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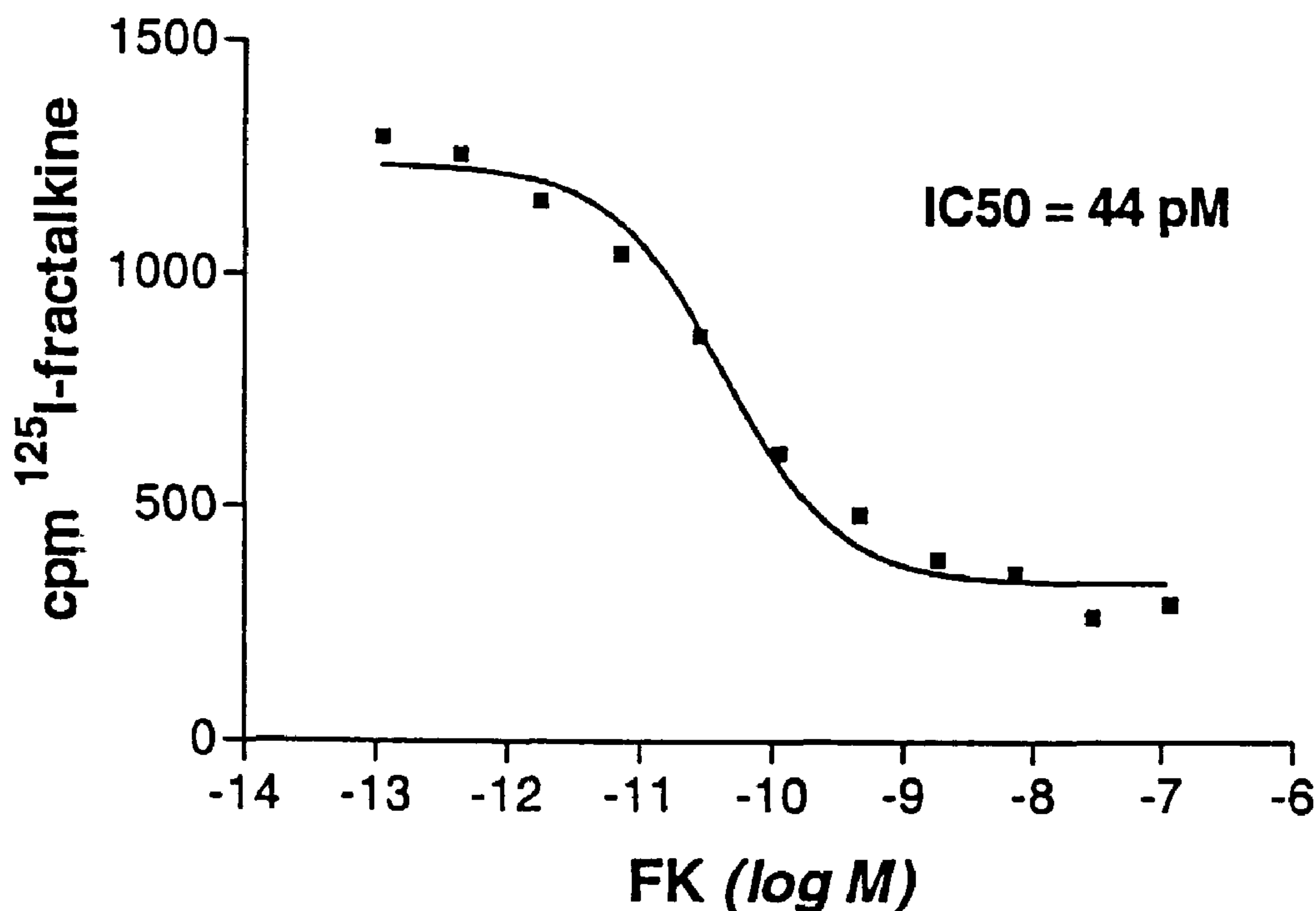
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Fractalkine Homologous Competition on Rh-CMV Infected Fibroblasts



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The invention provides methods and compositions for inhibiting CMV infection and dissemination in an animal, as well as in vitro and in vivo assay systems for identifying such compositions.

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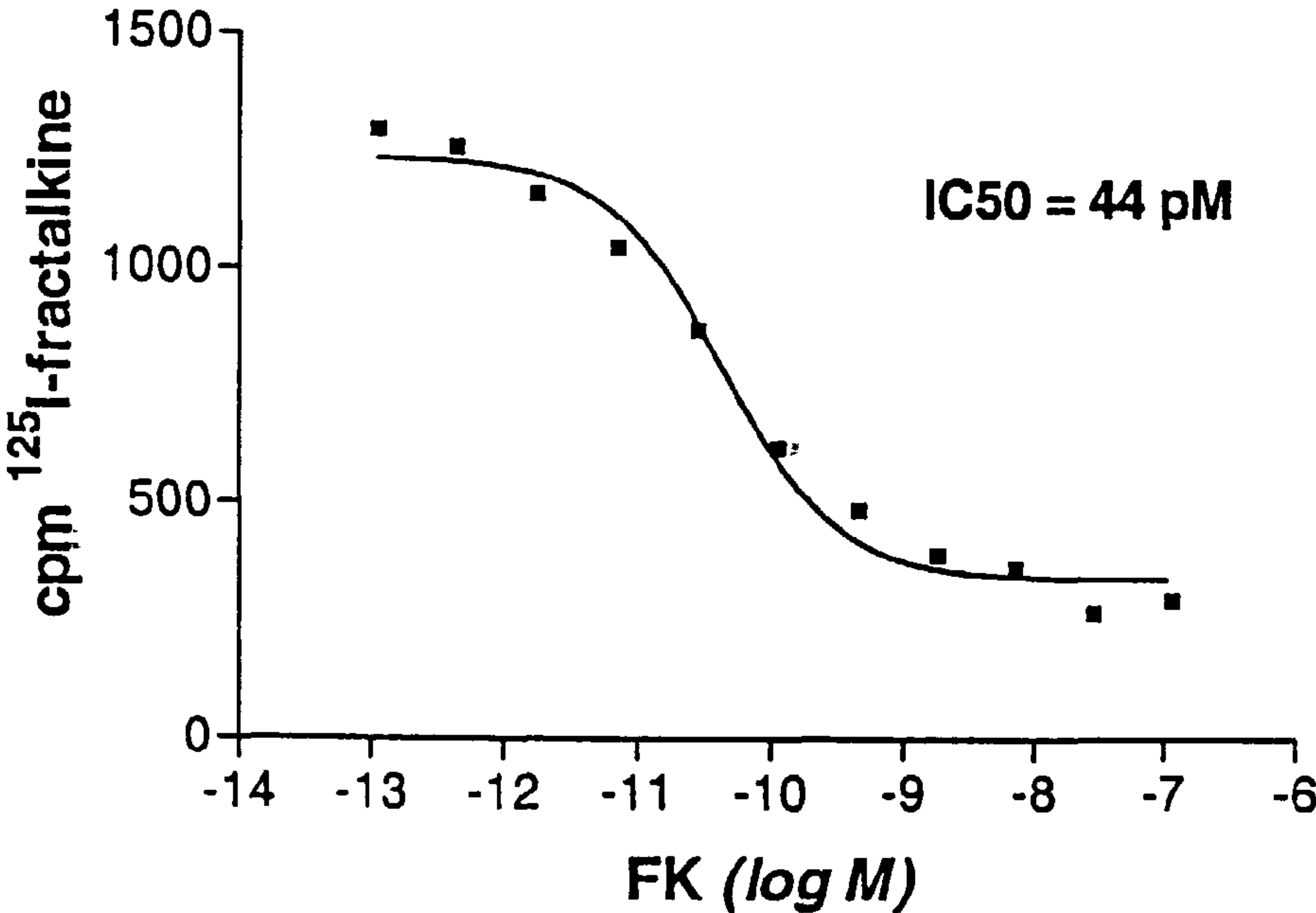
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(54) Title: INHIBITION OF CMV INFECTION AND DISSEMINATION

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and US, respectively), each of which is flanked by inverted repetitions. The entire HCMV genome has been sequenced (Chee, M.S., *et al.* (1990) *Curr. Top. Microbiol. Immunol.* 154:125-169) and appears to contain over 200 open reading frames.

One of these open reading frames is referred to as US28, which encodes a protein (also, "US28") that acts as a functional receptor for certain human and viral chemokines (see, e.g., Gao & Murphy, 1994, *J Biol Chem.* 269:28539-42). Upon infection of a cell by CMV, US28 is expressed on the surface of the infected cell and becomes capable of responding to chemokines in the environment. Three other open reading frames called US27, UL33 and UL78 encode for proteins having homology to US28 as shown in Table 1 below.

Table 1: Exemplary Viral Chemokine Elements and Immune-inhibitory Genes

CMV Chemokine Elements or Immune-inhibitory Genes	GenBank Accession No.	Reference
US27	X17403	Chee et al, 1990, <i>Nature</i> , 344:774
US28	L20501, AF073831-35	Neote et al, 1993, <i>Cell</i> , 72:415-25
UL33	X53293	Chee et al, 1990, <i>Nature</i> , 344:774
UL78	X17403	Chee et al, 1990, <i>Nature</i> , 344:774

Chemokine receptors such as US28 generally are G protein coupled receptors. Structurally these receptors have seven transmembrane segments that loop in and out of the cell membrane, as well as an intracellular tail that is coupled to a G protein signal transducing molecular complex.

The chemokines themselves constitute a subgroup of a larger class of signaling proteins and have the ability, among other things, to promote cellular migration (Zlotnik *et al.* (1999) *Crit. Rev. Immunol.* 19:1-47). The chemokines generally are divided into four groups based upon the arrangement of certain cysteine residues within the protein that can form disulfide bonds. One class of chemokines are the beta chemokines which are characterized by having two adjacent cysteines; this structure is referred to in shorthand form simply as CC. The beta chemokines are involved in attraction of monocytes and leukocytes. The alpha chemokines in contrast have a single amino acid separating the two cysteine residues, and thus their structure is designated as CXC. These chemokines are primarily involved in attracting polymorphonuclear cells. The fractalkines constitute a third class of chemokines and tend to be cell bound molecules. The two cysteines in this class

are separated by three amino acid residues, a structure designated as CX3C. This class of chemokines are expressed at high levels in the brain; some evidence indicates that the fractalkines are involved in neuron-glial cell interactions (see, e.g., Harrison, *et al.* (1998) *Proc. Natl. Acad. Sci. U.S.A.* 95:10896-10901; and Nishiyori, A. *et al.* (1998) *FEBS Lett.* 429:167-172). The structure of the final class of chemokines is simply referred to as C, because these chemokines contain only a single cysteine involved in a disulfide bond. The chemokine receptors have varying specificity for the different classes of chemokines. Some chemokine receptors can bind chemokines from different classes.

The US28 receptor of HCMV is characterized in part by its very strong affinity for fractalkine. It is unclear, however, whether this interaction is involved in the dissemination of the virus from the primary site of infection to other secondary sites. In fact, there is very little known concerning the mechanism by which HCMV is disseminated. Insight into this issue has been hampered primarily by the lack of assay systems, particularly *in vivo* assay systems, which are good models of viral dissemination in humans. Similarly, the lack of appropriate assay systems has hindered identification of inhibitors effective in reducing the spread of CMV infection.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1A shows the polynucleotide sequence of the US28 coding sequence (SEQ ID NO:1) and Figure 1B shows the amino acid sequence for the corresponding US28 polypeptide (SEQ ID NO:2). The extracellular domain is underlined.

Figure 2 is a sequence comparison of the amino acid sequences for human US28 (AD169) (upper sequence), rhesus US28.1 (second sequence), rhesus US28.2 (third sequence), rhesus US28.3 (fourth sequence), rhesus US28.3 (fourth sequence), rhesus US28.4 (fourth sequence) and rhesus US28.5 (bottom sequence). Regions of sequence similarity are indicated in the boxed regions as determined using the sequence comparison program, SeqVu, from the Garvan Institute, Sydney, Australia. Shaded regions correspond to regions of similar hydrophilicity or hydrophobicity as determined by the SeqVu program.

Figure 3 is a sequence comparison of the amino acid sequences for human UL78 [strain AD169 (Genebank Accession # X17403, see, e.g., Chee et al., 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169] (upper sequence) and rhesus UL78 (lower sequence). Regions of sequence similarity are indicated in the boxed regions as determined using the comparison program SeqVu, from the Garvan Institute, Sydney, Australia, with

shaded regions corresponding to regions of similar hydrophilicity or hydrophobicity as determined by the same program.

Figure 4 is a sequence comparison of the amino acid sequences for human UL33 [Genebank Accession # X17403; see, e.g., Chee et al., 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169] (upper sequence), human UL33 spliced (second sequence), rhesus UL33 (third sequence) and rhesus UL33 (lower sequence). Regions of sequence similarity are indicated in the boxed regions as determined using the comparison program SeqVu, from the Garvan Institute, Sydney, Australia; regions of similar hydrophilicity or hydrophobicity as determined by the same program are shaded.

Figure 5 is a binding plot showing fractalkine binding to human CMV virions.

Figure 6 is a binding plot showing fractalkine binding to rhesus dermal fibroblast cell infected with rhCMV.

Figure 7 is a binding plot showing fractalkine binding to human and rhCMV virions.

SUMMARY

Provided herein are compositions and prophylactic and therapeutic methods for reducing CMV dissemination in animals, particularly by interfering with the activity, function or expression of US28 or a US28 homolog. Screening methods to identify agents effective in such methods are also disclosed. These screening methods can include both *in vitro* and *in vivo* approaches.

The current inventors have unexpectedly found that strains of CMV that infect rhesus monkeys (rhCMV) include multiple open reading frames that encode US28 homologs. A group of five US28 homologs with direct homology to US28 are referred to herein as rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4 and rhUS28.5. Certain other US28 homologs have homology to the human US28 homologs UL33 and UL78, and thus are referred to as rhUL33 and rhUL78. Still other US28 homologs are splice variants of the foregoing reading frames. One such splice variant is a splice variant of rhUL33 and is referred to as rhUL33 spliced. Collectively, this group of eight exemplary US28 homologs are referred to as rhUS28 homologs.

Thus, isolated and recombinant nucleic acids that encode an entire US28 homolog or a variant or fragment which retains US28 activity are provided herein. More specifically, certain such nucleic acids include isolated, purified or recombinant nucleic acids

that encode a protein that is a US28 homolog, wherein the protein has an amino acid sequence at least 75% identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26 over a region at least 40 amino acids in length and binds a chemokine. Amino acid sequence identity can be compared, for example, using the BLASTP algorithm with a wordlength (W) of 3 and the BLOSUM62 scoring matrix. Certain nucleic acids encode a protein that has an amino acid sequence selected from the group of SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26. Specific examples of nucleic acids encoding rhUS28 homologs are the nucleic acids with a sequence as set forth in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25. Other nucleic acids include the foregoing nucleic acids that are operably linked to a promoter.

Also provided are vectors that contain the nucleic acids described herein and cells harboring such vectors.

Isolated proteins or recombinantly produced proteins encoded by rhUS28 homologs, or fragments or variants that retain a US28 activity (e.g., chemokine binding), are also disclosed herein. Certain such proteins include isolated or recombinant proteins comprising an amino acid sequence at least 75% identical to an amino acid sequence as set forth in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 or 26 over a region at least 40 amino acids in length, wherein the protein binds a chemokine. One example of a program that can be used to compare amino acid sequence identity is the BLASTP algorithm with a wordlength (W) of 3 using the BLOSUM62 scoring matrix. Certain of the proteins provided herein are encoded by a nucleic acid segment that hybridizes under stringent conditions to a nucleic acid having a sequence selected from the group consisting of SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25. Fragments of the full length protein are also provided which retain an activity of US28 (e.g., chemokine binding, such as ability to bind fractalkine). Certain such fragments are isolated proteins comprising at least 12 amino acids from one of the sequences set forth in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 or 26.

A variety of screening methods for identifying agents that reduce CMV dissemination in various human and non-human animals are also disclosed herein. Certain of these screening methods involve determining whether the agent inhibits the expression or activity of US28 or a US28 homolog, or a fragment or a variant of US28 or the US28 homolog. In some of these methods the US28 homolog is selected from the group consisting of human UL33, human UL33 spliced, human UL78, rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, rhUL33 spliced and rhUL78.

The screening methods can be conducted in cell-free, cell-based and *in vivo* formats. Certain *in vitro* methods involve contacting a chemokine and US28, the US28 homolog, the fragment or the variant, in the presence of a test agent and determining whether the agent inhibits binding between the chemokine and US28, the US28 homolog, the fragment or the variant. Such methods are typically conducted with a CX3C chemokine such as fractalkine or a CC chemokine such as MIP-1 α , MIP-1 β , MCP-1, eotaxin, vMIP-2 and RANTES. The agent being tested can be of a variety of different types including antibodies that specifically bind to US28, a US28 homolog or variants or fragments of US28 or the US28 homolog or a small molecule.

Cell based screening assays typically involve contacting a cell expressing US28, a US28 homolog, or a fragment or a variant of US28 or the US28 homolog, with a chemokine in the presence of a test agent and determining whether the agent inhibits binding between the chemokine and US28, the US28 homolog, the fragment or the variant. The cells in such assays can be infected with CMV or transfected with one of the nucleic acids provided herein which encodes for US28 or a US28 homolog or at least a fragment thereof (e.g., a nucleic acid that encodes at least 10 contiguous amino acids as set forth in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24 or 26).

The finding that rhCMV encodes US28 homologs means that *in vivo* assays can be conducted using rhesus monkeys. Previously, a good mammal model system for CMV dissemination was unavailable because CMV strains that infect certain other mammals such as rats and mice do not encode US28 homologs. Certain *in vivo* assays involve administering the agent to a non-human animal infected with CMV and determining whether the agent inhibits the dissemination of CMV from a primary site of infection in the non-human animal. The assays generally are conducted with a rhesus monkey infected with rhCMV.

In addition to the screening methods, a variety of prophylactic and therapeutic treatment methods are provided. These methods can be utilized to treat both human or non-human animals (e.g., rhesus monkeys) infected with CMV or at risk of infection by CMV. In general, the treatment methods typically involve administering to the animal an agent that interferes with the expression or activity of a target nucleic acid encoding US 28 or a US28 homolog. Certain treatment methods involves administering an agent that causes a reduction in expression of the target nucleic acid in cells of the animal. Such reduction can be achieved by administering an antisense nucleic acid that specifically

hybridizes to the target nucleic acid or a ribozyme that specifically recognizes the target nucleic acid.

In other treatment methods, the activity of US28 or the US28 homolog is inhibited by administering an agent that inhibits the binding of a ligand to US28 or the US28 homolog. Suitable agents for achieving this include, for example, an antibody that specifically binds to US28 or the US28 homolog or various small molecules.

Pharmaceutical compositions for treating CMV infections either therapeutically or prophylactically are also included. The active ingredients in such compositions can be identified, for example, through the various screening methods described herein. Other compositions are vaccines.

Certain vaccines include an immunogenic CMV polypeptide which is encoded by at least a region of a CMV genome in which the polynucleotide segment encoding US28 or a US28 homolog has been inactivated; and a pharmaceutically acceptable carrier. With some such vaccines, the immunogenic CMV polypeptide is an HCMV polypeptide encoded by at least a region of an HCMV genome in which the polynucleotide segment encoding US28, human UL33 and/or UL78 has been inactivated.

In other vaccines, the immunogenic CMV polypeptide is a rhCMV polypeptide encoded by at least a region of a rhCMV genome in which a polynucleotide segment encoding rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, or rhUL78 has been inactivated.

DETAILED DESCRIPTION

I. Definitions

As used in this specification and the appended claims, the singular forms “a,” “an” and “the” include plural references unless the content clearly dictates otherwise.

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton *et al.*, DICTIONARY OF MICROBIOLOGY AND MOLECULAR BIOLOGY (2d ed. 1994); THE CAMBRIDGE DICTIONARY OF SCIENCE AND TECHNOLOGY (Walker ed., 1988); THE GLOSSARY OF GENETICS, 5TH ED., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, THE HARPER COLLINS DICTIONARY OF BIOLOGY (1991).

Various biochemical and molecular biology methods are well known in the art. For example, methods of isolation and purification of nucleic acids are described in detail in WO 97/10365, WO 97/27317, Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation, (P. Tijssen, ed.) Elsevier, N.Y. (1993); Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part 1. Theory and Nucleic Acid Preparation, (P. Tijssen, ed.) Elsevier, N.Y. (1993); and Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, N.Y., (1989); and Current Protocols in Molecular Biology, (Ausubel, F.M. et al., eds.) John Wiley & Sons, Inc., New York (1987-1999), including supplements such as supplement 46 (April 1999).

As used herein, the following terms have the meanings ascribed to them unless specified otherwise:

As used herein, the term "cytomegalovirus (CMV)" has the normal meaning in the art and refers to one of a family of double stranded DNA viruses of the betaherpes group with positional and genomic similarity to human herpes virus 5 (cytomegalovirus) including, without limitation, human CMV AD169 (ATCC # VR 538), human CMV Towne (ATCC # VR 977), human CMV Davis (ATCC # VR 807), human CMV Toledo (Quinnan et al, 1984, *Ann Intern Med* 101: 478-83), monkey CMV Rh68.1 (ATCC # VR 677), monkey CMV CSG (ATCC # VR 706), rat CMV Priscott (ATCC # VR 991), mouse CMV Smith (ATCC # VR 1399) and others, such as various other mammals, for example. "ATCC" is the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, USA. The 230-kb dsDNA genome of human and murine CMV were sequenced (see, e.g., Chee *et al.*, 1990, *Curr. Top. Microbiol. Immunol.* 154:125-169; also see Rawlinson, 1996, *J Virol.* 70:8833-49, both incorporated herein in their entirety).

Various open reading frames from human CMV (HCMV) are referred to herein using the nomenclature of Chee *et al* [e.g., US28, US33, US78 (human US28, human US33, human US78, respectively)]. In general, reference to such reading frames from HCMV also refer to the sequences of sequence and positional homologs of such reading frames found in different HCMV strains, including sequences in any naturally occurring HCMV strain, and mutations to such strains. In some instances the term can also refer to various splice variants not yet characterized in the literature. With respect to the protein, the protein encoded by the HCMV reading frame refers to the protein having a native amino acid

sequence, as well as variants and fragments regardless of origin or mode of preparation.

Thus, for example, US28, US33 and US78 have the following meanings:

“US28” refers to open reading frame 28 in the unique short region of the genome of human strains of CMV and the protein encoded by this reading frame; while US28
5 can refer to either the coding region or the corresponding protein, in some instances the term US28 protein or US28 nucleic acid is used for the sake of increased clarity. Figures 1A and 1B show the nucleotide and amino acid sequences of US28 from one specific strain, namely CMV strain VHL/E (SEQ ID NOS:3 and 4), respectively; GenBank accession no. L20501)). US28 nucleotide and amino acid sequences from a second human CMV strain, the Toledo
10 strain, are set forth in SEQ ID NOS:1 and 2, respectively. This sequence is the same as US28 from human CMV strain AU4.1 (GenBank accession no. AF073831). The term US28 includes other US28 molecules, e.g., derived from other clinical strains of human CMV, that differ slightly in sequence (see, e.g., GenBank accession nos. AF 073832-35; see also M.S. Chee, et al. (1990) *Curr. Top. Microbiol. Immunol.* 154:125-69).

15 With respect to the protein, the term US28 refers to a protein having a native US28 amino acid sequence, as well as variants and fragments regardless of origin or mode of preparation. A US28 protein having a native amino acid sequence has the same amino acid sequence as a US28 as obtained from nature (i.e., a naturally occurring US28). The amino acid sequence for US28 from the VHL/E strain shown in FIG. 1B (SEQ ID NO:4) is one
20 specific example of a naturally occurring US28. US28 from the Toledo strain is another example of a protein having a native amino acid sequence (SEQ ID NO:2). Native US28 proteins can be isolated from nature or can be prepared using standard recombinant and/or synthetic methods. A native sequence US28 includes proteins following post-translational modifications such as glycosylation or phosphorylation of certain amino acid residues.

