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(54) **COMPOSITIONS COMPRISING AAV EXPRESSING DUAL ANTIBODY CONSTRUCTS AND USES THEREOF**

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(58) **Field of Classification Search**

CPC **A61K 38/00**; **C07K 16/00**; **C07K 2317/21**; **C07K 14/005**; **C12N 15/52**
See application file for complete search history.

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(57) **ABSTRACT**

A recombinant adeno-associated virus (AAV) having an AAV capsid and packaged therein a heterologous nucleic acid which expresses two functional antibody constructs in a cell is described. Also described are antibodies comprising a heavy chain and a light chain from a heterologous antibody. In one embodiment, the antibodies are co-expressed from a vector containing: a first expression cassette which encodes at least a first open reading frame (ORF) for a first immunoglobulin under the control of regulatory control sequences which direct expression thereof; and a second expression cassette which comprises a second ORF, a linker, and a third ORF under the control of regulatory control sequences which direct expression thereof, wherein the second and third ORF for a second and third immunoglobulin construct. The vector co-expressing these two antibody constructs is in one embodiment an AAV, in which the 5' and 3' ITRs flank the expression cassettes and regulatory sequences.

17 Claims, 8 Drawing Sheets

Specification includes a Sequence Listing.

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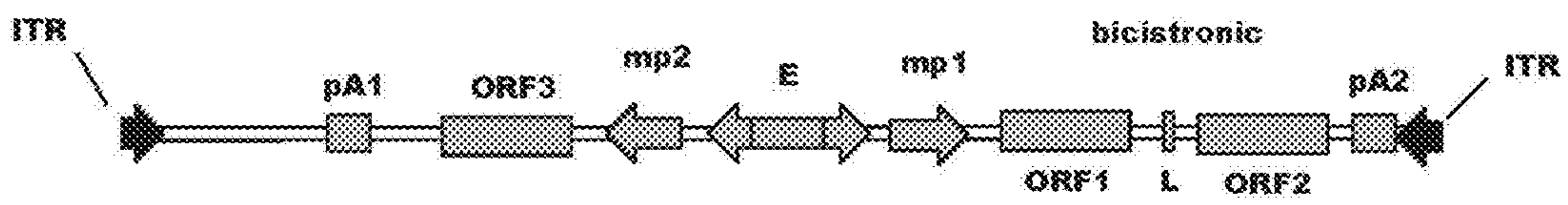


