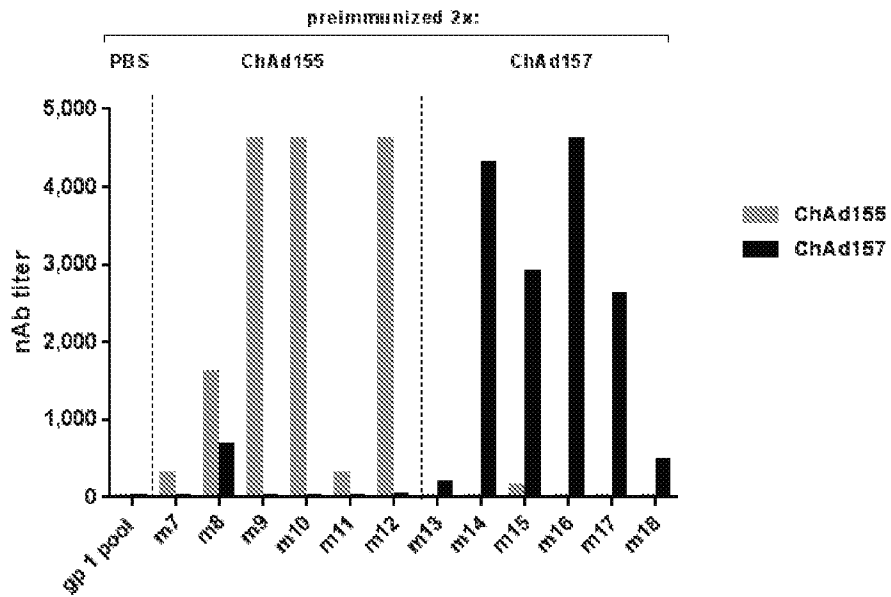
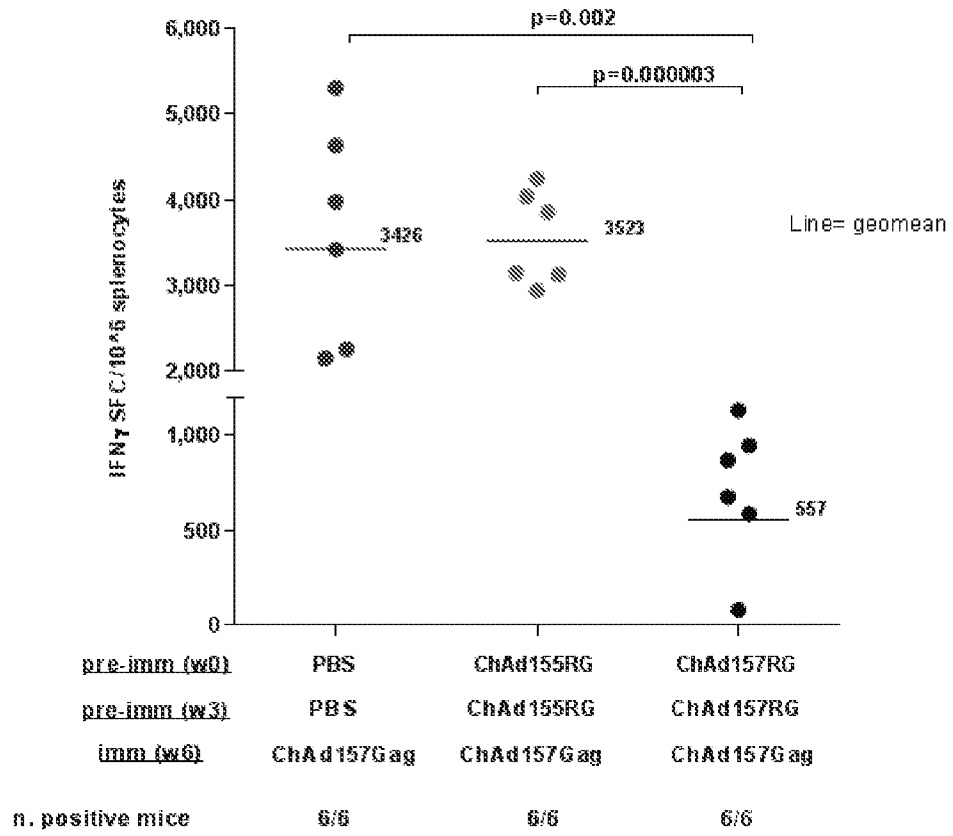


Figure 12



INTERNATIONAL SEARCH REPORT

International application No  
PCT/IB2017/057738

A. CLASSIFICATION OF SUBJECT MATTER  
INV. A61K39/12 A61K39/235 C07K14/075 C12N15/861  
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)  
A61K C07K C12N

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, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2005/071093 A2 (ANGELETTI P IST RICHERCHE BIO [IT]; CIRILLO AGOSTINO [IT]; COLLOCA STE) 4 August 2005 (2005-08-04) abstract page 4, line 3 - line 12 page 4, line 31 - page 5, line 5 page 6, line 12 - line 35 example 2 sequences 14, 15, 42, 56, 57, 83	1-71
A,P	WO 2016/198621 A1 (GLAXOSMITHKLINE BIOLOGICALS SA [BE]) 15 December 2016 (2016-12-15) cited in the application the whole document	1-71

Further documents are listed in the continuation of Box C.

See patent family annex.

\* Special categories of cited documents :

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
7 March 2018	20/03/2018

Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer  Chavanne, Franz
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# INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

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