25 The term “UL33” or “human UL33” refers to open reading frame 33 of the unique region of the genome of human strains of CMV and proteins encoded by this reading frame. The nucleotide and amino acid sequences for an exemplary UL33 are set forth in SEQ ID NOS:19 and 20, respectively. The term also includes various splice variants. For example, the term can include the splice variant having the nucleotide and amino acid
30 sequences of SEQ ID NOS:21 and 22, respectively. Those of skill can identify other such splice variants using programs designed to identify splice variants such as the “Genefinder”, “Genehunt” or “GRAIL” programs available at the CMS Molecular Biology resource found at [www. unl.edu](http://www.unl.edu).

Similarly the term “UL78” refers to the open reading frame 78 of the unique region of the genome of human strains of CMV and proteins encoded by this reading frame. The nucleotide and amino acid sequences for one exemplary UL78 are set forth in SEQ ID NOS:15 and 16, respectively.

5 The term “US28 homolog” refers to a nucleic acid or protein that has sequence homology with US28 and at least one activity of US28, typically the ability to bind a chemokine, especially fractalkine. The US28 homolog can be from CMV native to various animals, including various mammals (e.g., human and non-human primates, specifically monkeys, chimpanzee, gorilla, baboon and humans). Thus, US28 homologs can include, but
10 are not limited to, human US27, human UL33, and human UL78. Additional homologs from rhesus monkey (*macaca mulatta*) CMV can include rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33 and rhUL78.

 The terms “nucleic acid” “polynucleotide” and “oligonucleotide” are used interchangeably herein and refer to a deoxyribonucleotide or ribonucleotide polymer in either
15 single- or double-stranded form, and unless otherwise limited, encompasses known analogues of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally-occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence includes the complementary sequence thereof. A “subsequence” or “segment” refers to a sequence of nucleotides that comprise a part of a longer sequence of nucleotides.

20 A “primer” is a single-stranded polynucleotide capable of acting as a point of initiation of template-directed DNA synthesis under appropriate conditions (*i.e.*, in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer
25 but typically is at least 7 nucleotides long and, more typically range from 10 to 30 nucleotides in length. Other primers can be somewhat longer such as 30 to 50 nucleotides long. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template but must be sufficiently complementary to hybridize with a template. The term “primer site”
30 or “primer binding site” refers to the segment of the target DNA to which a primer hybridizes. The term “primer pair” means a set of primers including a 5' “upstream primer” that hybridizes with the complement of the 5' end of the DNA sequence to be amplified and a

3' "downstream primer" that hybridizes with the 3' end of the sequence to be amplified.

The term "complementary" means that one nucleic acid is identical to, or hybridizes selectively to, another nucleic acid molecule. Selectivity of hybridization exists when hybridization occurs that is more selective than total lack of specificity. Typically, selective hybridization will occur when there is at least about 55% identity over a stretch of at least 14-25 nucleotides, preferably at least 65%, more preferably at least 75%, and most preferably at least 90%. Preferably, one nucleic acid hybridizes specifically to the other nucleic acid. See M. Kanehisa, *Nucleic Acids Res.* 12:203 (1984).

A "native sequence" refers to the sequence of a naturally occurring nucleic acid or a protein, and includes allelic variants (and proteins encoded thereby) that may occur in nature.

The term "variant" when used in connection with a protein (e.g., US28 or US28 homolog) means proteins that are functional equivalents to a native sequence protein in that the protein has a similar sequence to the native sequence protein and retains, to some extent, one or more of the activities of the native protein. With US28 and the US28 homologs, an activity of the native protein can include, but is not limited to, the ability to bind to chemokines (e.g., fractalkine), immunological cross reactivity with antibodies that specifically bind to a native sequence US28 or US28 homolog (i.e., the fragment competes with the full-length US28); and immunogenicity (e.g., the protein retains an epitope that stimulates B- or T-cell responses against the protein). Preferred functional equivalents retain all of the activities of the native protein, although the activity of such equivalent proteins can be stronger or weaker when compared on a quantitative basis. Typically, functional equivalents have activities that are within 1% to 10,000% of the activity of a native sequence protein, while other functional equivalents have activities that are 10% to 1000%, or 50% to 500% of that of a native sequence protein.

Variants also include proteins having amino acid alterations such as deletions, insertions and/or substitutions. A "deletion" refers to the absence of one or more amino acid residues in the related protein. The term "insertion" refers to the addition of one or more amino acids in the related protein. A "substitution" refers to the replacement of one or more amino acid residues by another amino acid residue in the polypeptide. Typically, such alterations are conservative in nature such that the activity of the variant protein is substantially similar to a protein having a native sequence (see, e.g., Creighton (1984)

Proteins, W.H. Freeman and Company). In the case of substitutions, the amino acid replacing another amino acid usually has similar structural and/or chemical properties. Insertions and deletions are typically in the range of 1 to 5 amino acids, although depending upon the location of the insertion, more amino acids can be inserted or removed. Variants also include modified forms of a native sequence protein. Modified forms of proteins generally refer to proteins in which one or more amino acids of a native sequence US28 have been altered to a non-naturally occurring amino acid residue. Such modifications can occur during or after translation and include, but are not limited to, phosphorylation, glycosylation, cross-linking, acylation and proteolytic cleavage.

Variants can be prepared using methods known in the art such as site-directed mutagenesis (Carter, et al. (1986) Nucl. Acids Res. 13:4331; Zoller et al. (1987) Nucl. Acids Res. 10:6487), cassette mutagenesis (Wells et al. (1985) Gene 34:315), restriction selection mutagenesis (Wells, et al. (1986) Philos. Trans. R. Soc. London SerA 317:415), and PCR mutagenesis (Sambrook, et al. (1989) Molecular Cloning, Cold Spring Harbor Laboratory Press).

A "fragment" when used in reference to a protein refers to a subsequence of the native protein that retains one or more activities of the native sequence protein. As indicated *supra*, with respect to US28 and its homologs, such activities include, for example, the ability to bind to chemokines, the ability to bind to an antibody that specifically binds to the full-length US28 or US28 homolog; and immunogenicity.

The term "operably linked" refers to functional linkage between a nucleic acid expression control sequence (such as a promoter, signal sequence, or array of transcription factor binding sites) and a second polynucleotide, wherein the expression control sequence affects transcription and/or translation of the second polynucleotide.

A "heterologous sequence" or a "heterologous nucleic acid," as used herein, is one that originates from a source foreign to the particular host cell, or, if from the same source, is modified from its original form. Thus, a heterologous gene in a prokaryotic host cell includes a gene that, although being endogenous to the particular host cell, has been modified. Modification of the heterologous sequence can occur, *e.g.*, by treating the DNA with a restriction enzyme to generate a DNA fragment that is capable of being operably linked to the promoter. Techniques such as site-directed mutagenesis are also useful for modifying a heterologous nucleic acid.

The term “recombinant” when used with reference to a cell indicates that the cell replicates a heterologous nucleic acid, or expresses a peptide or protein encoded by a heterologous nucleic acid. Recombinant cells can contain genes that are not found within the native (non-recombinant) form of the cell. Recombinant cells can also contain genes found
5 in the native form of the cell wherein the genes are modified and re-introduced into the cell by artificial means. The term also encompasses cells that contain a nucleic acid endogenous to the cell that has been modified without removing the nucleic acid from the cell; such modifications include those obtained by gene replacement, site-specific mutation, and related techniques.

10 A “recombinant expression cassette” or simply an “expression cassette” is a nucleic acid construct, generated recombinantly or synthetically, that has control elements that are capable of affecting expression of a structural gene that is operably linked to the control elements in hosts compatible with such sequences. Expression cassettes include at least promoters and, optionally, transcription termination signals. Typically, the recombinant
15 expression cassette includes at least a nucleic acid to be transcribed (*e.g.*, a nucleic acid encoding US28 or a US28 homolog) and a promoter. Additional factors necessary or helpful in effecting expression can also be used as described herein. For example, transcription termination signals, enhancers, and other nucleic acid sequences that influence gene expression, can also be included in an expression cassette.

20 The term “disabled” or “inactivated” as used herein in the context of a gene sequence (*e.g.*, in a CMV genome), refers to a gene that is mutated, deleted or partially deleted in a coding or regulatory (*e.g.*, promoter) sequence, such that the gene product (*e.g.*, protein) that is encoded by the gene is not expressed or is not expressed in biologically active form.

25 The term “stringent conditions” refers to conditions under which a probe or primer will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence
30 at a defined ionic strength and pH. In other instances, stringent conditions are chosen to be about 20 °C or 25 °C below the melting temperature of the sequence and a probe with exact or nearly exact complementarity to the target. As used herein, the melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half-dissociated into single strands. Methods for calculating the T_m of nucleic acids are well

known in the art (see, *e.g.*, Berger and Kimmel (1987) *Methods in Enzymology*, vol. 152: Guide to Molecular Cloning Techniques, San Diego: Academic Press, Inc. and Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed., vols. 1-3, Cold Spring Harbor Laboratory), both incorporated herein by reference. As indicated by standard references, a
5 simple estimate of the T_m value can be calculated by the equation: $T_m = 81.5 + 0.41(\% G + C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (see *e.g.*, Anderson and Young, "Quantitative Filter Hybridization," in *Nucleic Acid Hybridization* (1985)). Other references include more sophisticated computations which take structural as well as sequence characteristics into account for the calculation of T_m . The melting temperature of a hybrid
10 (and thus the conditions for stringent hybridization) is affected by various factors such as the length and nature (DNA, RNA, base composition) of the probe or primer and nature of the target (DNA, RNA, base composition, present in solution or immobilized, and the like), and the concentration of salts and other components (*e.g.*, the presence or absence of formamide, dextran sulfate, polyethylene glycol). The effects of these factors are well known and are
15 discussed in standard references in the art, see *e.g.*, Sambrook, *supra*, and Ausubel, *supra*. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30 °C for short probes or primers (*e.g.*, 10 to 50 nucleotides) and at least about 60 °C for long probes or primers (*e.g.*, greater than 50
20 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide.

"Polypeptide" and "protein" are used interchangeably herein and include a molecular chain of amino acids linked through peptide bonds. The terms do not refer to a specific length of the product. Thus, "peptides," "oligopeptides," and "proteins" are included
25 within the definition of polypeptide. The terms include post-translational modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like. In addition, protein fragments, analogs, mutated or variant proteins, fusion proteins and the like are included within the meaning of polypeptide.

The terms "identical" or percent "identity," in the context of two or more
30 nucleic acids or polypeptides, refer to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using a sequence comparison algorithm such as those described below for example, or by visual inspection.

The phrase “substantially identical,” in the context of two nucleic acids or polypeptides, refers to two or more sequences or subsequences that have at least 75%, preferably at least 80% or 85%, more preferably at least 90%, 95% or higher nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using a sequence comparison algorithm such as those described below for example, or by visual inspection. Preferably, the substantial identity exists over a region of the sequences that is at least about 40-60 nucleotides or amino acids in length, in other instances over a region at least 60-80 nucleotides or amino acids in length, in still other instances at least 90-100 nucleotides or amino acids in length, and in yet other instances the sequences are substantially identical over the full length of the sequences being compared, such as the coding region of a nucleotide for example.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection [*see generally*, Current Protocols in Molecular Biology, (Ausubel, F.M. et al., eds.) John Wiley & Sons, Inc., New York (1987-1999, including supplements such as supplement 46 (April 1999))]. Use of these programs to conduct sequence comparisons are typically conducted using the default parameters specific for each program.

Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra.*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. For identifying whether a nucleic acid or polypeptide is within the scope of the invention, the default parameters of the BLAST programs are suitable. The BLASTN program (for nucleotide sequences) uses as defaults a word length (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix. The TBLASTN program (using protein sequence for nucleotide sequence) uses as defaults a word length (W) of 3, an expectation (E) of 10, and a BLOSUM 62 scoring matrix. (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.,* Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence. The phrase "hybridizing specifically to" or "specifically

hybridizing to”, refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

A further indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, as described below. The phrases “specifically binds to a protein” or “specifically immunoreactive with,” when referring to an antibody refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, a specified antibody binds preferentially to a particular protein and does not bind in a significant amount to other proteins present in the sample. Specific binding to a protein under such conditions requires an antibody that is selected for its specificity for a particular protein. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. *See, e.g.*, Harlow and Lane (1988) *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

“Conservatively modified variations” of a particular polynucleotide sequence refers to those polynucleotides that encode identical or essentially identical amino acid sequences, or where the polynucleotide does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance, the codons CGU, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are “silent variations,” which are one species of “conservatively modified variations.” Every polynucleotide sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by

standard techniques. Accordingly, each “silent variation” of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

A polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. A “conservative substitution,” when describing a protein, refers to a change in the amino acid composition of the protein that does not substantially alter the protein’s activity. Thus, “conservatively modified variations” of a particular amino acid sequence refers to amino acid substitutions of those amino acids that are not critical for protein activity or substitution of amino acids with other amino acids having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids do not substantially alter activity. Conservative substitution tables providing functionally similar amino acids are well-known in the art. *See, e.g.*, Creighton (1984) *Proteins*, W.H. Freeman and Company. In addition, individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also “conservatively modified variations.”

The term “naturally-occurring” as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism that can be isolated from a source in nature and which has not been intentionally modified by humans in the laboratory is naturally-occurring.

The term “antibody” as used herein includes antibodies obtained from both polyclonal and monoclonal preparations, as well as the following: (i) hybrid (chimeric) antibody molecules (see, for example, Winter *et al.* (1991) *Nature* 349:293-299; and U.S. Patent No. 4,816,567); (ii) F(ab’)₂ and F(ab) fragments; (iii) Fv molecules (noncovalent heterodimers, see, for example, Inbar *et al.* (1972) *Proc. Natl. Acad. Sci. USA* 69:2659-2662; and Ehrlich *et al.* (1980) *Biochem* 19:4091-4096); (iv) single-chain Fv molecules (sFv) (see, for example, Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883); (v) dimeric and trimeric antibody fragment constructs; (vi) humanized antibody molecules (see, for example, Riechmann *et al.* (1988) *Nature* 332:323-327; Verhoeyan *et al.* (1988) *Science* 239:1534-1536; and U.K. Patent Publication No. GB 2,276,169, published 21 September 1994); (vii) Mini-antibodies or minibodies (*i.e.*, sFv polypeptide chains that include oligomerization domains at their C-termini, separated from the sFv by a hinge region; see, *e.g.*, Pack *et al.* (1992) *Biochem* 31:1579-1584; Cumber *et al.* (1992) *J. Immunology* 149B:120-126); and,

(vii) any functional fragments obtained from such molecules, wherein such fragments retain specific-binding properties of the parent antibody molecule.

The phrases “specifically binds” when referring to a protein, “specifically immunologically cross reactive with,” or simply “specifically immunoreactive with” when referring to an antibody, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated conditions, a specified ligand binds preferentially to a particular protein and does not bind in a significant amount to other proteins present in the sample. A molecule or ligand (e.g., an antibody) that specifically binds to a protein has an association constant of at least 10^3 M^{-1} or 10^4 M^{-1} , sometimes 10^5 M^{-1} or 10^6 M^{-1} , in other instances 10^6 M^{-1} or 10^7 M^{-1} , in still other instances 10^8 M^{-1} to 10^9 M^{-1} , and in yet other instances, about 10^{10} M^{-1} to 10^{11} M^{-1} or higher. A variety of immunoassay formats can be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See, e.g., Harlow and Lane (1988) *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

The term “immunogen” has the normal meaning in the art and refers to a molecule that can elicit an adaptive immune response upon injection into a person or animal, typically a peptide, polypeptide, glycoprotein, lipopolysaccharide or glycosaminoglycan. Thus, the term “immunogenic” refers to the ability of a molecule to elicit an adaptive immune response. An “immunogenic polypeptide” is a polypeptide that is an immunogen.

As used herein, an “immune response” has the ordinary meaning in the art and, unless otherwise specified, refers to an adaptive immune response to a specific antigen. In one aspect, an immune response involves the concerted action of lymphocytes, antigen presenting cells, phagocytic cells, and various soluble macromolecules in defending the body against infection or other exposure to non-self molecules. The immune response can be detected and quantified (e.g., following immunization) by measuring cellular or humoral responses according to numerous assays known in the art (see, e.g., Coligan et al., 1991 (suppl. 1999), CURRENT PROTOCOLS IN IMMUNOLOGY, John Wiley & Sons (hereinafter, sometimes “Coligan”)). For example, to detect a cellular immune response, T cell effector effects against cells expressing the antigen are detected using standard assays, e.g., target-cell

killing, macrophage activation, B-cell activation or lymphokine production. Humoral responses are measured by detecting the appearance of, or increase in titer of, antigen-specific antibodies using routine methods such as ELISA. The progress of the antibody response can be determined by measuring class switching (*i.e.*, the switch from an early IgM response to a later IgG response).

The terms “isolated,” or “purified” means an object species (*e.g.*, a US28 protein or nucleic acid) has been purified from at least one other species present in a sample obtained from a natural source. In many instances, the terms mean that the object species is the predominant macromolecular species present (*i.e.*, on a molar basis it is more abundant than any other individual species in the composition), and preferably the object species comprises at least about 50 percent (on a molar basis) of all macromolecular species present. Such compositions are said to be “substantially pure.” Generally, an isolated, purified or substantially pure US28 protein or nucleic acid will comprise more than 80 to 90 percent of all macromolecular species present in a composition. Most preferably, the object species is purified to essential homogeneity (*i.e.*, contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

The term “detectably labeled” means that an agent (*e.g.*, a probe) has been conjugated with a label that can be detected by physical, chemical, electromagnetic and other related analytical techniques. Examples of detectable labels that can be utilized include, but are not limited to, radioisotopes, fluorophores, chromophores, mass labels, electron dense particles, magnetic particles, spin labels, molecules that emit chemiluminescence, electrochemically active molecules, enzymes, cofactors, and enzyme substrates.

The term “epitope” generally refers to that portion of an antigen that interacts with an antibody. More specifically, the term epitope includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Specific binding exists when the dissociation constant for antibody binding to an antigen is $\leq 1\mu\text{M}$, preferably $\leq 100\text{ nM}$ and most preferably $\leq 1\text{ nM}$. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids and typically have specific three-dimensional structural characteristics, as well as specific charge characteristics.

The term “patient” includes human and veterinary subjects.

II. General

Compositions and methods for treating or preventing viral dissemination from cytomegalovirus (CMV) infection are described herein. As indicated supra, as used herein the term "CMV" includes various strains of the virus that infect different animals, including various mammals such as humans and monkeys for example. Strains of CMV that infect humans are referred to as human CMV or simply HCMV. As described in the Background section, the HCMV genome contains an open reading frame designated US28, which encodes a receptor that binds certain human and viral chemokines.

The current inventors have unexpectedly found that the CMV strain that infects monkeys, specifically rhesus monkeys (i.e., rhCMV), includes several US28 homologs. This finding was unexpected for several reasons. First, the genome of CMV strains that infect various other mammals such as mice and rats lack a region encoding for a US28 homolog. Given this absence, one could not have predicted with any degree of certainty that the CMV strain that infects other animals such as monkeys would contain an open reading frame for a US28 homolog. Secondly, in HCMV there appears to be a limited number of proteins related to US28 (e.g., US27, UL33, and UL78). In contrast, rhCMV contains at least five US28 homologs, which the inventors refer to as rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5. Furthermore, the genome of rhCMV contains homologs of UL33 (i.e., rhUL33) and UL78 (i.e., rhUL78). In addition to the unexpectedly large number of US28 homologs in the rhCMV genome, it was also unexpected that as a group these various homologs would have relatively low homology (see Table 2A). Homology of other US28 homologs are shown in Table 2B. There is 29 percent identity between CMV (AD169) UL78 and the rhesus CMV (Rh68.1) UL78 homolog.

Table 2A. Percent identity of human CMV (Toledo) US28 and rhesus CMV (Rh68.1) US28 homologs.

RhUS28.1	RhUS28.2	RhUS28.3	RhUS28.4	RhUS28.5	
21	19	20	21	34	Toledo
	36	37	16	18	RhUS28.1
		33	15	16	RhUS28.2
			15	20	RhUS28.3
				18	RhUS28.4

Table 2B: Percent identity of human CMV (AD169) UL33 and rhesus CMV (Rh68.1) UL33 homologs, and exemplary splice variants.

Human UL33 splice	RhUL33	RhUL33 splice	
100	53.5	52.3	Human UL33
	53.5	51.2	Human UL33 splice
		100	RhUL33

5 The US28 homologs (both the genes and corresponding proteins) disclosed herein can be utilized in the development of a variety of *in vitro* and *in vivo* assays to study CMV pathology and mechanisms of viral dissemination. The absence of a non-human *in vivo* model system has meant that investigations of CMV have been limited only to *in vitro* systems. Thus, the finding that rhCMV encodes US28 homologs is an important advance
10 because it means that studies regarding modes of viral infection and dissemination can be performed using an *in vivo* model system which heretofore was not possible. The assays provided herein can be utilized to identify new agents that can inhibit the dissemination of viruses such as CMV. Such agents can subsequently be formulated as a pharmaceutical composition and used in the prophylactic and/or therapeutic treatment of CMV infections.
15 The *in vivo* system also means that one can rationally design and test CMV vaccines by inactivation or removal of segments of the viral genome thought to be involved in viral dissemination followed by a determination of the effect of such inactivation or removal on viral dissemination. Thus, vaccines against CMV and methods for making such vaccines are also disclosed.

20 Further studies described herein have also demonstrated that HCMV virions (viral particles) express US28 on their surface and that rhCMV virions likewise express one or more US28 homologs on their surface. This finding has important implications regarding viral dissemination given that US28 and US28 homologs bind certain chemokines. In particular, the virus could be transported to, or become anchored at, different locations in
25 the body by attachment to chemokines. Thus, for example, CMV in the blood could become attached to a cell expressing a chemokine such as fractalkine.

III. US28 Homologs – Nucleic Acids

The present inventors have identified a number of segments (open reading frames) of the rhCMV genome that encode US28 homologs; these homologs are referred to herein as rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4 and rhUS28.5. Other US28 homologs contained in the rhCMV genome are related to human UL33 and UL78 and thus are referred to as rhUL33 and rhUL78, respectively. Certain other homologs are splice variants of the foregoing. For example, various nucleic acids are splice variants of rhUL33. One such variant is referred to herein as rhUL33 spliced. Collectively, these eight nucleic acid sequences are referred to herein for the sake of simplicity as “rhesus US28 homologs.” Thus, isolated and/or recombinant nucleic acids that encode the entire length of one of the rhesus US28 homologs or a fragment or variant retaining US28 activity are provided herein. Table 3 below lists the various rhesus CMV homologs and the corresponding nucleotide and protein sequences.

Table 3: Sequence Identifiers for rhCMV Homologs

rhCMV Homolog	Nucleotide Sequence	Amino Acid Sequence
rhUS28.1	SEQ ID NO:5	SEQ ID NO:6
rhUS28.2	SEQ ID NO:7	SEQ ID NO:8
rhUS28.3	SEQ ID NO:9	SEQ ID NO:10
rhUS28.4	SEQ ID NO:11	SEQ ID NO:12
rhUS28.5	SEQ ID NO:13	SEQ ID NO:14
rhUL78	SEQ ID NO:17	SEQ ID NO:18
rhUL33	SEQ ID NO:23	SEQ ID NO:24
rhUL33 spliced	SEQ ID NO:25	SEQ ID NO:26

As described in greater detail below in Example 2, these sequences were identified by sequencing the entire rhCMV genome and then analyzing the resulting sequence for segments having homology to human US28 using the BLAST X program, as well as the BioNavigator bio-informatic program set (see Example 2 for additional details). The BioNavigator service is provided by Entigen of Sunnyvale, CA.