FIG. 1A

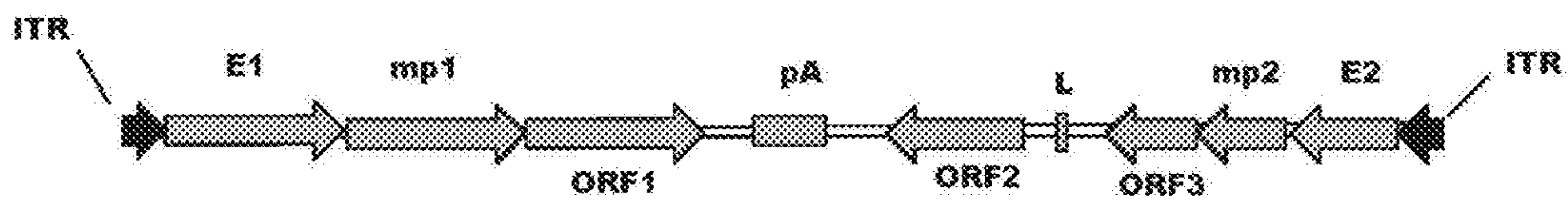


FIG. 1B

FIG 3

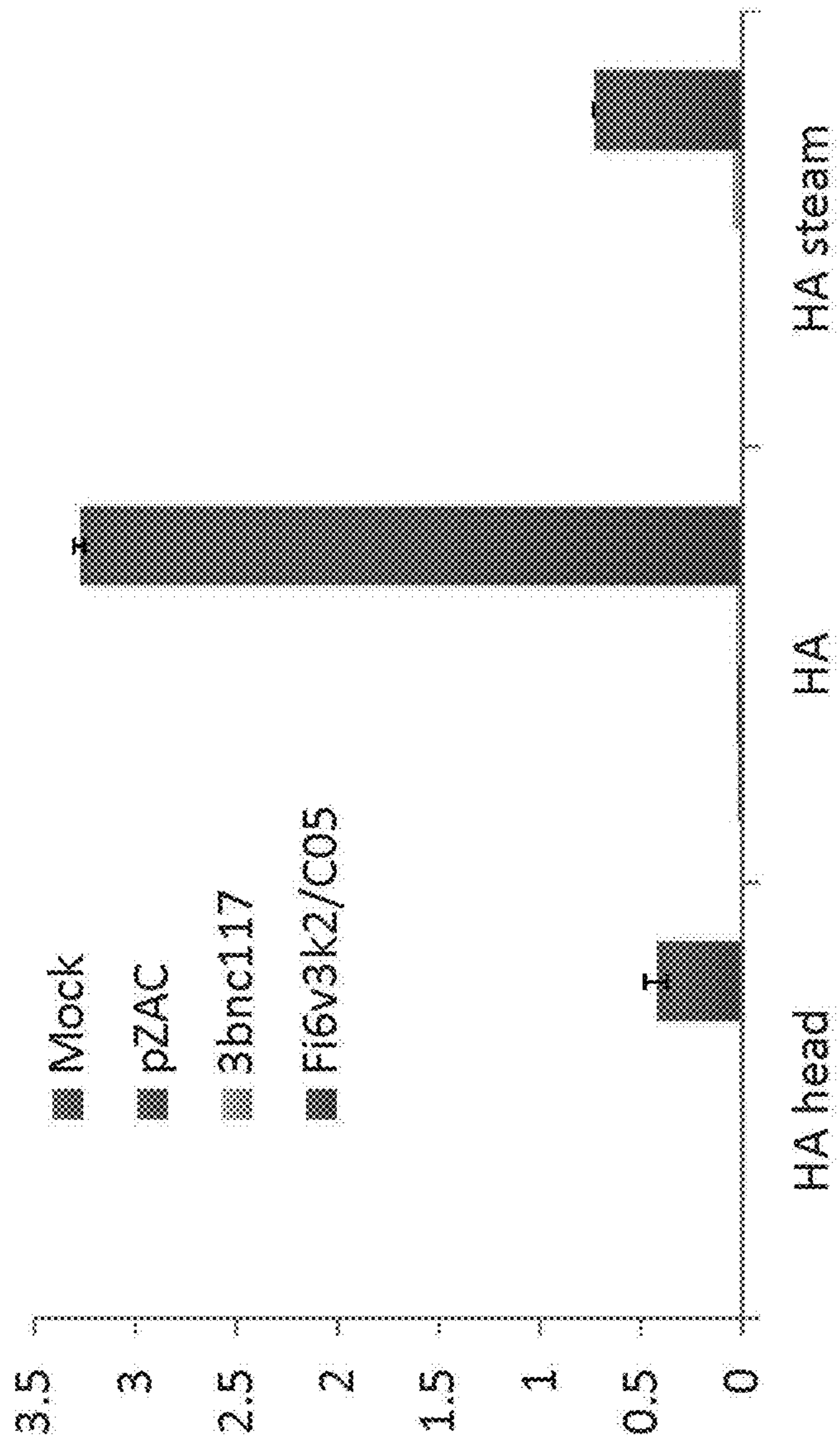


FIG 4B

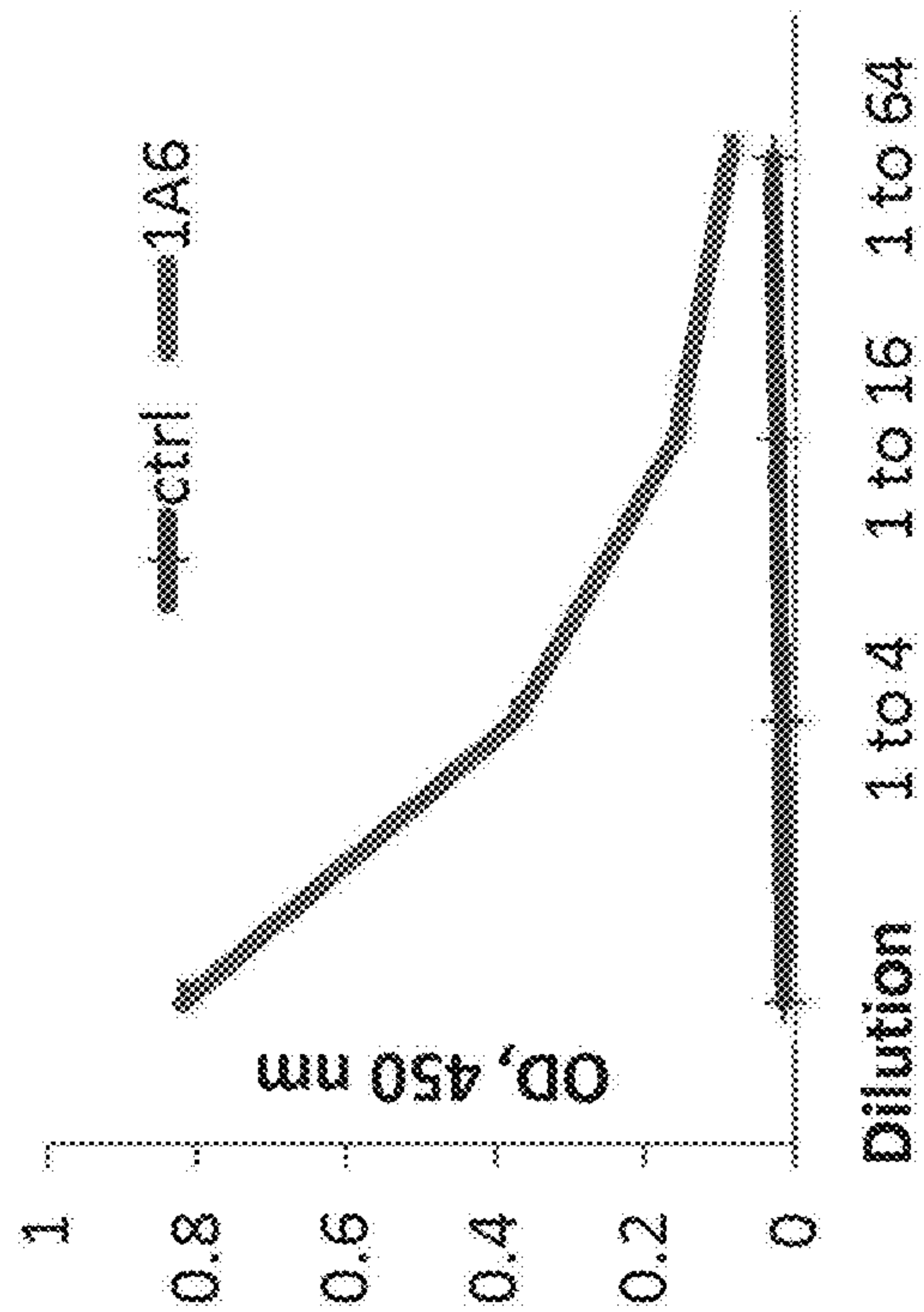


FIG 4A

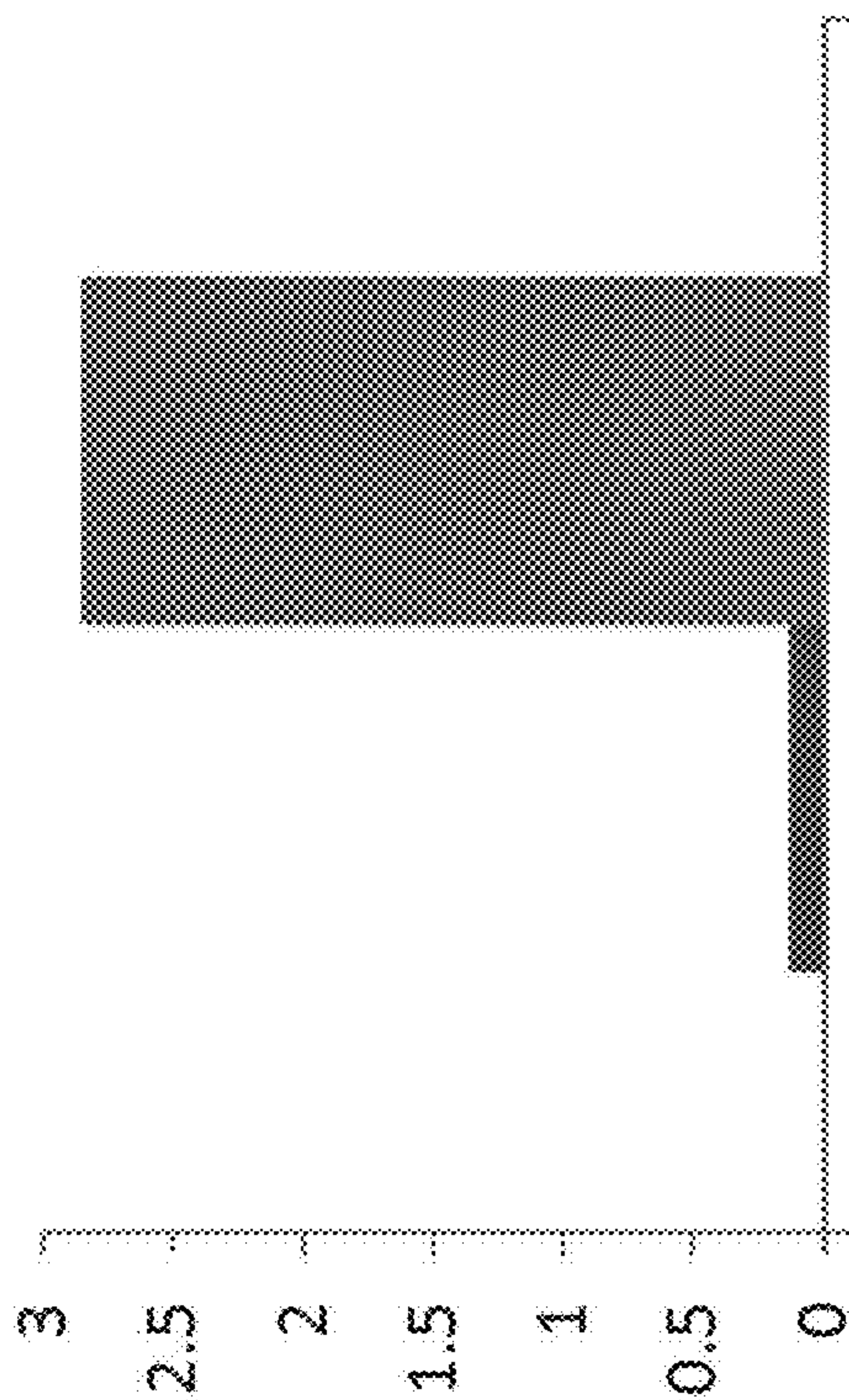


FIG 5

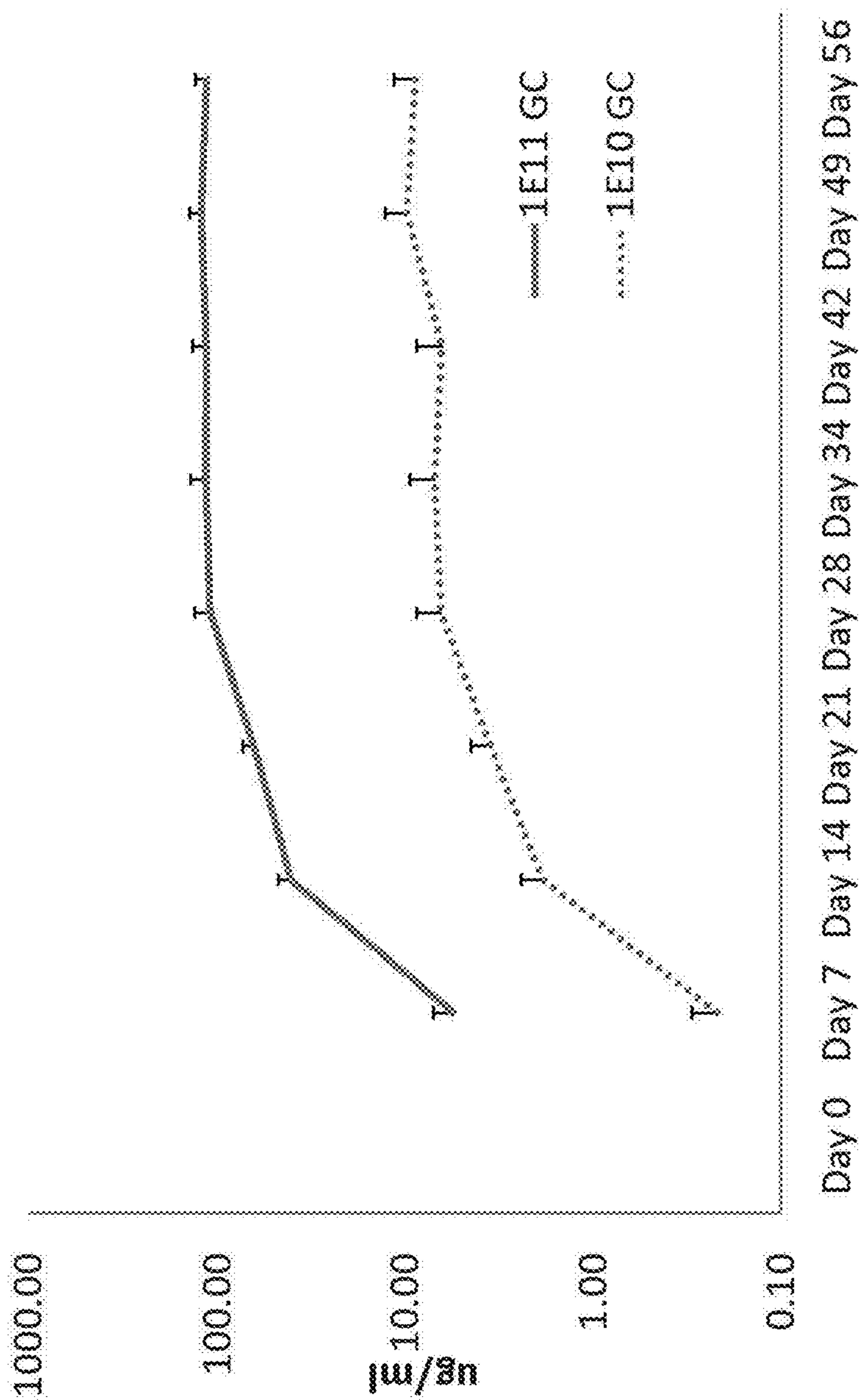


FIG 6B

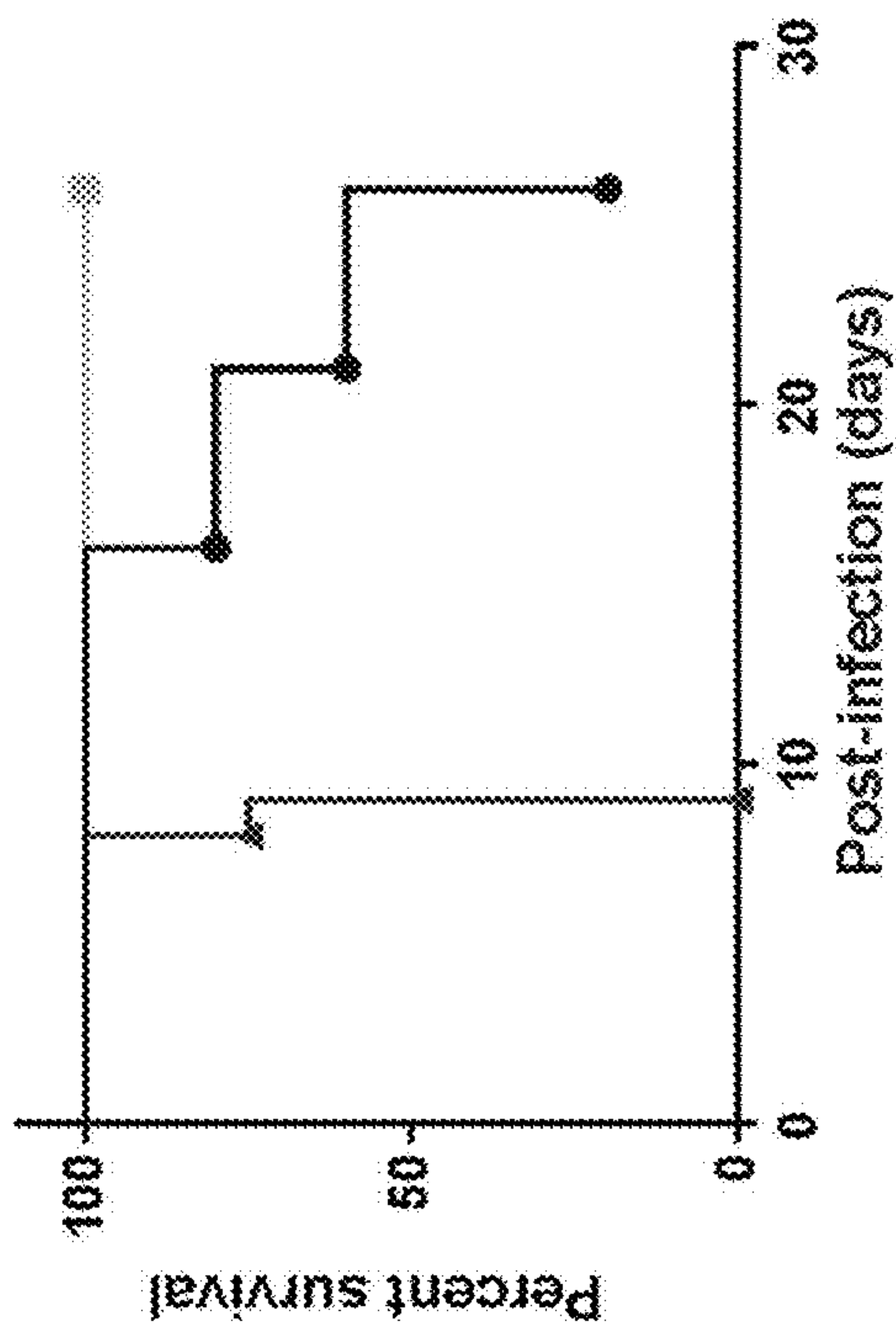


FIG 6A

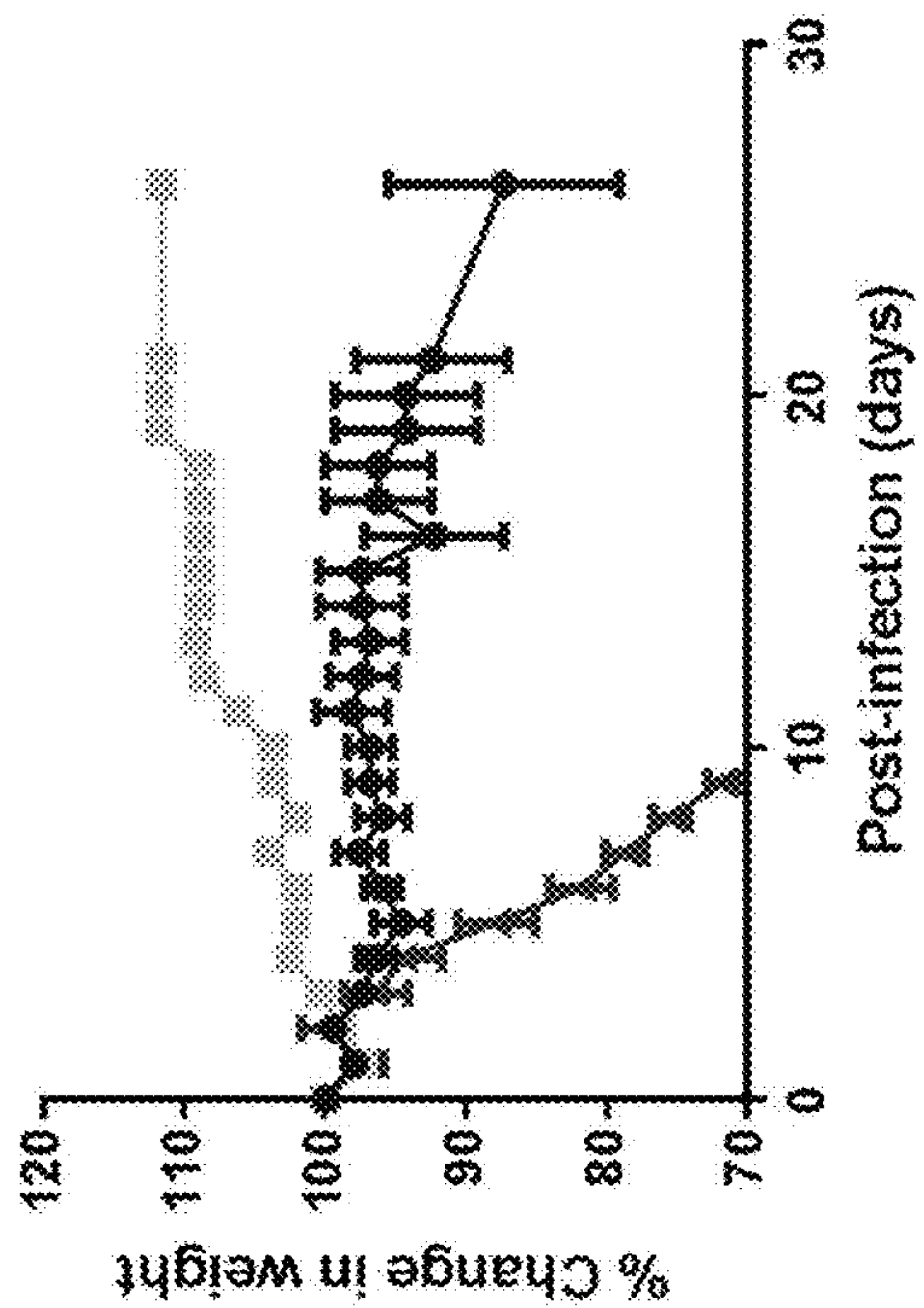


FIG. 7A

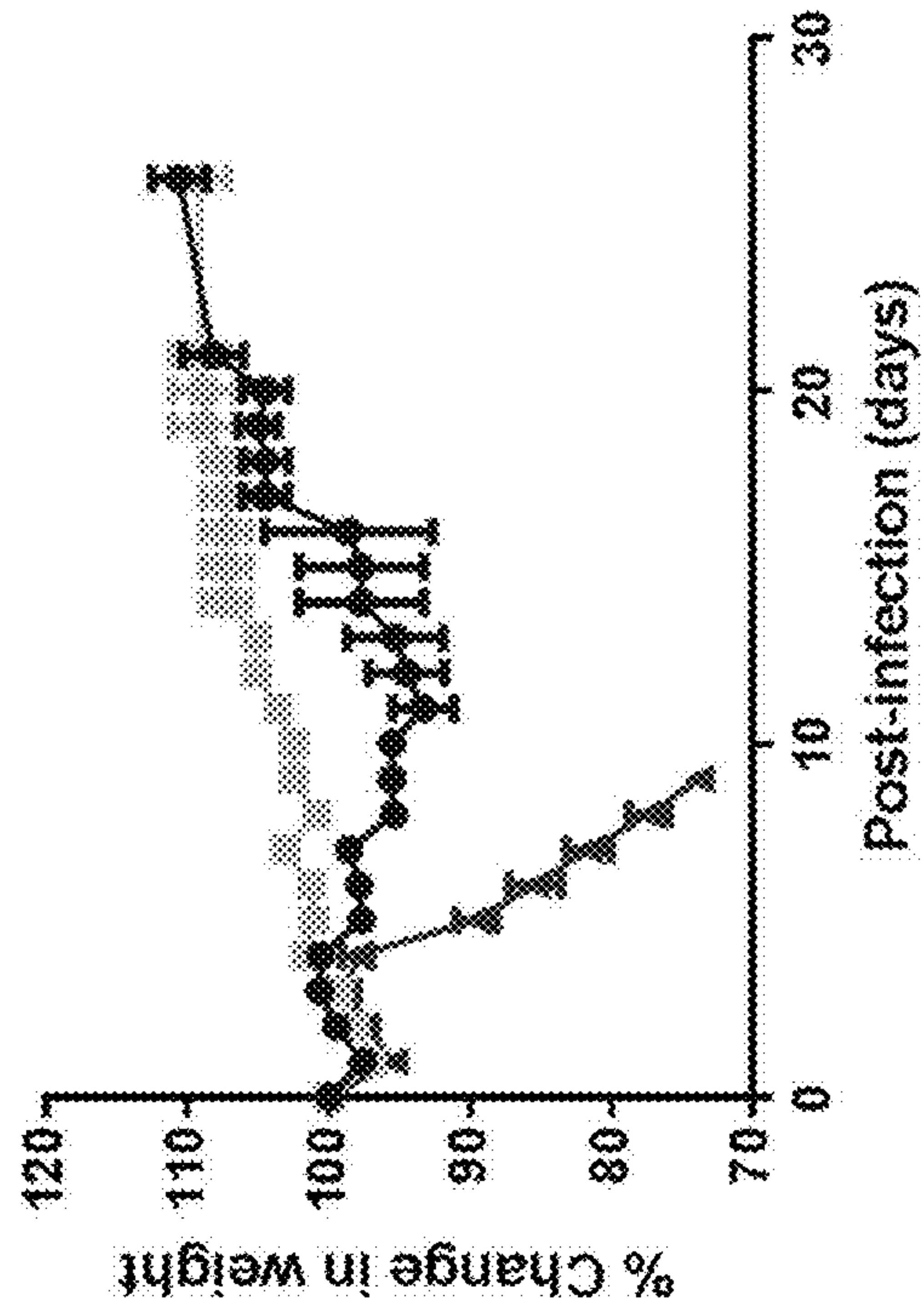
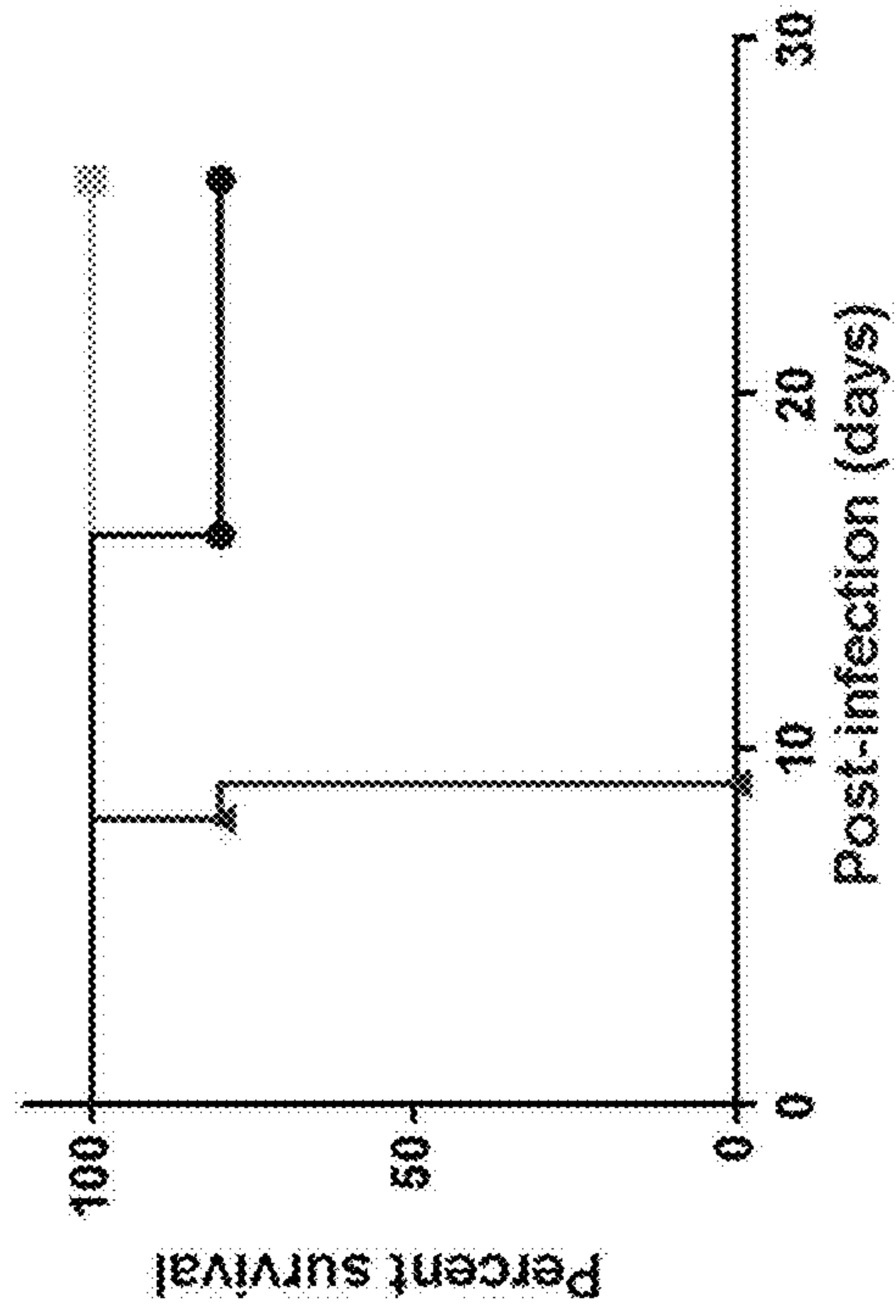


FIG. 7B



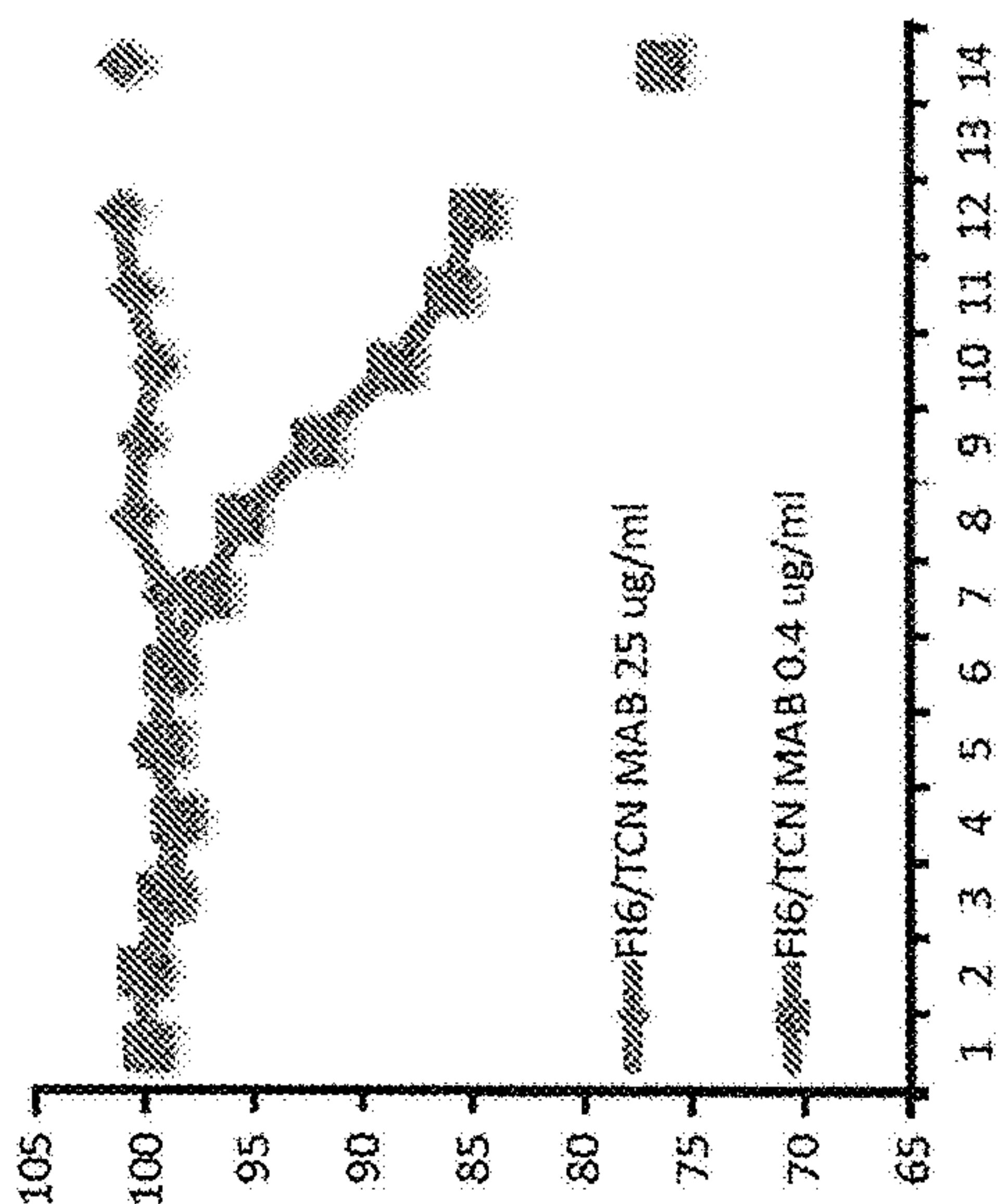


FIG 8A

FIG 8B

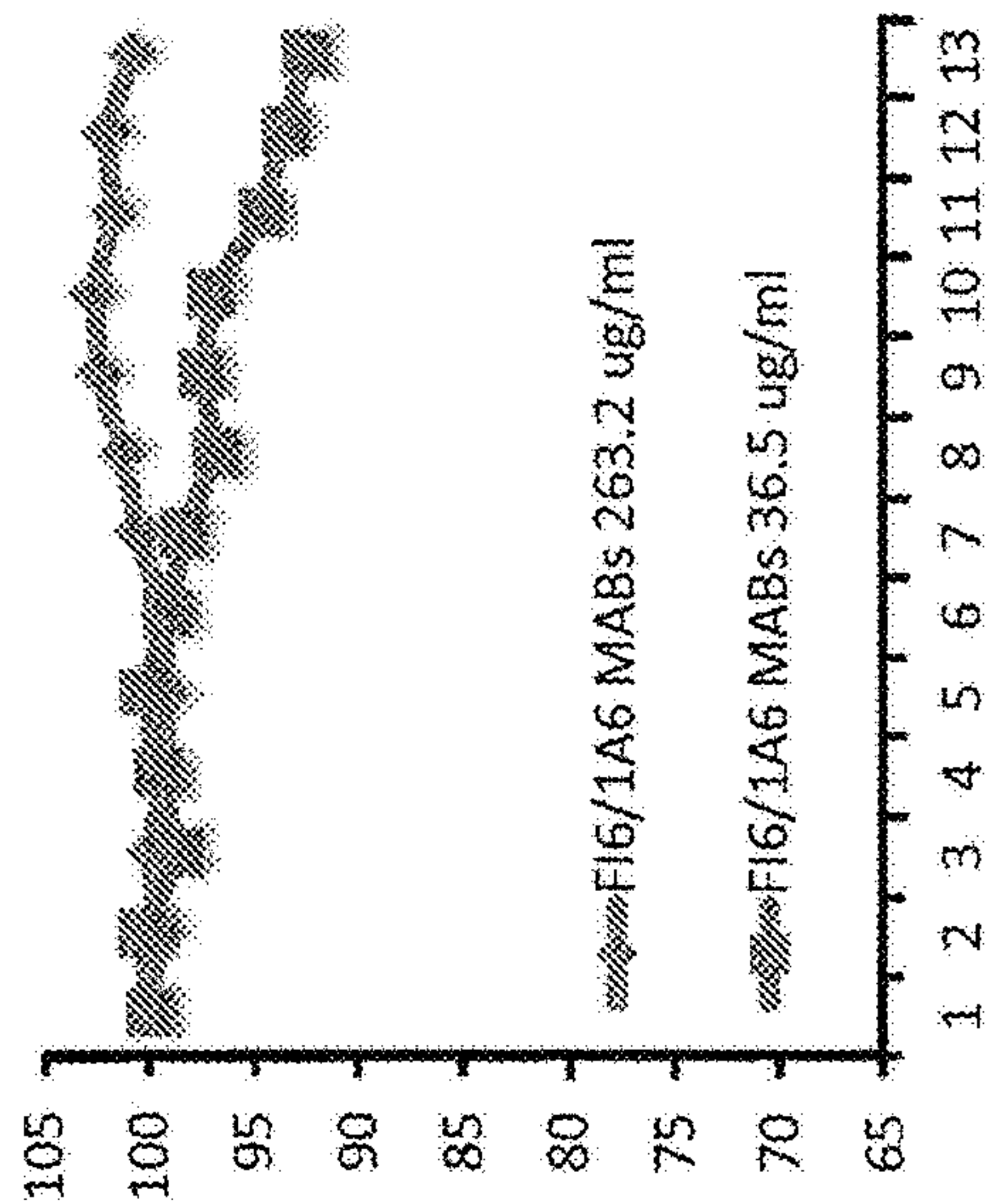
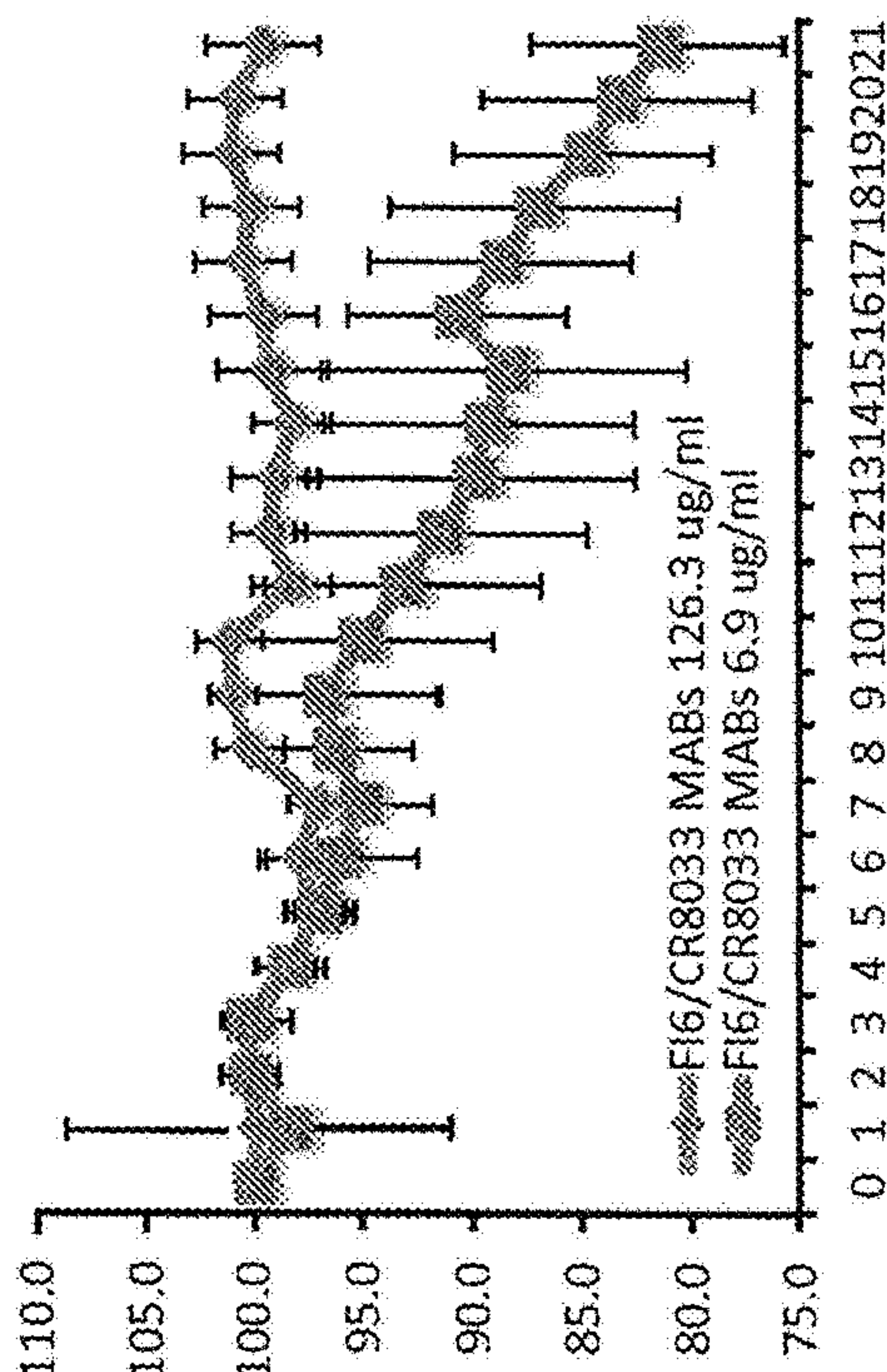


FIG 8C



1**COMPOSITIONS COMPRISING AAV
EXPRESSING DUAL ANTIBODY
CONSTRUCTS AND USES THEREOF****CROSS-REFERENCE TO RELATED
APPLICATIONS**

This is a continuation of U.S. patent application Ser. No. 15/310,555, filed Nov. 11, 2016, which is a national stage application under 35 USC 371 of PCT/US2015/030533, filed May 13, 2015, now expired, which claims the benefit under 35 USC 119(e) of U.S. Provisional Patent Application No. 61/992,649, filed May 13, 2014. Each of these applications is hereby incorporated by reference in its entirety.

**STATEMENT REGARDING FEDERALLY
SPONSORED RESEARCH OR DEVELOPMENT**

This invention was made with government support under grant number ARO No. 64047-LS-DRP awarded by Defense Advanced Research Projects Agency (DARPA). The government has certain rights in the invention.

**INCORPORATION-BY-REFERENCE OF
MATERIAL SUBMITTED IN ELECTRONIC
FORM**

Applicant hereby incorporates by reference the Sequence Listing material filed in electronic form herewith. This file is labeled "14-7032PCT_Seq_Listing_ST25.txt" and dated May 13, 2015 with a size of 220 KB.

BACKGROUND OF THE INVENTION

Monoclonal antibodies have been proven as effective therapeutics for cancer and other diseases. Current antibody therapy often involves repeat administration and long term treatment regimens, which are associated with a number of disadvantages, such as inconsistent serum levels and limited duration of efficacy per administration such that frequent re-administration is required and high cost. The use of antibodies as diagnostic tools and therapeutic modalities has found increasing use in recent years. The first FDA-approved monoclonal antibody for cancer treatment, Rituxan® (Rituximab) was approved in 1997 for the treatment of patients with non-Hodgkin's lymphoma and soon thereafter in 1995, Herceptin®, a humanized monoclonal antibody for treatment of patients with metastatic breast cancer, was approved. Numerous antibody-based therapies that are in various stages of clinical development are showing promise. Given the success of various monoclonal antibody therapies, it has been suggested the next generation of biopharmaceuticals will involve cocktails, i.e., mixtures, of antibodies.

One limitation to the widespread clinical application of antibody technology is that typically large amounts of antibody are required for therapeutic efficacy and the costs associated with production are significant. Chinese Hamster Ovarian (CHO) cells, SP20 and NSO2 myeloma cells are the most commonly used mammalian cell lines for commercial scale production of glycosylated human proteins such as antibodies. The yields obtained from mammalian cell line production typically range from 50-250 mg/L for 5-7 day culture in a batch fermenter or 300-1000 mg/L in 7-12 days in fed batch fermenters.

Adeno associated virus (AAV) is a desirable vector for delivering therapeutic genes due to its safety profile and capability of long term gene expression in vivo. Recombi-

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nant AAV vectors (rAAV) have been previously used to express single chain and full length antibodies in vivo. Due to the limited transgene packaging capacity of AAV, it has been a technical challenge to have a tightly regulated system to express heavy and light chains of an antibody using a single AAV vector in order to generate full length antibodies.

There remains a need in the art for delivering two antibodies in a single composition for therapeutic use.

SUMMARY OF THE INVENTION

A recombinant adeno-associated virus (AAV) having an AAV capsid which has packaged therein a heterologous nucleic acid which expresses two functional antibodies in a cell is provided herein. In one embodiment, the recombinant AAV contains an ORF encoding an immunoglobulin light chain, a second ORF encoding a first immunoglobulin heavy chain and a third ORF encoding a second heavy chain, whereby the expressed functional antibody constructs have two different heavy chains with different specificities which share a light chain. In one embodiment, the two antibodies with different specificities are co-expressed, with a third, bispecific antibody having the specificities of the two monospecific antibodies.

In one embodiment, the rAAV comprises: a 5' AAV inverted terminal repeat (ITR); a first expression cassette which encodes at least a first open reading frame (ORF) for a first immunoglobulin under the control of regulatory control sequences which direct expression thereof; a second expression cassette which comprises a second ORF, a linker, and a third ORF under the control of regulatory control sequences which direct expression thereof, wherein the second and third ORF encode for a second and third immunoglobulin construct; and a 3' AAV ITR.

A pharmaceutical composition is provided which comprises a recombinant AAV which expresses at least two functional antibody constructs and pharmaceutically acceptable carrier. In one embodiment, the at least two functional antibodies have different specificities. Optionally, also co-expressed is a bispecific antibody.

A composition comprising at least two functional antibodies having different specificities is provided, wherein each of the antibodies has the same light chain and a different heavy chain. The light chain is from a different source than the heavy chain for one or both of the antibodies. In one embodiment, two functional monospecific antibodies and a bifunctional antibody are expressed. In one embodiment, the ratio of antibodies is about 25:about 50:about 25, homodimeric:bispecific:homodimeric.

A method of delivering two functional antibodies to a subject is provided which comprises administering a recombinant AAV to the subject.

Still other aspects and advantages of the invention will be readily apparent from the following detailed description of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1A is a cartoon illustrating an exemplary arrangement for a vector expressing two monospecific antibody constructs containing a first and a second heavy chain and a light chain, which may be from an antibody heterologous to one or both of the antibodies from which the first and second heavy chain originate, and a third, bispecific antibody. This arrangement utilizes a shared enhancer which is bidirectional and which separates a first expression cassette and a second expression cassette. Three open reading frames

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(ORF) are illustrated. L refers to a linker. pA1 refers to a first polyA and pA2 refers to a second polyA. MP1 refers to a first minimal promoter and MP2 refers to a second minimal promoter. The polyA and the MP may be the same or different for each expression cassette.

FIG. 1B is a cartoon illustrating an alternative exemplary arrangement for a vector expressing two antibody constructs containing a first and a second heavy chain and a light chain, which may be from an antibody heterologous to one or both of the antibodies from which the first and second heavy chain originate, and a third, bispecific antibody. This arrangement utilizes a shared polyA. E1 refers to a first enhancer and E2 refers to a second enhancer. These may be same or different enhancers for each of the expression cassettes. Similarly MP1 and MP2 may be the same or different.

FIG. 2 illustrates a nucleic acid molecule carried by a plasmid for packaging into an AAV capsid, which is used for co-expression of an anti-TSG 101 heavy chain, FI6 influenza heavy chain, and FI6 light chain. These antibody chains utilize heterologous leader from interleukin 2 (IL2). The human CMV enhancer was used in conjunction with CMV promoters. The bicistronic expression cassette contains a furin recognition site and a 2A linker sequence separating the ORF containing the FI6 VL and CL regions from the ORF containing the FI6 heavy chain. The polyA for the expression cassette on the right is a shortened thymidine kinase polyA. The polyA for the expression cassette on the left is a synthetic polyA sequence.

FIG. 3 illustrates the binding ability of an FI6v3k2 antibody co-expressed with a C05 antibody from a recombinant AAV8 prepared as described herein. The results demonstrate the expected binding to full-length HA and the HA stem characteristic of FI6 and binding to HA and HA head only (no stem) characteristic of C05.

FIGS. 4A-4B illustrates the binding ability of an FI6v3k2 antibody co-expressed with a 1A6 antibody (anti-TSG 101) from a recombinant AAV8 prepared as described herein. FIG. 4A is a bar chart showing binding to protein A captures total monoclonal antibody in the mixture (negative control is represented by the bar on the left, antibody mixture by the bar on the right). FIG. 4B is a graph showing that binding to the TSG101 peptide captures only the MAB containing 1A6 heavy chain (upper line). These data demonstrate that when co-expressed with FI6v3k2, 1A6 antibody retained the binding specificity of antibody from which its heavy chains originated.

FIG. 5 illustrates systemic expression levels in mice administered FI6 co-expressed from an AAV vector with a second antibody at doses of 1×10^{11} genome copies (GC) or 1×10^{10} GC.

FIGS. 6A-6B illustrate the evaluation of the AAV9.BiD.FI6v3_CR8033mAb delivered intramuscularly (IM) at 1×10^{11} GC for protection against challenge with influenza strain PR8. FIG. 6A is a line graph showing percent change in weight. The circle represents the AAV9 construct with a bidirectional promoter expressing synthetic FI6v3 and CR8033 monoclonal antibodies having the same heterologous light chain. The square represents a positive control, i.e., AAV9 expressing a single antibody type FI6 also delivered at 1×10^{11} GC, and the triangle represents naïve animals FIG. 6B shows survival post-challenge.

FIGS. 7A-7B illustrate the evaluation of the AAV9.BiD.FI6v3_CR8033mAb delivered intramuscularly (IM) at 1×10^{11} GC for protection against challenge with influenza strain B/Lee/40. FIG. 7A is a line graph showing percent change in weight. The circle represents the AAV9

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construct with a bidirectional promoter expressing synthetic FI6 and CR8033 monoclonal antibodies having the same heterologous light chain. The square represents a positive control, i.e., AAV9 expressing a single antibody type CR8033 also delivered at 1×10^{11} GC, and the triangle represents naïve animals. FIG. 7B shows survival post-challenge.

FIG. 8A is a chart showing protection in a mouse model following administration of an AAV which expresses both FI6v3 and TCN monoclonal antibodies, as expressed by weight of the mouse over days. The top line (diamonds) represents a dose of 25 micrograms ($\mu\text{g/mL}$) and the bottom line represents 0.4 $\mu\text{g/mL}$.

FIG. 8B is a chart showing protection in a mouse model following administration of an AAV which expresses both FI6v3 and IA6 monoclonal antibodies, as expressed by weight of the mouse over days. The top line (diamonds) represents a dose of 263.2 micrograms ($\mu\text{g/mL}$) and the bottom line represents 36.5 $\mu\text{g/mL}$.

FIG. 8C is a chart showing protection in a mouse model following administration of an AAV which expresses both FI6v3 and CR8033 monoclonal antibodies, as expressed by weight of the mouse over days. The top line (diamonds) represents a dose of 126.3 micrograms ($\mu\text{g/mL}$) and the bottom line represents 6.9 $\mu\text{g/mL}$.

DETAILED DESCRIPTION OF THE INVENTION

A vector is provided herein which delivers at least two functional antibodies by co-expressing two different heavy chains and single light chain which when expressed in a cell form two functional antibodies with different specificities, i.e., which recognize different antigens (or ligands). A third functional antibody may also be expressed and is bispecific, having the heavy chain of each of the two monospecific antibodies. Typically, the third antibody is expressed at a lower level than the two monospecific antibodies. A vector may be used in vivo for efficient production of compositions which will utilize the at least two antibodies or an antibody-producing host cell may be engineered to contain the expression cassettes for the two, different heavy chains and a single type of light chain. Thus, the invention also encompasses a host cell expressing a mixture of two monospecific antibodies, wherein each antibody has a distinct specificity but contains the same light chain, and a third antibody which is bispecific. In one desired embodiment, the vector is designed to deliver the three different antibody constructs in a subject to which the vector is administered.

In one embodiment, the vector is a recombinant AAV which has packaged within an AAV capsid a nucleic acid molecule containing sequences encoding two different heavy chains and a single light chain, which when co-expressed forms two functional monospecific antibodies, i.e., first antibody with a first heavy chain and the light chain and a second antibody with the second heavy chain and the light chain, and a third antibody that has one of each of the heavy chains and the same light chain to make a bispecific antibody.

A “functional antibody” may be an antibody or immunoglobulin which binds to a selected target (e.g., an antigen on a cancer cell or a pathogen, such as a virus, bacteria, or parasite) with sufficient binding affinity to effect a desired physiologic result, which may be protective (e.g., passive immunization) or therapeutic.

The AAV vector provided herein may contain 1, 2, or 3 open reading frames (ORF) for up to ten immunoglobulin

domains. As used herein, an “immunoglobulin domain” refers to a domain of an antibody heavy chain or light chain as defined with reference to a conventional, full-length antibody. More particularly, a full-length antibody contains a heavy (H) chain polypeptide which contains four domains: one N-terminal variable (VH) region and three C-terminal constant (CH1, CH2 and CH3) regions and a light (L) chain polypeptide which contains two domains: one N-terminal variable (VL) region and one C-terminal constant (CL) region. An Fc region contains two domains (CH2-CH3). A Fab region may contain one constant and one variable domain for each the heavy and light chains.

In an AAV vector described herein, two full-length heavy chain polypeptides may be expressed (4 domains each) and a light chain polypeptide (two domains). In one desirable embodiment, the two heavy chain polypeptides have different specificities, i.e., are directed to different targets. Thus, the vectors are useful alone or in combination, for expressing mixtures of antibodies.

As used herein, “different specificities” indicates that the referenced immunoglobulin constructs (e.g., a full-length antibody, a heavy chain, or other construct capable of binding a specific target) bind to a different target site. Suitably, in a dual expressed antibody construct, the two specificities are non-overlapping and/or non-interfering, and may optionally enhance each other. Two antibody (immunoglobulin) constructs as described herein confer different specificity by binding to a different target site on the same pathogen or target site (e.g., a virus protein or tumor). Such different target antigens may be different strains of the same viral type (e.g., two different influenza strains), or two different antigens (e.g., an antiviral and anti-cancer, two different anti-cancer constructs, amongst others). For example, a first heavy chain polypeptide may combine with the light chain to form an antibody construct having a first specificity, the second heavy chain polypeptide may combine with the light chain to form a second antibody construct having a second specificity, and the first and second heavy chain may combine with the light chain to form a bispecific antibody. The antibodies may optionally both be directed to different antigenic sites (epitopes) on a single target (e.g., different target sites on a selected viral, bacterial, fungal or parasite pathogen) or to different targets. For example, heavy chains from the two antibodies may be directed to the influenza virus, and may be co-expressed to form two monospecific antibodies (e.g., heavy chains from influenza viruses FI6, CR8033 and C05 may be selected) and expressed with a selected light chain, and a bispecific antibody. Examples of suitable influenza antibody and other anti-airborne pathogen antibody constructs and a method for delivering same are described in, e.g., WO 2012/145572A1. The antibodies may also be directed to different targets (e.g., an anti-viral antibody, including chronic viral infections, viral infections associated with cancers, or different anti-neoplastic cell surface proteins or other targets. Examples of suitable viral targets include the influenza hemagglutinin protein or other viral proteins, human immunodeficiency virus (HIV), human papilloma virus (HPV), Epstein-Barr virus, human herpes virus, respiratory syncytial virus, amongst others. Thus, the invention is particularly well suited for use in therapeutics and passive prophylaxis for which combinations of antibodies are desired.

The term “immunoglobulin” is used herein to include antibodies, and functional fragments thereof. Antibodies may exist in a variety of forms including, for example, polyclonal antibodies, monoclonal antibodies, camelized single domain antibodies, intracellular antibodies (“intra-

bodies”), recombinant antibodies, multispecific antibody (bispecific), antibody fragments, such as, Fv, Fab, F(ab)₂, F(ab)₃, Fab', Fab'-SH, F(ab')₂, single chain variable fragment antibodies (scFv), tandem/bis-scFv, Fc, pFc', scFvFc (or scFv-Fc), disulfide Fv (dsfv), bispecific antibodies (bc-scFv) such as BiTE antibodies; camelid antibodies, resurfaced antibodies, humanized antibodies, fully human antibodies, single-domain antibody (sdAb, also known as NANOBODY®), chimeric antibodies, chimeric antibodies comprising at least one human constant region, and the like. “Antibody fragment” refers to at least a portion of the variable region of the immunoglobulin that binds to its target, e.g., the tumor cell. In one embodiment, immunoglobulin is an IgG. However, other types of immunoglobulin may be selected. In another embodiment, the IgG subtype selected is an IgG1. However, other isotypes may be selected. Further, any of the IgG1 allotypes may be selected.

The term “heterologous” when used with reference to a protein or a nucleic acid indicates that the protein or the nucleic acid comprises two or more sequences or subsequences which are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid. For example, in one embodiment, the nucleic acid has a promoter from one gene arranged to direct the expression of a coding sequence from a different gene. Thus, with reference to the coding sequence, the promoter is heterologous. The term “heterologous light chain” is a light chain containing a variable domain and/or constant domain from an antibody which has a different target specificity from the specificity of the heavy chain.

The two or more ORF(s) carried by the nucleic acid molecule packaged within the vector may be expressed from two expression cassettes, one or both of which may be bicistronic. Because the expression cassettes contain heavy chains from two different antibodies, it is desirable to introduce sequence variation between the two heavy chain sequences to minimize the possibility of homologous recombination. Typically there is sufficient variation between the variable domains of the two antibodies (VH-Ab1 and VH-Ab2). However, it is desirable to ensure there is sufficient coding sequence variation between the constant regions of the first antibody (Ab1) and the second antibody (Ab2), most preferably in each of the CH1, CH2, and CH3 regions. For example, in one embodiment, the heavy chain constant regions of a first antibody may have the sequence of nt 1 to 705 of SEQ ID NO: 1 (which encodes amino acids 1-233 of SEQ ID NO:2) or a sequence which is about 95% to about 99% identical thereto without any introducing any amino acid changes. In one embodiment, variation in the sequence of these regions is introduced in the form of synonymous codons (i.e., variations of the nucleic acid sequence are introduced without any changes at the amino acid level). For example, the second heavy chain may have constant regions which are at least 15%, at least about 25%, at least about 35%, divergent (i.e., about 65% to about 85% identical) over CH1, CH2 and/or CH3.

Once the target and immunoglobulin are selected, the coding sequences for the selected immunoglobulin (e.g., heavy and/or light chain(s)) may be obtained and/or synthesized. Methods for sequencing a nucleic acid (e.g., RNA and DNA) are known to those of skill in the art. Once the sequence of a nucleic acid is known, the amino acid can be deduced and subsequently, there are web-based and commercially available computer programs, as well as service based companies which back translate the amino acids

sequences to nucleic acid coding sequences. See, e.g., backtranseq by EMBOSS, www.ebi.ac.uk/Tools/st/; Gene Infinity (www.geneinfinity.org/sms/sms_backtranslation.html); ExPasy (www.expasy.org/tools/). In one embodiment, the RNA and/or cDNA coding sequences are designed for optimal expression in human cells. Methods for synthesizing nucleic acids are known to those of skill in the art and may be utilized for all, or portions, of the nucleic acid constructs described herein.

Codon-optimized coding regions can be designed by various different methods. This optimization may be performed using methods which are available on-line (e.g., GeneArt), published methods, or a company which provides codon optimizing services, e.g., as DNA2.0 (Menlo Park, Calif.). One codon optimizing algorithm is described, e.g., in WO 2015/012924, which is incorporated by reference herein. See also, e.g., US Patent Publication No. 2014/0032186 and US Patent Publication No. 2006/0136184. Suitably, the entire length of the open reading frame (ORF) for the product is modified. However, in some embodiments, only a fragment of the ORF may be altered. By using one of these methods, one can apply the frequencies to any given polypeptide sequence, and produce a nucleic acid fragment of a codon-optimized coding region which encodes the polypeptide.

A number of options are available for performing the actual changes to the codons or for synthesizing the codon-optimized coding regions designed as described herein. Such modifications or synthesis can be performed using standard and routine molecular biological manipulations well known to those of ordinary skill in the art. In one approach, a series of complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of the desired sequence are synthesized by standard methods. These oligonucleotide pairs are synthesized such that upon annealing, they form double stranded fragments of 80-90 base pairs, containing cohesive ends, e.g., each oligonucleotide in the pair is synthesized to extend 3, 4, 5, 6, 7, 8, 9, 10, or more bases beyond the region that is complementary to the other oligonucleotide in the pair. The single-stranded ends of each pair of oligonucleotides are designed to anneal with the single-stranded end of another pair of oligonucleotides. The oligonucleotide pairs are allowed to anneal, and approximately five to six of these double-stranded fragments are then allowed to anneal together via the cohesive single stranded ends, and then they ligated together and cloned into a standard bacterial cloning vector, for example, a TOPO® vector available from Invitrogen Corporation, Carlsbad, Calif. The construct is then sequenced by standard methods. Several of these constructs consisting of 5 to 6 fragments of 80 to 90 base pair fragments ligated together, i.e., fragments of about 500 base pairs, are prepared, such that the entire desired sequence is represented in a series of plasmid constructs. The inserts of these plasmids are then cut with appropriate restriction enzymes and ligated together to form the final construct. The final construct is then cloned into a standard bacterial cloning vector, and sequenced. Additional methods would be immediately apparent to the skilled artisan. In addition, gene synthesis is readily available commercially.

Optionally, amino acid substitutions may be introduced into a heavy chain constant region in order to increase sequence diversity between the two antibody heavy chains and/or for another purpose. Methods and computer programs for preparing such alignments are available and well known to those of skill in the art. Substitutions may also be written as (amino acid identified by single letter code)-

position #- (amino acid identified by single letter code) whereby the first amino acid is the substituted amino acid and the second amino acid is the substituting amino acid at the specified position. The terms “substitution” and “substitution of an amino acid” and “amino acid substitution” as used herein refer to a replacement of an amino acid in an amino acid sequence with another one, wherein the latter is different from the replaced amino acid. Methods for replacing an amino acid are well known to the skilled in the art and include, but are not limited to, mutations of the nucleotide sequence encoding the amino acid sequence. Methods of making amino acid substitutions in IgG are described, e.g., for WO 2013/046704, which is incorporated by reference for its discussion of amino acid modification techniques.

The term “amino acid substitution” and its synonyms described above are intended to encompass modification of an amino acid sequence by replacement of an amino acid with another, substituting amino acid. The substitution may be a conservative substitution. The term conservative, in referring to two amino acids, is intended to mean that the amino acids share a common property recognized by one of skill in the art. The term non-conservative, in referring to two amino acids, is intended to mean that the amino acids which have differences in at least one property recognized by one of skill in the art. For example, such properties may include amino acids having hydrophobic nonacidic side chains, amino acids having hydrophobic side chains (which may be further differentiated as acidic or nonacidic), amino acids having aliphatic hydrophobic side chains, amino acids having aromatic hydrophobic side chains, amino acids with polar neutral side chains, amino acids with electrically charged side chains, amino acids with electrically charged acidic side chains, and amino acids with electrically charged basic side chains. Both naturally occurring and non-naturally occurring amino acids are known in the art and may be used as substituting amino acids in embodiments. Thus, a conservative amino acid substitution may involve changing a first amino acid having a hydrophobic side chain with a different amino acid having a hydrophobic side chain; whereas a non-conservative amino acid substitution may involve changing a first amino acid with an acidic hydrophobic side chain with a different amino acid having a different side chain, e.g., a basic hydrophobic side chain or a hydrophilic side chain. Still other conservative or non-conservative changes can be determined by one of skill in the art. In still other embodiments, the substitution at a given position will be to an amino acid, or one of a group of amino acids, that will be apparent to one of skill in the art in order to accomplish an objective identified herein.

In order to express a selected immunoglobulin domain, a nucleic acid molecule may be designed which contains codons which have been selected for optimal expression of the immunoglobulin polypeptides in a selected mammalian species, e.g., humans. Further, the nucleic acid molecule may include a heterologous leader sequence for each heavy chain and light chain of the selected antibody, which encodes the wild-type or a mutated IL-2 signal leader peptide fused upstream of the heavy and light chain polypeptides composed of the variable and constant regions. However, another heterologous leader sequence may be substituted for one or both of the IL-2 signal peptide. Signal/leader peptides may be the same or different for each the heavy chain and light chain immunoglobulin constructs. These may be signal sequences which are natively found in an immunoglobulin (e.g., IgG), or may be from a heterologous source. Such heterologous sources may be a cytokine (e.g., IL-2, IL12, IL18, or the like), insulin, albumin, β -glu-

curonidase, alkaline protease or the fibronectin secretory signal peptides, amongst others.

As used herein, an “expression cassette” refers to a nucleic acid sequence which comprises at least a first open reading frame (ORF) and optionally a second ORF. An ORF may contain two, three, or four antibody domains. For example, the ORF may contain a full-length heavy chain. Alternatively, an ORF may contain one or two antibody domains. For example, the ORF may contain a heavy chain variable domain and a single heavy chain constant domain. In another example, the ORF may contain a light chain variable and a light chain constant region. Thus, an expression cassette may be designed to be bicistronic, i.e., to contain regulatory sequences which direct expression of the ORFs thereon from shared regulatory sequences. In this instance, the two ORFs are typically separated by a linker. Suitable linkers, such as an internal ribozyme binding site (IRES) and/or a furin-2a self-cleaving peptide linker (F2a), [see, e.g., Radcliffe and Mitrophanous, *Gene Therapy* (2004), 11, 1673-1674] are known in the art. Suitably, the ORF are operably linked to regulatory control sequences which direct expression in a target cell. Such regulatory control sequences may include a polyA, a promoter, and an enhancer. In order to facilitate co-expression from an AAV vector, at least one of the enhancer and/or polyA sequence may be shared by the first and second expression cassettes.

In one embodiment, the rAAV has packaged within the selected AAV capsid, a nucleic acid molecule comprising: a 5' ITR, a first expression cassette, a bidirectional enhancer, and a second expression cassette, where the bidirectional enhancer separates the first and second expression cassettes, and a 3' ITR. FIG. 1A is provided herein as an example of this embodiment. For example, in such an embodiment, a first promoter for a first expression cassette is located to the left of the bidirectional enhancer, followed by at least a first open reading frame, and a polyA sequence, and a second promoter. Further, a second promoter for the second expression cassette is located to the right of the bidirectional enhancer, followed by at least a second open reading frame and a polyA. The first and second promoters and the first and second polyA sequences may be the same or different. A minimal promoter and/or a minimal polyA may be selected in order to conserve space. Typically, in this embodiment, each promoter is located adjacent (either to the left or the right (or 5' or 3')) to the enhancer sequence and the polyA sequences are located adjacent to the ITRs, with the ORFs there between. While FIG. 1A is illustrative, the order of the ORFs may be varied, as may the immunoglobulin domains encoded thereby. For example, the light chain constant and variable sequences may be located to the left of the enhancer and the two heavy chains may be encoded by ORFs located to the right of the enhancer. Alternatively, one of the heavy chains may be located to the left of the enhancer and the ORFs to the right of the enhancer by encode a second heavy chain and a light chain. Alternatively, the opposite configuration is possible, and the expression cassette to the left of the enhancer may be bicistronic. Alternatively, depending upon what domains are encoded, both expression cassettes may be monocistronic (e.g., encoding two immunoadhesins), or both can be bicistronic (e.g., encoding two complete FABS).

In another embodiment, the rAAV has packaged within the selected AAV capsid, a nucleic acid molecule comprising: a 5' ITR, a first expression cassette, a polyA which functions bidirectionally, and a second expression cassette, where the bidirectional polyA separates and functions for both the first and the second expression cassettes, and a 3'

ITR. FIG. 1B is provided herein as an example of this embodiment. In this embodiment, a first enhancer and a first promoter (or enhancer/promoter combination) is located to the right of the 5' ITR, followed by the ORF(s) and the bidirectional polyA. The second expression cassette is separated from the first expression cassette by the bidirectional polyA and is transcribed in the opposite orientation. In this expression cassette, the enhancer and promoter (or promoter/enhancer combination) is located adjacent to the 3' ITR and the ORF(s) are adjacent to the bidirectional polyA. While FIG. 1B is illustrative, the order of the ORFs may be varied, as may the immunoglobulin domains encoded thereby. For example, the light chain constant and variable sequences may be located to the left of the polyA and the two heavy chains may be encoded by ORF(s) located to the right of the polyA. Alternatively, one of the heavy chains may be located to the left of the polyA and the ORFs to the right of the polyA encode a second heavy chain and a light chain. Alternatively, the opposite configuration is possible, and the expression cassette to the left of the polyA may be bicistronic. Alternatively, depending upon what domains are encoded, both expression cassettes may be monocistronic (e.g., encoding two immunoadhesins), or both can be bicistronic.

Optionally, the expression configuration exemplified in FIGS. 1A and 1B and described herein may be used to co-express other immunoglobulin constructs. For example, two immunoadhesins (IA) may be expressed from two monocistronic expression cassettes. An immunoadhesin includes a form of antibody that is expressed as single open reading frame containing a single chain variable fragment (scFv) unit (i.e., VH linked to VL or VL linked to VH) fused to an Fc domain (CH2-CH3), (e.g., VH-VL-CH2-CH3 or VL-VH-CH2-CH3). Alternatively, up to four scFvs could be expressed from two bicistronic expression cassettes. In another alternative, an IA may be co-expressed with a full-length antibody. In another alternative, one complete FABS may be co-expressed with a full-length antibody or two complete FABS may be co-expressed. In still another embodiment, other combinations of full-length antibody, IA, or FAB fragment may be co-expressed.

Suitable regulatory control sequences may be selected and obtained from a variety of sources. In one embodiment, a minimal promoter and/or a minimal polyA may be utilized to conserve size.

As used herein, the term “minimal promoter” means a short DNA sequence comprised of a TATA-box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. In one embodiment, a promoter refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. In one embodiment, the minimal promoter is a Cytomegalovirus (CMV) minimal promoter. In another embodiment, the minimal promoter is derived from human CMV (hCMV) such as the hCMV immediate early promoter derived minimal promoter (see, US 20140127749, and Gossen and Bujard (*Proc. Natl. Acad. Sci. USA*, 1992, 89: 5547-5551), which are incorporated herein by reference). In another embodiment, the minimal promoter is derived from a viral source such as, for example: SV40 early or late promoters, cytomegalovirus (CMV) immediate early promoters, or Rous Sarcoma Virus (RSV) early promoters; or from eukaryotic cell promoters, for example, beta actin

promoter (Ng, *Nuc. Acid Res.* 17:601-615, 1989; Quitsche et al., *J. Biol. Chem.* 264:9539-9545, 1989), GADPH promoter (Alexander, M. C. et al., *Proc. Nat. Acad. Sci. USA* 85:5092-5096, 1988, Ercolani, L. et al., *J. Biol. Chem.* 263:15335-15341, 1988), TK-1 (thymidine kinase) promoter, HSP (heat shock protein) promoters, UbB or UbC promoter, PGK, Efl-alpha promoter or any eukaryotic promoter containing a TATA box (US Published Application No. 2014/0094392). In another embodiment, the minimal promoter includes a mini-promoter, such as the CLDNS mini-promoter described in US Published Application No. 2014/0065666. In another embodiment, the minimal promoter is the Thymidine Kinase (TK) promoter. In one embodiment, the minimal promoter is tissue specific, such as one of the muscle-cell specific promoters, minimal TnISlow promoter, a minimal TnIFast promoter or a muscle creatine kinase promoter (US Published Application No. 2012/0282695). Each of these documents is incorporated herein by reference.