Although the degree of identity between certain of the homologs is not particularly high, there are several factors that indicate that the US28 homologs encode proteins having US28 activity. First, as shown in FIGS. 2-4, the rhUS28 homologs show a relatively high level of similarity with US28 or one of the corresponding human homologs of

US28 (e.g., UL33 or UL78). In particular, there is significant similarity in hydrophobicity/hydrophilicity alignments. The various rhUS28 homologs have hydrophobic and hydrophilic regions consistent with the class of 7 member G proteins of which US28 is a member. Additionally, the rhUS28 homologs have positional homology with US28.

5 The rhesus US28 homologs can include naturally occurring, synthetic, and intentionally manipulated polynucleotide sequences (e.g., site directed mutagenesis or use of alternate promoters for RNA transcription). The polynucleotide sequence for the rhesus US28 homologs includes antisense sequences, as well as sequences that are degenerate as a result of the degeneracy of the genetic code.

10 Hence, the nucleic acids encoding the various rhesus US28 homologs includes each of the nucleotide sequences as set forth in Table 3 and nucleic acid sequences complementary to those sequences. Also included are subsequences of the above-described nucleic acid sequences. Such subsequences include, for example, those that are at least 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length and which
15 specifically hybridize to a nucleic acid that encodes one of the rhesus US28 homologs. Other fragments are longer, such as at least 30, 35, 40, 45, 50, 55, 60, or 65 nucleotides in length.

 Thus, also provided herein are isolated or recombinant nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of (a) a deoxyribonucleotide sequence complementary to one of the rhesus US28 homologs; (b) a
20 ribonucleotide sequence complementary to one of the rhesus US28 homologs; (c) a nucleotide sequence complementary to the deoxyribonucleotide sequence of (a) or to the ribonucleotide sequence of (b); (d) a nucleotide sequence of at least 25 consecutive nucleotides capable of hybridizing to one of the rhesus US28 homologs; and (e) a nucleotide sequence capable of hybridizing to a nucleotide sequence of (d), wherein the nucleotide
25 sequences for the rhesus US28 homologs are as indicated in Table 3.

 Nucleic acid molecules that include a nucleotide sequence that encodes a polypeptide having an amino acid sequence that is substantially identical to the amino acid sequence of one of the rhesus US28 homologs are also provided (see Table 3). For example, the invention includes a nucleotide sequence that encodes a polypeptide having an amino
30 sequence that is at least 75 % identical to the amino acid sequence for one of the rhesus US28 homologs over a region of at least 40 amino acids in length. In other instances, the polypeptide encoded by the rhesus US28 homolog is at least 80, 82, 84, 86, 88 or 90% identical to the amino acid sequence of one of the rhesus US28 homologs; in still other instances, the polypeptide is at least 90% (e.g., 92 or 94%) or at least 95 % (e.g., 96 or 98%)

identical to the amino acid sequence of one of the rhesus US28 homologs over a region of at least 40 amino acids. In some instances, the region of percent identity extends over a region of 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 amino acids, and can extend over the full length of the amino acid sequence as shown in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26.

5 Sequence comparisons of the protein encoded by the nucleic acids of the invention can be performed visually or with a comparison algorithm. One such algorithm is the BLASTP algorithm using a wordlength (W) of 3 and the BLOSUM62 scoring matrix.

The polynucleotide sequences are typically substantially identical to one of the rhesus US28 homologs having a sequence as listed in Table 3 (i.e., SEQ ID NOS:5, 7, 9, 11,
10 13, 17, 23 and 25). For example, certain nucleic acids are at least 75% identical to the nucleic acid one of the rhesus US28 homologs over a region of at least 50 nucleotides in length. Other nucleic acids are at least 80, 82, 84, 86, 88 or 90% identical to the nucleic acid sequence of one of the rhesus US28 homologs of Table 3. Certain nucleic acids are at least 90% (e.g., 92 or 94%) or at least 95% (e.g., 96 or 98%) identical to the nucleic acid
15 sequences of one of the rhesus US28 homologs listed in Table 3 over a region of at least 50 amino acids. In some instances, the region of percent identity extends over a longer region than 50 nucleotides, such as 75, 100, 125, 150, 175, 200, 225 or 250 nucleotides, or over the full length of the encoding region.

As noted supra, the rhUS28 homologs can include splice variants of the
20 various open reading frames. A spliced variant form can be predicted by use of splice acceptor/donor site prediction programs commonly available to those skilled in the art, such as the "Genefinder", "Genehunt" or "GRAIL" programs available at the CMS Molecular Biology resource found at www.unl.edu. With such programs various spliced variants of a core sequence can be elucidated, and splicing at the N terminus of chemokine receptors such
25 as the rhUL28 homologs is not uncommon.

One example of such a splice variant is a splice variant of rhUL33, which is referred to herein as rhUL33 spliced (SEQ ID NO:25). This particular splice variant can be described with reference to the nucleotide sequence set forth in SEQ ID NO:27 which is a segment that extends roughly 1000 nucleotides upstream of the rhUL33 reading frame and
30 roughly a couple hundred nucleotides downstream. Assigning the first nucleotide of this sequence as nucleotide 1, with this particular splice variant, translation is initiated at nucleotide 603 through nucleotide 752, exon 1. An intron spanning nucleotide 753 to 830 is removed and exon 1 is joined to exon 2, nucleotide 831 to 2006. In contrast the unspliced gene runs through nucleotide 1017 to 2006 in this sequence.

To identify nucleic acids encoding one of the rhesus US28 homologs, one can employ a nucleotide sequence comparison algorithm such as are known to those of skill in the art. For example, one can use the BLASTN algorithm. Suitable parameters for use in BLASTN are wordlength (W) of 11, M=5 and N=-4. Specific examples of nucleic acids
5 which are provided herein include the nucleotide sequences as set forth in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.

Alternatively, one can identify a rhesus US28 homolog nucleic acid by hybridizing, under stringent conditions, the nucleic acid of interest to one of the rhesus US28 homologs as set forth in one of the following sequences, SEQ ID NOS: 5, 7, 9, 11, 13, 17, 23
10 and 25. Also provided are nucleic acids that encode a protein that is immunologically cross reactive with one of the rhesus US28 homologs or some fragment or variant thereof.

The foregoing nucleic acids can be obtained by any suitable method known in the art, including, for example, 1) hybridization of genomic or cDNA libraries with probes to detect homologous nucleotide sequences; 2) antibody screening of expression libraries to
15 detect cloned DNA fragments with shared structural features; 3) various amplification procedures such as polymerase chain reaction (PCR) using primers capable of annealing to the nucleic acid of interest; and 4) direct chemical synthesis.

In one embodiment, a rhesus US28 homolog is isolated by routine cloning methods. The nucleotide sequence of a gene or cDNA encoding one of the rhesus US28
20 homologs, is used to design probes that specifically hybridize to a rhesus US28 homolog cDNA in a cDNA library, a rhesus US28 homolog gene in a genomic DNA sample, or to a rhesus US28 homolog mRNA in a total RNA sample (e.g., in a Southern or Northern blot). Once the target nucleic acid is identified, it can be isolated according to standard methods known to those of skill in the art.

25 Rhesus US28 homologs can also be cloned using well-known amplification techniques. Examples of protocols sufficient to direct persons of skill through *in vitro* amplification methods, include: (i) the polymerase chain reaction (PCR), (ii) the ligase chain reaction (LCR), (iii) Q β -replicase amplification, and (iv) other RNA polymerase mediated techniques, are found in Berger, Sambrook, and Ausubel, as well as Mullis *et al.* (1987) U.S.
30 Patent No. 4,683,202; *PCR Protocols A Guide to Methods and Applications* (Innis *et al.* eds) Academic Press Inc. San Diego, CA (1990) (Innis); Arnheim & Levinson (October 1, 1990) *C&EN* 36-47; *The Journal Of NIH Research* (1991) 3: 81-94; (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86: 1173; Guatelli *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87: 1874;

Lomell *et al.* (1989) *J. Clin. Chem.* 35: 1826; Landegren *et al.* (1988) *Science* 241: 1077-1080; Van Brunt (1990) *Biotechnology* 8: 291-294; Wu and Wallace (1989) *Gene* 4: 560; and Barringer *et al.* (1990) *Gene* 89: 117. Improved methods of cloning *in vitro* amplified nucleic acids are described in Wallace *et al.*, U.S. Pat. No. 5,426,039.

5 Suitable primers for use in the amplification of the rhesus US28 homologs include, for example, those shown in Table 4 below:

Table 4: Primer sequences for amplifying rhUS28 homologs.

rhUS28 Homolog	Primer Sequence (Upper Strand)	SEQ ID NO:	Primer Sequence (Lower Strand)	SEQ ID NO:
rh28.1	TATGAATAACACATCTTGCAACTTC	28	CACACAGACCACATGTAC	29
rh28.2	ATTCAACATGACCAACGCCGG	30	GCATTTCCTGGATTTCG	31
rh28.3	CATGACCAACACTAAC	32	GAGTCTTTTGTGAGCC	33
rh28.4	TATGAATTCGAGCCAGCAC	34	GTACGCGACTAAGACAGAG	35
rh28.5	AAAGATGACTACCACCAC	36	ATAACCTAGCACCTCCCC	37
rh78	CTGAAACCATGATTACGG	38	CACGCAGCACAAGAGCAC	39
rh33	CATGACCAATCTTTACTC	40	GTGTCGCCACTCCTACCC	41
rh33 spliced	AAGTTAGTGATGGCAGTC	42	GTATGTAAACCCGTGGAG	43

10 As an alternative to cloning one of the rhesus US28 homologs, a suitable nucleic acid can be chemically synthesized. Direct chemical synthesis methods include, for example, the phosphotriester method of Narang *et al.* (1979) *Meth. Enzymol.* 68: 90-99; the phosphodiester method of Brown *et al.* (1979) *Meth. Enzymol.* 68: 109-151; the diethylphosphoramidite method of Beaucage *et al.* (1981) *Tetra. Lett.*, 22: 1859-1862; and
15 the solid support method of U.S. Patent No. 4,458,066. Chemical synthesis produces a single stranded oligonucleotide. This can be converted into double stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase using the single strand as a template. One of skill would recognize that while chemical synthesis of
20 DNA is often limited to sequences of about 100 bases, longer sequences can be obtained by the ligation of shorter sequences. Alternatively, subsequences can be cloned and the

appropriate subsequences cleaved using appropriate restriction enzymes. The fragments can then be ligated to produce the desired DNA sequence.

In certain methods that utilize rhesus US28 homologs, it may be desirable to modify the nucleotide sequence. One of skill will recognize many ways of generating alterations in a given nucleic acid construct. Such well-known methods include site-directed mutagenesis, PCR amplification using degenerate oligonucleotides, exposure of cells containing the nucleic acid to mutagenic agents or radiation, chemical synthesis of a desired oligonucleotide (*e.g.*, in conjunction with ligation and/or cloning to generate large nucleic acids) and other well-known techniques. *See, e.g.*, Gilman and Smith (1979) *Gene* 8:81-97, Roberts *et al.* (1987) *Nature* 328: 731-734.

IV. Rhesus US28 Homologs - Proteins

A. Protein Composition

Proteins encoded by the foregoing rhesus US28 homologs are also provided. More specifically, such proteins include rhesus US28 homologs that are isolated from natural sources, and/or prepared according to recombinant methods, and/or prepared by chemical synthesis, and/or using a combination of recombinant methods and chemical synthesis. The various US28 homologs are exemplified by the amino acid of SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26. Further provided are fragments and variants of these exemplary sequences.

Also included are isolated proteins having an amino acid sequence at least about 75% identical to an amino acid sequence of one of the rhesus US28 homologs. Generally, such proteins are at least 80, 82, 84, 86, 88 or 90% identical; other proteins are at least 90, 91, 92, 93, 94 or 95% identical to the amino acid sequence of one of the rhesus US28 homologs. The region of similarity between one of the rhesus US28 homologs and a related protein typically extends over a region of at least 40 amino acids in length, in other instances over a longer region than 40 amino acids such as 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 amino acids, and most preferably over the full length of the protein. One example of an algorithm that is useful for comparing a polypeptide to the amino acid sequence of US28 or a US28 homolog is the BLASTP algorithm; suitable parameters include a word length (W) of 3, and a BLOSUM62 scoring matrix.

Besides substantially full-length proteins, fragments of such proteins having biological activity are provided. Biological activity can include the ability to bind a chemokine, particularly a CX3C chemokine such as fractalkine, as well as other chemokines

such as CC chemokines. Other examples of significant biological activity include antibody binding (*e.g.*, the fragment competes with a full-length rhesus US28 homolog such as set forth in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26) and immunogenicity (*e.g.*, possession of epitopes that stimulate B- or T-cell responses against the fragment).

5 As alluded to supra, protein fragments are also provided herein. Such fragments typically include at least 5, 6, 7, 8, 9, or 10 contiguous amino acids; other fragments are somewhat longer and include at least 12, 13, 14, 15, 16, 17, 18, 19 or 20 contiguous amino acids. Certain fragments are still longer yet such as at least 25, 30, 40, 50, 60, 70, 80, 90 or 100 contiguous amino acids.

10 The proteins described herein also include particular regions or domains of the rhesus US28 homologs. The rhesus US28 homologs are typically encoded by nucleotide sequences that are substantially identical with the nucleotide sequences as set forth in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25. The nucleotides encoding the rhesus US28 homologs will also typically hybridize to a polynucleotide sequence as set forth in SEQ ID NOS: 5, 7, 9, 11,
15 13, 17, 23 and 25.

Often the rhesus US28 proteins will share at least one antigenic determinant in common with at least one of the amino acid sequences set forth in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26. The existence of such a common determinant is evidenced by cross-reactivity of the variant protein with an antibody prepared against rhesus US28 homolog.

20 Cross-reactivity can be tested using polyclonal sera against the rhesus US28 homolog, but can also be tested using one or more monoclonal antibodies against a rhesus US28 homolog.

The proteins provided herein include modified protein backbones. Illustrative examples of such modifications include chemical derivatizations of proteins, such as acetylations and carboxylations. Modifications also include glycosylation modifications and
25 processing variants of a typical polypeptide. Such processing steps specifically include enzymatic modifications, such as ubiquitination and phosphorylation. *See, e.g., Hershko & Ciechanover, Ann. Rev. Biochem.* 51:335-364 (1982).

B. Production of US28 Homolog Protein

30 1. Recombinant Technologies

Proteins encoded by US28 and US28 homologs (*e.g.*, SEQ ID NOS: 6, 8, 10, 12, 14, 18, 24 and 26) or fragments thereof can be prepared by recombinant means by expressing the proteins in host cells transfected with a vector in which the coding sequence for US28 or the US28 homolog is operably linked to an expression control sequence in an

expression vector. Expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors contain selection markers, *e.g.*, tetracycline resistance or hygromycin resistance, to permit detection and/or selection of those cells transformed with the desired DNA sequences
5 (*see, e.g.*, U.S. Patent 4,704,362).

Typically, the coding region for US28 or US28 homolog is placed under the control of a promoter that is functional in the desired host cell to produce relatively large quantities of the protein. An extremely wide variety of promoters are well-known, and can be used in the expression vectors provided herein, depending on the particular application.
10 Ordinarily, the promoter selected depends upon the cell in which the promoter is to be active. Other expression control sequences such as ribosome binding sites, transcription termination sites and the like are also optionally included. Constructs that include one or more of such control sequences are termed "expression cassettes." Accordingly, provided herein are expression cassettes into which nucleic acids encoding US28 or US28 homologs are
15 incorporated for high level expression of the corresponding protein in a desired host cell.

In certain instances, the expression cassettes are useful for expression of polypeptides in prokaryotic host cells. Commonly used prokaryotic control sequences (defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences) include such commonly used promoters as the
20 beta-lactamase (penicillinase) and lactose (*lac*) promoter systems (Change *et al.* (1977) *Nature* 198: 1056), the tryptophan (*trp*) promoter system (Goeddel *et al.* (1980) *Nucleic Acids Res.* 8: 4057), the *tac* promoter (DeBoer *et al.* (1983) *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25); and the lambda-derived P_L promoter and N-gene ribosome binding site (Shimatake *et al.* (1981) *Nature* 292: 128). In general, however, any available promoter that
25 functions in prokaryotes can be used.

For expression of polypeptides in prokaryotic cells other than *E. coli*, a promoter that functions in the particular prokaryotic species is required. Such promoters can be obtained from genes that have been cloned from the species, or heterologous promoters can be used. For example, the hybrid *trp-lac* promoter functions in *Bacillus* in addition to *E.*
30 *coli*.

For expression of the polypeptides in yeast, convenient promoters include GAL1-10 (Johnson and Davies (1984) *Mol. Cell. Biol.* 4:1440-1448) ADH2 (Russell *et al.* (1983) *J. Biol. Chem.* 258:2674-2682), PHO5 (*EMBO J.* (1982) 6:675-680), and MF α

(Herskowitz and Oshima (1982) in *The Molecular Biology of the Yeast Saccharomyces* (eds. Strathern, Jones, and Broach) Cold Spring Harbor Lab., Cold Spring Harbor, N.Y., pp. 181-209). Another suitable promoter for use in yeast is the ADH2/GAPDH hybrid promoter as described in Cousens *et al.*, *Gene* 61:265-275 (1987). Other promoters suitable for use in eukaryotic host cells are well-known to those of skill in the art.

For expression of the polypeptides in mammalian cells, convenient promoters include CMV promoter (Miller, *et al.*, *BioTechniques* 7:980), SV40 promoter (de la Luma, *et al.*, (1998) *Gene* 62:121), RSV promoter (Yates, *et al.*, (1985) *Nature* 313:812), and MMTV promoter (Lee, *et al.*, (1981) *Nature* 294:228).

For expression of the polypeptides in insect cells, the convenient promoter is from the baculovirus *Autographa Californica* nuclear polyhedrosis virus (NcMNPV) (Kitts, *et al.*, (1993) *Nucleic Acids Research* 18:5667).

Either constitutive or regulated promoters can be used in the expression systems. Regulated promoters can be advantageous because the host cells can be grown to high densities before expression of the polypeptides is induced. High level expression of heterologous proteins slows cell growth in some situations. For *E. coli* and other bacterial host cells, inducible promoters include, for example, the *lac* promoter, the bacteriophage lambda P_L promoter, the hybrid *trp-lac* promoter (Amann *et al.* (1983) *Gene* 25: 167; de Boer *et al.* (1983) *Proc. Nat'l. Acad. Sci. USA* 80: 21), and the bacteriophage T7 promoter (Studier *et al.* (1986) *J. Mol. Biol.*; Tabor *et al.* (1985) *Proc. Nat'l. Acad. Sci. USA* 82: 1074-8). These promoters and their use are discussed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, N.Y., (1989). Inducible promoters for other organisms are also well-known to those of skill in the art. These include, for example, the arabinose promoter, the *lacZ* promoter, the metallothionein promoter, and the heat shock promoter, as well as many others.

Construction of suitable vectors containing one or more of the above listed components employs standard ligation. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required. To confirm correct sequences in plasmids constructed, the plasmids can be analyzed by standard techniques such as by restriction endonuclease digestion, and/or sequencing according to known methods. A wide variety of cloning and *in vitro* amplification methods suitable for the construction of recombinant nucleic acids is described, for example, in Berger and

Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology*, Volume 152, Academic Press, Inc., San Diego, CA (Berger); and "Current Protocols in Molecular Biology," F.M. Ausubel *et al.*, eds., *Current Protocols*, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1998 Supplement) (Ausubel).

5 There are a variety of suitable vectors suitable for use as starting materials for constructing the expression vectors containing the nucleic acids encoding US28 or US28 homolog. For cloning in bacteria, common vectors include pBR322-derived vectors such as pBLUESCRIPT™, pUC18/19, and λ -phage derived vectors. In yeast, suitable vectors include Yeast Integrating plasmids (*e.g.*, YIp5) and Yeast Replicating plasmids (the YRp
10 series plasmids) pYES series and pGPD-2 for example. Expression in mammalian cells can be achieved, for example, using a variety of commonly available plasmids, including pSV2, pBC12BI, and p91023, pCDNA series, pCMV1, pMAMneo, as well as lytic virus vectors (*e.g.*, vaccinia virus, adenovirus), episomal virus vectors (*e.g.*, bovine papillomavirus), and retroviral vectors (*e.g.*, murine retroviruses). Expression in insect cells can be achieved using
15 a variety of baculovirus vectors, including pFastBac1, pFastBacHT series, pBluesBac4.5, pBluesBacHis series, pMelBac series, and pVL1392/1393, for example.

 The polypeptides encoded by the full-length genes or fragments thereof for US28 or US28 homolog can be expressed in a variety of host cells, including *E. coli*, other bacterial hosts, yeast, and various higher eukaryotic cells such as the COS, CHO, HeLa and
20 myeloma cell lines. The host cells can be mammalian cells, plant cells, insect cells or microorganisms, such as, for example, yeast cells, bacterial cells, or fungal cells. Examples of useful bacteria include, but are not limited to, *Escherichia*, *Enterobacter*, *Azotobacter*, *Erwinia*, *Klebsiella*.

 The expression vectors of the invention can be transferred into the chosen host
25 cell by well-known methods such as calcium chloride transformation for *E. coli* and calcium phosphate treatment or electroporation for mammalian cells. Cells transformed by the plasmids can be selected by resistance to antibiotics conferred by genes contained on the plasmids, such as the *amp*, *gpt*, *neo* and *hyg* genes.

 Once expressed, the recombinant polypeptides can be purified according to
30 standard procedures of the art, including ammonium sulfate precipitation, affinity columns, ion exchange and/or size exclusivity chromatography, gel electrophoresis and the like (*see*, generally, R. Scopes, *Protein Purification*, Springer-Verlag, N.Y. (1982), Deutscher,

Methods in Enzymology Vol. 182: Guide to Protein Purification., Academic Press, Inc. N.Y. (1990)). Typically, the polypeptides are purified to obtain substantially pure compositions of at least about 90 to 95% homogeneity; in other applications, the polypeptides are further purified to at least 98 to 99% or more homogeneity. To facilitate purification, the nucleic acids that encode the US28 or US28 polypeptide can be linked to a coding sequence for an epitope or "tag" for which an affinity binding reagent is available.

2. Non-Recombinant Methods

Alternatively, the polypeptides encoded by US28 or US28 homologs or fragments thereof can be synthesized by chemical methods or produced by *in vitro* translation systems using a polynucleotide template to direct translation. Methods for chemical synthesis of polypeptides and *in vitro* translation are well-known in the art, and are described further by Berger & Kimmel, *Methods in Enzymology, Volume 152, Guide to Molecular Cloning Techniques*, Academic Press, Inc., San Diego, CA, 1987 (incorporated by reference in its entirety).

V. Methods of Inhibiting CMV Dissemination

A. General

A variety of methods are provided herein for treating CMV infections by inhibiting the expression or function of US28 or US28 homolog; such treatments can reduce the extent or rapidity of CMV dissemination in an animal (e.g., a mammal, including, for example, a primate such as a human or a non-human primate such as an ape, monkey or chimpanzee). Several illustrative embodiments are described in the sections that follow. While the following examples are directed to methods of treating infections caused by HCMV and rhCMV, it should be understood that similar approaches could be taken in the treatment of other animals that are infected by CMV strains that contain a US28 homolog.

The methods typically utilize an agent that interferes with the function or expression of US28 or a US28 homolog such that viral dissemination during acute or re-emerging CMV infection and/or reactivation from latency is inhibited. As used herein, "dissemination" refers to a detectable increase in viral titer or amount at sites other than the site of primary infection (inoculation), e.g., by transmission of virus from sites of primary infection or reactivation to secondary sites (e.g., tissues or organs).

Virus dissemination typically involves transmission of virus from sites of primary infection (e.g. mucosal tissues such as oral or genital mucosal endothelia) or reactivation (e.g. blood leukocytes including myeloid progenitor cells in the bone marrow and peripheral blood monocytes) to secondary sites (e.g. tissues or organs including salivary glands, kidney, spleen, liver and lungs) where viral replication and amplification may occur. Dissemination is thought to be linked to the binding of US28 to various chemokines. For example, US28 has been shown to bind a variety of human, murine, and virus-encoded CC chemokines in a variety of assay formats (Kledal et al., 1997, *Science* 277:1656-9; Kuhn et al., 1995, *Biochem Biophys Res Commun.* 211:325-30). In addition, the CX3C chemokine, fractalkine, binds with a very high affinity ($K_I \sim 50$ pM) to US28 (Kledal et al., 1998, *FEBS Lett.* 441:209-14).

Thus, without intending to be bound by a particular mechanism, dissemination may involve assisted movement of virus from primary sites (e.g. by random or directed migration of infected cells), release of virus into the bloodstream and random or directed attachment of this virus to cells at secondary sites, or other modes. For instance, fractalkine is expressed on certain endothelial cell surfaces (e.g., vascular endothelial cells) and on populations of dendritic cells (DC), and may thus define a portal through which CMV infected cells or virions go from the circulation to the tissue space, as well as find residence in the DC. Expression of fractalkine on limited cell types can result in the formation of a solid phase chemotactic gradient. Cells infected with CMV and thus expressing US28 may then move along this gradient to tissues important in pathogenesis, immunity and latency.

As discussed briefly above, the current inventors have also established that CMV virions (both human and rhesus strains of the virus) express US28 or US28 homolog. Consequently, the virus could be transported through a circulatory system in the body and become anchored at a secondary site via binding to a chemokine located at a cell surface.

B. Inhibition of US28 Protein Expression

One general approach of the treatment methods provided herein is to reduce CMV dissemination by interfering with the expression of the US28 gene product (i.e., RNA or protein). Various techniques can be utilized to achieve this goal, including administering antisense nucleic acids and ribozymes. These methods are discussed in turn in the following sections.

1. Antisense

In certain treatment methods, antisense polynucleotides that specifically hybridize to a segment of US28 coding sequence or the US28 homolog coding sequence are administered to inhibit expression of US28 or the US28 homolog in an animal infected with CMV, or the antisense polynucleotide is administered prophylactically to an animal susceptible to infection with CMV. Methods relating to antisense polynucleotides are well known, see e.g., Melton, D., Ed, 1988, ANTISENSE RNA AND DNA, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; Dagle et al., 1991, *Nucleic Acids Research*, 19:1805; and Uhlmann et al., *Chem. Reviews*, 90:543-584 (1990).

Typically, the antisense polynucleotides used in the methods comprise an antisense sequence of typically at least about 10 contiguous nucleotides, in other instances at least 12 or 14 contiguous nucleotides, and in still other instances up to about 100 contiguous nucleotides that specifically hybridize to a sequence from a mRNA encoding US28 or a US28 homolog in the target organism. Thus, in the treatment of infections caused by human strains of CMV, appropriate polynucleotides sequences can be prepared based upon the nucleotide sequence for human US28 as set forth in SEQ ID NO:1 (FIG. 1A) and for human UL33 (SEQ ID NO:19), human UL33 spliced (SEQ ID NO:21) and human UL78 (SEQ ID NO:15). Likewise, in the treatment of infections caused by rhesus strains, appropriate polynucleotides can be prepared based upon the nucleotide sequences for the various rhesus US28 homologs as shown in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.

In general, the antisense polynucleotide should be long enough to form a stable duplex but short enough, depending on the mode of delivery, to be administered *in vivo*, if desired. The minimum length of a polynucleotide required for specific hybridization to a target sequence depends on several factors, such as G/C content, positioning of mismatched bases (if any), degree of uniqueness of the sequence as compared to the population of target polynucleotides, and chemical nature of the polynucleotide (e.g., methylphosphonate backbone, peptide nucleic acid, phosphorothioate), among other factors.

In some instances, the antisense sequence is complementary to relatively accessible sequences of the US28 mRNA or the US28 homolog mRNA (e.g., relatively devoid of secondary structure). This can be determined by analyzing predicted RNA secondary structures using, for example, the MFOLD program (Genetics Computer Group, Madison WI) and testing *in vitro* or *in vivo* as is known in the art. Another useful method

for optimizing antisense compositions uses combinatorial arrays of oligonucleotides (see, e.g., Milner et al., 1997, *Nature Biotechnology* 15:537).

The antisense nucleic acids (DNA, RNA, modified, analogues, and the like) can be made using any suitable method for producing a nucleic acid, such as the chemical synthesis and recombinant methods. Specific methods for preparing such sequences are referenced supra in the section on rhesus US28 nucleic acids.

2. Ribozymes

Ribozymes are also useful for inhibiting US28 or US28 homolog activity in an animal. Useful ribozymes can comprise 5'- and 3'-terminal sequences complementary to the US28 mRNA or US28 homolog mRNA and can be engineered by one of skill on the basis of the US28 mRNA sequence (see, e.g., SEQ ID NO:1; see FIG. 1A) and US28 homolog sequences disclosed herein (SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25).

Ribozymes that can be utilized in the treatment methods include those having characteristics of group I intron ribozymes (Cech, 1995, *Biotechnology* 13:323) and others of hammerhead ribozymes (Edgington, 1992, *Biotechnology* 10:256).

Ribozymes and antisense polynucleotides can be delivered directly as a drug in a suitable pharmaceutical formulation (see *infra*), or indirectly by means of introducing a nucleic acid into a cell, including liposomes, immunoliposomes, ballistics, direct uptake into cells, and the like as known in the art. Methods useful for delivery of polynucleotides for therapeutic purposes are described in U.S. Patent 5,272,065. In one embodiment, vectors (e.g., DNA vectors) encoding ribozyme or antisense polynucleotides are administered by injection (e.g., either transiently or as part of a gene therapy regimen).

B. Inhibiting Binding Between a Ligand and a US28 or US28 Homolog

Instead of inhibiting the expression of US28 or a US28 homolog, some treatment methods reduce viral dissemination by interfering with the interaction of a US28 or US28 homolog and a ligand that is naturally bound by US28 or the US28 homolog. Certain methods interfere with the interaction between the receptor and a chemokine. The chemokine typically is from either the CC or CX3C classes of chemokines. Thus, in some methods an agent is administered that interferes with binding between the receptor and a CX3C chemokine such as fractalkine. Other methods are based upon use of agents that

inhibit binding between receptor and CC type chemokines. Examples of CC chemokines include, but are not limited to , MIP-1 α , MIP-1 β , MCP-1, eotaxin, vMIP-2, or RANTES.

1. Antibodies

5 Antibodies are an example of one type of agent that can be used to inhibit binding between a chemokine and US28 or a US28 homolog. Such inhibition can be achieved, for example, through steric hindrance. Typically, the antibody specifically binds an epitope on the extracellular region of US28 (e.g., SEQ ID NO:1; see FIG. 1B) or one of the US28 homologs. Thus, certain treatments involve administering an antibody that
10 specifically binds to human UL33 (SEQ ID NO:19), human UL33 spliced (SEQ ID NO:33) or human UL78 (SEQ ID NO:15). Other treatment methods involve administering an antibody that specifically binds to one of the rhesus US28 homologs (i.e., SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26).

 The anti-US28 antibodies and anti-US28 homolog antibodies used in such
15 treatment approaches can be produced using a variety of routine methods. *See, e.g.,* , Harlow, 1988, ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York; Coligan, CURRENT PROTOCOLS IN IMMUNOLOGY, Wiley/Greene, NY (1991); Stites *et al.* (eds.) BASIC AND CLINICAL IMMUNOLOGY (7th ed.) Lange Medical Publications, Los Altos, CA, and references cited therein; Goding, MONOCLONAL ANTIBODIES:
20 PRINCIPLES AND PRACTICE (2d ed.) Academic Press, New York, NY (1986); Kohler and Milstein, 1975, *Nature* 256:495-97. In certain treatments, monoclonal anti-US28 antibodies are used; whereas, in other instances polyclonal antibody compositions are utilized. Useful anti-US28 and anti-US28 homolog binding compositions can also be produced using phage display technology (see, *e.g.*, Dower et al., WO 91/17271 and McCafferty et al., WO
25 92/01047).

 Using the foregoing methods, antibodies can be generated against the full-length amino acid sequences set forth for US28 or US28 homolog or some fragment thereof that is immunogenic. The fragment generally is at least 5-10 amino acids in length but can be longer. The antibodies which are produced are assayed for specific binding to US28 or
30 US28 homolog and for the ability to block receptor-ligand interactions.

2. Other Inhibitory Molecules

In addition to antibodies, a variety of compounds can be used to inhibit US 28 or US28 homolog receptor-ligand interactions, including, without limitation, polypeptides, oligopeptides, polysaccharides, polynucleotides, lipids, small organic molecules (e.g., MW < 800, more preferably 300-600), and the like. Small organic
5 molecules can be of a variety of chemical types including, but not limited to, sterols, nucleic acids, derivatives of purine and pyrimidine bases, β -lactams, aromatic compounds, heterocyclic compounds, carbocyclic compounds, oligo-N-substituted glycines, polycarbamates, oligosaccharides, lipids and amino acids, and derivatives and combinations thereof. Such compounds can be a natural product, a synthetic compound, or a chemical
10 compound, or a combination of two or more substances. Typically, compounds are identified by high-through put screening of large libraries of compounds (e.g., combinatorial libraries). Methods for creating and screening such libraries are established and are described, for example, by Dolle and Nelson, J. (1999) *Combinatorial Chemistry* 1:235-282; Needels, *et al. Proc. Natl. Acad. Sci. USA*, 90: 10700 (1993); Ni, *et al J. Med.*
15 *Chem.*, 39: 1601 (1996); and in PCT publications WO 95/12608, WO 93/06121, WO 94/08051, WO 95/35503 and WO 95/30642, each of the foregoing references being incorporated herein by reference in its entirety for all purposes.

Exemplary small molecules exhibiting inhibitory activity are described in commonly owned U.S. Application No. _____, filed August 31, 2001, entitled
20 "Modulators of US28," (Attorney Docket No. 019934-000310US/PC) which claims the benefit of U.S. Provisional Application No. 60/228,974, filed August 30, 2000; and in U.S. Provisional Patent Application Serial No. _____, filed August 30, 2001, entitled "Bicyclic Compounds as Inhibitors of Chemokine Binding to US 28" (Attorney Docket No. 019934-001000US); and in U.S. Application No. _____, filed August 30, 2001, entitled
25 "Reagents and Methods for the Diagnosis of CMV Dissemination" (Attorney Docket No. 019934-000910US/PCT), which claims the benefit of Ser. No. 60/229,191 filed August 30, 2000, the disclosures of each of the foregoing applications being incorporated herein by reference in their entirety for all purposes.

As used herein, the terms "compound" and "agent," are used interchangeably
30 when used in the context of inhibition of a US28 or US28 homolog-chemokine interaction.

3. Vaccines

The vaccines are generally designed to include CMV or some portion of the virion in which US28 or US28 homolog has been disabled such that US28 or US28 protein

is either not produced or is produced in inactive form. In some instances, this means that the segment of the genome encoding US28 or US28 homolog has been completely or substantially removed, either chemically, enzymatically or via recombination. Specific segments, or at least portions thereof, that can be removed for HCMV include those regions of the genome corresponding to US28 (SEQ ID NOS:1 and 3), UL33 (SEQ ID NO:19), UL33 spliced (SEQ ID NO:21) and UL78 (SEQ ID NO:17). For rhCMV, segments, or portions thereof, that can be removed include SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25).

In general the vaccines are administered as a composition that includes some type of pharmaceutically acceptable excipient (carrier). Additional details regarding methods for generating and administering the vaccines is provided in the section on vaccines *infra*.

VI. Assays for Agents that Inhibit Dissemination of CMV

A. General

A variety of assays are useful for identifying an agent capable of reducing CMV dissemination in a host animal, by determining whether the agent inhibits the binding of a ligand (e.g., a chemokine) to US28, US28 homolog, or a variant or fragment of US28 or the US28 homolog. Using assays such as described herein, agents which interfere with the binding between a chemokine and US28 or a US28 homolog can be identified. By interfering with such binding, the identified agents have utility as inhibitors of the dissemination of CMV. Agents identified by the assays inhibit the binding of a chemokine such as fractalkine to US28 with activity expressed as IC₅₀ (that amount of compound that reduces chemokine binding by 50%). Such agents typically have an IC₅₀ of approximately 50 µg/mL or less, in other instances 25 µg/mL or less, in still other instances 10 µg/mL or less, in yet other instances less than 1 µg/mL, and in other instances 50 ng/mL or less, 25 ng/mL or less, or 10 ng/mL or less. In addition to having strong binding characteristics, the agents should exhibit low levels of side effects.

The assays described herein fall into three general categories: non-cellular or *in vitro* assays, cell based assays and in vivo assays. Each of these is described in greater detail in the following sections.

B. Cell Based Assays

In general, cell-based assays involve contacting a cell that expresses US28, US28 homolog or fragment or variant thereof with a candidate agent and a chemokine in a competitive binding format. Typically, the candidate agent and/or chemokine is detectably labeled such that the amount of bound or free agent or chemokine can be determined.

5 Usually, the label will be a fluorescence label, a phosphorescence label, a radiolabel, a colorimetric label, or the like. In certain screening assays the labeled chemokine is a radiolabeled fractalkine (e.g., ¹²⁵I-fractalkine). Radiolabeled chemokines are available commercially (e.g., Amersham, New England Nuclear) or can be prepared using routine techniques.

10 1. Cells

Cells expressing US28 or US28 homolog can be prepared in primarily two ways. One option is to transfect cells with a nucleic acid that encodes US28 or the US28 homolog (e.g., SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 and 25). A number of
15 different cell lines can be utilized in the assays of this type. For example, in certain assays the cell line is a mouse cell line (e.g., NSO cells from R&D Systems, Minneapolis, Minnesota, USA). In other instances, the cell line is a human cell line, (e.g. human embryonic kidney 293 cells ("HEK293") (available from the American Tissue Culture Collection). Other mammalian cells that can be utilized include, but are not limited to
20 CHO, HeLa, HepG2, BaF-3, Schneider, COS, CV-1, HuTu80, and NTERA cell lines.

In general, such cell lines are transfected with an expression cassette including a promoter (e.g., CMV promoter) operably linked to US28 cDNA or US28 homolog cDNA using conventional methods, so as stably or transiently to express the US28 or US28 homolog gene product in the transfected cell. Thus, an expression cassette used to
25 transfect cells to express US28 includes a promoter and a nucleic acid sequence from SEQ ID NO:1 or 3 or subsequence thereof which encodes a protein retaining US28 activity. For cells transfected to express a US28 homolog, the expression cassette includes a promoter and a nucleic acid as set forth in SEQ ID NOS:5, 7, 9, 11, 13, 15, 17, 19, 21, 23 or 25), or a subsequence thereof which encodes a protein retaining an activity of the US28 homolog.

30 Instead of transfecting cells to obtain expression of US 28 or US28 homologs, cells can instead be infected with CMV. In assays systems of this type, the cell line is a primary cell line, e.g., rhesus monkey dermal fibroblast (available from the University of California at Davis Primate Center), primary human lung or foreskin fibroblasts (Clonetics, San Diego California), human diploid lung fibroblasts (MRC-5 and

WI-38), HUVECs, or the like. Cells can be infected with whole virus (CMV) and utilized in the assay following viral expression of the US28 or US28 homolog gene product (e.g., typically about 48-72 hours post infection). Cells typically are infected by contacting with an innoculum containing between 0.01 and 5 infectious particles per cell in minimal volume
5 for a period of 1 hour at 37 °C with gentle rocking. Innoculum is removed and replaced with fresh medium (DMEM + 10% FBS).

2. Chemokine

Some assays are conducted with CX3C chemokines such as fractalkine; such
10 assays can be utilized to identify tight binding inhibitors given the high affinity between fractalkine and the US28 receptor. Other assays are performed with chemokines from the CC class including, but not limited to, MIP-1 α , MIP-1 β , MCP-1, MCP-3, eotaxin, vMIP-2, or RANTES.

3. Methodology

Typically, cells are initially cultured in a suitable buffer (e.g., IMDM-5%
15 FBS, DMEM-10% FCS, HUVEC complete medium, and the like) then centrifuged and resuspended in assay buffer (e.g., HEPES with NaCl, CaCl₂, MgCl₂, and BSA) to a concentration of from about 5 x 10⁵ to about 5 x 10⁷, preferably from about 2 x 10⁵ to about 8 x 10⁵ cells/ml. Aliquots of the cells are then contacted with the candidate agent and
20 labeled chemokine.

After contacting the cells with one or more candidate agents in the presence of labeled chemokine, the assay mixture is typically incubated for a period of time of from about 1 to about 6 hours at a temperature of from about 1 to about 10 °C. Preferably the mixture is incubated for a period of from about 2 to about 4 hours at a temperature of about
25 4 °C. One of skill in the art will understand that a variety of assay conditions can be employed, depending on the cell line used, the concentrations of the compounds and chemokine and the concentration of the cells themselves, for example.

Following incubation, the assay wells can be harvested under vacuum using filter plates, pre-soaked with PEI solution (for those embodiments carried out on 96-, 384-,
30 1536-well or larger plates). Scintillation fluid (for radiolabel assays) is added, the plates are sealed and the wells are counted. Alternatively, other quantitative methods are employed when, for example, other types of detectably labeled chemokines or agents are used (e.g., fluorescent labels).

Other formats involve contacting a chemokine that is immobilized to a support with a labeled cell that expresses US28 or US28 homolog or a fragment or variant of US28 or the US28 homolog. The support can be made of essentially any material that is compatible with the conditions and components utilized to perform the assays. Exemplary materials include, but are not limited to, glass slides, microtiter wells, membranes and the like.

Another assay that can be used to identify agents that specifically inhibit the binding of chemokine (e.g., fractalkine) to US28 or US28 homolog is a cytoplasmic calcium mobilization assay. In certain methods, assays are performed by: (i) loading US28 or US28 homolog-expressing 293 cells with INDO-1 dye (45 min. at room temperature IN THE DARK), and (ii) washing with PBS, and resuspending into Ca²⁺ 'flux' buffer (HBSS with 1% fetal bovine serum). For each test, 1 x 10⁶ cells are incubated at 37 °C in the cuvette of a PTI spectrometer, excited at 350nm, and the ratio of 410/490 nm emission plotted over time (typically 2-3 minutes), with compounds added at 5 seconds, followed by chemokine (e.g., fractalkine) at 60 seconds. A rise in intracellular Ca²⁺ indicates that the US28 receptor has bound to the ligand, engaged a G-protein linked cascade which resulted in the mobilization of Ca²⁺ in the cytoplasm of the US28-bearing cells. Compounds that inhibit ligand (e.g., a chemokine such as fractalkine) binding are tested in this assay for the effects on Ca²⁺ in this system.

C. Cell-Free Assays

Alternatively, cell-free systems can be employed utilizing a full-length US28 or US28 homolog, or a fragment or a variant of US28 or US28 homolog (e.g., NH₂-terminal peptide, extracellular loops and the like). Such proteins can be used alone (or in combinations of fragments of US28 or US28 homologs) to assay binding levels of a chemokine in the presence of a candidate agent.

Cell-free assays can be conducted in a variety of formats. For example, in certain cell-free assays, expressed or synthesized receptor proteins of US28 are embedded in artificial membrane systems to assay for chemokine binding in the presence of a candidate agent (see for example, systems described in Kitaguchi, et al., 1999, *Biochem. Biophys. Res. Commun.* 261:784-89 and Myung, et al., 1999, *Anal. Biochem.* 270:303-13).

Other formats involve contacting a chemokine that is immobilized to a support with a labeled US28 protein or US28 homolog or fragment or variant thereof in the

presence of test agent and then detecting the formation of complex containing the label. Another format is one in which US28 or US28 homolog, or fragment or variant is attached to the support and the immobilized receptor, fragment or variant is contacted with a labeled chemokine in the presence of test agent, with subsequent detection of label bound by the
5 immobilized receptor.

D. In Vivo Assays

The discovery by the current inventors that the genome of rhCMV contains reading frames that encode proteins with homology to human US28 is important because it
10 provides a model system for studying the dissemination of human CMV and provides a means by which agents that are effective in arresting or reducing the dissemination of CMV *in vivo* can be identified. As explained earlier, the finding that rhCMV contained such reading frames was unexpected because the genome of several different CMV strains was found not to contain reading frames encoding proteins with homology to human US28 (e.g.,
15 rats and mice). Furthermore, it was not to be expected that the genome of rhCMV would be found to contain multiple different reading frames.

That the genome of rhCMV in fact does encode one or more US28 homologs has been confirmed at two levels. First, as described in greater detail in Example 3, rhesus cells infected with rhCMV express a protein that has binding affinity for the chemokine
20 fractalkine (see also FIG. 6). Secondly, the current inventors have shown that rhCMV virions, like human CMV virions, express at least one protein with fractalkine binding activity (i.e., a US28 homolog). Details of the experiments conducted to demonstrate this are provided in Example 4 and summarized in FIG. 7.

A list of the sequence identifiers for the nucleotide sequences of the open
25 reading frames encoding the rhesus US 28 homologs and the corresponding amino acid sequences are summarized in Table 3 *supra*. The actual nucleotide and amino acid sequences of the rhesus US28 homologs are shown in SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25 (nucleotide sequences) and 6, 8, 10, 12, 14, 18, 24 and 26 (amino acid sequences).

The *in vivo* screening assays generally involve administering a test agent to a
30 non-human animal such as a monkey (e.g., a rhesus monkey) infected with CMV and then determining whether the test agent inhibits the function or activity of the US28 homolog or fragment or variant thereof. In general this involves a determination of whether the test agent causes a detectable reduction in the dissemination of CMV in the non-human animal. More specifically, certain assay methods involve introduction of CMV into the animal and

then a determination of the degree to which the virus spreads from a primary site to one or more secondary sites.

If the animals being utilized are not already infected, CMV can be introduced by oral inoculation, intravenous injection and other methods known to those of skill in the art. The test agent that is administered can be of any of the types discussed *supra* including, but not limited to, antibodies, vaccines, antisense nucleic acids, ribozymes and small molecules. The test agent can be administered to the animal in a number of different ways. Exemplary modes of administration include, but are not limited to, parenteral injection either intravenously, subcutaneously or intramuscularly (single or multiple doses), orally, and by the use of an osmotic pump (e.g., the Alzet Osmotic Pump, DURECT Corporation, Cupertino, CA). Other approaches are described in the section on pharmaceutical compositions.

Determination of the extent to which the CMV virus is disseminated or spreads from the site of primary infection can be accomplished in a number of different ways. One method is to collect sterile blood, saliva and/or urine samples prior to infection of the animal and then again periodically thereafter. Viral titer can then be determined according to established protocols (see, e.g., Spaete and Mocarski, 1985, *J Virol* 56:135-43). In a second approach, blood samples obtained before and after infection are assayed for viral DNA by nested PCR using primers that are specific for CMV (kits containing such primers are available from, for example, Qiagen, CA). A third alternative involves direct detection of CMV in various tissues by performing a necropsy on the infected animals approximately 15 to 30 days after administration of virus. Tissue and blood samples are taken and DNA purified from these samples, typically using commercially available kits (e.g., those from Qiagen, CA). The resulting purified DNA then serves as a template for nested PCR as just described.

Histological analyses can also be conducted by staining tissue samples with antibody that specifically binds to CMV (e.g., rhCMV). Inhibition of CMV dissemination is demonstrated by a difference of viral titer or kinetics (as described *supra*) as assessed by levels of viral antigens in specific tissues or organs of experimental animals compared to control animals. Another alternative is to determine the levels of reactive leukocytes in the peripheral blood of the infected animal (e.g., by FACS analysis of blood samples). Inhibition of CMV dissemination is demonstrated by fewer activated T cells or memory T cells in peripheral blood of experimental animals compared to control animals. Suitable

assays for conducting such an analysis is described by Lockridge et al. (1999) *J Virol.* 73:9576-83.

Further details regarding the performance of *in vivo* assays including a more detailed description of the foregoing approaches for detecting reduction in CMV dissemination are provided in Example 5.