In one embodiment, the polyadenylation (poly(A)) signal is a minimal poly(A) signal, i.e., the minimum sequence required for efficient polyadenylation. In one embodiment, the minimal poly(A) is a synthetic poly(A), such as that described in Levitt et al, *Genes Dev.*, 1989 July, 3(7):1019-25; and Xia et al, *Nat Biotechnol.* 2002 October; 20(10):1006-10. Epub 2002 Sep. 16. In another embodiment, the poly(A) is derived from the rabbit beta-globin poly(A). In one embodiment, the polyA acts bidirectionally (An et al, 2006, *PNAS*, 103(49): 18662-18667). In one embodiment, the poly(A) is derived from the SV40 early poly A signal sequence. Each of these documents is incorporated herein by reference.

As described herein, in one embodiment, a single enhancer, or the same enhancer, may regulate the transcription of multiple heterologous genes in the plasmid construct. Various enhancers suitable for use in the invention are known in the art and include, for example, the CMV early enhancer, Hoxc8 enhancer, nPE1 and nPE2. Additional enhancers useful herein are described in Andersson et al, *Nature*, 2014 March, 507(7493):455-61, which is incorporated herein by reference. Still other enhancer elements may include, e.g., an apolipoprotein enhancer, a zebrafish enhancer, a GFAP enhancer element, and tissue specific enhancers such as described in WO 2013/1555222, woodchuck hepatitis post-transcriptional regulatory element. Additionally, or alternatively, other, e.g., the hybrid human cytomegalovirus (HCMV)-immediate early (IE)-PDGR promoter or other promoter-enhancer elements may be selected. To enhance expression the other elements can be introns (like promega intron or chimeric chicken globin-human immunoglobulin intron). Other promoters and enhancers useful herein can be found in the Mammalian Promoter/Enhancer Database found at promoter.cdb.riken.jp/.

The constructs described herein may further contain other expression control or regulatory sequences such as, e.g., include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. A promoter may be selected from amongst a constitutive promoter, a tissue-specific promoter, a cell-specific promoter, a promoter responsive to physiologic cues, or an regulatable promoter [see, e.g., WO 2011/126868 and WO 2013/049492].

These control sequences are "operably linked" to the immunoglobulin construct gene sequences. As used herein, the term "operably linked" refers to 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.

Examples of constitutive promoters suitable for controlling expression of the antibody domains include, but are not limited to chicken β -actin (CB) or beta actin promoters from other species, human cytomegalovirus (CMV) promoter, the early and late promoters of simian virus 40 (SV40), U6 promoter, metallothionein promoters, EFl α promoter, ubiquitin promoter, hypoxanthine phosphoribosyl transferase (HPRT) promoter, dihydrofolate reductase (DHFR) promoter (Scharfmann et al., *Proc. Natl. Acad. Sci. USA* 88:4626-4630 (1991)), adenosine deaminase promoter, phosphoglycerol kinase (PGK) promoter, pyruvate kinase promoter phosphoglycerol mutase promoter, the β -actin promoter (Lai et al., *Proc. Natl. Acad. Sci. USA* 86: 10006-10010 (1989)), UbB, UbC, the long terminal repeats (LTR) of Moloney Leukemia Virus and other retroviruses, the thymidine kinase promoter of Herpes Simplex Virus and other constitutive promoters known to those of skill in the art. Examples of tissue- or cell-specific promoters suitable for use in the present invention include, but are not limited to, endothelin-I (ET-I) and Flt-I, which are specific for endothelial cells, FoxJ1 (that targets ciliated cells).

Inducible promoters suitable for controlling expression of the antibody domains include promoters responsive to exogenous agents (e.g., pharmacological agents) or to physiological cues. These response elements include, but are not limited to a hypoxia response element (HRE) that binds HIF-1 α and β , a metal-ion response element such as described by Mayo et al. (1982, *Cell* 29:99-108); Brinster et al. (1982, *Nature* 296:39-42) and Searle et al. (1985, *Mol. Cell. Biol.* 5:1480-1489); or a heat shock response element such as described by Nouer et al. (in: *Heat Shock Response*, ed. Nouer, L., CRC, Boca Raton, Fla., pp167-220, 1991).

In one embodiment, expression of an open reading frame is controlled by a regulatable promoter that provides tight control over the transcription of the ORF (gene), e.g., a pharmacological agent, or transcription factors activated by a pharmacological agent or in alternative embodiments, physiological cues. Examples of regulatable promoters which are ligand-dependent transcription factor complexes that may be used include, without limitation, members of the nuclear receptor superfamily activated by their respective ligands (e.g., glucocorticoid, estrogen, progestin, retinoid, ecdysone, and analogs and mimetics thereof) and rTTA activated by tetracycline. Examples of such systems, include, without limitation, the ARGENTTM Transcriptional Technology (ARIAD Pharmaceuticals, Cambridge, Mass.). Examples of such promoter systems are described, e.g., in WO 2012/145572, which is incorporated by reference herein.

Still other promoters may include, e.g., human cytomegalovirus (CMV) immediate-early enhancer/promoter, the SV40 early enhancer/promoter, the JC polymavirus promoter, myelin basic protein (MBP) or glial fibrillary acidic protein (GFAP) promoters, herpes simplex virus (HSV-1) latency associated promoter (LAP), rouse sarcoma virus (RSV) long terminal repeat (LTR) promoter, neuron-specific promoter (NSE), platelet derived growth factor (PDGF) promoter, hSYN, melanin-concentrating hormone (MCH) promoter, CBA, matrix metalloprotein promoter (MPP), and the chicken beta-actin promoter. The promoters may be the same or different for each expression cassette.

For use in producing an AAV viral vector (e.g., a recombinant (r) AAV), the expression cassettes can be carried on any suitable vector, e.g., a plasmid, which is delivered to a packaging host cell. The plasmids useful in this invention may be engineered such that they are suitable for replication and packaging in prokaryotic cells, mammalian cells, or both. Suitable transfection techniques and packaging host cells are known and/or can be readily designed by one of skill in the art.

Methods for generating and isolating AAVs suitable for use as vectors are known in the art. See generally, e.g., Grieger & Samulski, 2005, "Adeno-associated virus as a gene therapy vector: Vector development, production and clinical applications," *Adv. Biochem. Engin/Biotechnol.* 99: 119-145; Buning et al., 2008, "Recent developments in adeno-associated virus vector technology," *J. Gene Med.* 10:717-733; and the references cited below, each of which is incorporated herein by reference in its entirety. For packaging a transgene into virions, the ITRs are the only AAV components required in cis in the same construct as the nucleic acid molecule containing the expression cassettes. The cap and rep genes can be supplied in trans.

As described above, the term "about" when used to modify a numerical value means a variation of $\pm 10\%$, unless otherwise specified.

As used throughout this specification and the claims, the terms "comprise" and "contain" and its variants including, "comprises", "comprising", "contains" and "containing", among other variants, is inclusive of other components, elements, integers, steps and the like. The term "consists of" or "consisting of" are exclusive of other components, elements, integers, steps and the like.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., any one of the modified ORFs provided herein) when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site or the like). As another example, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1, herein incorporated by reference. Generally, these programs are used at default settings, although one skilled in the art can alter these settings as needed. Alternatively, one of skill in the art can utilize another algorithm or computer program that provides at least the level of identity or alignment as that provided by the referenced algorithms and programs. This definition also refers to, or can be applied to, the complement of a sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25, 50, 75, 100, 150, 200 amino acids or nucleotides in length, and oftentimes over a region that is

225, 250, 300, 350, 400, 450, 500 amino acids or nucleotides in length or over the full-length of an amino acid or nucleic acid sequences.

Typically, when an alignment is prepared based upon an amino acid sequence, the alignment contains insertions and deletions which are so identified with respect to a reference AAV sequence and the numbering of the amino acid residues is based upon a reference scale provided for the alignment. However, any given AAV sequence may have fewer amino acid residues than the reference scale. In the present invention, when discussing the parental sequence, the term "the same position" or the "corresponding position" refers to the amino acid located at the same residue number in each of the sequences, with respect to the reference scale for the aligned sequences. However, when taken out of the alignment, each of the proteins may have these amino acids located at different residue numbers. Alignments are performed using any of a variety of publicly or commercially available Multiple Sequence Alignment Programs. Sequence alignment programs are available for amino acid sequences, e.g., the "Clustal X", "MAP", "PIMA", "MSA", "BLOCK-MAKER", "MEME", and "Match-Box" programs. Generally, any of these programs are used at default settings, although one of skill in the art can alter these settings as needed. Alternatively, one of skill in the art can utilize another algorithm or computer program which provides at least the level of identity or alignment as that provided by the referenced algorithms and programs. See, e.g., J. D. Thomson et al, *Nucl. Acids. Res.*, "A comprehensive comparison of multiple sequence alignments", 27(13):2682-2690 (1999).

In one embodiment, the expression cassettes described herein are engineered into a genetic element (e.g., a shuttle plasmid) which transfers the immunoglobulin construct sequences carried thereon into a packaging host cell for production a viral vector. In one embodiment, the selected genetic element may be delivered to a an AAV packaging cell by any suitable method, including transfection, electroporation, liposome delivery, membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion. Stable AAV packaging cells can also be made. Alternatively, the expression cassettes may be used to generate a viral vector other than AAV, or for production of mixtures of antibodies in vitro. The methods used to make such constructs are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, e.g., *Molecular Cloning: A Laboratory Manual*, ed. Green and Sambrook, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (2012).

AAV Vectors

A recombinant AAV vector (AAV viral particle) may comprise, packaged within an AAV capsid, a nucleic acid molecule containing a 5' AAV ITR, the expression cassettes described herein and a 3' AAV ITR. As described herein, an expression cassette may contain regulatory elements for an open reading frame(s) within each expression cassette and the nucleic acid molecule may optionally contain additional regulatory elements.

The AAV vector may contain a full-length AAV 5' inverted terminal repeat (ITR) and a full-length 3' ITR. A shortened version of the 5' ITR, termed Δ ITR, has been described in which the D-sequence and terminal resolution site (trs) are deleted. The abbreviation "sc" refers to self-complementary. "Self-complementary AAV" refers a construct in which a coding region carried by a recombinant AAV nucleic acid sequence has been designed to form an intra-molecular double-stranded DNA template. Upon infec-

tion, rather than waiting for cell mediated synthesis of the second strand, the two complementary halves of scAAV will associate to form one double stranded DNA (dsDNA) unit that is ready for immediate replication and transcription. See, e.g., D M McCarty et al, "Self-complementary recombinant adeno-associated virus (scAAV) vectors promote efficient transduction independently of DNA synthesis", *Gene Therapy*, (August 2001), Vol 8, Number 16, Pages 1248-1254. Self-complementary AAVs are described in, e.g., U.S. Pat. Nos. 6,596,535; 7,125,717; and 7,456,683, each of which is incorporated herein by reference in its entirety.

Where a pseudotyped AAV is to be produced, the ITRs are selected from a source which differs from the AAV source of the capsid. For example, AAV2 ITRs may be selected for use with an AAV capsid having a particular efficiency for a selected cellular receptor, target tissue or viral target. In one embodiment, the ITR sequences from AAV2, or the deleted version thereof (Δ ITR), are used for convenience and to accelerate regulatory approval. However, ITRs from other AAV sources may be selected. Where the source of the ITRs is from AAV2 and the AAV capsid is from another AAV source, the resulting vector may be termed pseudotyped. However, other sources of AAV ITRs may be utilized.

A variety of AAV capsids have been described. Methods of generating AAV vectors have been described extensively in the literature and patent documents, including, e.g., WO 2003/042397; WO 2005/033321, WO 2006/110689; U.S. Pat. No. 7,588,772 B2. The source of AAV capsids may be selected from an AAV which targets a desired tissue. For example, suitable AAV may include, e.g., AAV9 [U.S. Pat. No. 7,906,111; US 2011-0236353-A1], rh10 [WO 2003/042397] and/or hu37 [see, e.g., U.S. Pat. No. 7,906,111; US 2011-0236353-A1]. However, other AAV, including, e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, [U.S. Pat. No. 7,790,449; U.S. Pat. No. 7,282,199] and others. However, other sources of AAV capsids and other viral elements may be selected, as may other immunoglobulin constructs and other vector elements.

A single-stranded AAV viral vector is provided. Methods for generating and isolating AAV viral vectors suitable for delivery to a subject are known in the art. See, e.g., U.S. Pat. No. 7,790,449; U.S. Pat. No. 7,282,199; WO 2003/042397; WO 2005/033321, WO 2006/110689; and U.S. Pat. No. 7,588,772 B2]. In one system, a producer cell line is transiently transfected with a construct that encodes the transgene flanked by ITRs and a construct(s) that encodes rep and cap. In a second system, a packaging cell line that stably supplies rep and cap is transiently transfected with a construct encoding the transgene flanked by ITRs. In each of these systems, AAV virions are produced in response to infection with helper adenovirus or herpesvirus, requiring the separation of the rAAVs from contaminating virus. More recently, systems have been developed that do not require infection with helper virus to recover the AAV—the required helper functions (i.e., adenovirus E1, E2a, VA, and E4 or herpesvirus ULS, ULB, UL52, and UL29, and herpesvirus polymerase) are also supplied, in trans, by the system. In these newer systems, the helper functions can be supplied by transient transfection of the cells with constructs that encode the required helper functions, or the cells can be engineered to stably contain genes encoding the helper functions, the expression of which can be controlled at the transcriptional or posttranscriptional level. In yet another system, the transgene flanked by ITRs and rep/cap genes are introduced into insect cells by infection with baculovirus-based vectors. For reviews on these production systems, see generally, e.g.,

Zhang et al., 2009, "Adenovirus-adeno-associated virus hybrid for large-scale recombinant adeno-associated virus production," *Human Gene Therapy* 20:922-929, the contents of each of which is incorporated herein by reference in its entirety. Methods of making and using these and other AAV production systems are also described in the following U.S. patents, the contents of which is incorporated herein by reference in its entirety: U.S. Pat. Nos. 5,139,941; 5,741,683; 6,057,152; 6,204,059; 6,268,213; 6,491,907; 6,660,514; 6,951,753; 7,094,604; 7,172,893; 7,201,898; 7,229,823; and 7,439,065.

Uses and Regimens

The rAAV, preferably suspended in a physiologically compatible carrier, may be administered to a human or non-human mammalian patient. Suitable carriers may be readily selected by one of skill in the art in view of the indication for which the transfer virus is directed. For example, one suitable carrier includes saline, which may be formulated with a variety of buffering solutions (e.g., phosphate buffered saline). Other exemplary carriers include sterile saline, lactose, sucrose, maltose, and water. The selection of the carrier is not a limitation of the present invention. Optionally, the compositions of the invention may contain, in addition to the rAAV and carrier(s), other conventional pharmaceutical ingredients, such as preservatives, or chemical stabilizers.

Methods for using these rAAV, e.g., for passive immunization are described, e.g., in WO 2012/145572. Other methods of delivery and uses will be apparent to one of skill in the art. For example, a regimen as described herein may comprise, in addition to one or more of the combinations described herein, further combination with one or more of a biological drug, a small molecule drug, a chemotherapeutic agent, immune enhancers, radiation, surgery, and the like. A biological drug as described herein, is based on a peptide, polypeptide, protein, enzyme, nucleic acid molecule, vector (including viral vectors), or the like.

In a combination therapy, the AAV-delivered immunoglobulin construct described herein is administered before, during, or after commencing therapy with another agent, as well as any combination thereof, i.e., before and during, before and after, during and after, or before, during and after commencing the therapy. For example, the AAV can be administered between 1 and 30 days, preferably 3 and 20 days, more preferably between 5 and 12 days before commencing radiation therapy. In another embodiment of the invention, chemotherapy is administered concurrently with or, more preferably, subsequent to AAV-mediated immunoglobulin (antibody) therapy. In still other embodiments, the compositions of the invention may be combined with other biologics, e.g., recombinant monoclonal antibody drugs, antibody-drug conjugates, or the like. Further, combinations of different AAV-delivered immunoglobulin constructs such as are discussed above may be used in such regimens.

Any suitable method or route can be used to administer AAV-containing compositions as described herein, and optionally, to co-administer other active drugs or therapies in conjunction with the AAV-mediated antibodies described herein. Routes of administration include, for example, systemic, oral, intravenous, intraperitoneal, subcutaneous, or intramuscular administration.

Targets for the immunoglobulin constructs described herein may be selected from a variety of pathogens, including, e.g., bacterial, viral, fungal and parasitic infectious agents. Suitable targets may further include cancer or cancer-associated antigens, or the like. Still other targets may

include an autoimmune condition such as rheumatoid arthritis (RA) or multiple sclerosis (MS).

Examples of viral targets include influenza virus from the orthomyxoviridae family, which includes: Influenza A, Influenza B, and Influenza C. The type A viruses are the most virulent human pathogens. The serotypes of influenza A which have been associated with pandemics include, H1N1, which caused Spanish Flu in 1918, and Swine Flu in 2009; H2N2, which caused Asian Flu in 1957; H3N2, which caused Hong Kong Flu in 1968; H5N1, which caused Bird Flu in 2004; H7N7; H1N2; H9N2; H7N2; H7N3; and H10N7.

Broadly neutralizing antibodies against influenza A have been described. As used herein, a "broadly neutralizing antibody" refers to a neutralizing antibody which can neutralize multiple strains from multiple subtypes. For example, CR6261 [The Scripps Institute/Crucell] has been described as a monoclonal antibody that binds to a broad range of the influenza virus including the 1918 "Spanish flu" (SC1918/H1) and to a virus of the H5N1 class of avian influenza that jumped from chickens to a human in Vietnam in 2004 (Viet04/H5). CR6261 recognizes a highly conserved helical region in the membrane-proximal stem of hemagglutinin, the predominant protein on the surface of the influenza virus. This antibody is described in WO 2010/130636, incorporated by reference herein. Another neutralizing antibody, F10 [XOMA Ltd] has been described as being useful against H1N1 and H5N1. [Sui et al, Nature Structural and Molecular Biology (Sui, et al. 2009, 16(3):265-73)] Other antibodies against influenza, e.g., Fab28 and Fab49, may be selected. See, e.g., WO 2010/140114 and WO 2009/115972, which are incorporated by reference. Still other antibodies, such as those described in WO 2010/010466, US Published Patent Publication US/2011/076265, and WO 2008/156763, may be readily selected.

Other target pathogenic viruses include, arenaviruses (including funin, machupo, and Lassa), filoviruses (including Marburg and Ebola), hantaviruses, picornaviridae (including rhinoviruses, echovirus), coronaviruses, paramyxovirus, morbillivirus, respiratory syncytial virus, togavirus, coxsackievirus, parvovirus B19, parainfluenza, adenoviruses, reoviruses, variola (Variola major (Smallpox)) and Vaccinia (Cowpox) from the poxvirus family, and varicella-zoster (pseudorabies).

Viral hemorrhagic fevers are caused by members of the arenavirus family (Lassa fever) (which family is also associated with Lymphocytic choriomeningitis (LCM)), filovirus (ebola virus), and hantavirus (puremala). The members of picornavirus (a subfamily of rhinoviruses), are associated with the common cold in humans. The coronavirus family includes a number of non-human viruses such as infectious bronchitis virus (poultry), porcine transmissible gastroenteric virus (pig), porcine hemagglutinin encephalomyelitis virus (pig), feline infectious peritonitis virus (cat), feline enteric coronavirus (cat), canine coronavirus (dog). The human respiratory coronaviruses, have been putatively associated with the common cold, non-A, B or C hepatitis, and sudden acute respiratory syndrome (SARS). The paramyxovirus family includes parainfluenza Virus Type 1, parainfluenza Virus Type 3, bovine parainfluenza Virus Type 3, rubulavirus (mumps virus), parainfluenza Virus Type 2, parainfluenza virus Type 4, Newcastle disease virus (chickens), rinderpest, morbillivirus, which includes measles and canine distemper, and pneumovirus, which includes respiratory syncytial virus (RSV). The parvovirus family includes feline parvovirus (feline enteritis), feline panleucopeniavirus, canine parvovirus, and porcine parvovirus.

The adenovirus family includes viruses (EX, AD7, ARD, O.B.) which cause respiratory disease.

A neutralizing antibody construct against a bacterial pathogen may also be selected for use in the present invention. In one embodiment, the neutralizing antibody construct is directed against the bacteria itself. In another embodiment, the neutralizing antibody construct is directed against a toxin produced by the bacteria. Examples of airborne bacterial pathogens include, e.g., *Neisseria meningitidis* (meningitis), *Klebsiella pneumonia* (pneumonia), *Pseudomonas aeruginosa* (pneumonia), *Pseudomonas pseudomallei* (pneumonia), *Pseudomonas mallei* (pneumonia), *Acinetobacter* (pneumonia), *Moraxella catarrhalis*, *Moraxella lacunata*, *Alkaligenes*, *Cardiobacterium*, *Haemophilus influenzae* (flu), *Haemophilus parainfluenzae*, *Bordetella pertussis* (whooping cough), *Francisella tularensis* (pneumonia/fever), *Legionella pneumonia* (Legionnaires disease), *Chlamydia psittaci* (pneumonia), *Chlamydia pneumoniae* (pneumonia), *Mycobacterium tuberculosis* (tuberculosis (TB)), *Mycobacterium kansasii* (TB), *Mycobacterium avium* (pneumonia), *Nocardia asteroides* (pneumonia), *Bacillus anthracis* (anthrax), *Staphylococcus aureus* (pneumonia), *Streptococcus pyogenes* (scarlet fever), *Streptococcus pneumoniae* (pneumonia), *Corynebacteria diphtheria* (diphtheria), *Mycoplasma pneumoniae* (pneumonia).

The causative agent of anthrax is a toxin produced by *Bacillus anthracis*. Neutralizing antibodies against protective agent (PA), one of the three peptides which form the toxoid, have been described. The other two polypeptides consist of lethal factor (LF) and edema factor (EF). Anti-PA neutralizing antibodies have been described as being effective in passively immunization against anthrax. See, e.g., U.S. Pat. No. 7,442,373; R. Sawada-Hirai et al, J Immune Based Ther Vaccines. 2004; 2: 5. (on-line 2004 May 12). Still other anti-anthrax toxin neutralizing antibodies have been described and/or may be generated. Similarly, neutralizing antibodies against other bacteria and/or bacterial toxins may be used to generate an AAV-delivered anti-pathogen construct as described herein.

Other infectious diseases may be caused by airborne fungi including, e.g., *Aspergillus* species, *Absidia corymbifera*, *Rhizopus stolonifer*, *Mucor plumbeus*, *Cryptococcus neoformans*, *Histoplasma capsulatum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Penicillium* species, *Micropolyspora faeni*, *Thermoactinomyces vulgaris*, *Alternaria alternate*, *Cladosporium* species, *Helminthosporium*, and *Stachybotrys* species.

In addition, passive immunization may be used to prevent fungal infections (e.g., athlete's foot), ringworm, or viruses, bacteria, parasites, fungi, and other pathogens which can be transmitted by direct contact. In addition, a variety of conditions which affect household pets, cattle and other livestock, and other animals. For example, in dogs, infection of the upper respiratory tract by canine sinonasal aspergillosis causes significant disease. In cats, upper respiratory disease or feline respiratory disease complex originating in the nose causes morbidity and mortality if left untreated. Cattle are prone to infections by the infectious bovine rhinotracheitis (commonly called IBR or red nose) is an acute, contagious virus disease of cattle. In addition, cattle are prone to Bovine Respiratory Syncytial Virus (BRSV) which causes mild to severe respiratory disease and can impair resistance to other diseases. Still other pathogens and diseases will be apparent to one of skill in the art. See, e.g., U.S. Pat. No. 5,811,524, which describes generation of anti-respiratory syncytial virus (RSV) neutralizing antibodies. The techniques described therein are applicable to other

pathogens. Such an antibody may be used intact or its sequences (scaffold) modified to generate an artificial or recombinant neutralizing antibody construct. Such methods have been described [see, e.g., WO 2010/13036; WO 2009/115972; WO 2010/140114].

Anti-neoplastic immunoglobulins as described herein may target a human epidermal growth factor receptor (HER), such as HER2. For example, trastuzumab is a recombinant IgG1 kappa, humanized monoclonal antibody that selectively binds with high affinity in a cell-based assay (Kd=5 nM) to the extracellular domain of the human epidermal growth factor receptor protein. The commercially available product is produced in CHO cell culture. See, e.g., www.drugbank.ca/drugs/DB00072. The amino acid sequences of the trastuzumab light chains 1 and 2 and heavy chains 1 and 2, as well as sequences obtained from a study of the x-ray structure of trastuzumab, are provided on this database at accession number DB00072, which sequences are incorporated herein by reference. See, also, 212-Pb-TCMC-trastuzumab [Areva Med, Bethesda, Md.]. Another antibody of interest includes, e.g., pertuzumab, a recombinant humanized monoclonal antibody that targets the extracellular dimerization domain (Subdomain II) of the human epidermal growth factor receptor 2 protein (HER2). It consists of two heavy chains and two light chains that have 448 and 214 residues respectively. FDA approved Jun. 8, 2012. The amino acid sequences of its heavy chain and light chain are provided, e.g., in www.drugbank.ca/drugs/DB06366 (synonyms include 2C4, MOAB 2C4, monoclonal antibody 2C4, and rhuMAb-2C4) on this database at accession number DB06366. In addition to HER2, other HER targets may be selected.