VII. Vaccines

A. Background

Immune-modulation by CMV genes plays a crucial role in pathogenesis, persistence and immunity. The ability of US28 and US28 homologs to bind chemokines such as fractalkine indicates a role for these proteins in the alteration of migration/activation of immune cells that are near CMV infected cells and in trafficking of infected cells via some type of US28 mediated migration. Thus, modification of viral coding regions which control the magnitude of immune responses and influence viral dissemination in the host are key targets to achieve the correct balance between attenuation and immune-stimulation. Alterations at these loci can be used to produce an acceptable vaccine profile.

Thus, the general approach for vaccine development is to produce rhCMV in which one or more of these immuno-modulatory loci are altered. In this way attenuated forms of the virus can be produced which are non-pathogenic but which are still able to induce a recipient's immune system, preferably by generating cell mediated immunity such as the induction of CD8⁺ cells. CMV altered at such loci is then evaluated by introducing the altered CMV into a rhesus monkey (*macaca mulatta*) and determining the resulting phenotype. More specifically, vaccines are generally designed to include CMV or some portion of the virion in which US28 or US28 homolog has been removed such that US28 or US28 protein is either not produced or is produced in inactive form. In some instances, this means that the segment of the genome encoding US28 or US28 homolog has been completely or substantially removed, either chemically, enzymatically or via recombination. Specific segments, or at least portions thereof, that can be removed include those regions of the genome encoding for US28 (SEQ ID NOS:1 and 3) or US28 homolog (SEQ ID NOS:5, 7, 9, 11, 13, 15, 17, 19, 21, 23 or 25).

Candidate vaccines showing good efficacy in the rhesus model system can then serve as candidates in humans. Alternatively, similar vaccines can be prepared from human CMV.

B. Exemplary Method for Making Non-Pathogenic Forms of CMV

One approach for generating rhCMV that is altered at the regions encoding the rhesus US28 homologs involves the following strategy:

1. A cloning vector carrying an insertion containing a sequence that is homologous to one of the rhesus US28 homologs is constructed. The vector includes the desired modifications to the segment(s) encoding the US 28 homolog(s) under evaluation and a selective marker (e.g., green fluorescent protein (GFP) and/or puromycin).
2. Wild type CMV DNA and the recombinant vector from step (1) are co-transfected into rhesus dermal fibroblasts (DF) using calcium phosphate transfection protocols. The rhesus DF are propagated in DMEM and 10% FBS.
3. Cellular recombination of the wild type DNA with the homologous regions in the vector results in a small number of cells infected with a recombinant genome.
4. Cells containing recombinant virus are isolated by selection of the marker (e.g., by FACS detection of GFP or puromycin selection).
5. Plaques containing infected cells are then purified and the recombinant virus subsequently amplified in rh DF.

Recombinant viruses may also be constructed utilizing cosmid technology (see, e.g., Kemble G, Duke G, Winter R, Spaete R., (1996) J. Virol. 70:2044-8) or by bacterial artificial chromosome technology (see, e.g., Borst EM, et al. (1999) J. Virol. 73:8320-9). Other methods are discussed in commonly owned U.S. Provisional Application No. 60/265,925, which is incorporated herein by reference in its entirety for all purposes.

C. Evaluation of Candidate Vaccines

The resulting amplified viral recombinants are initially analyzed *in vitro* to confirm the nature of the recombinant. Rhesus CMV DNA is prepared by SDS/proteinase K digestion of supernatant virions, followed by phenol/chloroform extraction and ethanol precipitation.

Restriction fragment analysis and Southern blot comparison of the viral recombinants to parental DNA as well as sequencing is used to confirm the altered genotype (i.e., that some or all of region encoding the US28 homolog has been removed). Growth characteristics of the recombinants are compared to the parental strain at both high (5 pfu/cell) and low (0.01 pfu/cell) MOI (multiplicity of infection). Rhesus DF are separately inoculated with parental and recombinant virus, harvested at various time points (0 –4 days

high MOI and 0-10 days low MOI) and total cellular viral load of these samples determined by serial dilution and plaque assay in rhesus DF.

The phenotype of the US28 recombinant can be assessed using chemokine binding assays. In such assays, recombinant and parental virus infected rhesus DF, as well as
5 density gradient purified virions (see Examples *infra*), are incubated with ^{125}I labeled fractalkine and increasing concentrations of cold competitor in a competition binding experiment. Cells or virions are then immobilized on a support (e.g., glass filters), and unbound label is washed away, such that bound label can then be quantified by scintillation counting. IC_{50} values for the US28/fractalkine interaction is determined from this
10 competitive binding analysis (see Examples 1, 3 and 4 for additional details). Abrogation of fractalkine binding to recombinant US28 virions containing a deletion one of the coding regions for a US28 homolog and infected cells is evidence that the loci corresponding to the US28 homolog being investigated has in fact been modified.

CMV virions confirmed to have the desired modification can then be
15 formulated as a vaccine and administered to a rhesus monkey. The effectiveness of the vaccine in inducing an immune response and inhibiting CMV dissemination can be assessed, for example, using any of the various dissemination assays described in the *in vivo* assay section *supra*.

20 D. Formulation and Administration

Candidate forms of the virus identified by the screening procedures described *supra* are typically combined with a pharmaceutically acceptable excipient (carrier) for administration to a patient.

A variety of different excipients or carriers can be utilized in the vaccines
25 including, for example, adjuvants and compounds that stimulate T-cells, such as Freund's adjuvant, Ribi adjuvant (Ribi, et al., *Clin. Immunol. Newsletter*, 6:33-36, 1985) and BCG. Other excipients include Montanide ISA51 and Alum adjuvants (previously approved for use in primates and humans, respectively). Other suitable adjuvants include aluminum phosphate, aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP),
30 N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), and N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxy-phosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE). The effectiveness of an adjuvant can be determined by measuring the amount of cross-reactive

antibodies directed against the immunogenic antigen. In certain instances, cyclophosphamide, an inhibitor of suppressor T-cell response, is included with the vaccine.

The vaccines described herein can be used to induce a therapeutic or protective immune response in a patient and in methods for treating diseases such as those described *infra*. Such methods include administering to a patient a therapeutically effective amount of a vaccine of the invention. A therapeutically effective amount of the vaccine is an amount sufficient to elicit a therapeutic or protective immune response, such as inducing the formation of antibodies and/or other cellular immune responses (e.g., the induction of helper T cells; cytotoxic killer T-cells, anomalous killer cells (AK cells) and/or antibody-dependent cytotoxic cells).

Doses, methods of administering, and suitable pharmaceutical carriers can be determined readily by the skilled artisan. For example, appropriate doses can be extrapolated from dose-response studies in animals, including non-human primates. An appropriate immunization schedule can be determined by a skilled artisan but generally depends upon the susceptibility of the host or patient to immunization with the vaccine and is typically continued until sufficient antibody is detectable in whole serum.

The vaccines can be administered in a variety of different ways including, for example, by oral, intranasal, intraperitoneal, intravenous, intramuscular, subcutaneous, subdermal and transdermal methods. It has been found in some instances that although similar immunologic responses are generated by either intraperitoneal or subcutaneous administration that the latter form of administration is capable of inducing higher T-cell responses.

VIII. Additional Pharmaceutical Compositions

25 A. Active Component

In addition to the vaccines just described, other inhibitory agents described herein or identified using the screening assays disclosed herein can be formulated as part of a pharmaceutical composition for use in preventing CMV dissemination in a host. As described *supra*, such agents can include, for example, antisense nucleic acids, ribozymes, antibodies and small molecules. Typically, the compositions contain from about 0.1% to about 99% by weight of active compound, and in other instances from about 10% to about 60% by weight depending on which method of administration is employed.

Certain agents that are identified can serve as lead compounds for the synthesis of analog compounds that exhibit even higher activity (e.g., increased inhibition of

CMV dissemination). Typically, the analog compounds are synthesized to have an electronic configuration and a molecular conformation similar to that of the lead compound.

Identification of analog compounds can be performed through use of techniques such as self-consistent field (SCF) analysis, configuration interaction (CI) analysis, and normal mode
5 dynamics analysis. Computer programs for implementing these techniques are available. See, e.g., Rein et al. (1989) *Computer-Assisted Modeling of Receptor-Ligand Interactions* (Alan Liss, New York).

Once analogs have been prepared, they can be screened using the methods disclosed *supra* to identify those analogs that exhibit an increased ability to inhibit
10 dissemination of CMV. Such compounds can then be subjected to further analysis to identify those compounds that appear to have the greatest potential as pharmaceutical agents. Alternatively, analogs shown to have activity through the screening methods can serve as lead compounds in the preparation of still further analogs, which can be screened by the methods disclosed herein. The cycle of screening, synthesizing analogs and rescreening can
15 be repeated multiple times to further optimize the activity of the analog.

Further guidance on the synthesis of analog compounds and lead optimization is provided by, for example: Iwata, Y., *et al.* (2001) *J. Med. Chem.* 44:1718-1728; Prokai, L., *et al.* (2001) *J. Med. Chem.* 44:1623-1626; Roussel, P. *et al.*, (1999) *Tetrahedron* 55:6219-6230; Bunin, B.A., *et al.* (1999) *Ann. Rep. Med. Chem.* 34:267-286; Venkatesh, S., *et al.*
20 (2000) *J. Pharm. Sci.* 89:145-154; and Bajpai, M. and Adkinson, K.K. (2000) *Curr. Opin. Drug Discovery and Dev.* 3:63-71.

B. Compositions

In general the pharmaceutical compositions include an active ingredient such
25 as just described in combination with a pharmaceutically acceptable carrier as part of a formulation or medicament for the treatment of various conditions related to CMV infection, although certain active ingredients can be administered without formulation with a carrier.

Some compositions can also include other antiviral agents that are either
30 therapeutic or prophylactic agents, and different from the foregoing active ingredients. The compositions can also include and be used in combination with agents that treat or induce conditions often associated with the viral infections that are sensitive to the present compounds, such as anti-HIV agents or immunosuppressive agents. In many instances, administration in conjunction with the subject compositions enhances the efficacy of such

agents. Exemplary antiviral agents include ganciclovir, foscarnet and cidofovir. Exemplary anti-HIV agents include indinavir, ritonavir, AZT, lamivudine and saquinavir. Exemplary immunosuppressive agents include cyclosporin and FK-506. The compositions can also be used as antiviral prophylactic treatment in combination with immunosuppressive protocols
5 such as bone-marrow destruction (either by radiation or chemotherapy).

The compositions can also include various agents to enhance delivery and stability of the active ingredients. Thus, for example, the compositions can also include, depending on the formulation desired, pharmaceutically-acceptable, non-toxic carriers or diluents, which are defined as vehicles commonly used to formulate pharmaceutical
10 compositions for animal or human administration. The diluent is selected so as not to affect the biological activity of the combination. Examples of such diluents are distilled water, buffered water, physiological saline, PBS, Ringer's solution, dextrose solution, and Hank's solution. In addition, the pharmaceutical composition or formulation can include other carriers, adjuvants, or non-toxic, nontherapeutic, nonimmunogenic stabilizers, excipients and
15 the like. The compositions can also include additional substances to approximate physiological conditions, such as pH adjusting and buffering agents, toxicity adjusting agents, wetting agents and detergents.

The composition can also include any of a variety of stabilizing agents, such as an antioxidant, for example. When the pharmaceutical composition includes a
20 polypeptide, the polypeptide can be complexed with various well-known compounds that enhance the in vivo stability of the polypeptide, or otherwise enhance its pharmacological properties (e.g., increase the half-life of the polypeptide, reduce its toxicity, enhance solubility or uptake). Examples of such modifications or complexing agents include sulfate, gluconate, citrate and phosphate. Polypeptides can also be complexed with molecules that
25 enhance their in vivo attributes. Such molecules include, for example, carbohydrates, polyamines, amino acids, other peptides, ions (e.g., sodium, potassium, calcium, magnesium, manganese), and lipids.

The proportion of each carrier, diluent or adjuvant is determined by the solubility and chemical nature of the compound and the route of administration according to
30 standard pharmaceutical practice. In order to obtain consistency of administration, however, it is preferred that a composition of the invention is in the form of a unit dose. For example, the unit dose presentation forms for oral administration may be tablets and capsules and may contain conventional excipients such as binding agents (e.g., acacia, gelatin, sorbitol, or polyvinylpyrrolidone), fillers (e.g., lactose, sugar, maize-starch, calcium

phosphate, sorbitol or glycine), tableting lubricants (e.g., magnesium stearate), disintegrants (e.g., starch, polyvinylpyrrolidone, sodium starch glycoallate or microcrystalline cellulose), or pharmaceutically acceptable wetting agents (e.g., sodium lauryl sulfate).

The components used to formulate the pharmaceutical compositions are preferably of high purity and are substantially free of potentially harmful contaminants (e.g., at least National Food (NF) grade, generally at least analytical grade, and more typically at least pharmaceutical grade). Moreover, compositions intended for *in vivo* use are usually sterile. To the extent that a given compound must be synthesized prior to use, the resulting product is typically substantially free of any potentially toxic agents, particularly any endotoxins, which may be present during the synthesis or purification process. Compositions for parental administration are also sterile, substantially isotonic and made under GMP conditions.

Further guidance regarding formulations that are suitable for various types of administration can be found in Remington's Pharmaceutical Sciences, Mace Publishing Company, Philadelphia, PA, 17th ed. (1985). For a brief review of methods for drug delivery, see, Langer, Science 249:1527-1533 (1990).

C. Dosage

The pharmaceutical compositions can be administered as part of a prophylactic and/or therapeutic treatments. A "therapeutically effective" amount refers to an amount that is sufficient to remedy a disease state or symptoms, particularly symptoms associated with CMV infection, or otherwise prevent, hinder, retard, or reverse the progression of disease or any other undesirable symptoms in any way whatsoever. A "prophylactically effective" amount refers to an amount administered to an individual susceptible to or otherwise at risk of a particular condition associated with CMV or CMV infection to prevent, retard or lessen the progression of the disease or the undesirable symptoms associated with the disease.

A CMV dissemination-inhibiting amount is that amount of active compound required to slow the progression of viral dissemination or reduce the amount of viral dissemination from that which would otherwise occur without administration of the compound, e.g., as determined according to the assays described herein. Or, it is an amount of active compound required to slow the progression or reduce the intensity of symptoms resulting from CMV infection or elimination thereof.

Toxicity and therapeutic efficacy of the active ingredient can be determined according to standard pharmaceutical procedures in cell cultures and/or experimental animals, including, for example, determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds that exhibit large therapeutic indices are preferred.

The data obtained from cell culture and/or animal studies can be used in formulating a range of dosages for humans. More specifically, the effective doses as determined in cell culture and/or animal studies can be extrapolated to determine doses in other species, such as humans for example. The dosage of the active ingredient typically lines within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. What constitutes an effective dose also depends upon the nature of the disease, the general state of an individual's health and the specific properties (e.g., IC₅₀) of the agent. In general terms, however, the amount of active ingredient will generally be approximately about 0.05 mg/kg to about 20 mg/kg, more preferably in the range of about 0.05 mg/kg to about 2 mg/kg, most preferably in the range of about 0.05 mg/kg to about 0.2 mg per kg of body weight per day. 0.01 to 250 mg/kg/day, often about 0.5 to 30 mg/kg/day, more often about 1 to 20 mg/kg/day, and most often about 1-10 mg/kg/day or less.

D. Administration

The compositions and the inhibitory agents disclosed herein as well as pharmaceutically acceptable salts thereof can be administered in any effective way such as via oral, parenteral or topical routes.

The compounds may be injected parenterally; this being intramuscularly, intravenously, or subcutaneously. For parenteral administration, the compound may be used in the form of sterile solutions containing other solutes, for example, sufficient saline or glucose to make the solution isotonic.

The compounds can be administered orally in the form of tablets, capsules, or granules containing suitable excipients such as starch, lactose, white sugar and the like, in the form of solutions, or sublingually. The amount of active ingredient administered orally will depend on bioavailability of the specific compound. The solid oral compositions may

be prepared by conventional methods of blending, filling, tableting, or the like. Oral liquid preparations can be in the form of emulsions, syrups, or elixirs, or can be presented as a dry product for reconstitution with water or other suitable vehicle before use. Such liquid preparations may or may not contain conventional additives.

5 The compositions can also be administered in the form of suppositories for rectal administration of the drug. For topical use, creams, ointments, jellies, solutions or suspensions, etc., containing the active ingredients are employed. As used herein, topical application is also meant to include the use of mouth washes and gargles.

10 In some instances, the active ingredient can be provided in the form of a pro-drug, that can be metabolically or chemically converted to the active ingredient by the recipient host. A wide variety of pro-drug derivatives are known in the art such as those that rely on hydrolytic cleavage or oxidative activation of the prodrug.

15 Therapeutic and prophylactic methods of involve treating patients in a pharmaceutically acceptable manner with those compounds or compositions. Such compositions may be in the form of tablets, capsules, caplets, powders, granules, lozenges, suppositories, reconstitutable powders, or liquid preparations, such as oral or sterile parenteral solutions or suspensions. The pharmaceutical compositions described herein can also be administered via an intraocular implant for treating retinitis as a result of CMV infection. In particular, active ingredients can be embedded in a polymer based implant
20 which is released into the eye over an extended period of time.

 Physicians can determine the dosage of the present therapeutic agents which will be most suitable. As described *supra*, dosages may vary with the mode of administration and the particular compound chosen. In addition, the dosage may vary with the particular patient under treatment. The dosage of the compound used in the treatment
25 will vary, depending on viral load, the weight of the patient, the relative efficacy of the compound and the judgment of the treating physician. Such therapy may extend for several weeks or months, in an intermittent or uninterrupted manner.

IX. Exemplary Utilities

30 As indicated in the Background section, CMV is an opportunistic pathogen that infects primarily fetuses *in utero* and immunocompromised adults. In the case of neonates that become infected *in utero*, the infection can cause mental retardation, deafness and various neurological sequelae. Thus, the pharmaceutical compositions and vaccines

described herein can be utilized as a prophylactic to prevent primary infection of women during pregnancy, thereby preventing transmission of the virus during gestation and birth.

Acute or re-emerging infections of CMV can result in retinitis, encephalitis and pneumocystis. Administration of the pharmaceutical compositions and vaccines
5 provided herein can be used prophylactically or therapeutically to treat such diseases.

The pharmaceutical compositions and vaccines disclosed herein can also be utilized to treat a number of diseases to which immunocompromised individuals are susceptible. Examples of such diseases include artery occlusion following heart transplants, and arthrectomy and restenosis following angioplasty. There is some evidence to suggest
10 that the arterial wall may be a site of latent CMV and that CMV induces atherosclerotic lesions. It also appears that CMV can play a role in chronic rejection syndrome and graft versus host disease. Thus, the compositions provided can be used to treat these diseases as well. Of course, other systemic sequelae associated with CMV can be treated as well using the compositions provided herein.

15 The following examples are provided to illustrate certain aspects of the methods and compositions provided herein and are not to be construed to limit the scope of these methods and compositions.

20 EXAMPLE 1

Demonstration of Expression of US28 by CMV Virions

I. Background

To gain insight into the mechanism by which CMV is disseminated, this set
25 of experiments was conducted to determine whether human CMV viral particles express US28. If so, the virus may be transported from the site of primary infection by being transported (e.g., in the circulatory system of the infected host) from the primary site of infection to another site where the viral particle becomes attached via the US28 receptor to a chemokine (e.g., fractalkine) expressed at the cell surface.

30 II. Experimental

Human dermal fibroblasts were infected with HCMV strain Toledo or HCMV TolΔUS28 (Streblow et al., 1999, *Cell* 99:511-20) at an MOI of 0.01 and

maintained at 37°C and 5% CO₂ in Dulbecco's minimal essential medium with 10% fetal calf serum and fed as necessary. At day 15 post infection supernatant was collected and clarified by two rounds of centrifugation at 400g. Virions from the clarified supernatant were pelleted at 10,000g, resuspended in TN (50 mM TRIS-Cl pH 7.5, 100 mM NaCl), and
5 purified over two consecutive 20-70% sucrose gradients by standard techniques (Britt WJ., 1984, *Virology* 135:369-78). Virions were resuspended in 500 ul of assay buffer (20 mM HEPES, 140 mM NaCl, 1 mM CaCl₂, 5 mM MgCl₂, and with 0.2% bovine serum albumin) and 0.09 mL added to each well of assay plates containing serial dilutions of fractalkine (concentrations between 0-250 nM) in triplicate.

10 Then 0.09 mL of ¹²⁵I-fractalkine diluted in assay buffer (final concentration ~2-10 fM, with ~30,000 cpm per well) was added, the plates sealed and incubated for approximately 3 hours at 4°C on a shaker platform. The assay plates were harvested using Packard filter plates, pre-soaked in PEI solution, on the vacuum harvest apparatus. Scintillation fluid (35 µL) was added to all wells, the plates were sealed and counted in a
15 Top Count scintillation counter. Control wells containing either diluent only (for total counts) or excess fractalkine (1 µg/mL, for non-specific binding) were used to calculate the percent of total inhibition for each set of compounds.

In wild type virions (Toledo), labeled fractalkine bound strongly to the virions and was competed off by unlabeled fractalkine with an IC₅₀ of about 4x10⁻¹¹.

20 However virions from a virus identical except for deletion of US28 from the genome (TolΔUS28) had virtually no binding to the labeled fractalkine (see FIG. 5).

III. Results/Conclusion

These results demonstrate that US28 is a virion molecule capable of
25 interacting with fractalkine.

EXAMPLE 2

Identification of Rhesus US28 Homologs

I. Background

30 Given the role that US28 appears to play in CMV dissemination, an *in vivo* system for conducting further studies on the receptor would be useful. However, the CMV strain infecting rats as well as the CMV that infects mice were found to lack a US28

homolog. This investigation was conducted to determine whether the genome of rhCMV contains regions having homology with the coding region for human US28.

II. Experimental

5 Rhesus dermal fibroblasts (RhDF) were infected at an MOI of 3 with rhesus CMV strain 68.1 (see ATCC # VR-677). At 96 hours post infection supernatants were collected. Supernatants were cleared by two spins at 1,500 rpm for 5 minutes in a bench top centrifuge. Virions were pelleted from the supernatant for 30 minutes at 10,000 rpm in a Beckman JA-21 or J-14 centrifuge or similar centrifuge and resuspended in 0.5 ml TN buffer
10 (0.05 M Tris/HCl, pH 7.4, 0.1M NaCl) then layered onto a 5 ml sucrose density gradient (20% to 70% w/v sucrose in TN) in a SW 50 centrifuge tube. Gradients were spun 90 minutes at 24,000 rpm in Beckman SW50 at 10 °C. The virion band was collected by piercing the tube with a needle just below band and recovered in minimal volume, then diluted 4 fold in TN buffer and spun 30 minutes at 20,000 rpm in a Beckman SW50
15 centrifuge at 10 °C to pellet virions.

The isolated virions were resuspended in TE buffer (Tris HCl 10 mM, 0.5 mM EDTA) and proteinase K added to a final concentration of 0.2ug/ml, SDS to a final concentration of 1% and RnaseA to a final concentration of 10ug/ml. The resulting mixture was incubated for 2 hours at 65 °C. The mixture was then subjected to one phenol extraction,
20 one phenol/chloroform extraction and one chloroform extraction according to standard techniques (see, e.g., Sambrook et al., 2001, MOLECULAR CLONING, A LABORATORY MANUAL, 3D ED., Cold Spring Harbor, New York; and Ausubel et al. (eds). CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Green/Wiley, N.Y. (1994-1998 and periodic supplements through year 2000).

25 Viral DNA is precipitated with ethanol in accordance with established techniques and then resuspend in sterile TE. The resulting suspension was provided to Genome Therapeutics, MA for sequencing. The DNA was used to create a shot gun library using hydroshearing and producing inserts of about 3,000 bp in length. Individual clones were sequenced using ABI Prism BigDye terminator chemistry. The 220 kb genome was
30 covered to an average accuracy of 6x sequence. Individual reads were assembled into contiguous fragments. Homologs of human CMV genes were elucidated using the BLAST X program. Sequence was further analyzed using the BioNavigator™ bio-informatic program set (Entigen Corp, CA).

III. Results/Conclusion

Analysis of the rhCMV genome indicated the presence of a number of open reading frames having homology with the human CMV US28 open reading frame. As indicated supra, the present inventors refer to these regions of homology as rhUS28.1 (SEQ ID NO:5), rhUS28.2 (SEQ ID NO:7), rhUS28.3 (SEQ ID NO:9), rhUS28.4 (SEQ ID NO:11), and rhUS28.5 (SEQ ID NO:13). Other regions having homology to human UL33 and human UL 78 were also identified and named rhUL33 (SEQ ID NO:23), rhUL33 spliced (SEQ ID NO:25) and rhUL78 (SEQ ID NO:15).

EXAMPLE 3

Expression of rhCMV US28 Homolog on Surface of CMV Infected Cells

I. Background

Having shown in Example 2 that rhesus CMV genome contained regions with homology to human US28, this study was conducted to determine whether rhesus cells infected with rhCMV express a receptor having chemokine binding activity similar to that with human cells infected with human CMV.

II. Experimental

Radioligand binding assays were carried out in the following manner. The target cells typically used in these assays were Rhesus dermal fibroblasts which had been infected with Rhesus CMV for 3-7 days. Lots of cells verified for fractalkine binding were frozen until ready for use. For the assay, cells were thawed, washed, and resuspended in assay buffer (20 mM HEPES pH 7.1, 140 mM NaCl, 1 mM CaCl₂, 5 mM MgCl₂, and 0.2% bovine serum albumin) to a concentration of from 4×10^5 to 5×10^6 cells/ml.

Serial dilutions of unlabeled fractalkine were prepared as a 10X solution in 20% DMSO, and 0.02 ml was placed in assay plates. Next 0.09 ml of cells was added to the assay plates containing the unlabeled fractalkine. Lastly, 0.09 ml of ¹²⁵I-fractalkine diluted in assay buffer (final concentration ~50 pM, with 20,000-50,000 cpm per well) was added, the plates sealed and incubated for 2-4 hours at 4 °C on a shaker platform. Assay plates were harvested using Packard GF/B filter plates (pre-soaked in 0.3% polyethyleneimine (PEI) solution) on a Packard vacuum cell harvester. Scintillation fluid was added to all wells, the plates were sealed and then counted in a Top Count scintillation counter. Control wells

containing either diluent only (for total counts) or excess unlabeled fractalkine (1 μ g/ml, for non-specific binding) were used to calculate the percent of total inhibition. IC_{50} values are those concentrations required to reduce the binding of labeled fractalkine to the receptor by 50%, and were determined by nonlinear regression curve-fitting of the dose-response assays.

5

III. Results/Conclusion

Figure 6 shows a binding plot showing that rhesus cells infected with rhCMV express a receptor protein that has binding characteristics related to those of human US28, namely the ability to bind fractalkine with high affinity ($IC_{50} = 44$ picomolar). This result is consistent with the conclusion reached in sequence studies described in Example 2 that rhCMV contains an open reading frame with homology to human US28.

10

EXAMPLE 4

Demonstration of Expression of rhesus US28 Homologs by rhCMV Virions

15

I. Background

This investigation was undertaken to determine whether rhCMV virions express a surface receptor having US28 binding characteristics similar to that of human CMV virions. As with the human virions, such expression would have important implications for the way the virus is disseminated.

20

II. Experimental

Human dermal fibroblast (HDF) were infected at an MOI of 3 with human CMV strain Toledo or a Toledo strain in which the US28 gene had been replaced with a green fluorescent protein/gpt resistance cassette (Toledo deltaUS28) (see, e.g., Vieira, J. et al. (1998) *J. Virol.* 72:8158-65). Alternatively, rhesus dermal fibroblasts (RhDF) were infected at an MOI of 3 with rhesus CMV strain 68.1 (see ATCC # VR-677). At 96 hours post infection supernatants were collected.

25

Supernatants were cleared by two spins at 1,500 rpm for 5 minutes in a bench top centrifuge. Virions were pelleted from the supernatant for 30 minutes at 10,000 rpm in a Beckman JA-21 or J-14 centrifuge or other similar centrifuge and resuspended in 0.5 ml TN buffer (0.05 M Tris/HCl, pH 7.4, 0.1M NaCl) then layered onto a 5 ml sucrose density gradient (20% to 70% w/v sucrose in TN) in a SW 50 centrifuge tube. Gradients were spun

30

90 minutes at 24,000 rpm in a Beckman SW50 centrifuge at 10 °C. The virion band was collected by piercing the tube with a needle just below the band and recovered in minimal volume, then diluted 4 fold in TN buffer and spun 30 minutes at 20,000 rpm in a Beckman SW50 centrifuge at 10 °C to pellet virions. TN/sucrose was removed and virions from the
5 HDF cells and the RhDF cells separately resuspended in PBS.

Aliquots of the virions from the two cell types were then separately contacted with ¹²⁵I-labeled fractalkine (available from, for example, Amersham and New England Nuclear) and varying concentrations of unlabeled fractalkine. These assay mixtures were then incubated for 3 hours at 4 °C.

10 Following incubation, the assay wells were harvested under vacuum using filter plates, pre-soaked with PEI solution. Scintillation fluid was added, the plates sealed and the radioactivity in the various wells counted.

III. Results/Conclusion

15 A binding plot showing the extent of binding of the various viral particles to radiolabeled fractalkine is shown in FIG. 7. The results show that HCMV virions lacking US28 do not bind fractalkine. Wild type HCMV virions expressing US28, however, do bind fractalkine tightly as expected in view of the results presented in Example 1. The chart also shows that virions purified from RhDF cells also bind to fractalkine. Thus, these
20 results demonstrate that rhCMV virions, like human CMV virions, express a protein able to bind fractalkine. This result supports the finding from the sequence comparison analysis that rhCMV contains coding regions with homolog to US28.

EXAMPLE 5

25 Inhibition of CMV Dissemination by Administration of an
Inhibitor of a US28-Receptor Interaction

I. Background

Collectively, the results from the foregoing examples demonstrate that rhesus
30 monkeys infected with rhCMV can serve as an excellent *in vivo* model system for studies on CMV dissemination. This example describes methods for conducting *in vivo* studies utilizing rhesus monkeys as such a model system.

II. Experimental

In an exemplary assay, Rhesus CMV strain 68.1 (e.g., $10^4 - 10^7$ pfu, usually 10^6 pfu, in excipient) is administered by oral inoculation (or intravenous injection) to CMV-negative animals. In “experimental” animals, an inhibitor or putative inhibitor of US28-fractalkine interaction (e.g., octoclotheptin) is also administered, while “control” animals do not receive the inhibitor. The inhibitor is administered at the same time as the virus or, alternatively, prior to or after administration of the virus (e.g., one day prior or up to 2 days post-inoculation). The inhibitor or putative inhibitor can be administered intravenously, subcutaneously or by other modes. Single or multiple injections can be administered. A slow release apparatus such as an Alzet pump (an osmotic pump) can also be utilized.

Viral infection and dissemination in experimental and control animals is determined by analyzing spread of the virus from the site of primary inoculation. Suitable assays for detecting CMV are described in Lockridge et al. (1999) *J. Virol.* 73:9576-83. Sterile blood, saliva and urine samples are collected at the time of virus administration and thereafter periodically (e.g., every day or every 3 days) and assayed for virus. According to one suitable assay, viral titer is measured in saliva, urine and blood samples, by co-cultivation of serial dilutions of sterile samples with a cell permissive for CMV replication (e.g., human dermal fibroblasts) for a period of about 2 weeks, and counting of viral plaques, using standard techniques (Spaete and Mocarski, 1985, *J Virol* 56:135-43). Inhibition of CMV dissemination is demonstrated by a 5-fold or greater (e.g., at least 10-fold) reduction in the overall titer of infectious virus in at least one, sometimes two or three of these fluids in experimental animals compared to control animals when assayed at timepoints after administration of the inhibitor (e.g., 3, 6, 9, 12, or 15 days or 1 month following administration). Inhibition of CMV dissemination can alternatively be shown by a delay in appearance of detectable virus in at least one, sometimes two or three of the these fluids in experimental animals compared to control animals.

In another suitable assay, blood is assayed for viral DNA by PCR using CMV specific primers. For example, in one embodiment, DNA is purified from plasma (e.g., using commercially available kits from Qiagen, CA), then used as template for nested PCR with primers able to amplify the rhCMV immediate early 2 gene (5' GCC AAT GCA TCC TCT GGA TGT ATT GTG A 3' (SEQ ID NO:44) and 5' TGC TTG GGG AAT CTC TGC AC 3' (SEQ ID NO:45) then 5' CCC TTC CTG ACT ACT AAT GTA C 3' (SEQ ID NO:46) and 5' TTG GGG AAT CTC TGC ACA AG 3' (SEQ ID NO:47) (see, e.g., Tarantal et al., 1998, *J Infect Dis* 177:446-50). Inhibition of CMV dissemination is demonstrated by

a difference of viral titer or kinetics (as described *supra*) as assessed by levels of viral DNA in peripheral blood.

Assays for viral dissemination can also be carried out by direct detection of CMV in tissues including lung, spleen thymus, salivary gland, bone marrow, pancreas, kidney, tonsil, liver, parotid gland, esophagus and others. Thus, in embodiment, animals are necropsied 15 to 30 days after administration of virus (e.g., day 30) and complete tissue and blood samples taken. DNA is purified from tissue (e.g. using commercially available kits from Qiagen, CA), then used as template for nested PCR as described *supra*. Dissemination can also be assayed by histology. Typically, tissue is fixed in paraformaldehyde and embedded in paraffin, or frozen in OCT for frozen sections (see, e.g., by Luna, L.G., THE MANUAL OF HISTOLOGIC STAINING METHODS OF THE ARMED FORCES INSTITUTE OF PATHOLOGY, , McGraw-Hill, 3rd edition, 1968). Sections are stained using an antibody specific for CMV (e.g., rhCMV). Inhibition of CMV dissemination is demonstrated by a difference of viral titer or kinetics (as described *supra*) as assessed by levels of viral antigens in specific tissues or organs of experimental animals compared to control animals.

In another suitable assay, levels of reactive leukocytes are assayed, e.g., by FACS analysis of blood samples. Suitable assays are described in Lockridge et al., *J Virol.* 73:9576-83, *supra*. Briefly, activated T cells are identified by dual fluorescent staining for CD3 (T cell marker, Pharmingen, clone SP34) and CD69 (very early activation marker, Becton Dickinson, clone L78) while memory T cells are identified by dual fluorescent staining for CD3 (T cell marker, Pharmingen, clone SP34) and CD45RO (memory cell marker, Dako, clone UCHL1). Inhibition of CMV dissemination is demonstrated by fewer activated T cells or memory T cells in peripheral blood of experimental animals compared to control animals (e.g., at least about 30% or about 50% fewer, often at least 80% fewer when measured following administration (e.g., 3, 6, 9, 12, or 15 days or 1 month following administration of the agent).

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

SEQUENCE LISTING

SEQ ID NO:1

5 Nucleotide sequence for HCMV Toledo US28 (same sequence as AU4.1)

ATGACACCGACGACGACGACCGCGGAACTCACGACGGAGTTTGACTACGATGAA
 GCCGCGACTCCTTGTGTTTTACCGACGTGCTTAATCAGTCAAAGCCGGTTACGT
 TGTTTCTGTACGGCGTTGTCTTTCTGTTCGGTTCATCGGCAACTTCTTGGTGATC
 TTCACCATCACCTGGCGACGTCGGATTCAATGCTCCGGCGATGTTTACTTTATCA
 10 ACCTCGCGGCCGCGCGATTGCTTTTCGTTTGTACACTACCTCTGTGGATGCAATAC
 CTCCTAGATCACAACCTCCCTAGCCAGCGTGCCGTGTACGTTACTCACTGCCTGTTT
 CTACGTGGCTATGTTTGCCAGTTTGTGTTTTATCACGGAGATTGCACTCGATCGCT
 ACTACGCTATTGTTTACATGAGATATCGGCCTGTAAACAGGCCTGCCTTTTCAG
 TATTTTTTGGTGGATCTTTGCCGTGATCATCGCCATTCCACATTTTATGGTGGTGA
 15 CCAAAAAAGACAATCAATGTATGACCGACTACGACTACTTAGAGGTCAGCTACC
 CGATCATCCTCAACGTAGAACTCATGCTCGGTGCTTTCGTGATCCCGCTCAGTGT
 CATCAGCTACTGCTACTACCGCATTTCAGAAATCGTTGCGGTGTCTCAGTCGCGC
 CACAAAGGTCGCATTGTACGGGTACTTATAGCGGTCGTGCTTGTCTTTATCATCTT
 TTGGCTGCCGTACCACCTAACGCTGTTTGTGGACACGTTAAAACTCCTCAAATGG
 20 ATCTCCAGCAGCTGCGAGTTCGAAAGATCGCTCAAACGTGCGCTCATCTTGACCG
 AGTCGCTCGCCTTTTGTCACTGTTGTCTCAATCCGCTGCTGTACGTCTTCGTGGGC
 ACCAAGTTTCGGCAAGAACTGCACTGTCTGCTGGCCGAGTTTCGCCAGCGACTCT
 TTTCCCGCGATGTATCCTGGTACCACAGCATGAGCTTTTCGCGTCGGAGCTCGCC
 GAGCCGAAGAGAGACATCTTCCGACACGCTGTCCGACGAGGTGTGTCGCGTCTC
 25 ACAAATTATACCGTAA

SEQ ID NO:2

Amino acid sequence for HCMV Toledo US28 (same sequence as AU4.1)

MTPTTTTAEALTTEFDYDEAATPCVFTDVLNQSKPVTFLYGVVFLFGSIGNFLVIFTIT
 30 WRRRIQCSGDVYFINLAAADLLFVCTLPLWMQYLLDHNSLASVPCTLLTACFYVAM
 FASLCFITEIALDRYYAIVYMRYRPVKQACLFSIFWWIFAVIIAIPHFMVVTKKDNQC
 MTDYDYLEVSYPIILNVELMLGAFVIPLSVISYCYRISRIVAVSQRHKGRIVRVLIA
 VVLVFIIFWLPYHLTLFVDTLKLLKWISSSCEFERSLKRALILTESLAFCHCCLNPLLY

VFVGTKFRQELHCLLAEFRQRLFSRDVSWYHSMFSRRSSPSRRETSSDTLSDEVCRV
SQIIP*

5 SEQ ID NO:3

Nucleotide sequence for HCMV VHL/E US28

ATGACACCGACGACGACGACCGCGGAACTCACGACGGAGTTTGACTACGACGAT
GAAGCGACTCCCTGTGTCCTACCGACGTGCTTAATCAGTCGAAGCCAGTCACGT
TGTTTCTGTACGGCGTTGTCTTTCTCTTCGGTTCCATCGGCAACTTCTTGGTGATCT
10 TCACCATCACCTGGCGACGTCGGATTCAATGTTCCGGCGATGTTTACTTTATCAA
CCTCGCGGCCGCCGATTTGCTTTTCGTTTGTACACTACCTCTGTGGATGCAATACC
TCCTAGATCACAACCTCCCTAGCCAGCGTGCCGTGTACGTTACTCACTGCCTGTTTC
TACGTGGCTATGTTTGCCAGTTTGTGTTTTATCACGGAGATTGCACTCGATCGCTA
CTACGCTATTGTTTACATGAGATATCGGCCTGTAAACAGGCCTGCCTTTTTCAGT
15 ATTTTTTGGTGGATCTTTGCCGTGATCATCGCCATTCCACACTTTATGGTGGTGAC
CAAAAAGACAATCAATGTATGACCGACTACGACTACTTAGAGGTCAGTTACCC
GATCATCCTCAACGTAGAACTCATGCTCGGTGCTTTCGTGATCCCGCTCAGTGTC
ATCAGCTACTGCTACTACCGCATTTCAGAAATCGTTGCGGTGTCTCAGTCGCGCC
ACAAAGGCCGCATTGTACGGGTACTTATAGCGGTGCTGCTTGTCTTTATCATCTTT
20 TGGCTGCCGTACCACCTGACGCTGTTTGTGGACACGTTGAAACTGCTCAAATGGA
TCTCCAGCAGCTGCGAGTTCGAAAAATCACTCAAGCGCGCGCTCATCTTGACCGA
GTCACTCGCCTTTTGTCACTGTTGTCTCAATCCGCTGCTGTACGTCTTCGTGGGCA
CCAAGTTTCGGCAAGAACTGCACTGTCTGCTGGCCGAGTTTCGCCAGCGACTGTT
TTCCCGCGATGTATCCTGGTACCACAGCATGAGCTTTTCGCGTCCGAGCTCGCCG
25 AGCCGAAGAGAGACGTCTTCCGACACGCTGTCCGACGAGGCGTGTCGCGTCTCA
CAAATTATACCGTAA

SEQ ID NO:4

Amino acid sequence for HCMV VHL/E US28

30 MTPTTTTAELTTEFDYDDEATPCVLTDVLNQSKPVTFLYGVVFLFGSIGNFLVIFTIT
WRRRIQCSGDVYFINLAAADLLFVCTLPLWMQYLLDHNSLASVPCTLLTACFYVAM
FASLCFITEIALDRYYAIVYMRYRPVKQACLFSIFWWIFAVIIAIPHFMVVTKKDNQC
MTDYDYLEVSYPIILNVELMLGAFVIPLSVISYCYRISRIVAVSQSRHKGRIVRVLIA
VVLVFIIFWLPYHLTLFVDTLKLLKWISSSCEFESLKRALILTESLAFCHCCLNPLLY

VFVGTKFRQELHCLLAEFRQRLFSRDVSWYHSMFSRRSSPSRRETSSDTLSDEACRV
SQIIP*

5 SEQ ID NO:5

Nucleotide sequence for RhUS28.1

ATGAATAACACATCTTGCAACTTCAACGTCACTCTCAACGCATCGGCACCAAGCC
GATACATAGCTATTGCTATGTACAGCATTGTTATCTGTATCGGGTTGGTTGGAAA
CCTGCTGTTATGCATCGTGTTAGTCAAGAAACGCAAACCTGCGATATTCCAGCGAT
10 GTTTATTTTTTCCACGCCTCTATGGCCGACCTCGTCAGCACTGTCATGCTACCGCT
CTGGCTACATTATGTCCTCAACTTTGCCCAACTCTCTCGAGGAGCCTGTATCAGCT
TTTCGGTGACTTTCTATGTTCCCCTTTTCGTTTCAGGCCTGGTTACTCATTTCATCG
CTATGGAGCGATATTCCAACCTTAGTATGGATGGCACCCATTAGCGTTAAGACGGC
CTTTAAACACTGCATAGGAACCTGGATCGTATCTGCCTTCGTGGCATCACCCCTAC
15 TACGCATACAGAACTCACACGACGAACACGAATGCATTCTAGGAACTACACT
TGGCACATTAACGAACCGCTACACACGTGTATGGATGTGGTGATCATAGTATGGA
CCTTTTTGGCCCCAGTACTGGTAACCATTATAGCAAGCGTCAAAATGAGACGAAC
GACCTGGGGCAATACTAGGTAAACGAAAAGAACAGCGACATTCTTATAGTACT
AGTTGTCATGACAGTGTTCTTTTGGGGACCGTTTAATATCGTGTTGGTTATTGACA
20 ATATTTTACAGAGATACTATGATACCACGAATTGCGATGTAGAAAAGATTAAAC
ATATCATGGCTATGATCTCAGAAGCCATTGTTTATTTTCGCGGTATTACAGCACCT
ATTATTTATGTAGGGATTAGTGGCAGATTTTCGCGAAGAGATTTACTCTCTGTTTA
GACGCCAGCCGTATAACGATTTGGACCCCGATGCCAATCAATTCATGATTGAACT
CACTAGCCAGGGAAGAAGTAGAAATAGAAATGCTAGACAATCGGAAAGCAATG
25 TACCGCAACCAGAAGAATGCTTCTGGTAA

SEQ ID NO:6

Amino acid sequence for RhUS28.1

MNNTSCNFNVTNLNASAPSRYIAIAMYSIVICIGLVGNLLLCIVLVKKRKLRYSSDVYFF
30 HASMADLVSTVMLPLWLHYVLNFAQLSRGACISFSVTFYVPLFVQAWLLISIAMERY
SNLVWMAPISVKTAFAKHCIGTWIVSAFVASPYAYRNSHDEHECILGNYTWHINEPL
HTCMDVVIIVWTFLAPVLVTIIASVKMRRTTWGNTRLNEKNSDILIVLVMTVFFWG
PFNIVLVIDNILQRYYYDTTNC DVEKIKHIMAMISEAIVYFRGITAPIIYVGISGRFREEIY
SLFRRQPYNDLDPDANQFMIELTSQGRSRNRNARQSES NVPQPEECFW*

SEQ ID NO:7

Nucleotide sequence for RhUS28.2

5 ATGACCAACGCCGGACACTGTCACATAAACGAAAGTCTCGCGTCGTATGGAATC
 GCTCCCGCAGCTACCATTACCTTATACAGCATTGCGGGAATCTGCGGTGTCACGG
 GAAATCTGTTAATACTTTTGGTTTTGTTACGAGACGCATACACTGGTTCGCAAA
 TGACATCTACTATCTCAACATGATCTTTACAGACTTTCTTGTTTTTCATTACATTAC
 CCGCCTGGGTTTACTACCTGCTGAATTACACACAACCTCTCACACTATGCCTGCATT
 10 GCTCTATCATTTGTTTTTTTACGTTTCCATTTTTTATTCAAGCTGACTTTATGGTAGCA
 GTGGCTATCGAGCGTTATCGAAGCCTAGTGAAAAACAAACCCCTTAGCGTAAAA
 AAAGCCAGCGTCAGCTGCGCGTGCATCTGGATCATTGTTATTATAGTGTCTTCAC
 CATACTACATGTTTAGATCGCAACACGAAACAAATTCTTGCAATTCTAGGAAACTA
 CACCTGGCATATGAACAGTCCTTTTCGCACCACAATGGACGCATCCATTAAACATT
 15 TGGTCTTTTGTCTGTTCCGGCCGTGACGACCTTGTTAATAGCCAGACGAATTTATGT
 ATGTACTTCAGGCAACAAAAAAATGAACGCCAGAGCCAGTGGTTTGTTAGAGGC
 CATGGTGATTAGCATGTTATTCTTCGGAGGACTTTTCAACCTGAACATCTTTCGAG
 ACATAGTTTCGGACACATCGGAAGACAATAAAGACTGCACATATCTTAAGCAGG
 AACACTTTATTTCGCATGGTCGGTGTGGCCCTCGTTTACGGGCGCGCTATATTCAA
 20 CCCTTTTATGTATATGTGTGTGAGTACCAGATTGCGCCAAGAAATAAAATGTTTG
 TTTATGCGAATACCTTATGAAACACTAGATGCAGAACACGCTAAACTCATGGTTA
 ATTTAAAAAACAGAAATGCTAATGTACCCGATCCTAAACCTCGTGAATATGAATC
 TGTGTTATAG

25 SEQ ID NO:8

Amino acid sequence for RhUS28.2

MTNAGHCHINESLASYGIAPAATITLYSIAGICGVTGNLLILLVLFTRRIHWFANDIYY
 LNMIFTDLFLVFITLPAWVYYLLNYTQLSHYACIALSFVIFYVSIFIQADFMVAVAIERYR
 SLVKNKPLSVKKASVSCACIWIIVIVSSPYMFRSQHETNSCILGNYTWHMNSPFRTT
 30 MDASINIWSFVVPVAVTTLLIARRIYVCTSGNKKMNARASGLLEAMVISMLFFGGLFN
 LNIFRDIVSDTSEDNKKDCTYLKQEHFIRMVGVALVYGRAIFNPFMVMCVSTRRLRQEI
 CLFMRIPIYETLDAEHAKLMVNLKNRNANVPDPKPREYESVL*