For example, MM-121/SAR256212 is a fully human monoclonal antibody that targets the HER3 receptor [Merimack's Network Biology] and which has been reported to be useful in the treatment of non-small cell lung cancer (NSCLC), breast cancer and ovarian cancer. SAR256212 is an investigational fully human monoclonal antibody that targets the HER3 (ErbB3) receptor [Sanofi Oncology]. Another anti-Her3/EGFR antibody is RG7597 [Genentech], described as being useful in head and neck cancers. Another antibody, margetuximab (or MGAH22), a next-generation, Fc-optimized monoclonal antibody (mAb) that targets HER [MacroGenics], may also be utilized.

Alternatively, other human epithelial cell surface markers and/or other tumor receptors or antigens may be targeted. Examples of other cell surface marker targets include, e.g., 5T4, CA-125, CEA (e.g., targeted by labetuzumab), CD3, CD19, CD20 (e.g., targeted by rituximab), CD22 (e.g., targeted by epratuzumab or velutuzumab), CD30, CD33, CD40, CD44, CD51 (also integrin avf33), CD133 (e.g., glioblastoma cells), CTLA-4 (e.g., Ipilimumab used in treatment of, e.g., neuroblastoma), Chemokine (C-X-C Motif) Receptor 2 (CXCR2) (expressed in different regions in brain; e.g., Anti-CXCR2 (extracellular) antibody #ACR-012 (Alomene Labs)); EpCAM, fibroblast activation protein (FAP) [see, e.g., WO 2012020006 A2, brain cancers], folate receptor alpha (e.g., pediatric ependymal brain tumors, head and neck cancers), fibroblast growth factor receptor 1 (FGFR1) (see, et al, WO2012125124A1 for discussion treatment of cancers with anti-FGFR1 antibodies), FGFR2 (see, e.g., antibodies described in WO2013076186A and WO2011143318A2), FGFR3 (see, e.g., antibodies described in U.S. Pat. No. 8,187,601 and WO2010111367A1), FGFR4 (see, e.g., anti-FGFR4 antibodies described in WO2012138975A1), hepatocyte growth factor (HGF) (see, e.g., antibodies in WO2010119991A3), integrin $\alpha_5\beta_1$, IGF-1

receptor, ganglioside GD2 (see, e.g., antibodies described in WO2011160119A2), ganglioside GD3, transmembrane glycoprotein NMB (GPNMB) (associated with gliomas, among others and target of the antibody glembatumumab (CR011), mucin, MUC1, phosphatidylserine (e.g., targeted by bavituximab, Peregrine Pharmaceuticals, Inc), prostatic carcinoma cells, PD-L1 (e.g., nivolumab (BMS-936558, MDX-1106, ONO-4538), a fully human gG4, e.g., metastatic melanoma], platelet-derived growth factor receptor, alpha (PDGFR α) or CD140, tumor associated glycoprotein 72 (TAG-72), tenascin C, tumor necrosis factor (TNF) receptor (TRAIL-R2), vascular endothelial growth factor (VEGF)-A (e.g., targeted by bevacizumab) and VEGFR2 (e.g., targeted by ramucirumab).

Other antibodies and their targets include, e.g., APN301 (hu14.19-IL2), a monoclonal antibody [malignant melanoma and neuroblastoma in children, Apeiron Biologics, Vienna, Austria]. See, also, e.g., monoclonal antibody, 8H9, which has been described as being useful for the treatment of solid tumors, including metastatic brain cancer. The monoclonal antibody 8H9 is a mouse IgG1 antibody with specificity for the B7H3 antigen [United Therapeutics Corporation]. This mouse antibody can be humanized. Still other immunoglobulin constructs targeting the B7-H3 and/or the B7-H4 antigen may be used in the invention. Another antibody is S58 (anti-GD2, neuroblastoma). Cotara™ [Peregrine Pharmaceuticals] is a monoclonal antibody described for treatment of recurrent glioblastoma. Other antibodies may include, e.g., avastin, ficlatuzumab, med-575, and olaratumab. Still other immunoglobulin constructs or monoclonal antibodies may be selected for use in the invention. See, e.g., Medicines in Development Biologics, 2013 Report, pp. 1-87, a publication of PhRMA's Communications & Public Affairs Department. (202) 835-3460, which is incorporated by reference herein.

For example, immunogens may be selected from a variety of viral families. Example of viral families against which an immune response would be desirable include, the picornavirus family, which includes the genera rhinoviruses, which are responsible for about 50% of cases of the common cold; the genera enteroviruses, which include polioviruses, coxsackieviruses, echoviruses, and human enteroviruses such as hepatitis A virus; and the genera aphoviruses, which are responsible for foot and mouth diseases, primarily in non-human animals. Within the picornavirus family of viruses, target antigens include the VP1, VP2, VP3, VP4, and VPG. Another viral family includes the calcivirus family, which encompasses the Norwalk group of viruses, which are an important causative agent of epidemic gastroenteritis. Still another viral family desirable for use in targeting antigens for inducing immune responses in humans and non-human animals is the togavirus family, which includes the genera alphavirus, which include Sindbis viruses, Ross River virus, and Venezuelan, Eastern & Western Equine encephalitis, and rubivirus, including Rubella virus. The flaviviridae family includes dengue, yellow fever, Japanese encephalitis, St. Louis encephalitis and tick borne encephalitis viruses. Other target antigens may be generated from the Hepatitis C or the coronavirus family, which includes a number of non-human viruses such as infectious bronchitis virus (poultry), porcine transmissible gastroenteric virus (pig), porcine hemagglutinating encephalomyelitis virus (pig), feline infectious peritonitis virus (cats), feline enteric coronavirus (cat), canine coronavirus (dog), and human respiratory coronaviruses, which may cause the common cold and/or non-A, B or C hepatitis. Within the coronavirus family, target antigens include the E1 (also called M or matrix protein), E2 (also

called S or Spike protein), E3 (also called HE or hemagglutinin-esterase) glycoprotein (not present in all coronaviruses), or N (nucleocapsid). Still other antigens may be targeted against the rhabdovirus family, which includes the genera vesiculovirus (e.g., Vesicular Stomatitis Virus), and the general lyssavirus (e.g., rabies).

Within the rhabdovirus family, suitable antigens may be derived from the G protein or the N protein. The family filoviridae, which includes hemorrhagic fever viruses such as Marburg and Ebola virus, may be a suitable source of antigens. The paramyxovirus family includes parainfluenza Virus Type 1, parainfluenza Virus Type 3, bovine parainfluenza Virus Type 3, rubulavirus (mumps virus), parainfluenza Virus Type 2, parainfluenza virus Type 4, Newcastle disease virus (chickens), rinderpest, morbillivirus, which includes measles and canine distemper, and pneumovirus, which includes respiratory syncytial virus. The influenza virus is classified within the family orthomyxovirus and is a suitable source of antigen (e.g., the HA protein, the N1 protein). The bunyavirus family includes the genera bunyavirus (California encephalitis, La Crosse), phlebovirus (Rift Valley Fever), hantavirus (pneumonia is a hantavirus fever virus), nairovirus (Nairobi sheep disease) and various unassigned bunyaviruses. The arenavirus family provides a source of antigens against LCM and Lassa fever virus. The reovirus family includes the genera reovirus, rotavirus (which causes acute gastroenteritis in children), orbiviruses, and cultivivirus (Colorado Tick fever, Lebombo (humans), equine encephalosis, blue tongue).

The retrovirus family includes the sub-family oncorivirinal which encompasses such human and veterinary diseases as feline leukemia virus, HTLV I and HTLV II, lentivirinal (which includes human immunodeficiency virus (HIV), simian immunodeficiency virus (SIV), feline immunodeficiency virus (FIV), equine infectious anemia virus, and spumavirinal). Among the lentiviruses, many suitable antigens have been described and can readily be selected as targets. Examples of suitable HIV and SIV antigens include, without limitation the gag, pol, Vif, Vpx, VPR, Env, Tat, Nef, and Rev proteins, as well as various fragments thereof. For example, suitable fragments of the Env protein may include any of its subunits such as the gp120, gp160, gp41, or smaller fragments thereof, e.g., of at least about 8 amino acids in length. Similarly, fragments of the tat protein may be selected. [See, U.S. Pat. No. 5,891,994 and U.S. Pat. No. 6,193,981.] See, also, the HIV and SIV proteins described in D. H. Barouch et al, *J. Virol.*, 75(5):2462-2467 (March 2001), and R. R. Amara, et al, *Science*, 292:69-74 (6 Apr. 2001). In another example, the HIV and/or SIV immunogenic proteins or peptides may be used to form fusion proteins or other immunogenic molecules. See, e.g., the HIV-1 Tat and/or Nef fusion proteins and immunization regimens described in WO 01/54719, published Aug. 2, 2001, and WO 99/16884, published Apr. 8, 1999. The invention is not limited to the HIV and/or SIV immunogenic proteins or peptides described herein. In addition, a variety of modifications to these proteins has been described or could readily be made by one of skill in the art. See, e.g., the modified gag protein that is described in U.S. Pat. No. 5,972,596.

The papovavirus family includes the sub-family polyomaviruses (BKU and JCU viruses) and the sub-family papillomavirus (associated with cancers or malignant progression of papilloma). The adenovirus family includes viruses (EX, AD7, ARD, O.B.) which cause respiratory disease and/or enteritis. The parvovirus family includes feline parvovirus (feline enteritis), feline panleucopeniavi-

rus, canine parvovirus, and porcine parvovirus. The herpesvirus family includes the sub-family alphaherpesvirinae, which encompasses the genera simplexvirus (HSV I, HSV II), varicellovirus (pseudorabies, varicella zoster) and the sub-family betaherpesvirinae, which includes the genera cytomegalovirus (HCMV, muromegalovirus) and the sub-family gammaherpesvirinae, which includes the genera lymphocryptovirus, EBV (Burkitts lymphoma), infectious rhinotracheitis, Marek's disease virus, and rhadinovirus. The poxvirus family includes the sub-family chordopoxvirinae, which encompasses the genera orthopoxvirus (Variola (Smallpox) and Vaccinia (Cowpox)), parapoxvirus, avipoxvirus, capripoxvirus, leporipoxvirus, suipoxvirus, and the sub-family entomopoxvirinae. The hepadnavirus family includes the Hepatitis B virus. One unclassified virus which may be suitable source of antigens is the Hepatitis delta virus. Still other viral sources may include avian infectious bursal disease virus and porcine respiratory and reproductive syndrome virus. The alphavirus family includes equine arteritis virus and various Encephalitis viruses.

Other pathogenic targets for antibodies may 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. Examples of bacterial pathogens include pathogenic gram-positive cocci include pneumococci; staphylococci; and streptococci. Pathogenic gram-negative cocci include meningococcus; gonococcus. Pathogenic enteric gram-negative bacilli include enterobacteriaceae; *pseudomonas*, *acinetobacteria* and *eikenella*; *melioidosis*; *salmonella*; *shigella*; *haemophilus*; *moraxella*; *H. ducreyi* (which causes chancroid); *brucella*; *Francisella tularensis* (which causes tularemia); *yersinia (pasteurella)*; *streptobacillus moniliformis* and *spirillum*; Gram-positive bacilli include *listeria monocytogenes*; *erysipelothrix rhusiopathiae*; *Corynebacterium diphtheria* (diphtheria); cholera; *B. anthracis* (anthrax); donovanosis (granuloma inguinale); and bartonellosis. Diseases caused by pathogenic anaerobic bacteria include tetanus; botulism; other clostridia; tuberculosis; leprosy; and other mycobacteria. Pathogenic spirochetal diseases include syphilis; treponematoses: yaws, pinta and endemic syphilis; and leptospirosis. Other infections caused by higher pathogen bacteria and pathogenic fungi include actinomycosis; nocardiosis; cryptococcosis, blastomycosis, histoplasmosis and coccidioidomycosis; candidiasis, aspergillosis, and mucormycosis; sporotrichosis; paracoccidioidomycosis, petriellidiosis, torulopsosis, mycetoma and chromomycosis; and dermatophytosis. Rickettsial infections include Typhus fever, Rocky Mountain spotted fever, Q fever, and Rickettsialpox. Examples of *mycoplasma* and chlamydial infections include: *mycoplasma pneumoniae*; lymphogranuloma venereum; psittacosis; and perinatal chlamydial infections. Pathogenic eukaryotes encompass pathogenic protozoa and helminthes and infections produced thereby include: amebiasis; malaria; leishmaniasis; trypanosomiasis; toxoplasmosis; *Pneumocystis carinii*; *Trichans*; *Toxoplasma gondii*; babesiosis; giardiasis; trichinosis; filariasis; schistosomiasis; nematodes; trematodes or flukes; and cestode (tapeworm) infections.

Many of these organisms and/or toxins produced thereby have been identified by the Centers for Disease Control [(CDC), Department of Health and Human Services, USA], as agents which have potential for use in biological attacks. For example, some of these biological agents, include, *Bacillus anthracis* (anthrax), *Clostridium botulinum* and its toxin (botulism), *Yersinia pestis* (plague), variola major (smallpox), *Francisella tularensis* (tularemia), and viral

hemorrhagic fevers [filoviruses (e.g., Ebola, Marburg), and arenaviruses [e.g., Lassa, Machupo]], all of which are currently classified as Category A agents; *Coxiella burnetti* (Q fever); *Brucella* species (brucellosis), *Burkholderia mallei* (glanders), *Burkholderia pseudomallei* (meloidosis), *Ricinus communis* and its toxin (ricin toxin), *Clostridium perfringens* and its toxin (epsilon toxin), *Staphylococcus* species and their toxins (enterotoxin B), *Chlamydia psittaci* (psittacosis), water safety threats (e.g., *Vibrio cholerae*, *Cryptosporidium parvum*), Typhus fever (*Rickettsia powazekii*), and viral encephalitis (alphaviruses, e.g., Venezuelan equine encephalitis; eastern equine encephalitis; western equine encephalitis); all of which are currently classified as Category B agents; and Nipah virus and hantaviruses, which are currently classified as Category C agents. In addition, other organisms, which are so classified or differently classified, may be identified and/or used for such a purpose in the future. It will be readily understood that the viral vectors and other constructs described herein are useful to target antigens from these organisms, viruses, their toxins or other by-products, which will prevent and/or treat infection or other adverse reactions with these biological agents.

The following examples are illustrative only and are not a limitation on the invention described herein.

Example 1: Generation of Vectors Containing Full-Length Antibody Co-Expression Cassettes

A series of cis-plasmids were prepared for use in generating an AAV viral particle containing a nucleic acid molecule for delivery to a host target cell. The nucleic acid molecules comprise AAV2 5' and 3' ITR sequences at each terminus, a shared CMV enhancer flanked by two expression cassettes in opposite orientations, where a first expression cassette is controlled by a first minimal CMV promoter and a second expression cassette is controlled by a second minimal CMV promoter. All sequences located between AAV2 ITRs were de novo synthesized by a commercial vendor (GeneArt). All coding sequences for immunoglobulin variable domains were flanked with the unique restriction enzymes to allow convenient shuttling of the desired variable domains. To create constructs with heterologous light chain sequence (kgl), a coding sequence encoding germline light chain (IGKV4-1*01) was de novo synthesized and used to replace FI6 variable light sequence.

An exemplary antibody co-expression shuttle is illustrated in FIG. 2. This shuttle contains to the left of the enhancer a first expression cassette which contains, from right to left, a CMV minimal promoter, a heterologous IL2 leader sequence linked to an anti-TSG101 antibody (IA6) variable heavy (VH) domain, a CH1 domain, and a CH2-3 domain which has been optimized for expression in humans, and a synthetic polyA. To the right of the enhancer is located a CMV minimal promoter, a heterologous IL2 leader sequence, a FI6k2 (anti-influenza antibody) light chain variable domain and a light chain constant domain, furin cleavage site, the 2a linker from the foot-and-mouth disease virus, an IL2 leader sequence, the FI6v3 VH, CH1, CH2-3, and a thymidine kinase short polyA sequence. CH designations refer to the known antibody allotype G1m17,1.

SEQ ID NO: 1 provides sequences of the FI6 constant regions. The amino acid sequences of the FI6 amino acid light chain is provided in SEQ ID NO: 2.

The cis-plasmid of FIG. 2 was used in a triple transfection method as previously described in, e.g., in U.S. patent application Ser. No. 12/226,558, to generate AAV8 and AAV9 vectors which were used in subsequent studies

described herein. The resulting plasmid, pN509_ACE Fi6-1A6 MAB_p3160, is 7722 bp in length, the sequence of which is provided in SEQ ID NO: 3, which is incorporated herein by reference together with its features. The encoded sequences for the FI6 variable light (VL) chain [SEQ ID NO:4], FI6 variable heavy [SEQ ID NO: 5], CH1 (SEQ ID NO: 6), CH2-3 [SEQ ID NO: 7] are also provided.

Similar antibody co-expression cis-plasmids were generated by subcloning a seasonal flu antibody (CR8033) or a pandemic flu antibody (C05), or an anti-M2e antibody (TCN-032) in the place of 1A6 heavy variable domain in FIG. 2 using pre-positioned unique restriction sites that allow easy shuffling of the variable domains. These cis-plasmids were in turn used in triple transfection (e.g., performed as described in U.S. patent application Ser. No. 12/226,588) to generate AAV8 and AAV9 vectors used for subsequent studies. Sequences for the pN510_ACE Fi6-C05 MAB shuttle are provided in SEQ ID NO:8; the amino acids sequence of the variable light chain is provided in SEQ ID NO: 9, the constant light is provided in SEQ ID NO: 10, the FI6 variable heavy chain is provided in SEQ ID NO: 11, the CH1 is provided in SEQ ID NO:12 and the CH2-3 is provide in SEQ ID NO: 13. Sequences for the pN514_ACE Fi6-C05 MAB shuttle are provided in SEQ ID NO:19; the amino acids sequence of the constant light is provided in SEQ ID NO: 20, the FI6 variable heavy chain is provided in SEQ ID NO: 21, the CH1 is provided in SEQ ID NO:22 and the CH2-3 is provide in SEQ ID NO: 23. These shuttles were in turn used to generate AAV8 and AAV9 vectors which were used for subsequent studies.

Example 2: Characterization of Products Expressed from AAV8 Vectors Co-Expressing FI6 Monoclonal Antibody (mAb) and IA6 mAb

A series of ELISA assays were performed to characterize expression levels and to assess binding of the FI6 MAB co-expressed with the IA6 MAB from the cis plasmid generated as described in Example 1 after transfection into HEK 293 cells. TSG101 peptide was synthesized using f-Moc chemistry by Mimotopes. All flu antigens were procured from a commercial supplier, ImmuneTechnologies, Inc. ProteinA was purchased from Sigma-Aldrich and was used to monitor expression of total human IgG1. Detection of human IgG1 in tissue culture supernatants was measured by either antigen-specific or proteinA capture ELISA. High binding ELISA plates were coated with 2 µg/ml of HA proteins or peptides, or with 5 µg/ml proteinA diluted in PBS and incubated overnight at 4° C. Wells were washed 5-8 times and blocked with 1 mM EDTA, 5% heat inactivated PBS, 0.07% Tween 20 in PBS for one hour at room temperature. Tissue culture supernatants were added to the plates at various dilutions in duplicates and incubated at 37° C. for one hour. Plates were washed, blocked, and Bio-SP-conjugated Affinipures Goat Anti-Human IgG antibody (Jackson ImmunoResearch Laboratories, Inc., West Grove, Pa., USA) was added at a 1:10,000 dilution. After one hour, plates were washed and streptavidin-conjugated horseradish peroxidase (HRP) was added at a 1:30,000 dilution. After one hour, plates were washed 3,3',5,5'-tetramethylbenzidine (TMB) was added. The reaction was stopped after 30 minutes at room temperature using 2N sulfuric acid and plates were read at 450 nm using a BioTek µQuant plate reader (Winooski, Vt., USA).

As expected, no binding is observed of FI6 to the TSG101 peptide, the HA (B/Malaysia/2506/2/004), or the HA (Head region only of influenza strain A/Brisbane/59/2007). FI6

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binding is observed for this same strain of influenza when the full-length HA is present, as well as for influenza strain HA(dTM)(A/Beijing/01/2009, H1N1)). As expected, FI6 binding is also observed for Protein A.

According to published reports, FI6 produced according to prior art methods binds to full-length HA and to HA stem, but not to the head only region. These data demonstrate that the co-expressed FI6 monoclonal antibody retains its characteristic binding profile.

Example 3: Characterization of Products Expressed from AAV8 Vectors Co-Expressing Fi6 Monoclonal Antibody (mAb) and Pandemic Flu mAb C05

The possibility of differential detection of two different monoclonal antibodies was assessed in a capture assay. Monoclonal antibodies FI6 and C05 co-expressed from a cis-plasmid prepared as described in Example 1 and transfected into HEK293 cells were assessed for binding. FI6 is expected to bind to full-length HA and to HA stem, but not to the head only region. The results of the binding study illustrated in FIG. 3 demonstrate that the co-expressed antibodies retain their characteristic binding. More particularly, binding to full-length HA and the HA stem characteristic of FI6 is observed and binding to HA and HA head only (no stem) characteristic of C05 is also observed. ELISA assays were performed as described in Example 2.

Example 4: Characterization of Products Expressed from AAV8 Vectors Co-Expressing Fi6 Monoclonal Antibody (mAb) and a Second Full-Length mAb

6-8 weeks old male RAG KO mice (The Jackson Laboratory Bar Harbor, Me., USA) were housed under pathogen-free conditions at the University of Pennsylvania's Translational Research Laboratories. All animal procedures and protocols were approved by the Institutional Animal Care and Use Committee. Mice were sacrificed by carbon dioxide asphyxiation and death was confirmed by cervical dislocation. For vector administration, mice were anaesthetized with a mixture of 70 mg/kg of body weight ketamine and 7 mg/kg of body weight xylazine by intraperitoneal (IP) injection. Vectors were diluted in phosphate buffered saline (PBS) and IM injections were performed using a Hamilton syringe. Serum was collected weekly via retro-orbital bleeds.

Detection of human IgG1 in tissue culture supernatants was measured by proteinA capture ELISA. High binding ELISA plates were coated with 5 µg/ml proteinA diluted in PBS and incubated overnight at 4° C. Wells were washed 5-8 times and blocked with 1 mM EDTA, 5% heat inactivated PBS, 0.07% Tween 20 in PBS. Mouse serum samples were heat inactivated and added to the plates at various dilutions in duplicates and incubated at 37° C. for one hour. Plates were washed, blocked, and Bio-SP-conjugated Affinipures Goat Anti-Human IgG antibody (Jackson ImmunoResearch Laboratories, Inc., West Grove, Pa., USA) was added at a 1:10,000 dilution. After one hour, plates were washed and incubated with streptavidin-conjugated horseradish peroxidase (HRP) at a 1:30,000 dilution. After one hour, plates were washed 3,3',5,5'-tetramethylbenzidine (TMB) was added. The reaction was stopped after 30 minutes at room temperature using 2N sulfuric acid and plates were read at 450 nm using a BioTek µQuant plate reader (Winooski, Vt., USA).

FIG. 5 illustrates systemic expression levels for total human IgG1 in mice administered an AAV vector co-expressing FI6 with IA6 antibody. Mice were injected intramuscularly at doses of 1×10^{11} genome copies (GC) or 1×10^{10} GC. Expression levels were assessed at day 7, 15, 21,

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28, 34, 42, 49 and 56 and measured at a concentration of micrograms/mL. A dose dependent increase in expression was observed.

Example 5: Characterization of Products Expressed from AAV8 Vectors Co-Expressing Fi6 Monoclonal Antibody (mAb) and Three Different Full-Length Monoclonal Antibodies

The tables below showing expression levels in mice administered an AAV vector co-expressing FI6 with full-length CR8033, C05, or 1A6 monoclonal antibody. RAG knock-out (KO) mice were injected intramuscularly at doses of 1×10^{11} genome copies (GC) or 1×10^{10} GC as described in the previous example. Expression levels were assessed weekly at days 7, 15, 21, 28, 34, 42, and 49 and measured at a concentration of micrograms/mL. A dose dependent increase in expression was observed for expressed antibodies. The capture antigen used for the assay is Protein A ELISA as described in the previous example

Test	Fi6v3k2 mAb + CR8033 mAb			
	1.00×10^{11}		1.00×10^{10}	
Article	average	stdev.	average	stdev.
Dose				
Day 0	0.00	0.00	0.00	0.00
Day 7	2.92	0.48	0.04	0.07
Day 14	18.30	4.79	1.24	0.66
Day 21	33.69	7.45	2.09	0.88
Day 28	43.38	10.92	2.84	1.81
Day 35	66.45	16.61	4.47	1.86
Day 42	64.25	12.06	4.37	2.35
Day 49	51.36	11.90	3.57	1.52

Test	Fi6v3k2 mAb + CO5 mAb			
	1.00×10^{11}		1.00×10^{10}	
Article	average	stdev.	average	stdev.
Dose				
Day 0	0.00	0.00	0.00	0.00
Day 7	1.73	0.42	0.00	0.00
Day 14	9.95	3.39	0.24	0.22
Day 21	24.74	11.66	0.81	0.24
Day 28	22.32	4.77	1.11	0.17
Day 35	31.67	7.93	1.53	0.28
Day 42	34.69	14.46	1.83	0.29
Day 49	26.14	5.85	1.46	0.49

Test	Fi6v3k2 mAb + 1A6 mAb			
	1.00×10^{11}		1.00×10^{10}	
Article	average	stdev.	average	stdev.
Dose				
Day 0	0	0	0	0
Day 7	2.70	0.75	0	0
Day 14	5.01	0.06	1.58	.055
Day 21	30.16	13.31	1.71	0.52
Day 28	38.18	15.99	2.16	0.59
Day 35	55.18	18.52	4.09	1.53
Day 42	50.49	16.61	3.69	0.94
Day 49	46.66	15.59	3.73	1.09

Example 6: Anti-Viral Effect is Conferred by Dual Full-Length Antibodies Expressed from a Single AAV9 and/or AAV8 Vector Intramuscularly

A. AAV9.BiD.FI6_CR8033mAb and Influenza A Challenge

BALB/c mice were injected with AAV9.BiD.FI6_CR8033mAb delivered intramuscularly (IM) at 1×10^{11} GC. Two weeks later the mice were challenged intranasally with 5LD50 of mouse adapted PR8 (influenza A). The circle represents the AAV9 construct with a bidirectional promoter expressing synthetic FI6 and CR8033 monoclonal antibodies having the same heterologous light chain. The square represents a positive control, i.e., AAV9 expressing a single antibody type FI6 also delivered at 1×10^{11} GC, and the triangle represents naïve animals FIG. 6B shows survival post-challenge. Administration of the AAV9.BiD.FI6_CR8033mAb at 10^{11} GC/mouse dose allowed partial protection with a significant delay in the weight loss.