SEQ ID NO:9

Nucleotide sequence for RhUS28.3

ATGACCAACACTAACAATACGACTTGTCATCTCAACGGAACCTTTCGAAACTTTTA
 AAATCACCCGTCCAGTAGCCATCAGCGCCTACACTGTACTCGTGGTTATCGGACT
 TTTGGGAAACATTGTGCTGCTCAGCGTGCTCGTCGTGAAACGCAAGCTCAAGTTT
 5 CCGAATGACATTTACTTTTTCAACGCGTCTTTGGCAGACGTTTTTGCCGTCTGCAT
 GTTGCCCGCCTGGGTAACTATGCACTGGACTCCACACAACCTTAGCAAGTTCTCA
 TGTATCACTTTTACGTTTGGTTTTTACGTCTCCCTGTTCATCCAGGCCTGGATGCT
 CATTCTGGTCACCCTGGAGCGATACGGATCTCTAGTCTGGATCGCCCCGATCACC
 AGAAACAAAGCCATAGCGAATTGTGTACTCTTTTGGCTTGTTTCCATCTTCTTGGC
 10 CGCACCTTACTACTCTTTTAGAAACGAAAGCAACGAACACCAATGCATCATGAG
 AAACCTATACCTGGAGCGTTGGTGAAACATGGCACATAGCCCTGGATTTCTTAATT
 ACGCTCATTACATTTATCATGCCAGTGACTATTGTGTTAGCTCTGAGTTTCAAAT
 GGCCAGATGGTCAACCTTTGGTTACAGAAACCTCACCAGCAGAACCAGTCTTATC
 CTTATTTTGATACTGACAGTAGCAGCAGGGTTCTGGGGACCTTTTCACCTATTTAT
 15 GTTTATAGAAAACGTGGCAGGGCAGATTTACCACATTCAAAGGATTGCTGGTA
 CTTACAGCTCAGACACTTGTGTAGCTTGATGACCGAAACCCTAGTGTTTCTACGT
 TCAGTTTTTAACCCTTATATTTATATGATAATCAGTTACAAGTTTAGGCAGCAGGT
 GCGCAGTCTACTCAAGCGTACTCAGTATGATGCTTTGGACACGACTCAGTTAGCA
 GAAACTATGCAGCTGAAAGCGAAAGGTGTGCCGGTGTCCGACCCCGCGCCGCAT
 20 GACTGCGAATGCTTTTTGTAA

SEQ ID NO:10

Amino acid sequence for RhUS28.3

MTNTNNTTCHLNGTFETFKITRPVAISAYTVLVVIGLLGNIVLLSVLVVKRKLKFPNDI
 25 YFFNASLADVFAVCMLPAWVNYALDSTQLSKFSCITFTFGFYVSLFIQAWMLILVTLE
 RYGSLVWIAPITRNKAIANCVLFWLVSIFLAAPYYSFERNESNEHQCIMRNYTWSVGE
 TWHIALDFLITLITFIMPVTIVLALSFKMARWSTFGYRNLTSTRSLILILILTVAAGFWG
 PFHLFMFIENVAGQIYHIQKDCWYLQLRHLCSLMTETLVFLRSVFNPYIYMIISYKFR
 QQVRSLLKRTQYDALD TTQLAETMQLKAKGVPSDPAPHDCECFL*

30

SEQ ID NO:11

Nucleotide sequence for RhU28.4

ATGAATTCGAGCCAGCACAAACATAAGCGTGTTTCTCTCCATTGGAGCAGGGCCCG
 TCATTACCGGATACACGTGCGTTTTTCTGTTCGGGATTCTGGGACACTTTTACTTG

TATTGGAAAAACCATCAGAGACGACACCGGACAAACAGTTTCAGTGATGTTTTAT
 TTCGACATCTCATGATCACCGAAGAGGTCTTTACCCTCACCATTCCCGTCTGGGC
 GTATCACTTAACACTACTCACGGCAACTTACCGGGGCTCGTGGTGCCGAAGTCTCACC
 TTCGTTTTTTTATCTAACGGTATTCGCTCGTGCCTTCTTTTACCTGCTCCTCATCTGG
 5 GACCGATACAGCGTAATCATCTGCAGACACCCTCTCCCCGTTAATCTGAACTACA
 GTCAGGTCATAGGCCTGTCTGTCTGGCTGGTTGCCGTACTGTCAGCATCACCGTT
 CTCCATTTTTTAACGGAAGTGTGAAACAATGCCTGGGCAACATGGGCAGCATACCC
 AGCGAATCGTCTGCCGTTCTTAACCTGGAAGTGCACCTGTGCTCCTTCTGGTTACC
 GCTCATCATGTCTGGCTAACTGTTACTACCAAGCAAAACGCCGAGCATCGCCTGAC
 10 CAACTCCACGAACCTTTACCGATGCAGTTTGCTAATTACCATTATCACAACCTTACG
 CTATCGTATGGTTTCCTTTCCATCTCGCTTTACTCATAGACGCCCTGATTAGCATA
 AGCCATGTAGAACCCTCTAGCGCTCTCCACTGGGCATCCATTGTCGTTACCTGTA
 AATCATTTACATTTGTATATGCGGGCATAAGCCCACTAGTGTATTTACATGCTG
 CCCCACCGTACGTCGCGAACTGCTGATGTCTCTACGTCCATTCTTCACCTGGATTT
 15 CCAGCAAAACGCGGCGAGGCTACGCTCCGATTAAACACAACCTTTAAACATCC
 CCGACGAGCCGATAGATAACAAGTCACCGCACCTGTAAACGAATAA

SEQ ID NO:12

Amino acid sequence for RhU28.4

20 MNSSQHNISVFLSIGAGPVITGYTCVFLFGILGHFYLYWKNHQRRHRTNSFSDVLFRRH
 LMITEEVFTLTIPVWAYHLTTHGNLPGSWCRSLTFVFYLTVFARAFFYLLLIWDRYSV
 IICRHPLPVNLNYSQVIGLSVWLVAVLSPFSIFNGSVKQCLGNMGSIPESSAVLNL
 EVHLCSEFWLPLIMSANCYYQAKRRASPDQLHELYRCSLLITIITYAIVWFPFHLALLI
 DALISISHVEPSSALHWASIVVTCKSFVYAGISPLVYFTCCPTVRRELLMSLRPFFT
 25 WISSKTRRGYAPIKTQPLNIPDEPIDNKSPHLLNE*

SEQ ID NO:13

Nucleotide sequence for RhUS28.5

30 ATGACTACCACCACAATGAGTGCTACCACGAATTCCAGTACCACGCCTCAAGCA
 AGCAGCACCACGATGACAACGAAGACAAGCACTCCTGGCAATACAACACTACTGGC
 ACTACGTCCACCCTGACAACGATATCAACAACCTTCTAATGCTACCAGCATAACGT
 CTAATTTAAGCACTACCGGAAACCAAACCTGCAACTACCAATGCTACTACCTTCAG
 TTCCACATTAACAACATCTACAAATATAAGCAGTACATTTTCGACAGTTTCTACC

GTCGCATCCAATGCAACATGTAATTCTACAATCACAACGAATATTACAACCTGCTT
 TTA CTACAGCAGCAAACACTACCGCAAGCAGCCTCACCAGCATCGTAACTTCACT
 TGCCACTACCATTGAAACCACATCATTTGATTATGATGAGTCAGCAGAAGCTTGC
 AACTTAACAGACATCGTTCATACTACTAGATCAGTGACAGTTACTTTCTATACTA
 5 TCATATTCATACTCGGCCTTTTGGGAAACTTTCTGGTTCTTATGACCATCATTTGG
 AACCGTCGCATTTTCCTTTATGGTTGAAATATATTTTCGTTAATCTAGCAATCTCCGA
 TCTTATGTTTGTATGTACTTTACCATTTTGGATAATGTATCTTCTTGAGCACGACG
 TCATGTCACATGCATCCTGTGTAGCAATGACAGCCATTTTTTTATTGCGCGCTGTTT
 GCCAGCACTGTTTTCTCTTGCTAATTGTTTTAGACAGATGTTACGCTATTCTATT
 10 AGGTACAGAAAAAGCAAATAGACGTTTATTGCGCAATGCTGTTTCTGGATGCATG
 CTCATGTGGGGATTGTGTTTCATTTTAGCATTACCTCATTTTATCTTTATGAAGAA
 AGGAACCAACGTATGTGTAGCAGAGTATGAACCAGGACTTAACAATTTCTATGTT
 ATTTTTATCAATACTGAGGTGAACCTATGCACCCTAGTTTTGCCAGCCGCAGCCA
 TTATCTACTGGTATCTTAAACTAACCAAAGCACTCAAACCCATGAACGACTGCG
 15 TCATAGGCTAACGTCTCTAAACATAGTGTTAGCTGTTGTCATTGTATTTGCTTTGT
 TTTGGCTGCCGTATAATCTCATGCTTATGATGTATAGCTTAGTTCACATGCAGATA
 CCTTGGGAATGCAGCTCTGAAAAAATACTGAGACGAAGTTTAATTATTACAGAAT
 CCATCGCCCTCAGTCACTGTTGCATCAACCCCATATCTACTTGCTCTTCGGACCT
 CGCTGTCGAAGCGAGTTCTGTCACCTGTTGCGATGTTGCTTTACGCGCTTATGTCC
 20 ACACAGATCCTGGAGTTCCATACGTGCAGAGACGGTGTCCATCAGTCTCAGTCAC
 TCACAGGTATCTGCATCATCTGAGGATGATGACAACGATGTGCATGATGAATTGC
 AATTTTAAATTGA

SEQ ID NO:14

25 Amino acid sequence for RhUS28.5
 MTTTMSATTNSSTTPQASSTMTTKTSTPGNTTTGTTSTLTTISTTSNATSITSNLSTT
 GNQTATTNATTFSSLTSTNISSTFSTVSTVASNATCNSTITTNITTAFTTAANTTASS
 LTSIVTSLATTIETTSFDYDESAEACNLTDIVHTTRSVTVTFYTIIFILGLLGNFLVLMTH
 WNRRISFMVEIYFVNLAISDLMFVCTLFPFWIMYLLEHDMVSHASCVAMTAIFYCALF
 30 ASTVFLLLIVLDRCYAILLGTEKANRRLLRNAVSGCMLMWGLCFILALPHFIFMKKG
 TNVCVAEYEPGLNNFYVIFINTEVNLCTLVLPAAAIYWYLKLTALKTHERLRHRLT
 SLNIVLAVVIVFALFWLPYNLMLMMYSLVHMQIPWECSSEKILRRSLITESIALSHCC
 INPIIYLLFGPRCRSEFCHLLRCCFTRLCPHRSWSSIRAETVSISLSHSQVSASSEDNDN
 DVHDELQFLI*

SEQ ID NO:15

Nucleotide sequence for HCMV AD169 UL78

5 ATGTCCCCTTCTGTGGAGGAGACTACCTCAGTCACCGAGTCCATCATGTTCGCTA
TTGTGAGTTTCAAACACATGGGCCCCGTTCTGAAGGCTACTCTATGTCGGCCGATCG
CGCCGCCTCGGATCTACTCATCGGCATGTTCGGCTCCGTTAGCCTGGTCAACCTG
CTGACTATCATCGGTTGCCTCTGGGTGTTGCGTGTTACGCGGCCGCCCGTGTCCGT
GATGATTTTTACTTGAATCTGGTACTTAGTCAGTTTTTTTTCCATCCTGGCCACCA
10 TGTTGTCCAAGGGTATCATGCTGCGTGGCGCTCTAAATCTCAGCCTCTGTGCGCTTA
GTGCTCTTTGTGCGACGACGTGGGCCTATATTCGACGGCGTTGTTTTTCCTCTTTCT
GATACTGGATCGTCTGTGCGGCCATATCTTACGGCCGTGATCTCTGGCATCATGAG
ACGCGCGAAAACGCCGGCGTGGCGCTCTACGCGGTCGCCTTTGCCTGGGTCTTT
CCATCGTAGCCGCTGTGCCCACCGCCGCTACGGGTTCCTGGACTACCGTTGGCT
15 AGGCTGTCAGATCCCTATACAGTATGCCGCGGTGGACCTCACCATCAAGATGTGG
TTTTTGCTGGGGGCGCCCATGATCGCCGTACTGGCTAACGTGGTAGAGTTGGCCT
ACAGCGATCGGCGCGACCACGTCTGGTCCTACGTGGGTCTGTGTCTGCACCTTCTA
CGTGACGTGTCTCATGCTGTTTGTGCCCTACTACTGCTTCAGAGTCCTACGCGGTG
TACTGCAGCCCGCTAGCGCGGCCGGCACCGGTTTCGGCATTATGGATTACGTGGA
20 ATTGGCTACGCGTACCCTTCTCACCATGCGTCTTGGCATTCTGCCGCTCTTTATCA
TTGCGTTCTTCTCCCGCGAGCCCAAGGATCTGGATGACTCCTTTGATTATCTG
GTCGAGAGATGTCAGCAAAGCTGCCACGGTCATTTTCGTACGTCGGTTGGTGCAGG
CGTTGAAGCGGGCTATGTATAGCGTGGAGCTGGCCGTGTGTTACTTTTCTACGTC
CGTCCGAGACGTCGCCGAGGCGGTGAAAAAGTCCTCCAGCCGTTGTTACGCCGA
25 CGCGACGTCGGCGGCCGTTGTGGTAACGACAACCACGTCGGAGAAAGCCACGTT
GGTGGAGCACGCGGAAGGCATGGCTTCCGAAATGTGTCCTGGGACTACGATCGA
TGTTTCGGCCGAAAGTTCCTCCGTCTCTGCACCGACGGCGAAAACACCGTCGCG
TCGGACGCGACGGTGACGGCATTATGA

30 SEQ ID NO:16

Amino acid sequence for HCMV AD169 UL78

MSPSVEETTSVTESIMFAIVSFKHMGPFEGYSMSADRAASDLLIGMFGSVSLVNLLTII
GCLWVLRVTRPPVSVMIFTWNLVLSQFFSILATMLSKGIMLRGALNLSLCRLVLFVD
DVGLYSTALFFLFLILDRLSAISYGRDLWHHETRENAGVALYAVAFWVLSIVAAMP

TAATGSLDYRWLGCQIQYAAVDLTIKMWFLLGAPMIAVLANVVELAYSDDRRDHV
 WSYVGRVCTFYVTCLMLFVPYYCFRVLRGVLQPASAAGTGFGIMDYVELATRTLLT
 MRLGILPLFIIAFFSREPTKDLDDSFYDLVERCQQSCHGHFVRRLVQALKRAMYSVEL
 AVCYFSTSVRDVAEAVKKSSSRCYADATSAAVVVTTTTSEKATLVEHAEGMASEMC
 5 PGTTIDVSAESSSVLCTDGENTVASDATVTAL*

SEQ ID NO:17

Nucleotide sequence for RhUL78

10 ATGATTACGGAGCGCGTCCTCGCAGGCATCCTCGCGGGCATGACGGCCGCGGGG
 AGTTTGGTCATTCTCCTCGCGGTTGTTATGTGGTTGAACATGTTAGATCGCGCTGG
 CATGCCAATGGCCGTTGGGCATTACACAGGGAACCTGGTGTGACTCAGGTCATC
 TGTATCTTCTCCATGCTGGCGTCTAAAATTGTTGGCATGACGAGTGCGGCCAACA
 TGGGCTTCTGCGGCATCGTGGTTTTTCTGGAAGACACTGGCCTCTATGTCACCTCG
 15 CTGCTCTTCATGTTTATGATCCTGGATCGCATGGCGGGCTTTTCTTAACGGGGCGTCT
 TTTCTGGAGGCAGCAGACGACGAAGCAGAATCTGAGTACAAGCGTGTACATTAT
 TCTGTTTTGCTGGGTGTTGGGAATGGCCGCGGCTGTTCCCAGCGCGGCTGTGGCT
 GCACCCAATTCCAGGTGGGAACGCTGCGAAATTCCAGTGTCATATGCCGCAATCG
 ACATGATTGTGAAGCTCTGGTTTGTGCTGTTGGCACCCGTCGTGCTGATTATGGCT
 20 GTGATCATTCAATCTTCCTATCATCGTGATCGGGAGAGGATCTGGTACTATGCCA
 GACGTGTGTTTCATGTTCTACACGGCCTGCTTTGTCATGATGGTGCCTTATTACTTC
 GTCAGAGTCATGCTGAGCGACTTTGCTTTGGTTGATATAAAAACAAAACGGCG
 AACAGCGACGGTTGTGATTCGACATTTCTTGATTATCTGAACATGTTCACTCACG
 TGATTTACAGTTTTTAAGTTGGTGGTGTGTTTGTCTTTGTTTCATTGTCCTGTTTTGCTCCA
 25 TAAACCCGATGGAAACGCTGGAAGAATGCTTGGAGAGGGCCGATGCTGAGAGGC
 AAAGTCGGTCAGAAGCATCCCAGGGTGAAAGGAGGCTGCCAATCAACACATGCT
 GTATAAAGTTGATTGAATTGATAAAGCAGTATGTAAGCACTCTCTCTAAAGCCAC
 GAGGGACAATTCTGGCGAAAGGGCCAATTTGCCAGAGAATGCTGAAGATATTGG
 AACAACTGGCAGTGATCAGCTACCGACTGAGGTCACCGTGACCCCAAATTCATC
 30 GGCTGTGTTTAGCACTGGAGGAACGGTGTCTCCAGTCTAA

SEQ ID NO:18

Amino acid sequence for RhUL78

MITERVLAGILAGMTAAGSLVILLAVVMWLNMLDRAGMPMAVGHYTGNLVLTQVI
 CIFSMLASKIVGMTSAANMGFCGIVVFLED TGLYVTSLLFMFMILDRMAAFLNGRLF
 WRQQTTKQNLSTSVYIILFCWVLGMAAAVPSAAVAAPNSRWERCEIPVSYAAIDMIV
 KLWFLVLLAPVVLIMAVIIQSSYHRDRERIWYYARRVFMFYTACFVMMVPYYFVRVM
 5 LSDFALVDIKTKTANS DGCDSTFLDYLNMFT HVIYSFKLVVFALFIVLFCSINPMETLE
 ECLERADAERQSRSEASQGERRLPINTCCIKLIELIKQYVSTLSKATRDN SGERANLPE
 NAEDIGTTGSDQLPTEVTVPNSSAVFSTGGTVSPV*

10 SEQ ID NO:19

Nucleotide sequence for HCMV AD169 UL33

ATGACAGGGCCGCTATTCGCCATTCTGAACCACCGAAGCCGTACTCAACACATTCA
 TCATCTTCGTGGGCGGTCCACTTAACGCCATAGTGTTGATCACGCAGCTGCTCAC
 GAATCGCGTGCTTGGCTATTCGACGCCCACCATTACATGACCAACCTCTACTCT
 15 ACTAATTTTCTCACGCTTACTGTGCTACCCTTTATCGTACTCAGCAACCAGTGGCT
 GTTGCCGGCCGGCGTGCCCTCGTGTAATTTCTATCGGTGATCTACTACTCAAGC
 TGCACAGTGGGCTTTGCCACCGTAGCTCTGATCGCCGCCGATCGTTATCGCGTCC
 TTCATAAACGAACATACGCACGCCAATCATACCGTTCAACCTATATGATTTTGCT
 ATTGACATGGCTCGCTGGACTAATTTTTTCCGTGCCCGCAGCTGTTTACACCACG
 20 GTGGTGATGCATCACGATGCCAACGATACCAATAATACTAATGGGACACGCCACC
 TGTGTACTGTACTTCGTAGCTGAAGAAGTGACACACAGTGCTGCTTTCGTGGAAAG
 TGCTGCTGACGATGGTATGGGGTGCCGCACCCGTGATAATGATGACGTGGTTCTA
 CGCATTCTTCTACTCAACCGTACAGCGCACGTCACAGAAACAAAGGAGTCGTACC
 TTAACCTTTGTTAGCGTGCTACTCATCTCCTTCGTGGCGCTACAAACTCCCTACGT
 25 CTCTCTCATGATCTTCAACAGTTATGCCACAACCGCCTGGCCCATGCAGTGTGAA
 CACCTCACACTGCGACGCACCATTTGGCACGCTGGCGCGTGTGGTGCCCCACCTAC
 ACTGCCTCATTAATCCCATCCTGTACGCGCTGCTGGGTCATGATTTTCTGCAACGC
 ATGCGGCAGTGTTTCCGCGGTGAGTTGCTGGACCGCCGCGCTTTCCTGAGATCGC
 AGCAGAATCAGCGAGCTACAGCGGAGACAAATCTAGCGGCTGGCAACAATTCAC
 30 AATCAGTGGCTACGTCATTAGACACCAATAGCAAAAACCTACAATCAGCACGCCA
 AACGCAGCGTGTCTTTCAATTTTCCCAGCGGTACGTGGAAAGGCGGGCCAGAAAA
 CCGCGTCCAACGACACATCCACAAAAATCCCCCATCGACTCTCACAATCGCATCA
 TAACCTCAGCGGGGTATGA

SEQ ID NO:20

Amino acid sequence for HCMV AD169 UL33

MTGPLFAIRTTEAVLNTFIIFVGGPLNAIVLITQLLTNRVLGYSTPTIYMTNLYSTNFLT
5 LTVLPFIVLSNQWLLPAGVASCKFLSVIYYSSCTVGFATVALIAADRYRVLHKRTYAR
QSYRSTYMILLLTWLAGLIFSVPAAVYTTVVMHHDANDTNNTNGHATCVLYFVAEE
VHTVLLSWKVLLTMVWGAAPVIMMTWFYAFFYSTVQRTSQKQRSRTLTFVSVLLIS
FVALQTPYVSLMIFNSYATTAWPMQCEHLTLRRTIGTLARVVPHLHCLINPILYALLG
HDFLQRMQRQCFRGQLLDRRAFLRSQQNQRATAETNLAAGNNSQSVATSLDTNSKNY
10 NQHAKRSVSFNFPSGTWKGGQKTASNDTSTKIPHRLSQSHHNLSGV*

SEQ ID NO:21

Nucleotide sequence for HCMV AD169 UL33 spliced

15 ATGGACACCATCATCCACAACCTCGACCCGCAACAACACTCCTCCGCACATCAATG
ACACTTGCAACATGACAGGGCCGCTATTCGCCATTCTGAACCACCGAAGCCGTACT
CAACACATTCATCATCTTCGTGGGCGGTCCACTTAACGCCATAGTGTTGATCACG
CAGCTGCTCACGAATCGCGTGCTTGGCTATTCGACGCCACCATTTACATGACCA
ACCTCTACTCTACTAATTTTCTCACGCTTACTGTGCTACCCTTTATCGTACTCAGC
20 AACCAGTGGCTGTTGCCGGCCGGCGTGGCCTCGTGTAATTTCTATCGGTGATCT
ACTACTCAAGCTGCACAGTGGGCTTTGCCACCGTAGCTCTGATCGCCGCCGATCG
TTATCGCGTCCTTCATAAACGAACATACGCACGCCAATCATACCGTTCAACCTAT
ATGATTTTGCTATTGACATGGCTCGCTGGACTAATTTTTTCCGTGCCCCGCAGCTGT
TTACACCACGGTGGTGATGCATCACGATGCCAACGATACCAATAATACTAATGG
25 GCACGCCACCTGTGTACTGTACTTCGTAGCTGAAGAAGTGACACACAGTGCTGCTT
TCGTGGAAAGTGCTGCTGACGATGGTATGGGGTGCCGCACCCGTGATAATGATG
ACGTGGTTCTACGCATTCTTCTACTCAACCGTACAGCGCACGTACAGAAACAAA
GGAGTCGTACCTTAACCTTTGTTAGCGTGCTACTCATCTCCTTCGTGGCGCTACAA
ACTCCCTACGTCTCTCTCATGATCTTCAACAGTTATGCCACAACCGCCTGGCCCAT
30 GCAGTGTGAACACCTCACACTGCGACGCACCATTTGGCACGCTGGCGCGTGTGGT
GCCCCACCTACACTGCCTCATTAATCCCATCCTGTACGCGCTGCTGGGTCATGATT
TTCTGCAACGCATGCGGCAGTGTTTCCGCGGTCAGTTGCTGGACCGCCGCGCTTT
CCTGAGATCGCAGCAGAATCAGCGAGCTACAGCGGAGACAAATCTAGCGGCTGG
CAACAATTCACAATCAGTGGCTACGTCATTAGACACCAATAGCAAAAACCTACAA