B. AAV9.BiD.FI6_CR8033mAb and Influenza B Challenge

For AAV9 vector injection: BALB/c female mice were anesthetized by an intramuscular injection of a 100 mg/kg ketamine/10 mg/kg xylazine mixture in PBS, and AAV9.BiD.FI6_CR8033mAb vector was injected intramuscularly (IM) at 1×10^{11} GC per mouse. BiD vector was compared to an AAV9 expressing a single antibody type CR8033 also delivered at 1×10^{11} GC, and a negative control (naïve animals). FIG. 7B shows survival post-challenge. For influenza challenge, two weeks after vector treatment, AAV-treated and naïve BALB/c mice were weighed and tails color-coded, anesthetized as described above, suspended by their dorsal incisors with their hind limbs supported on a platform, and administered intranasally with 5LD50 of B/Lee/40 (influenza B) in a total volume of 50 μ l of PBS as described above. Mice were then weighed daily and monitored for signs of disease or distress. Animals that exhibited behavioral signs of distress or lost 30% of their initial body weight were euthanized by CO₂ asphyxiation.

FIG. 7A is a line graph showing percent change in weight. These data show that full protective effect was conferred by the dual expressed antibodies at this dose. FIG. 7B shows survival post-challenge.

C. AAV8.F16-TCN032, AAV8.F16-1A6, and AAV8.F16-CR8033 Vectors Administered IM and Mouse Adapted PR8 Influenza A Challenge.

These vectors were made as described in Example 1. 6-8 weeks old male RAG KO mice (The Jackson Laboratory Bar Harbor, Me., USA) were housed under pathogen-free conditions at the University of Pennsylvania's Translational Research Laboratories. All animal procedures and protocols were approved by the Institutional Animal Care and Use Committee. For vector administration, mice were anaesthetized with a mixture of 70 mg/kg of body weight ketamine and 7 mg/kg of body weight xylazine by intraperitoneal (IP) injection. Vectors were diluted in phosphate buffered saline (PBS) and IM injections were performed using a Hamilton syringe. Serum was collected weekly via retro-orbital bleeds.

Detection of human IgG1 in tissue culture supernatants was measured by proteinA capture ELISA. High binding ELISA plates were coated with 5 μ g/ml proteinA diluted in PBS and incubated overnight at 4° C. Wells were washed 5-8 times and blocked with 1 mM EDTA, 5% heat inactivated PBS, 0.07% Tween 20 in PBS. Mouse serum samples were heat inactivated and added to the plates at various dilutions

in duplicates and incubated at 37° C. for one hour. Plates were washed, blocked, and Bio-SP-conjugated Affinipures Goat Anti-Human IgG antibody (Jackson ImmunoResearch Laboratories, Inc., West Grove, Pa., USA) was added at a 1:10,000 dilution. After one hour, plates were washed and incubated with streptavidin-conjugated horseradish peroxidase (HRP) at a 1:30,000 dilution. After one hour, plates were washed 3,3',5,5'-tetramethylbenzidine (TMB) was added. The reaction was stopped after 30 minutes at room temperature using 2N sulfuric acid and plates were read at 450 nm using a BioTek μ Quant plate reader (Winooski, Vt., USA).

With reference to FIG. 8C, on all panels, expression levels are indicated on Day 56 after vector administration. Couple days after the last orbital bleed on Day 56, mice were weighed and tails color-coded, anesthetized as described above, suspended by their dorsal incisors with their hind limbs supported on a platform, and administered intranasally with 5LD₅₀ of mouse adapted PR8 (influenza A) in a total volume of 50 μ l of PBS as described above. Mice were then weighed daily and monitored for signs of disease or distress. Animals that exhibited behavioral signs of distress or lost 30% of their initial body weight were euthanized by CO₂ asphyxiation and death was confirmed by cervical dislocation. FIG. 8A shows that systemic expression of as little as 25 μ g/ml of anti-influenza antibody is sufficient to afford protection in PR8 challenge, but expression of 0.4 μ g/ml is insufficient for protection.

D. AAV9. FI6_IA6 mAbs and Influenza A Challenge

An AAV9 vector expressing artificial FI6 and an anti-HIV immunoadhesin, IA6, were assessed for protection against challenge with influenza A as described above. FIG. 8B shows that expressing 36.5 μ g/ml of anti-influenza antibody is sufficient to provide complete protection against challenge with PR8. FIG. 8C shows expressing 6.9 μ g/ml of anti-influenza antibodies is not sufficient to protect against PR8 challenge.

Example 7—Generation of Vectors Containing Two Immunoadhesin Co-Expression Cassettes

Using a shuttle vector similar to that illustrated in FIG. 2, vectors containing two immunoadhesins have been generated.

In one embodiment, a vector containing FI6 and C05 immunoadhesins was created. The sequences from a plasmid carrying the FI6 and C05 immunoadhesin expression cassettes are provided in SEQ ID NO: 36; with the translated encoded sequences provided in SEQ ID NO: 37 (FI6 variable heavy chain), SEQ ID NO: 38 (FI6 variable light chain), and SEQ ID NO: 39 (CH2-3). These sequences and their features are incorporated by reference.

In another embodiment, a vector containing FI6 and CR8033 immunoadhesins was created. The sequences from a plasmid containing the FI6 and CR8033 immunoadhesins are provided in SEQ ID NO:40; with the translated encoded sequences provided in SEQ ID NO: 41 (FI6 VH) and SEQ ID NO: 42 (FI6 variable light). These sequences and their features are incorporated by reference.

AAV may be generated from the immunoadhesin shuttle plasmids described above using techniques known to those of skill in the art.

Additional illustrative shuttle plasmids are as follows.

The sequence of a plasmid pN512_ACE FI6v3kg1-1A6 MAB_p3184 containing a kappa germline light chain that is heterologous to the source of both heavy chains, 1A6 and FI6v3 is provided in SEQ ID NO: 14. The translated encode

sequences are provide in SEQ ID NO: 15 (constant light), SEQ ID NO: 16 (FI6 variable heavy), SEQ ID NO: 17 (CH1), and SEQ ID NO: 18 (CH2-3).

The sequences of an intermediate vector which carries the TCN032 heavy and light chain immunoglobulins are provided in SEQ ID NO: 30. The translated amino acid sequences encoded by this plasmid include the TCN032 heavy chain in SEQ ID NO: 31; the CH1 sequence in SEQ ID NO: 32; the F16 VH chain in SEQ ID NO: 33; the CH1 sequence in SEQ ID NO: 34 and the CH2-3 sequence in SEQ ID NO: 35.

The sequence of a plasmid carrying the TCN032 and F16 heavy chains and co-expressing two antibodies having these specificities is provided in SEQ ID NO: 43. The translated amino acids of the TCN032 variable heavy chain are in SEQ ID NO: 44, the CH1 is in SEQ ID NO: 45, the hinge-CH2'-CH3' is in SEQ ID NO: 46, the Fi6 VH is in SEQ ID NO: 47, the CH1 is in SEQ ID NO: 48, the CH2-3 is in SEQ ID NO: 49, and the ampicillin resistance gene is in SEQ ID NO: 50. These sequences and their features are incorporated herein by reference.

SEQUENCE LISTING FREE TEXT

The following information is provided for sequences containing free text under numeric identifier <223>.

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	<221> CDS <222> (3556)..(3888) <223> FI6\VL <220>	30
	<221> CDS <222> (3892)..(4560) <223> CH2-3 <220>	
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	<221> CDS <222> (3526)..(3858) <223> FI6\VL <220>
	<221> misc_feature <222> (3862)..(4530) <223> CH2-3 <220>
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	<221> misc_feature <222> (261)..(267) <223> stop cassette (complement) <220>
	<221> misc_feature <222> (268)..(588) <223> constant light (on complementary strand) <220>
	<221> misc_feature <222> (967)..(971) <223> Kozak (located on complementary strand) <220>
	<221> misc_feature <222> (972)..(1019) <223> c-myc 5' UTR (located on complementary strand) <220>
	<221> misc_feature <222> (1026)..(1094) <223> CMV\mp2 <220>
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	<222> (2460)..(3152)			<223> Amp-R
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This application contains sequences and a sequence listing, which is hereby incorporated by reference. All publications, patents, and patent applications cited in this application, and U.S. Provisional Patent Application No. 61/992,649, filed May 13, 2014, the priority of which is claimed, are hereby incorporated by reference in their entireties as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications can be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

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<221> NAME/KEY: CDS

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<223> OTHER INFORMATION: FI6 constant

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gcc cct gaa ctg ctg gga ggc ccc agc gtg ttc ctg ttc ccc cca aag 96
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
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ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc gtg 144
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
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gtg gtg gac gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg tac 192
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
      50                55                60

gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag ccc aga gag gaa 240
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
      65                70                75                80

cag tac aac agc acc tac cgg gtg gtg tcc gtg ctg acc gtg ctg cac 288
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
      85                90                95

cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac aag 336
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
      100                105                110

gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc cag 384
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
      115                120                125

ccc cgc gag cct cag gtg tgc aca ctg ccc ccc agc cgg gaa gag atg 432
Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
      130                135                140

acc aag aac cag gtg tcc ctg acc tgc ctg gtc aag ggc ttc tac ccc 480
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
      145                150                155                160

agc gat atc gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac aac 528
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
      165                170                175

tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc ctg 576
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
      180                185                190

tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac gtg 624
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
      195                200                205

ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc cag 672
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
      35      40      45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
      50      55      60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
      65      70      75      80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
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Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
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 130 135 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 145 150 155 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
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cataacttac ggtaaatggc ccgctggct gaccgcccc cgacccccgc ccattgacgt   1860
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ccttatggga	ctttcctact	tggcagtaca	tctactgtatt	agtcacgct	attaccatgg	2100
tgatgcgggt	ttggcagtac	atcaatgggc	gtggatagcg	gtttgactca	cggggatttc	2160
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Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr						
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atc aac tgc aag agc agc cag agc gtg acc ttc aac tac aag aac tac						2552
Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr Lys Asn Tyr						
	25		30		35	
ctg gcc tgg tac cag cag aag cca gga cag cca cca aag ctg ctg atc						2600
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile						
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Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly						
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agc gga agc gga acc gat ttc acc ctg acc atc agc agc ctg cag gcc						2696
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala						
	70		75		80	
gag gat gtg gcc gtg tac tac tgc cag cag cac tac cgg acc cca cca						2744
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro Pro						
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acc ttc gga cag gga acc aag gtg gag atc aag cgtacggtgg ccgccccaa						2797
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys						
	105		110			
cgtgttcate	ttcccaccaa	gcgatgagca	gctgaagagc	ggaaccgcca	gcgtggtgtg	2857
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			Gln Val Gln Leu Val Glu Ser Gly Gly			
			115		120	
gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc gcc agc						3317
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser						
	125		130		135	
gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag gcc cca						3365
Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro						
	140		145		150	
gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc aac tac						3413
Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala Asn Tyr						
	155		160		165	
aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc cgg gat						3461

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Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	
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gaa agt aac ggc cag cct gag aat aac tac aag act acc cct cca gtg	4469
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	
505 510 515 520	
ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg aca gtg gac	4517
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp	
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Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	
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Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	
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Gly Lys	
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<210> SEQ ID NO 4
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 4

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
          20          25          30
Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
          35          40          45
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
          50          55          60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65          70          75          80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
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Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 5

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 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
 100 105 110
 Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125

Ser

<210> SEQ ID NO 6
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 6

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 100 105

<210> SEQ ID NO 7
 <211> LENGTH: 223
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 7

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 1 5 10 15

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
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Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
      35                               40                               45
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
      50                               55                               60
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
      65                               70                               75                               80
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
      85                               90                               95
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
      100                              105                              110
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
      115                              120                              125
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
      130                              135                              140
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
      145                              150                              155                              160
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
      165                              170                              175
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
      180                              185                              190
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
      195                              200                              205
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
      210                              215                              220

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<210> SEQ ID NO 8
<211> LENGTH: 7773
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid encoding FI6 and C05 monoclonal
antibodies
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (204)..(252)
<223> OTHER INFORMATION: synthetic\polyA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (259)..(927)
<223> OTHER INFORMATION: complement - CH'2-3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (928)..(1248)
<223> OTHER INFORMATION: complement - CH'1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1251)..(1668)
<223> OTHER INFORMATION: complement - C05\VH
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1669)..(1719)
<223> OTHER INFORMATION: complement - leader
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<222> LOCATION: (1729)..(1979)
<223> OTHER INFORMATION: complement - CMV\mp2
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1798)..(2266)
<223> OTHER INFORMATION: Enhancer
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<222> LOCATION: (2267)..(2392)
<223> OTHER INFORMATION: CMV\mp2

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<220> FEATURE:
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<223> OTHER INFORMATION: FI6\VL
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<222> LOCATION: (2842)..(3162)
<223> OTHER INFORMATION: CL
<220> FEATURE:
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<222> LOCATION: (3247)..(3306)
<223> OTHER INFORMATION: leader
<220> FEATURE:
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<222> LOCATION: (3307)..(3693)
<223> OTHER INFORMATION: FI6\ VH
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3694)..(4014)
<223> OTHER INFORMATION: CH1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (4015)..(4683)
<223> OTHER INFORMATION: CH2-3
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (4690)..(4767)
<223> OTHER INFORMATION: TKpAshort

<400> SEQUENCE: 8

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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac      180
gtagccatgc tctaggaaga tctcacacaa aaaaccaaca cacagatgta atgaaaataa      240
agatatatta ttttatcact tcccggggct caggctcagg gacttctggg tgtagtggtt      300
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	Asp Ile Val
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atg acc cag agc cca gat agc ctg gcc gtg agc ctg gga gag cgg gcc	2565
Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala	
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Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr Lys Asn	
20 25 30 35	
tac ctg gcc tgg tac cag cag aag cca gga cag cca cca aag ctg ctg	2661
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu	
40 45 50	
atc tac tgg gcc agc acc cgg gag agc gga gtg cca gat cgg ttc agc	2709
Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser	
55 60 65	
gga agc gga agc gga acc gat ttc acc ctg acc atc agc agc ctg cag	2757
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln	
70 75 80	
gcc gag gat gtg gcc gtg tac tac tgc cag cag cac tac cgg acc cca	2805
Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro	
85 90 95	
cca acc ttc gga cag gga acc aag gtg gag atc aag cgt acg gtg gcc	2853
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala	
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gcc cca agc gtg ttc atc ttc cca cca agc gat gag cag ctg aag agc	2901
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser	
120 125 130	
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Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu	
135 140 145	
gcc aag gtg cag tgg aag gtg gat aac gcc ctg cag agc gga aac agc	2997
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser	
150 155 160	
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Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys	
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Val Val Val Asp Val Ser His Glu Glu Pro Asp Val Lys Phe Asn Trp	
495 500 505	
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Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
510 515 520	
gag cag tat aat agt aca tac cga gtc gtg tca gtc ctg aca gtg ctg	4269
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
525 530 535	
cac cag gat tgg ctg aac ggc aag gag tat aag tgc aag gtg tct aac	4317
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
540 545 550 555	
aag gcc ctg ccc gcc cct atc gag aaa aca att agc aag gcc aaa ggg	4365
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
560 565 570	
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Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu	
575 580 585	
ctg act aag aac cag gtc agc ctg acc tgt ctg gtg aaa ggc ttc tac	4461
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
590 595 600	
ccc agc gac atc gcc gtg gag tgg gaa agt aac ggc cag cct gag aat	4509
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
605 610 615	
aac tac aag act acc cct cca gtg ctg gat agc gac ggg tcc ttc ttc	4557
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
620 625 630 635	
ctg tat agc aag ctg aca gtg gac aaa tcc cgc tgg cag cag gga aac	4605
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
640 645 650	
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Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	
655 660 665	
cag aag agt ctg tca ctg agc ccc ggc aaa tgataaaagg aaccgcgct	4703
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
670 675	
atgacggcaa taaaaagaca gaataaaacc cacgggtggtt gggctggttg ttcataaacc	4763
cgggatogat aaggatcttc ctagagcatg gctacgtaga taagtagcat ggcggggttaa	4823
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7773

<210> SEQ ID NO 9
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 9

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 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
 20 25 30
 Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
 85 90 95
 Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 10
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 10

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 20 25 30
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> SEQ ID NO 11
 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 11

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 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

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Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Ser	Tyr	Asp	Ala	Asn	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90						95
Ala	Lys	Asp	Ser	Gln	Leu	Arg	Ser	Leu	Leu	Tyr	Phe	Glu	Trp	Leu	Ser
			100					105						110	
Gln	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			

Ser

<210> SEQ ID NO 12
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 12

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
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Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70					75					80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
				85					90						95
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His					
		100						105							

<210> SEQ ID NO 13
 <211> LENGTH: 223
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 13

Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val
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Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			20					25					30		
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Glu	Pro	Asp
		35					40					45			
Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
	50					55				60					
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
65					70					75					80
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys

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85					90					95					
Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile
			100					105					110		
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		115					120					125			
Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		130					135					140			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
145					150					155					160
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
				165					170					175	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			180					185					190		
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
		195					200					205			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
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<210> SEQ ID NO 14
 <211> LENGTH: 7728
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Plasmid encoding synthetic FI6 and 1A6
 monoconals
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (191)..(239)
 <223> OTHER INFORMATION: synthetic\polyA
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (246)..(914)
 <223> OTHER INFORMATION: complement - CH'2-3
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (915)..(1235)
 <223> OTHER INFORMATION: complement - CH'1
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1236)..(1598)
 <223> OTHER INFORMATION: complement - 1A6\VH
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1599)..(1655)
 <223> OTHER INFORMATION: complement - leader
 <220> FEATURE:
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 <222> LOCATION: (1665)..(1733)
 <223> OTHER INFORMATION: complement - CMV\mp2
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1732)..(2202)
 <223> OTHER INFORMATION: Enhancer
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (2203)..(2328)
 <223> OTHER INFORMATION: CMV\mp1
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (2388)..(2444)
 <223> OTHER INFORMATION: leader
 <220> FEATURE:
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 <222> LOCATION: (2445)..(2789)
 <223> OTHER INFORMATION: KGL
 <220> FEATURE:
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 <222> LOCATION: (2784)..(3104)
 <223> OTHER INFORMATION: CL
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
 <222> LOCATION: (3189)..(3248)
 <223> OTHER INFORMATION: leader
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (3249)..(3635)
 <223> OTHER INFORMATION: FI6\VH
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (3636)..(3956)
 <223> OTHER INFORMATION: CH1
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (3957)..(4625)
 <223> OTHER INFORMATION: CH2-3
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (4632)..(4709)
 <223> OTHER INFORMATION: TKpAshort

<400> SEQUENCE: 14

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aggggttccct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct    180
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gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala 150 155 160	3413
aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser 165 170 175	3461
cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg 180 185 190	3509
gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg 195 200 205 210	3557
agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp 215 220 225	3605
gga cag gga acc ctg gtg acc gtg agc agc gct agc acc aag gga cca Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro 230 235 240	3653
agc gtg ttc cca ctg gcc cca agc agc aag agc acc agc gga gga acc Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr 245 250 255	3701
gcc gcc ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg acc Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 260 265 270	3749
gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc cca Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 275 280 285 290	3797
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gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg aac Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 310 315 320	3893
cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag agc His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser 325 330 335	3941
tgc gat aag acc cac acg tgc cct cct tgt cca gcc ccc gaa ctg ctg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 340 345 350	3989
ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca ctg Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 355 360 365 370	4037
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cac gaa gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg gag His Glu Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 390 395 400	4133
gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt aca Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 405 410 415	4181
tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg aac Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 420 425 430	4229
ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc cct Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 435 440 445 450	4277
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455	460	465	
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atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca ctg Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 550 555 560			4613
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<210> SEQ ID NO 15
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<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 15

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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20           25           30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35           40           45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50           55           60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65           70           75           80

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Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<210> SEQ ID NO 16
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 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 16

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
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Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
 100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125

Ser

<210> SEQ ID NO 17
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 17

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
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<210> SEQ ID NO 18
 <211> LENGTH: 223
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

 <400> SEQUENCE: 18

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 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 20 25 30

 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
 35 40 45

 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 50 55 60

 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 65 70 75 80

 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 85 90 95

 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 100 105 110

 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 115 120 125

 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 130 135 140

 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 145 150 155 160

 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 165 170 175

 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 180 185 190

 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 195 200 205

 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215 220

 <210> SEQ ID NO 19
 <211> LENGTH: 7746
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Plasmid carrying FI6 and CR8033 monoclonals
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (173)..(221)
 <223> OTHER INFORMATION: synthetic\polyA
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (228)..(896)
 <223> OTHER INFORMATION: complement - CH'2-3
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (897)..(1217)
 <223> OTHER INFORMATION: complement - CH'1
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1218)..(1604)
 <223> OTHER INFORMATION: complement - CR8033\VH
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 <222> LOCATION: (1605)..(1655)
 <223> OTHER INFORMATION: complement - leader
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 <222> LOCATION: (1665)..(1733)
 <223> OTHER INFORMATION: complement - CMV\mp2
 <220> FEATURE:

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 <220> FEATURE:
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 <222> LOCATION: (2203)..(2328)
 <223> OTHER INFORMATION: CMV\mp1
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
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 <223> OTHER INFORMATION: KGL
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (2784)..(3104)
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 <223> OTHER INFORMATION: leader
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 <222> LOCATION: (3249)..(3635)
 <223> OTHER INFORMATION: FI6\VH
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 <222> LOCATION: (3636)..(3956)
 <223> OTHER INFORMATION: CH1
 <220> FEATURE:
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 <222> LOCATION: (3957)..(4625)
 <223> OTHER INFORMATION: CH2-3
 <220> FEATURE:
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 <222> LOCATION: (3968)..(3968)
 <223> OTHER INFORMATION: A -> T
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (4632)..(4709)
 <223> OTHER INFORMATION: TKpAshort

<400> SEQUENCE: 19

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aaaccaaac acagatgtaa tgaaaataaa gatattttat tttatcactt cccggggctc    240
aggctcaggg acttctgggt gtagtggttg tgcaggcct cgtgcatcac gctgcagctg    300
aacacgttgc cctgctgcca ccggctcttg tccacggtea gcttgctata caggaagaat    360
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agggaaaccaa ggtggagatc aag cgt acg gtg gcc gcc cca agc gtg ttc atc 2813
                Arg Thr Val Ala Ala Pro Ser Val Phe Ile
                1             5             10

ttc cca cca agc gat gag cag ctg aag agc gga acc gcc agc gtg gtg 2861
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                15             20             25

tgc ctg ctg aac aac ttc tac cca cgg gag gcc aag gtg cag tgg aag 2909
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
                30             35             40

gtg gat aac gcc ctg cag agc gga aac agc cag gag agc gtg acc gag 2957
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
                45             50             55

cag gat agc aag gat agc acc tac agc ctg agc agc acc ctg acc ctg 3005
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
                60             65             70

agc aag gcc gat tac gag aag cac aag gtg tac gcc tgc gag gtg acc 3053
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                75             80             85             90

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cac cag gga ctg agc agc cca gtg acc aag agc ttc aac cgc gga gag	3101
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu	
95 100 105	
tgc cggaagcggc gggccccagt gaagcagacc ctgaacttcg atctgctgaa	3154
Cys	
gctggccgga gatgtggaga gcaacccagg accaatgtac agaatgcagc tgctgagctg	3214
catcgccctg agcctggccc tggtgaccaa cagc cag gtg caa cta gtg gag agc	3269
Gln Val Gln Leu Val Glu Ser	
110	
gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc	3317
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala	
115 120 125 130	
gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag	3365
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln	
135 140 145	
gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc	3413
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala	
150 155 160	
aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc	3461
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser	
165 170 175	
cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg	3509
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg	
180 185 190	
gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg	3557
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg	
195 200 205 210	
agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg	3605
Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp	
215 220 225	
gga cag gga acc ctg gtg acc gtg agc agc gct agc acc aag gga cca	3653
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
230 235 240	
agc gtg ttc cca ctg gcc cca agc agc aag agc acc agc gga gga acc	3701
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	
245 250 255	
gcc gcc ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg acc	3749
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
260 265 270	
gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc cca	3797
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
275 280 285 290	
gcc gtg ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg acc	3845
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
295 300 305	
gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg aac	3893
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn	
310 315 320	
cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag agc	3941
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser	
325 330 335	
tgc gat aag acc cac acg tgc cct cct tgt cca gcc ccc gaa ctg ctg	3989
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	
340 345 350	
ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca ctg	4037
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
355 360 365 370	
atg att agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg tcc	4085
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	

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375	380	385	
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gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt aca Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 405 410 415			4181
tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg aac Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 420 425 430			4229
ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc cct Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 435 440 445 450			4277
atc gag aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 455 460 465			4325
gtc tac act ctg cca ccc tca aga gat gaa ctg act aag aac cag gtc Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val 470 475 480			4373
agc ctg acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc gtg Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 485 490 495			4421
gag tgg gaa agt aac ggc cag cct gag aat aac tac aag act acc cct Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 500 505 510			4469
cca gtg ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg aca Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr 515 520 525 530			4517
gtg gac aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct gtg Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 535 540 545			4565
atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca ctg Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 550 555 560			4613
agc ccc ggc aaa tgataaaagg aaccgcgct atgacggcaa taaaaagaca Ser Pro Gly Lys 565			4665
gaataaaacc cacgggtgtt gggtcgttt ttcataaacc cgggatcgat aaggatcttc			4725
ctagagcatg gctacgtaga taagtagcat ggcggggtta tcattaacta caaggaaccc			4785
ctagtgatgg agttggccac tccctctctg cgcgctcgt cgctcactga ggccgggcca			4845
ccaaaggctg cccgacgcc gggctttgcc cgggcggcct cagtgagcga gcgagcgcgc			4905
agccttaatt aacctaatc actggccgtc gttttacaac gtcgtgactg ggaaaaccct			4965
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gaagaggccc gcaccgatcg ccttcccaa cagttgcgca gcctgaatgg cgaatgggac			5085
gcgccctgta gcggcgcat aagcgcggcg ggtgtggtgg ttacgcgcag cgtgaccgct			5145
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gggattttgc cgatttcggc ctattgggta aaaaatgagc tgatttaaca aaaatttaac			5505
gcgaatttta acaaaatatt aacgcttaca atttaggtg cacttttcgg ggaaatgtgc			5565

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gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg ctcatgagac 5625
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tgatgagcac ttttaaagtt ctgctatgtg gcgcggtatt atcccgtatt gacgcccggc 5925
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<210> SEQ ID NO 20

<211> LENGTH: 107

<212> TYPE: PRT

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<213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 20

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> SEQ ID NO 21
 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 21

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
 100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125

Ser

<210> SEQ ID NO 22
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 22

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
    35                40                45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                55                60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                70                75                80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    85                90                95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
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<210> SEQ ID NO 23
<211> LENGTH: 223
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 23

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    20                25                30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
    35                40                45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    50                55                60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65                70                75                80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
    85                90                95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    100                105                110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    115                120                125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                135                140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                150                155                160

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
    165                170                175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    180                185                190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    195                200                205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                215                220

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<210> SEQ ID NO 24
<211> LENGTH: 7740
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid carrying FI6 and CR8033 monoclonal
antibodies
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (191)..(239)
<223> OTHER INFORMATION: synthetic polyA

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (246)..(914)
<223> OTHER INFORMATION: complement - CH'2-3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (915)..(1235)
<223> OTHER INFORMATION: complement - CH'1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1236)..(1622)
<223> OTHER INFORMATION: complement - CR8033\ VH
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1623)..(1673)
<223> OTHER INFORMATION: complement - leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1683)..(1751)
<223> OTHER INFORMATION: CMV\mp2
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1752)..(2220)
<223> OTHER INFORMATION: Enhancer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2221)..(2346)
<223> OTHER INFORMATION: CMV\mp1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2406)..(2462)
<223> OTHER INFORMATION: leader
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2463)..(2795)
<223> OTHER INFORMATION: FI6\VL
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2796)..(3116)
<223> OTHER INFORMATION: CL
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3201)..(3260)
<223> OTHER INFORMATION: leader
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3261)..(3647)
<223> OTHER INFORMATION: FI6\ VH
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3648)..(3968)
<223> OTHER INFORMATION: CH1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3969)..(4637)
<223> OTHER INFORMATION: CH2-3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3980)..(3980)
<223> OTHER INFORMATION: A -> T
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (4644)..(4721)
<223> OTHER INFORMATION: TKpAshort

<400> SEQUENCE: 24

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aggggttctt tgtagttaat gattaaccgc ccatgctact tatctacgta gccatgctct 180
aggaagatct cacacaaaa accaacacac agatgtaatg aaaataaaga tattttattt 240
tatcaacttc cggggctcag gctcagggac ttctgggtgt agtgggttg cagggcctcg 300
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gc gat atc gtc atg acc cag agc cca gat agc ctg gcc gtg agc ctg	2507
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu	
1 5 10 15	
gga gag cgg gcc acc atc aac tgc aag agc agc cag agc gtg acc ttc	2555
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe	
20 25 30	
aac tac aag aac tac ctg gcc tgg tac cag cag aag cca gga cag cca	2603

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Asn	Tyr	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro		
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cca	aag	ctg	ctg	atc	tac	tgg	gcc	agc	acc	cgg	gag	agc	gga	gtg	cca		2651
Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	Pro		
		50					55					60					
gat	cgg	ttc	agc	gga	agc	gga	agc	gga	acc	gat	ttc	acc	ctg	acc	atc		2699
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile		
	65				70					75							
agc	agc	ctg	cag	gcc	gag	gat	gtg	gcc	gtg	tac	tac	tgc	cag	cag	cac		2747
Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	His		
					85					90					95		
tac	cgg	acc	cca	cca	acc	ttc	gga	cag	gga	acc	aag	gtg	gag	atc	aag		2795
Tyr	Arg	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys		
					100					105					110		
cgt	acg	gtg	gcc	gcc	cca	agc	gtg	ttc	atc	ttc	cca	cca	agc	gat	gag		2843
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu		
			115					120						125			
cag	ctg	aag	agc	gga	acc	gcc	agc	gtg	gtg	tgc	ctg	ctg	aac	aac	ttc		2891
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe		
		130						135					140				
tac	cca	cgg	gag	gcc	aag	gtg	cag	tgg	aag	gtg	gat	aac	gcc	ctg	cag		2939
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln		
	145					150					155						
agc	gga	aac	agc	cag	gag	agc	gtg	acc	gag	cag	gat	agc	aag	gat	agc		2987
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser		
					165					170					175		
acc	tac	agc	ctg	agc	agc	acc	ctg	acc	ctg	agc	aag	gcc	gat	tac	gag		3035
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu		
					180					185					190		
aag	cac	aag	gtg	tac	gcc	tgc	gag	gtg	acc	cac	cag	gga	ctg	agc	agc		3083
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser		
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cca	gtg	acc	aag	agc	ttc	aac	cgc	gga	gag	tgc	cggaagcggc	gggccccagt					3136
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
			210					215									
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	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly		
		220						225					230				
cgg	agc	ctg	cgg	ctg	agc	tgc	gcc	gcc	agc	gga	ttc	acc	ttc	agc	acc		3353
Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr		
		235					240						245				
tac	gcc	atg	cac	tgg	gtg	cgg	cag	gcc	cca	gga	aag	gga	ctg	gag	tgg		3401
Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp		
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gtg	gcc	gtg	atc	agc	tac	gat	gcc	aac	tac	aag	tac	tac	gcc	gat	agc		3449
Val	Ala	Val	Ile	Ser	Tyr	Asp	Ala	Asn	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser		
					270					275					280		
gtg	aag	gga	cgg	ttc	acc	atc	agc	cgg	gat	aac	agc	aag	aac	acc	ctg		3497
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu		
					285					290					295		
tac	ctg	cag	atg	aac	agc	ctg	cgg	gcc	gag	gat	acc	gcc	gtg	tac	tac		3545
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr		
			300					305							310		
tgc	gcc	aag	gat	agc	cag	ctg	cgg	agc	ctg	ctg	tac	ttc	gag	tgg	ctg		3593
Cys	Ala	Lys	Asp	Ser	Gln	Leu	Arg	Ser	Leu	Leu	Tyr	Phe	Glu	Trp	Leu		
			315				320								325		

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agc cag gga tac ttc gat tac tgg gga cag gga acc ctg gtg acc gtg	3641
Ser Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val	
330 335 340 345	
agc agc gct agc acc aag gga cca agc gtg ttc cca ctg gcc cca agc	3689
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
350 355 360	
agc aag agc acc agc gga gga acc gcc gcc ctg gga tgc ctg gtg aag	3737
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
365 370 375	
gat tac ttc cca gag cca gtg acc gtg agc tgg aac agc gga gcc ctg	3785
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
380 385 390	
acc agc gga gtg cac acc ttc cca gcc gtg ctg cag agc agc gga ctg	3833
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
395 400 405	
tat agc ctg agc agc gtg gtg acc gtg cca agc agc agc ctg gga acc	3881
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
410 415 420 425	
cag acc tac atc tgc aac gtg aac cac aag cca agc aac acc aag gtg	3929
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
430 435 440	
gat aag aag gtg gag cca aag agc tgc gat aag acc cac acg tgc cct	3977
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
445 450 455	
cct tgt cca gcc ccc gaa ctg ctg ggc ggg cct agc gtg ttc ctg ttt	4025
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	
460 465 470	
ccc cct aag cct aaa gat aca ctg atg att agt aga acc cca gag gtc	4073
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
475 480 485	
aca tgc gtg gtc gtg gac gtg tcc cac gaa gag cct gac gtg aag ttc	4121
Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp Val Lys Phe	
490 495 500 505	
aac tgg tac gtg gat ggc gtg gag gtg cac aat gct aag act aaa cca	4169
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
510 515 520	
cgc gaa gag cag tat aat agt aca tac cga gtc gtg tca gtc ctg aca	4217
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
525 530 535	
gtg ctg cac cag gat tgg ctg aac ggc aag gag tat aag tgc aag gtg	4265
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
540 545 550	
tct aac aag gcc ctg ccc gcc cct atc gag aaa aca att agc aag gcc	4313
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
555 560 565	
aaa ggg cag cca cgg gaa ccc cag gtc tac act ctg cca ccc tca aga	4361
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
570 575 580 585	
gat gaa ctg act aag aac cag gtc agc ctg acc tgt ctg gtg aaa ggc	4409
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
590 595 600	
ttc tac ccc agc gac atc gcc gtg gag tgg gaa agt aac ggc cag cct	4457
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
605 610 615	
gag aat aac tac aag act acc cct cca gtg ctg gat agc gac ggg tcc	4505
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
620 625 630	
ttc ttc ctg tat agc aag ctg aca gtg gac aaa tcc cgc tgg cag cag	4553
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
635 640 645	

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tgcaaacaaa aaaaccaccg ctaccagcgg tggtttgttt gccggatcaa gagctaccaa 6807
ctctttttcc gaaggtaact ggcttcagca gagcgcagat accaaatact gttcttctag 6867
tgtagccgta gttaggccac cacttcaaga actctgtagc accgcctaca tacctcgctc 6927
tgctaatect gttaccagtg gctgctgcca gtggcgataa gtcgtgtctt accgggttgg 6987
actcaagacg atagttaccg gataaggcgc agcggtcggg ctgaacgggg ggttcgtgca 7047
cacagcccag cttggagcga acgacctaca ccgaactgag atacctacag cgtgagctat 7107
gagaaagcgc cacgcttccc gaagggagaa aggcggacag gtatccggta agcggcaggg 7167
tcggaacagg agagcgcacg agggagcttc cagggggaaa cgcctggtat ctttatagtc 7227
ctgtcggggtt tcgccacctc tgacttgagc gtcgattttt gtgatgctcg tcaggggggc 7287
ggagcctatg gaaaaacgcc agcaacgcgg cctttttacg gttcctggcc ttttgctggc 7347
cttttgctca catgttcttt cctgcgttat ccctgatc tgtggataac cgtattaccg 7407
cctttgagtg agctgatacc gctcgcgcga gccgaacgac cgagcgcagc gagtcagtga 7467
gcgaggaagc ggaagagcgc ccaatacgcga aaccgcctct ccccgcgctg tggccgatc 7527
attaatgcag ctggcacgac aggtttcccg actggaaagc gggcagtgag cgcaacgcaa 7587
ttaatgtgag ttagctcact cattagcac cccaggcttt acactttatg cttccggctc 7647
gtatgttggtg tggaaattgtg agcggataac aatttcacac aggaaacagc tatgacctg 7707
attacgccag atttaattaa ggccttaatt agg 7740

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<210> SEQ ID NO 25
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 25

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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1           5           10          15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
          20          25          30
Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
          35          40          45
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
          50          55          60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65          70          75          80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
          85          90          95
Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          100         105         110

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<210> SEQ ID NO 26
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 26

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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1           5           10          15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

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20					25					30					
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
		35					40					45			
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
	50					55					60				
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
65						70					75				80
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
				85					90					95	
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
			100					105							

<210> SEQ ID NO 27
 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 27

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Ser	Tyr	Asp	Ala	Asn	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65						70					75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Lys	Asp	Ser	Gln	Leu	Arg	Ser	Leu	Leu	Tyr	Phe	Glu	Trp	Leu	Ser
			100					105					110		
Gln	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			

Ser

<210> SEQ ID NO 28
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 28

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1				5					10					15	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65						70					75				80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys

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85	90	95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His		
100	105	
<210> SEQ ID NO 29		
<211> LENGTH: 223		
<212> TYPE: PRT		
<213> ORGANISM: Artificial sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic Construct		
<400> SEQUENCE: 29		
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val		
1	5	10
		15
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr		
	20	25
		30
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp		
	35	40
		45
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys		
	50	55
		60
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser		
65	70	75
		80
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys		
	85	90
		95
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile		
	100	105
		110
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro		
	115	120
		125
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu		
	130	135
		140
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn		
145	150	155
		160
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser		
	165	170
		175
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg		
	180	185
		190
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
	195	200
		205
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	210	215
		220

<210> SEQ ID NO 30
 <211> LENGTH: 7782
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: EcoRV
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (201)..(252)
 <223> OTHER INFORMATION: complement - synthetic\polyA
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (268)..(588)
 <223> OTHER INFORMATION: complement - CL
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (589)..(909)
 <223> OTHER INFORMATION: complement - TCN032\VL
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (910)..(966)

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<223> OTHER INFORMATION: complement - leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1026)..(1094)
<223> OTHER INFORMATION: complement - CMV\mp2
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1095)..(1563)
<223> OTHER INFORMATION: Enhancer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1564)..(1689)
<223> OTHER INFORMATION: CMV p1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1749)..(1805)
<223> OTHER INFORMATION: leader
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1806)..(2165)
<223> OTHER INFORMATION: TCN032\VH
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2166)..(2459)
<223> OTHER INFORMATION: CH1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2460)..(3152)
<223> OTHER INFORMATION: hinge-CH2'-CH3'
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3239)..(3296)
<223> OTHER INFORMATION: leader
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3297)..(3683)
<223> OTHER INFORMATION: FI6\VH
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3684)..(4004)
<223> OTHER INFORMATION: CH1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (4005)..(4673)
<223> OTHER INFORMATION: CH2-3
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (4693)..(4770)
<223> OTHER INFORMATION: TKpAshort

<400> SEQUENCE: 30

ggccttaatt aggctgcgcg ctgctcgct cactgaggcc gcccgggcaa agccccgggcg      60
tcgggcgacc tttggtcgcc cggcctcagt gagcgagcga gcgcgagag agggagtggc      120
caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatget acttatctac      180
gtagccatgc tctaggaaga tctcacacaa aaaaccaaca cacagatgta atgaaaataa      240
agatatttta ttgcccgcgc tttatcagca ctctccgagg ttgaagctct tggtcactgg      300
gctgctcagt ccctggtggg tcacctcgca ggcgtacacc ttgtgcttct cgtaatcggc      360
cttgctcagg gtcagggtgc tgctcaggct gtaggtgcta tccttgctat cctgctcggc      420
cacgctctcc tggtgtttc cgtctgcag ggcgttatcc accttccact gcaccttggc      480
ctcccgtggg tagaagttgt tcagcaggca caccacgctg gcggttccgc tcttcagctg      540
ctcatcgctt ggtggaaga tgaacacgct tggggcgccc accgtacgct tgatctccac      600
ccgggttcc cctccgaagg tcagtgggtg gctgtagctc tgctggcagt agtaggtggc      660
gaaatcctct ggctgcaggc tggatgatgg cagggtgaaa tcggttccgc ttccgcttcc      720
gctgaaccgg cttggcactc cgtctgcag tccgctggcg gcgctgatca gtccctttgg      780
ggcctttcct ggccgctgct ggtaccagtt caggtacttg tagatgttct ggctggcccg      840

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gcaggtgatg gtcacccgat ctcccacgct ggcgctcagg ctgcttgggc tctgggtcat 900
ctggatateg ctgttggtca ccagggccag gctcagggcg atcagcagca gcagctgcat 960
tctcatggtg gagagtcgcg tccttgctcg ggtgttgtaa gttccagtgc aaagtgcccc 1020
aattggcgat ctgacgggtc actaaacgag ctctgcttat ataggcctcc caccgtacac 1080
gccacctcga catacctagt tattaatagt aatcaattac ggggtcatta gttcatagcc 1140
catatatgga gttccgcgtt acataactta cggtaaattgg cccgcctggc tgaccgcccc 1200
acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaatagggg 1260
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aagtgtatca tatgccaaat acgcccccta ttgacgtcaa tgacggtaaa tggccccgct 1380
ggcattatgc ccagtacatg accttatggg actttcctac ttggcagtac atctacgtat 1440
tagtcatcgc tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc 1500
ggtttgactc acggggattt ccaagtctcc acccattga cgtcaatggg agtttgtttt 1560
ggcaccaaaa tcaacgggac tttccaaaat gtcgtaacaa ctccgcccc ttgacgcaaa 1620
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agatccgctg ctagegggca ctttgactg gaacttacia caccgagca aggacgcgac 1740
tctccaccat gcgcatgcag ctgctgctgc tgatcgccct gagcctggcc ctggtgacca 1800
acagc cag gtg cag ctg cag gag agc gga cca gga ctg gtg aag cca agc 1850
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15
gag acc ctg agc ctg acc tgc acc gtg agc gga agc agc atc agc aac 1898
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn
20 25 30
tac tac tgg agc tgg atc cgg cag agc cca gga aag gga ctg gag tgg 1946
Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
35 40 45
atc gga ttc atc tac tac gga gga aac acc aag tac aac cca agc ctg 1994
Ile Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu
50 55 60
aag agc cgg gtg acc atc agc cag gat acc agc aag agc cag gtg agc 2042
Lys Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser
65 70 75
ctg acc atg agc agc gtg acc gcc gcc gag agc gcc gtg tac ttc tgc 2090
Leu Thr Met Ser Ser Val Thr Ala Ala Glu Ser Ala Val Tyr Phe Cys
80 85 90 95
gcc cgg gcc agc tgc agc gga gga tac tgc atc ctg gat tac tgg gga 2138
Ala Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly
100 105 110
cag gga acc ctg gtg acc gtg agc agc gcg tcg acc aag gga cct tcg 2186
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 2234
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 2282
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 2330
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
160 165 170 175
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 2378
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

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180	185	190	
ccc tcc agc agc ttg ggc acc cag	acc tac atc tgc aac gtg aat cac		2426
Pro Ser Ser Ser Leu Gly Thr Gln	Thr Tyr Ile Cys Asn Val Asn His		
195	200	205	
aag ccc agc aac acc aag gtg gac	aag aaa gtt gaaccaaaga gctgcgacaa		2479
Lys Pro Ser Asn Thr Lys Val Asp	Lys Lys Val		
210	215		
gaccacacg tgtccccct gccctgcccc	tgaactgctg ggaggcccca gcgtgttct		2539
gttccccca aagcccaagg acaccctgat	gatcagccgg acccccgaag tgacctgcgt		2599
ggtggtggac gtgtcccacg aggaccctga	agtgaagttt aattggtacg tggacggcgt		2659
ggaagtgcac aacgccaaga ccaagcccag	agaggaacag tacaacagca cctaccgggt		2719
ggtgtccgtg ctgacctgc tgcaccagga	ctggctgaac ggcaaagagt acaagtgcaa		2779
ggtgtccaac aaggccctgc ctgccccat	cgagaaaacc atcagcaagg ccaagggcca		2839
gccccgag cctcaggtct acacactgcc	cccagccgg gaagagatga ccaagaacca		2899
ggtgtccctg acctgctgg tcaagggctt	ctaccccagc gacatcgccg tggaatggga		2959
gagcaacggc cagccccgaga acaactaaa	gaccaccccc cctgtgctgg acagcgacgg		3019
ctcattcttc ctgtatagca agctgaccgt	ggacaagagc cgggtggcagc agggcaacgt		3079
gttcagctgc agcgtgatgc acgaggccct	gcacaaccac tacaccaga agtccctgag		3139
cctgagcccc ggcagaaagc ggagagcccc	cgtgaagcag accctgaact tgcacctgct		3199
gaagctggcc ggcgacgtgg aaagcaacc	tggccctatg tacagaatgc agctgctgag		3259
ctgcatcgcc ctgagcctgg ccctggtgac	caacagc cag gtg caa cta gtg gag		3314
	Gln Val Gln Leu Val Glu		
	220		
agc gga gga gga gtg gtg cag cca	gga cgg agc ctg cgg ctg agc tgc		3362
Ser Gly Gly Gly Val Val Gln Pro	Gly Arg Ser Leu Arg Leu Ser Cys		
225	230	235	240
gcc gcc agc gga ttc acc ttc agc	acc tac gcc atg cac tgg gtg cgg		3410
Ala Ala Ser Gly Phe Thr Phe Ser	Thr Tyr Ala Met His Trp Val Arg		
245	250	255	
cag gcc cca gga aag gga ctg gag	tgg gtg gcc gtg atc agc tac gat		3458
Gln Ala Pro Gly Lys Gly Leu Glu	Trp Val Ala Val Ile Ser Tyr Asp		
260	265	270	
gcc aac tac aag tac tac gcc gat	agc gtg aag gga cgg ttc acc atc		3506
Ala Asn Tyr Lys Tyr Tyr Ala Asp	Ser Val Lys Gly Arg Phe Thr Ile		
275	280	285	
agc cgg gat aac agc aag aac acc	ctg tac ctg cag atg aac agc ctg		3554
Ser Arg Asp Asn Ser Lys Asn Thr	Leu Tyr Leu Gln Met Asn Ser Leu		
290	295	300	
cgg gcc gag gat acc gcc gtg tac	tac tgc gcc aag gat agc cag ctg		3602
Arg Ala Glu Asp Thr Ala Val Tyr	Tyr Cys Ala Lys Asp Ser Gln Leu		
305	310	315	320
cgg agc ctg ctg tac ttc gag tgg	ctg agc cag gga tac ttc gat tac		3650
Arg Ser Leu Leu Tyr Phe Glu Trp	Leu Ser Gln Gly Tyr Phe Asp Tyr		
325	330	335	
tgg gga cag gga acc ctg gtg acc	gtg agc agc gcc agc acc aag ggg		3698
Trp Gly Gln Gly Thr Leu Val Thr	Val Ser Ser Ala Ser Thr Lys Gly		
340	345	350	
ccc agc gtg ttc cca ctg gcc cca	agc agc aag agc acc agc gga gga		3746
Pro Ser Val Phe Pro Leu Ala Pro	Ser Ser Lys Ser Thr Ser Gly Gly		
355	360	365	
acc gcc gcc ctg gga tgc ctg gtg	aag gat tac ttc cca gag cca gtg		3794
Thr Ala Ala Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro Glu Pro Val		
370	375	380	

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acc gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc	3842
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe	
385 390 395 400	
cca gcc gtg ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg	3890
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val	
405 410 415	
acc gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg	3938
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val	
420 425 430	
aac cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag	3986
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys	
435 440 445	
agc tgc gat aag acc cac acg tgc cct cca tgt cca gcc ccc gaa ctg	4034
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu	
450 455 460	
ctg ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca	4082
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	
465 470 475 480	
ctg atg att agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg	4130
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	
485 490 495	
tcc cac gaa gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg	4178
Ser His Glu Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val	
500 505 510	
gag gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt	4226
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	
515 520 525	
aca tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg	4274
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	
530 535 540	
aac ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc	4322
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala	
545 550 555 560	
cct atc gag aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc	4370
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	
565 570 575	
cag gtc tac act ctg cca ccc tca aga gat gaa ctg act aag aac cag	4418
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln	
580 585 590	
gtc agc ctg acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc	4466
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala	
595 600 605	
gtg gag tgg gaa agt aac ggc cag cct gag aat aac tac aag act acc	4514
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr	
610 615 620	
cct cca gtg ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg	4562
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu	
625 630 635 640	
aca gtg gac aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct	4610
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser	
645 650 655	
gtg atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca	4658
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser	
660 665 670	
ctg agc ccc ggc aaa tgataaaaag cttctcgaga aggaaccgc gctatgacgg	4713
Leu Ser Pro Gly Lys	
675	
caataaaaag acagaataaa acccacgggt gttgggtcgt ttgttcataa acccggaag	4773

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<210> SEQ ID NO 31
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 31

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn Tyr
20          25          30
Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35          40          45
Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys
50          55          60
Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser Leu
65          70          75          80
Thr Met Ser Ser Val Thr Ala Ala Glu Ser Ala Val Tyr Phe Cys Ala
85          90          95
Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly Gln
100         105         110
Gly Thr Leu Val Thr Val Ser Ser
115         120

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<210> SEQ ID NO 32
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 32

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1           5           10           15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20          25          30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35          40          45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50          55          60

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Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
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Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> SEQ ID NO 33
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 33

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser

<210> SEQ ID NO 34
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 34

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
100 105

<210> SEQ ID NO 35
<211> LENGTH: 223
<212> TYPE: PRT

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<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 35

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1           5           10           15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
20           25           30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
35           40           45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50           55           60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65           70           75           80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
85           90           95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
100          105          110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
115          120          125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
130          135          140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145          150          155          160

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
165          170          175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
180          185          190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
195          200          205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210          215          220

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<210> SEQ ID NO 36
<211> LENGTH: 7814
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<223> OTHER INFORMATION: FI6 and CO5 immunoadhesins
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (201)..(432)
<223> OTHER INFORMATION: complement - SV40\polyA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (453)..(1121)
<223> OTHER INFORMATION: complement - CH'2-3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1125)..(1457)
<223> OTHER INFORMATION: complement - C05\VL
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1458)..(1502)
<223> OTHER INFORMATION: SL rom[3]bn201co
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1503)..(1916)
<223> OTHER INFORMATION: complement - C05\VH
<220> FEATURE:
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<222> LOCATION: (1965)..(1973)
<223> OTHER INFORMATION: leader

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2371)..(2412)
<223> OTHER INFORMATION: complement - CMV\mp2
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2413)..(2881)
<223> OTHER INFORMATION: enhancer
<220> FEATURE:
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<222> LOCATION: (2882)..(3007)
<223> OTHER INFORMATION: CMV\mp1
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<222> LOCATION: (3067)..(3055)
<223> OTHER INFORMATION: leader
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<222> LOCATION: (3124)..(3510)
<223> OTHER INFORMATION: FI6\ VH
<220> FEATURE:
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<222> LOCATION: (3511)..(3555)
<223> OTHER INFORMATION: SL\from\3bn201co
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3556)..(3888)
<223> OTHER INFORMATION: FI6\VL
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3892)..(4560)
<223> OTHER INFORMATION: CH2-3
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (4581)..(4812)
<223> OTHER INFORMATION: SV40\polyA

<400> SEQUENCE: 36

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tcgggcgacc tttggtcgcc cggcctcagt gacgagcga gcgcgcagag agggagtggc      120
caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac      180
gtagccatgc tctaggaaga tcattttacc acattttagt aggttttact tgctttaaaa      240
aacctcccac atctcccctt gaacctgaaa cataaaatga atgcaattgt tgttgtaaac      300
ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaat      360
aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat      420
catgtctgct cgaagcggcc gcaagcttat cacttcccgg ggctcaggct cagggacttc      480
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cccaccatgc	gcatgcagct	gctgctgctg	atcgccctga	gcctggccct	ggtgaccaac	3120										
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	1			5						10					15	
cgg	agc	ctg	cgg	ctg	agc	tgc	gcc	gcc	agc	gga	ttc	acc	ttc	agc	acc	3216
Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	
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tac	gcc	atg	cac	tgg	gtg	cgg	cag	gcc	cca	gga	aag	gga	ctg	gag	tgg	3264
Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
			35					40					45			
gtg	gcc	gtg	atc	agc	tac	gat	gcc	aac	tac	aag	tac	tac	gcc	gat	agc	3312
Val	Ala	Val	Ile	Ser	Tyr	Asp	Ala	Asn	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	
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Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu	
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tac ctg cag atg aac agc ctg cgg gcc gag gat acc gcc gtg tac tac	3408
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr	
80 85 90 95	
tgc gcc aag gat agc cag ctg cgg agc ctg ctg tac ttc gag tgg ctg	3456
Cys Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu	
100 105 110	
agc cag gga tac ttc gat tac tgg gga cag gga acc ctg gtg acc gtg	3504
Ser Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val	
115 120 125	
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Ser Ser Asp Ile	
130	
gtc atg acc cag agc cca gat agc ctg gcc gtg agc ctg gga gag cgg	3609
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg	
135 140 145	
gcc acc atc aac tgc aag agc agc cag agc gtg acc ttc aac tac aag	3657
Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr Lys	
150 155 160	
aac tac ctg gcc tgg tac cag cag aag cca gga cag cca cca aag ctg	3705
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu	
165 170 175	
ctg atc tac tgg gcc agc acc cgg gag agc gga gtg cca gat cgg ttc	3753
Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe	
180 185 190 195	
agc gga agc gga agc gga acc gat ttc acc ctg acc atc agc agc ctg	3801
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu	
200 205 210	
cag gcc gag gat gtg gcc gtg tac tac tgc cag cag cac tac cgg acc	3849
Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg Thr	
215 220 225	
cca cca acc ttc gga cag gga acc aag gtg gag atc aag gcc acg tgc	3897
Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Cys	
230 235 240	
cct cca tgt cca gcc ccc gaa ctg ctg ggc ggg cct agc gtg ttc ctg	3945
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu	
245 250 255	
ttt ccc cct aag cct aaa gat aca ctg atg att agt aga acc cca gag	3993
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu	
260 265 270	
gtc aca tgc gtg gtc gtg gac gtg tcc cac gaa gag cct gac gtg aag	4041
Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp Val Lys	
275 280 285 290	
ttc aac tgg tac gtg gat ggc gtg gag gtg cac aat gct aag act aaa	4089
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys	
295 300 305	
cca cgc gaa gag cag tat aat agt aca tac cga gtc gtg tca gtc ctg	4137
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu	
310 315 320	
aca gtg ctg cac cag gat tgg ctg aac ggc aag gag tat aag tgc aag	4185
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys	
325 330 335	
gtg tct aac aag gcc ctg ccc gcc cct atc gag aaa aca att agc aag	4233
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys	
340 345 350	
gcc aaa ggg cag cca cgg gaa ccc cag gtc tac act ctg cca ccc tca	4281
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser	

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Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys				
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ggc ttc tac ccc agc gac atc gcc gtg gag tgg gaa agt aac ggc cag				4377
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln				
	390	395	400	
cct gag aat aac tac aag act acc cct cca gtg ctg gat agc gac ggg				4425
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly				
	405	410	415	
tcc ttc ttc ctg tat agc aag ctg aca gtg gac aaa tcc cgc tgg cag				4473
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln				
	420	425	430	
cag gga aac gtc ttt tcc tgt tct gtg atg cat gag gcc ctg cac aat				4521
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn				
	435	440	445	450
cat tac acc cag aag agt ctg tca ctg agc ccc ggc aaa tgataagctt				4570
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
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ttaa 7814

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<210> SEQ ID NO 37
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 37

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20           25           30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35           40           45
Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
50           55           60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser

<210> SEQ ID NO 38
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 38

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
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Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
85 90 95

Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 39
<211> LENGTH: 223
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 39

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
20 25 30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50 55 60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65 70 75 80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
85 90 95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
100 105 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
115 120 125

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Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 130                               135                       140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                               150                       155                       160

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                               165                       170                       175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                               180                       185                       190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
                               195                       200                       205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210                               215                       220

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<210> SEQ ID NO 40
<211> LENGTH: 7784
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<223> OTHER INFORMATION: FI6 and CR8033 immunoadhesins
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (201)..(432)
<223> OTHER INFORMATION: complement - SV40\polyA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (453)..(1121)
<223> OTHER INFORMATION: complement - CH'2-3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1125)..(1460)
<223> OTHER INFORMATION: complement - 033\VL
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1461)..(1505)
<223> OTHER INFORMATION: SL\from\3bn201co
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1506)..(1886)
<223> OTHER INFORMATION: complement - 033\VH
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1935)..(1946)
<223> OTHER INFORMATION: complement - leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2341)..(2382)
<223> OTHER INFORMATION: complement - CMV\mp2
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2383)..(2851)
<223> OTHER INFORMATION: enhancer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2852)..(2977)
<223> OTHER INFORMATION: CMV\mp1
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<222> LOCATION: (3073)..(3045)
<223> OTHER INFORMATION: leader
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<222> LOCATION: (3094)..(3480)
<223> OTHER INFORMATION: FI6\VH
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3481)..(3525)
<223> OTHER INFORMATION: SL\from\3bn201co
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3526)..(3858)
<223> OTHER INFORMATION: FI6\VL
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (3862)..(4530)
<223> OTHER INFORMATION: CH2-3
<220> FEATURE:
<221> NAME/KEY: polyA_signal
<222> LOCATION: (4551)..(4782)
<223> OTHER INFORMATION: SV40\polyA

<400> SEQUENCE: 40

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tcgggcgacc tttggtcgcc cggcctcagt gagcgagcga gcgcgagag agggagtggc      120
caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac      180
gtagccatgc tctaggaaga tcattttacc acattttagt aggttttact tgctttaaaa      240
aacctcccac atctccccct gaacctgaaa cataaaatga atgcaattgt tgttgtaaac      300
ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat      360
aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat      420
catgtctgct cgaagcggcc gcaagcttat cacttcccgg ggctcaggct cagggacttc      480
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agcacagggg ggggtgtctt gtagttgttc tcgggctggc cgttgctctc ccattccacg      660
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Gln Val Gln Leu Val Glu Ser	
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gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc	3162
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala	
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gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag	3210
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln	
25 30 35	
gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc	3258
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala	
40 45 50 55	
aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc	3306
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser	
60 65 70	
cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg	3354
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg	
75 80 85	
gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg	3402
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg	
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Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp	
105 110 115	
gga cag gga acc ctg gtg acc gtg agc agc ggcggaggag gcagcggagg	3500
Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
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Asp Ile Val Met Thr Gln Ser Pro Asp	
130 135	
agc ctg gcc gtg agc ctg gga gag cgg gcc acc atc aac tgc aag agc	3600
Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser	
140 145 150	
agc cag agc gtg acc ttc aac tac aag aac tac ctg gcc tgg tac cag	3648
Ser Gln Ser Val Thr Phe Asn Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln	
155 160 165 170	

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cgg gag agc gga gtg cca gat cgg ttc agc gga agc gga agc gga acc	3744
Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr	
190 195 200	
gat ttc acc ctg acc atc agc agc ctg cag gcc gag gat gtg gcc gtg	3792
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val	
205 210 215	
tac tac tgc cag cag cac tac cgg acc cca cca acc ttc gga cag gga	3840
Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro Pro Thr Phe Gly Gln Gly	
220 225 230	
acc aag gtg gag atc aag gccacgtgcc ctccatgtcc agccccgaa	3888
Thr Lys Val Glu Ile Lys	
235 240	
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ttcgagcaga catgataaga tacattgatg agtttgaca aaccacaact agaatgcagt	4608
gaaaaaatg ctttatttgt gaaatttgtg atgctattgc tttatttga accattataa	4668
gctgcaataa acaagttaac aacaacaatt gcattcattt tatgtttcag gttcaggggg	4728
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ttataaggga ttttgccgat ttcggcctat tggttaaaa atgagctgat ttaacaaaa	5568
tttaacgcga attttaacaa aatattaacg cttacaattt aggtggcact tttcggggaa	5628

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atgtgcgcgg aaccctatt tgtttatfff tctaaataca ttcaaatacg tatccgctca 5688
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<210> SEQ ID NO 41

<211> LENGTH: 129

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

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<400> SEQUENCE: 41

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 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
 100 105 110
 Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125

Ser

<210> SEQ ID NO 42

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 42

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
 20 25 30
 Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
 85 90 95
 Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 43

<211> LENGTH: 7782

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Plasmid carrying TCN032 and Fi6 monoclonal antibodies

<220> FEATURE:

<221> NAME/KEY: repeat_region

<222> LOCATION: (14)..(143)

<220> FEATURE:

<221> NAME/KEY: polyA_signal

<222> LOCATION: (204)..(252)

<223> OTHER INFORMATION: synthetic polyA

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (261)..(267)

<223> OTHER INFORMATION: stop cassette (complement)

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (268)..(588)
<223> OTHER INFORMATION: constant light (on complementary strand)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (967)..(971)
<223> OTHER INFORMATION: Kozak (located on complementary strand)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (972)..(1019)
<223> OTHER INFORMATION: c-myc 5' UTR (located on complementary strand)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1026)..(1094)
<223> OTHER INFORMATION: CMV\mp2
<220> FEATURE:
<221> NAME/KEY: enhancer
<222> LOCATION: (1026)..(1094)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1564)..(1689)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1696)..(1743)
<223> OTHER INFORMATION: c-myc 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1744)..(1748)
<223> OTHER INFORMATION: Kozak
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1749)..(1805)
<223> OTHER INFORMATION: leader
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1806)..(2165)
<223> OTHER INFORMATION: TCN032 variable heavy
<220> FEATURE:
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<222> LOCATION: (1845)..(4974)
<223> OTHER INFORMATION: inverted terminal repeat
<220> FEATURE:
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<222> LOCATION: (1845)..(4974)
<223> OTHER INFORMATION: inverted terminal repeat (located on complement)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2166)..(2459)
<223> OTHER INFORMATION: CH1
<220> FEATURE:
<221> NAME/KEY: misc
<222> LOCATION: (2166)..(2459)
<223> OTHER INFORMATION: CH1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2460)..(3152)
<223> OTHER INFORMATION: hinge-CH2'-CH3'
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3153)..(3164)
<223> OTHER INFORMATION: furin cleavage site
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3165)..(3236)
<223> OTHER INFORMATION: F2A linker
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3239)..(3296)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3239)..(3296)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3297)..(3683)
<223> OTHER INFORMATION: FI6 VH
<220> FEATURE:
<221> NAME/KEY: CDS

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<222> LOCATION: (3684)..(4004)
 <223> OTHER INFORMATION: CH1
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (4005)..(4673)
 <223> OTHER INFORMATION: CH2-3
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (4674)..(4680)
 <223> OTHER INFORMATION: Stop cassette
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (4674)..(4680)
 <220> FEATURE:
 <221> NAME/KEY: polyA_signal
 <222> LOCATION: (4693)..(4770)
 <223> OTHER INFORMATION: TKpAshort
 <220> FEATURE:
 <221> NAME/KEY: rep_origin
 <222> LOCATION: (5151)..(5606)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (5737)..(6594)
 <223> OTHER INFORMATION: Amp-R
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (6768)..(7356)
 <223> OTHER INFORMATION: col\E1\origin

<400> SEQUENCE: 43

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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac      180
gtagccatgc tctaggaaga tctcacacaa aaaaccaaca cacagatgta atgaaaataa      240
agatatatta ttgcccgcgc tttatcagca ctctccggcg ttgaagctct tggtcactgg      300
gtgctcagtc ccctggtggg tcacctcgca ggcgtacacc ttgtgcttct cgtaatcggc      360
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gctgaaccgg cttggcactc cgtctcgcag tccgctggcg gcgctgatca gtccccttgg      780
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gcaggtgatg gtcacccgat ctcccacgct ggcgctcagg ctgcttgggc tctgggtcat      900
ctggatatcg ctggttggtc ccagggccag gctcagggcg atcagcagca gcagctgcat      960
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aagtgtatca tatgccaaat acgcccccta ttgacgtcaa tgacggtaaa tggccccgct     1380
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agatccgctg ctagecgggca ctttgactg gaacttaca caccgagca aggacgcgac	1740
tctccaccat gcgcatgcag ctgctgctgc tgatcgccct gagcctggcc ctggtgacca	1800
acagc cag gtg cag ctg cag gag agc gga cca gga ctg gtg aag cca agc	1850
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser	
1 5 10 15	
gag acc ctg agc ctg acc tgc acc gtg agc gga agc agc atc agc aac	1898
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn	
20 25 30	
tac tac tgg agc tgg atc cgg cag agc cca gga aag gga ctg gag tgg	1946
Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp	
35 40 45	
atc gga ttc atc tac tac gga gga aac acc aag tac aac cca agc ctg	1994
Ile Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu	
50 55 60	
aag agc cgg gtg acc atc agc cag gat acc agc aag agc cag gtg agc	2042
Lys Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser	
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ctg acc atg agc agc gtg acc gcc gcc gag agc gcc gtg tac ttc tgc	2090
Leu Thr Met Ser Ser Val Thr Ala Ala Glu Ser Ala Val Tyr Phe Cys	
80 85 90 95	
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Ala Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly	
100 105 110	
cag gga acc ctg gtg acc gtg agc agc gcg tcg acc aag gga cct tcg	2186
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
115 120 125	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	2234
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
130 135 140	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	2282
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
145 150 155	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	2330
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
160 165 170 175	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	2378
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
180 185 190	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	2426
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	
195 200 205	
aag ccc agc aac acc aag gtg gac aag aaa gtt gaa cca aag agc tgc	2474
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	
210 215 220	
gac aag acc cac acg tgt ccc ccc tgc cct gcc cct gaa ctg ctg gga	2522
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly	
225 230 235	
ggc ccc agc gtg ttc ctg ttc ccc cca aag ccc aag gac acc ctg atg	2570
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	
240 245 250 255	
atc agc cgg acc ccc gaa gtg acc tgc gtg gtg gtg gac gtg tcc cac	2618
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His	
260 265 270	

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gag gac cct gaa gtg aag ttt aat tgg tac gtg gac ggc gtg gaa gtg	2666
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
275 280 285	
cac aac gcc aag acc aag ccc aga gag gaa cag tac aac agc acc tac	2714
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
290 295 300	
cgg gtg gtg tcc gtg ctg acc gtg ctg cac cag gac tgg ctg aac ggc	2762
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
305 310 315	
aaa gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gcc ccc atc	2810
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile	
320 325 330 335	
gag aaa acc atc agc aag gcc aag ggc cag ccc cgc gag cct cag gtc	2858
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
340 345 350	
tac aca ctg ccc ccc agc cgg gaa gag atg acc aag aac cag gtg tcc	2906
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser	
355 360 365	
ctg acc tgc ctg gtc aag ggc ttc tac ccc agc gac atc gcc gtg gaa	2954
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu	
370 375 380	
tgg gag agc aac ggc cag ccc gag aac aac tac aag acc acc ccc cct	3002
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
385 390 395	
gtg ctg gac agc gac ggc tca ttc ttc ctg tat agc aag ctg acc gtg	3050
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
400 405 410 415	
gac aag agc cgg tgg cag cag ggc aac gtg ttc agc tgc agc gtg atg	3098
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
420 425 430	
cac gag gcc ctg cac aac cac tac acc cag aag tcc ctg agc ctg agc	3146
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
435 440 445	
ccc ggc agaaagcggg gagccccgt gaagcagacc ctgaacttcg acctgctgaa	3202
Pro Gly	
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Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala	
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Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln	
475 480 485	
gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc	3461
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala	
490 495 500	
aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc	3509
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser	
505 510 515 520	
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Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg	
525 530 535	
gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg	3605
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg	
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cattaactac aaggaacccc tagtgatgga gttggcact ccctctctgc gcgctcgctc	4893
gctcactgag gccgggagac caaaggctgc ccgacgccg ggctttgcc gggcggcctc	4953
agtgagcgag cgagcgcgca gccttaatta acctaattca ctggcctcg ttttacaacg	5013
tcgtgactgg gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt	5073
cgccagctgg cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag	5133
cctgaatggc gaatgggacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt	5193
tacgcgcagc gtgaccgcta cacttgccag cgcctagcg cccgctcctt tcgctttctt	5253
cccttccttt ctgcccagct tcgcccgtt tccccgtcaa gctctaaatc gggggctccc	5313
tttagggttc cgatttagtg ctttacggca cctcgacccc aaaaaacttg attaggggta	5373
tggttcacgt agtgggcat cgccctgata gacggttttt cgcccttga cgttggagtc	5433
cacgttcttt aatagtggac tcttgttcca aactggaaca aactcaacc ctatctcggc	5493
ctattctttt gatttataag ggattttgcc gatttcggcc tattggtaa aaaatgagct	5553
gatttaacaa aaatttaacg cgaattttaa caaaatatta acgcttaciaa tttaggtggc	5613
acttttcggg gaaatgtgcg cggaaccctt atttgtttat ttttctaat acattcaaat	5673
atgtatccgc tcatgagaca ataaccctga taaatgcttc aataatattg aaaaggaag	5733
agt atg agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala 910 915 920	5781
gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa gta Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val 925 930 935	5829
aaa gat gct gaa gat cag ttg ggt gca cga gtg ggt tac atc gaa ctg Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu 940 945 950 955	5877
gat ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg 960 965 970	5925
ttt cca atg atg agc act ttt aaa gtt ctg cta tgt ggc gcg gta tta Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu 975 980 985	5973
tcc cgt att gac gcc ggg caa gag caa ctc ggt cgc cgc ata cac tat Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr 990 995 1000	6021
tct cag aat gac ttg gtt gag tac tca cca gtc aca gaa aag cat Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His 1005 1010 1015	6066
ctt acg gat ggc atg aca gta aga gaa tta tgc agt gct gcc ata Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile 1020 1025 1030	6111
acc atg agt gat aac act gcg gcc aac tta ctt ctg aca acg atc	6156

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actttatgct tccggctcgt atgttggtg gaattgtgag cggataacaa tttcacacag 7744
 gaaacagcta tgaccatgat tacgccagat ttaattaa 7782

<210> SEQ ID NO 44
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 44

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser Leu
 65 70 75 80
 Thr Met Ser Ser Val Thr Ala Ala Glu Ser Ala Val Tyr Phe Cys Ala
 85 90 95
 Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 45
 <211> LENGTH: 98
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val

<210> SEQ ID NO 46
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 46

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

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1	5	10	15												
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
		20						25					30		
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75					80
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				85					90					95	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100						105					110		
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120						125		
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr
	130					135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
145					150					155					160
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly									
225					230										

<210> SEQ ID NO 47

<211> LENGTH: 129

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 47

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Ser	Tyr	Asp	Ala	Asn	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Asp	Ser	Gln	Leu	Arg	Ser	Leu	Leu	Tyr	Phe	Glu	Trp	Leu	Ser
			100					105					110		
Gln	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			

Ser

-continued

<210> SEQ ID NO 48
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

 <400> SEQUENCE: 48

 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 100 105

<210> SEQ ID NO 49
 <211> LENGTH: 223
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Construct

 <400> SEQUENCE: 49

 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 1 5 10 15
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 20 25 30
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
 35 40 45
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 50 55 60
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 65 70 75 80
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 85 90 95
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 100 105 110
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 115 120 125
 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 130 135 140
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 145 150 155 160
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 165 170 175
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 180 185 190
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu

a 3' AAV ITR, and

wherein the encoded immunoglobulin chains form the at least two functional monospecific antibodies and wherein the at least two expressed monospecific antibodies have different specificities.

2. The method according to claim 1, wherein the recombinant AAV comprises a bidirectional enhancer located between the first expression cassette and the second expression cassette.

3. The method according to claim 1, wherein at least one of the immunoglobulin chains contain modified Fc coding sequences.

4. The method according to claim 1, wherein the linker in the second cassette comprises a linker selected from an IRES or an F2A.

5. The method according to claim 1, wherein the regulatory control sequences for the first expression cassette and/or the second cassette comprise a minimal promoter.

6. The method according to claim 1, wherein the regulatory control sequences for the first expression cassette and/or the second expression cassette comprise a minimal or synthetic polyA.

7. The method according to claim 1, wherein the first expression cassette further encodes a linker and a fourth immunoglobulin chain.

8. The method according to claim 1, wherein each of the immunoglobulin chain comprises an scFv.

9. The method according claim 1, wherein the vector comprises a bidirectional polyA between the first expression cassette and the second expression cassette.

10. The method according to claim 1, wherein the first expression cassette comprises an enhancer and a minimal promoter.

11. The method according to claim 1, wherein the second expression cassette comprises an enhancer and a minimal promoter.

12. The method according to claim 1, wherein the first and second expression cassettes together express two F(ab')₂.

13. The method according to claim 1, wherein the at least two expressed monospecific antibodies are independently selected from a monoclonal antibody, an immunoadhesin, a Fab, a bifunctional antibody, and combinations thereof.

14. The method according to claim 1, wherein the immunoglobulin chains are an immunoglobulin light chain, a first immunoglobulin heavy chain, and a second immunoglobulin heavy chain, wherein the first expressed monospecific antibody comprises the immunoglobulin light chain and the first immunoglobulin heavy chain, and wherein the second expressed monospecific antibody comprises the immunoglobulin light chain and the second immunoglobulin heavy chain.

15. The method according to claim 14, wherein the first expression cassette encodes an antibody light chain, the second expression cassette encodes a first antibody heavy chain and a second antibody heavy chain, whereby the expressed functional antibodies have two different heavy chains with different specificities which share the light chain.

16. The method according to claim 14, wherein the first expression cassette encodes a first antibody heavy chain, the second expression cassette encodes an antibody light chain and a second antibody heavy chain, whereby the expressed functional antibodies have two different heavy chains with different specificities which share the light chain.

17. The method according to claim 1, wherein the recombinant AAV expresses a first monoclonal antibody having a first specificity, a second monoclonal antibody having a specificity different from the first monoclonal antibody, and a bispecific antibody.

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