TCAGCACGCCAAACGCAGCGTGTCTTTCAATTTTCCCAGCGGTACGTGGAAAGGC
 GGCCAGAAAACCGCGTCCAACGACACATCCACAAAAATCCCCCATCGACTCTCA
 CAATCGCATCATAACCTCAGCGGGGTATGA

5

SEQ ID NO:22

Amino acid sequence for HCMV AD169 UL33 spliced

MDTIHNS¹TRNNTPPHINDTCNMTGPLFAIRTTEAVLNTFIIFVGGPLNAIVLITQLLTN
 RVLGYSTPTIYMTNLYSTNFLTLTVLPFIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF
 10 ATVALIAADRYRVLHKRTYARQSYRSTYMILLTWLAGLIFSVPAAVYTTVVMHHD
 ANDTNNTNGHATCVLYFVAEEVHTVLLSWKVLLTMVWGAAPVIMMTWFYAFFYS
 TVQRTSQKQRSRTLTFVSVLLISFVALQTPYVSLMIFNSYATTAWPMQCEHLTLRRTI
 GTLARVVP²PHLHCLINPILYALLGHDFLQRM³RQCFRGQLLDRRAFLRSQQNQRATAET
 NLAAGNNSQSVATSLDTNSKNYNQHAKRSVSFNFPSGTWKGGQKTASNDTSTKIPH
 15 RLSQSHHNLSGV*

SEQ ID NO:23

Nucleotide sequence for RhUL33

20 ATGACCAATCTTTACTCTGCCAATTTTCTCACCTTGATAGTACTTCCTTTTATCGTT
 TTAAGCAATCAACACCTTTTACCTGCCAGTGCAGTAACCTGTAAATTTCTCTCCCT
 GTTGTACTACTCTAGCTGCAGCGTAGGTTTTGCTACAGTGGCACTGATAGCGGCC
 GACCGATACCGAGTGATTCATCGCCGA⁴ACTCAAGCTCGCCAATCCTACCGTAACA
 CATATATGATAGTAGGCTTAACGTGGCTCATTGGCTTGATCTGCGCTACCCCCGG
 25 GGGGGTCTACACAACCATTGTAGCTCACCGCGATGGGGAAAGTGATGCTCAAAG
 ACACAATACTTGCATTATGCACTTTGCGTATGATGAAGTTTACGTCCTCATGGTCT
 GGAAACTTCTCATCGTTTTTAGTCTGGGGCATAGTGCCAGTTGTCATGATGAGCTG
 GTTTTACGCGTTTTTTTTACAATACTGTACAAAGAACAGCCAAAAACAACAACGT
 ACGTTGAAATTCGTAAAGGTATTACTCCTGTCATTCATCATCATCAA⁵ACTCCCTA
 30 TGTGTCAATCATGATTTTTTAACACGTATGCCACCGTAGGATGGCCGATGGAATGC
 GCCGATCTAACTAGACGCCGAGTCATCAACACGTTTTTCCCGTCTCGTCCCCAATC
 TACATTGCATGGTCAACCCCATCCTCTACGCTCTCATGGGAAATGACTTTGTGTCT
 AAAGTGGGCCAATGCTTTCGGGGGGGA⁶ACTCACGAACCGTCGAACTTTTCTGCGTT
 CCAAGCAACAAGCCCGCAACTCGGACGATGTACCGACAATTGTCAGTCAACAAC

CCGCCACACCCACCATCGTCAATAAGCCCGAAAAAAACCCGCACGTAAAACGCG
 GTGTATCTTTCAGCGTCAGCGCATCTCCGAACTCGCAGCGGCCAAAAAAGCCAA
 AGACAAAGCCAAGCGGCTTTCATGTCCCACCAAAACCTACGTCTGACGTGA

5

SEQ ID NO:24

Amino acid sequence for RhUL33

MTNLYSANFLTLIVLPFIVLSNQHLLPASAVTCKFLSLLYYSSCSVGFATVALIAADRY
 RVIHRRTQARQSYRNTYMIVGLTWLIGLICATPGGVYTTIVAHRDGESDAQRHNTCI
 10 MHFAYDEVYVLMVWKLIVLVWGIVPVVMMMSWFYAFFYNTVQRTAKKQQRTLKF
 VKVLLLSFIIIQTPYVSIMIFNTYATVGWPMECADLTRRRVINTFSRLVPNLHCMVNPI
 LYALMGNDFVSKVGQCFRGELTNRRTFLRSKQQARNSDDVPTIVSQQPATPTIVNKP
 EKNPHVKRGVSFSVSASSELAATAKKAKDKAKRLSMHQNLRLT*

15

SEQ ID NO:25

Nucleotide sequence for RhUL33 spliced

ATGGCAGTCACTTTACGAGGCGGCAGCCCGATAAACTTTAACTCATGATTGTCA
 GCCACAGAAACCGGAAATTTACGAGATACGGCTGTTTCAGCGTTCTGCTATCCG
 20 TCCAGGCGGGTTATGGAAACCATTTCTTACAACCGAACGAGTGAAACTAATTCCA
 TTTTGCACATCAACACCACCTGCAATGTGACCGACTCACTGTACGCCGCCAAACT
 AGGCGAAGCCCTCGTGAACAGCGCGCTAGCTTTATTCGGTACCCCCCTCAACGCC
 ATCGTCCTCGTCACACAGCTATTGGCCAACCGAGTTCATGGATACTCCACCCCGA
 TTATCTACATGACCAATCTTTACTCTGCCAATTTTCTCACCTTGATAGTACTTCCTT
 25 TTATCGTTTTAAGCAATCAACACCTTTTACCTGCCAGTGCAGTAACCTGTAAATT
 CTCTCCCTGTTGTACTACTCTAGCTGCAGCGTAGGTTTTGCTACAGTGGCACTGAT
 AGCGGCCGACCGATAACCGAGTGATTCATCGCCGAACCTCAAGCTCGCCAATCCTAC
 CGTAACACATATATGATAGTAGGCTTAACGTGGCTCATTGGCTTGATCTGCGCTA
 CCCCCGGGGGGGTCTACACAACCATTTAGCTCACCGCGATGGGGGAAAGTGATG
 30 CTCAAAGACACAATACTTGCATTATGCACTTTGCGTATGATGAAGTTTACGTCCT
 CATGGTCTGGAAACTTCTCATCGTTTTTAGTCTGGGGCATAGTGCCAGTTGTCATG
 ATGAGCTGGTTTTACGCGTTTTTTTACAATACTGTACAAAGAACAGCCAAAAAAC
 AACAACGTACGTTGAAATTCGTAAAGGTATTACTCCTGTCATTCATCATCATCCA
 AACTCCCTATGTGTCAATCATGATTTTTTAACACGTATGCCACCGTAGGATGGCCG

ATGGAATGCGCCGATCTAACTAGACGCCGAGTCATCAACACGTTTTCCCGTCTCG
TCCCCAATCTACATTGCATGGTCAACCCCATCCTCTACGCTCTCATGGGAAATGA
CTTTGTGTCTAAAGTGGGCCAATGCTTTCGGGGGGAACTCACGAACCGTCGAACT
TTTCTGCGTTCCAAGCAACAAGCCCGCAACTCGGACGATGTACCGACAATTGTCA
5 GTCAACAACCCGCCACACCCACCATCGTCAATAAGCCCGAAAAAAACCCGCACG
TAAAACGCGGTGTATCTTTCAGCGTCAGCGCATCTTCCGAACTCGCAGCGGCCAA
AAAAGCCAAAGACAAAGCCAAGCGGCTTTCATGTCCCACCAAAACCTACGTCT
GACGTGA

10 SEQ ID NO:26

Amino acid sequence for RhUL33 spliced

MAVTLRGGSPINFKLMIVSHRNRKFHEIRLFQRSAIRPGGLWKPFFTTERETNSILHIN
TTCNVTDSELYAAKLGEALVNSALALFGTPLNAIVLVTQLLANRVHGYSTPIIYMTNL
YSANFLTIVLPFIVLSNQHLLPASAVTCKFLSLLYSSCSVGFATVALIAADRYRVIH
15 RRTQARQSYRNTYMIVGLTWLIGLICATPGGVYTTIVAHRDGEDAQRHNTCIMHFA
YDEVYVLMVWKLLIVLVWGIVPVMMMSWFYAFFYNTVQRTAKKQQRTLKFKVL
LLSFIIIQTPYVSIMIFNTYATVGWPMECADLTRRRVINTFSRLVPNLHCMVNPILYAL
MGNDFVSKVGQCFRGELTNRRTFLRSKQQARNSDDVPTIVSQQPATPTIVNKPEKNP
HVKRGVSFSVSASSELAACKAKDKAKRL'SMSHQNLRLT*

20

SEQ ID NO:27

CGGCCAAGATGTCCCAAGAGGTTCTGACATGAACAATCACTTTTCCGAGATAGAT
GAGTTTGTAGTGGCATTACCAGAGAACTATTGGAGTGACGCTCAAGATGAAGC
25 TTCCTGGCCGTATTTGGAACATATTGTTAGATATAGCTAGTAAAGAATCTTCTA
AAGCCATGACGTCTTTCTGACGAAGTTGAATAAATTCTATCTCACCAGTACCCAA
AGGCTGACACTCAGACAACTTTGCCAAGGCCGTTGCACCCACCATGGCATTCTGA
ATCACAGTAACATCCGTCCGAGAATCGTCACCAAAAACGGTGGCCTCCAAAGTT
CGCAGGTGAGGCCGAGCCTTTACTGGATCTCGGAAGGGATACATGTGTGCTCGCC
30 GAGTGACAGCATTAGCATTAACCTCAAACCTCATCTAAAAGCGATGATAAATCAG
GAATATGATAGCGCAATTCTCGATAGTAGGCCAACCAGAGGACTAATTGGTTGA
ACAGACAGCTCCGTCTGTGCAAAAACCTTTTCGCCGCATTTTCTGAGAATTTTAGG
ATGCTGCTCTAAATCTACGTTCTTTAGTCGGCAGGGTCTTTAAAAAGTTAGTG
ATGGCAGTCACTTTACGAGGCGGCAGCCCGATAAACTTTAAACTCATGATTGTCA

GCCACAGAAACCGGAAATTTACGAGATACGGCTGTTTCAGCGTTCTGCTATCCG
TCCAGGCGGGTTATGGAAACCATTTCTTCACAACCGAACGGTGAGTGACATTTAAG
ACAGTTTAATAGCCAACACTCGTAACGTCTCGGAAGCTGATAAGTTTCGTTTTTC
CACAGAGTGAAACTAATTCCATTTTGCACATCAACACCACCTGCAATGTGACCGA
5 CTCACTGTACGCCGCCAAACTAGGGCGAAGCCCTCGTGAACAGCGCGCTAGCTTTA
TTCGGTACCCCCCTCAACGCCATCGTCCTCGTCACACAGCTATTGGCCAACCGAG
TTCATGGATACTCCACCCCGATTATCTACATGACCAATCTTTACTCTGCCAATTTT
CTCACCTTGATAGTACTTCCTTTTATCGTTTTTAAGCAATCAACACCTTTTACCTGC
CAGTGCAGTAACCTGTAAATTTCTCTCCCTGTTGTACTACTCTAGCTGCAGCGTAG
10 GTTTTGCTACAGTGGCACTGATAGCGGCCGACCGATACCGAGTGATTCATCGCCG
AACTCAAGCTCGCCAATCCTACCGTAACACATATATGATAGTAGGCTTAACGTGG
CTCATTGGCTTGATCTGCGCTACCCCCGGGGGGGTCTACACAACCATTGTAGCTC
ACCGCGATGGGGAAAGTGATGCTCAAAGACACAATACTTGCATTATGCACTTTGC
GTATGATGAAGTTTACGTCCTCATGGTCTGGAAACTTCTCATCGTTTTTAGTCTGGG
15 GCATAGTGCCAGTTGTCATGATGAGCTGGTTTTACGCGTTTTTTTTACAATACTGTA
CAAAGAACAGCCAAAAACAACAACGTACGTTGAAATTCGTAAAGGTATTACTC
CTGTCATTCATCATCATCCAAACTCCCTATGTGTCAATCATGATTTTTTAACACGTA
TGCCACCGTAGGATGGCCGATGGAATGCGCCGATCTAACTAGACGCCGAGTCAT
CAACACGTTTTTCCCGTCTCGTCCCCAATCTACATTGCATGGTCAACCCCCATCCTCT
20 ACGCTCTCATGGGAAATGACTTTGTGTCTAAAGTGGGCCAATGCTTTCGGGGGGA
ACTCACGAACCGTCGAACTTTTCTGCGTTCCAAGCAACAAGCCCGCAACTCGGAC
GATGTACCGACAATTGTCAGTCAACAACCCGCCACACCCACCATCGTCAATAAGC
CCGAAAAAAACCCGCACGTAAAACGCGGTGTATCTTTCAGCGTCAGCGCATCTTC
CGAACTCGCAGCGGCCAAAAAAGCCAAAGACAAAGCCAAGCGGCTTTCCATGTC
25 CCACCAAACCTACGTCTGACGTGAATTTTCCTAGAGGCTGCCTCCACGGGGTTTA
CATACATATCTCGGTACTTGCTACACTTGATCACTTTACTGCGGACACCACGGCC
AATCGCATC

WHAT IS CLAIMED IS:

1. A method for identifying an agent that reduces CMV dissemination in an animal, the assay comprising determining whether the agent inhibits the expression or
5 activity of US28 or a US28 homolog, or a fragment or a variant of US28 or the US28 homolog.
2. The method of claim 1, wherein the US28 homolog is selected from the group consisting of human UL33, human UL33 spliced, human UL78, rhUS28.1, rhUS28.2,
10 rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, rhUL33 spliced and rhUL78.
3. The method of claim 1, wherein the determining step comprises
 - (a) contacting a chemokine and US28, the US28 homolog, the fragment or the variant in the presence of the agent; and
 - 15 (b) determining whether the agent inhibits binding between the chemokine and US28, the US28 homolog, the fragment or the variant.
4. The method of claim 3, wherein the chemokine is a CX3C chemokine.
- 20 5. The method of claim 4, wherein the chemokine is fractalkine.
6. The method of claim 3, wherein the chemokine is a CC chemokine.
7. The method of claim 6, wherein the chemokine is selected from the group
25 consisting of MIP-1 α , MIP-1 β , MCP-1, eotaxin, vMIP-2 and RANTES.
8. The method of claim 3, wherein the agent is an antibody that specifically binds to US28, the US28 homolog, the fragment or the variant.
- 30 9. The method of claim 3, wherein the agent is a small molecule.
10. The method of claim 1, wherein the determining step comprises

(a) contacting a cell expressing US28, the US28 homolog, the fragment or the variant with a chemokine in the presence of the agent; and

(b) determining whether the agent inhibits binding between the chemokine and US28, the US28 homolog, the fragment or the variant.

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11. The method of claim 10, wherein the cell is infected with CMV.

12. The method of claim 10, wherein the cell is transfected with a heterologous nucleic acid encoding US28, the US28 homolog, the fragment or the variant.

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13. The method of claim 12, wherein US28, the US28 homolog, the fragment or the variant comprises at least 10 contiguous amino acids from the group of amino acid sequences as shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24 or 26 and binds to the chemokine.

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14. The method of claim 10, wherein the chemokine is a CX3C chemokine.

15. The method of claim 14, wherein the chemokine is fractalkine.

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16. The method of claim 10, wherein the chemokine is a CC chemokine.

17. The method of claim 16, wherein the chemokine is selected from the group consisting of MIP-1 α , MIP-1 β , MCP-1, eotaxin, vMIP-2 and RANTES.

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18. The method of claim 10, wherein the agent is an antibody that specifically binds to US28, the US28 homolog, the fragment or the variant.

19. The method of claim 10, wherein the agent is a small molecule.

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20. The method of claim 1, wherein the determining step comprises

(a) administering the agent to a non-human animal infected with CMV;

and

(b) determining whether the agent inhibits the dissemination of CMV from a primary site of infection in the non-human animal.

21. The method of claim 20, wherein the animal is a non-human primate.

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22. The method of claim 21, wherein the primate is a rhesus monkey, the CMV is rhCMV and the US28 homolog is selected from the group of rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, rhUL33 spliced and rhUL78.

10 23. The method of claim 20, wherein the agent is an antibody that specifically binds to the US28 homolog.

15 24. The method of claim 20, wherein the agent is an antisense nucleic acid that specifically hybridizes to a segment of a nucleic acid encoding the US28 homolog or a ribozyme that specifically recognizes a nucleic acid encoding the US28 homolog.

25. The method of claim 20, wherein the agent is a small molecule.

20 26. The method of claim 20, wherein the determining step (b) comprises determining whether viral titer in a saliva, urine or blood sample obtained from the non-human animal is detectably less than viral titer in a corresponding sample obtained from the saliva, urine or blood of a control animal.

25 27. The method of claim 20, wherein the determining step (b) comprises (i) obtaining a peripheral blood sample from the non-human animal; (ii) amplifying a region of CMV which is present in the sample with a set of primers that specifically hybridize to a segment of the CMV genome to form amplified product; and

(iii) detecting amplified product.

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28. The method of claim 20, wherein the determining step (b) comprises obtaining a tissue sample from the non-human animal and staining the tissue with an antibody that specifically binds to CMV.

29. The method of claim 20, wherein the determining step (b) comprises detecting activated T cells and/or memory cells in a peripheral blood sample taken from the non-human animal.

5 30. A method for treating an animal infected with cytomegalovirus (CMV) or at risk for infection by cytomegalovirus (CMV), comprising administering to the animal an agent that interferes with the expression or activity of US 28 or a US28 homolog.

10 31. The method of claim 30, wherein the animal is a human and the US28 homolog is selected from the group consisting of human UL33, human UL33 spliced and human UL78.

32. The method of claim 31, wherein the US28 homolog is human UL33.

15 33. The method of claim 31, wherein the US28 homolog is human UL78.

34. The method of claim 30, wherein the animal is a rhesus monkey and the US28 homolog is selected from the group consisting of rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, rhUL33 spliced and rhUL78.

20 35. The method of claim 34, wherein the US28 homolog is rhUS28.1.

36. The method of claim 34, wherein the US28 homolog is rhUS28.2.

25 37. The method of claim 34, wherein the US28 homolog is rhUS28.3.

38. The method of claim 34, wherein the US28 homolog is rhUS28.4.

39. The method of claim 34, wherein the US28 homolog is rhUS28.5.

30 40. The method of claim 34, wherein the US28 homolog is rhUL33.

41. The method of claim 34, wherein the US28 homolog is rhUL78.

42. The method of claim 30, wherein the agent interferes with expression of a target nucleic acid encoding US28 or the US28 homolog in cells of the animal.

43. The method of claim 42, wherein interference is achieved by
5 administering an antisense nucleic acid that specifically hybridizes to the target nucleic acid.

44. The method of claim 42, wherein interference is achieved by administering a ribozyme that specifically recognizes the target nucleic acid.

10 45. The method of claim 42, wherein the target nucleic acid encodes US28.

46. The method of claim 42, wherein the target nucleic acid encodes human UL33 or human UL78.

15 47. The method of claim 42, wherein the target nucleic acid encodes rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, rhUL33 spliced or rhUL78.

48. The method of claim 30, wherein the agent inhibits the binding of a chemokine to US28 or the US28 homolog.

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49. The method of claim 48, wherein the agent is an antibody that specifically binds to US28 or the US28 homolog.

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50. The method of claim 48, wherein the agent is a small molecule.

51. The method of claim 48, wherein the agent inhibits binding of the chemokine to US28.

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52. The method of claim 48, wherein the US28 homolog is human UL33 or human UL78.

53. The method of claim 48, wherein the US28 homolog is rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, rhUL33 spliced or rhUL78.

54. The method of claim 48, wherein the chemokine is a CX3C chemokine.

55. The method of claim 54, wherein the chemokine is fractalkine.

5 56. The method of claim 48, wherein the chemokine is a CC chemokine.

57. The method of claim 56, wherein the chemokine is selected from the group consisting of MIP-1 α , MIP-1 β , MCP-1, eotaxin, vMIP-2 and RANTES.

10 58. The method of claim 30, wherein the agent is a vaccine which generates an immune response in the animal, and wherein the vaccine is attenuated through inhibition of expression or activity of US28 or US28 homolog.

15 59. The method of claim 58, wherein the vaccine comprises an immunogenic HCMV polypeptide encoded by at least a region of an HCMV genome in which the polynucleotide segment encoding US28 has been inactivated.

20 60. The method of claim 58, wherein the vaccine comprises an immunogenic HCMV polypeptide encoded by at least a region of an HCMV genome in which the polynucleotide segment encoding human UL33 or human UL78 has been inactivated.

25 61. The method of claim 58, wherein the vaccine comprises an immunogenic rhCMV polypeptide encoded by at least a region of a rhCMV genome in which the polynucleotide segment encoding rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, or rhUL78 has been inactivated.

62. The method of claim 30, wherein CMV titer is reduced by 5-fold or greater as measured in blood, saliva, or urine following administration of the agent.

30 63. The method of claim 30, wherein interference results in a delay in appearance or reduction of levels of reactive leukocytes in the peripheral blood of the animal.

64. An isolated, purified or recombinant nucleic acid that encodes a protein that is a US28 homolog, wherein said protein

- (a) has an amino acid sequence at least 75% identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26; and
- (b) binds a chemokine.

65. The nucleic acid of claim 64, wherein the protein has a sequence selected from the group consisting of SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 and 26.

66. The nucleic acid of claim 64, wherein the nucleic acid has a sequence selected from the group consisting of SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.

67. A vector comprising the nucleic acid of claim 64.

68. A cell comprising the nucleic acid of claim 64.

69. An isolated or recombinant protein comprising an amino acid sequence having at least 75% identical to an amino acid sequence as set forth in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 or 26 over a region at least 40 amino acids in length, and wherein the protein can bind a chemokine.

70. The protein of claim 69, that is encoded by a nucleic acid segment that hybridizes under stringent conditions to a nucleic acid having a sequence selected from the group consisting of SEQ ID NOS:5, 7, 9, 11, 13, 17, 23 and 25.

71. An isolated protein comprising at least 12 amino acids from one of the sequences set forth in SEQ ID NOS:6, 8, 10, 12, 14, 18, 24 or 26.

72. A vaccine, comprising

- (a) an immunogenic CMV polypeptide which is encoded by at least a region of a CMV genome in which the polynucleotide segment encoding US28 or a US28 homolog has been inactivated; and
- (b) a pharmaceutically acceptable carrier.

73. The vaccine of claim 72, wherein the immunogenic CMV polypeptide is an HCMV polypeptide encoded by at least a region of an HCMV genome in which the polynucleotide segment encoding US28 has been inactivated.

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74. The vaccine of claim 72, wherein the immunogenic CMV polypeptide is an HCMV polypeptide encoded by at least a region of an HCMV genome in which the polynucleotide segment encoding human UL33 or human UL78 has been inactivated.

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75. The vaccine of claim 72, wherein the immunogenic CMV polypeptide is a rhCMV polypeptide encoded by at least a region of a rhCMV genome in which the polynucleotide segment encoding rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4, rhUS28.5, rhUL33, or rhUL78 has been inactivated.

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76. The vaccine of claim 75, wherein the immunogenic CMV polypeptide is a rhCMV polypeptide encoded by at least a region of a rhCMV genome in which the polynucleotide segment encoding rhUS28.1, rhUS28.2, rhUS28.3, rhUS28.4 or rhUS28.5 is inactivated.

20

VH/E 1 ATGACACCGACGACGACGACCGCGGAACTCACG 33
VH/E 34 ACGGAGTTTGACTACGACGATGAAGCGACTCCC 66
VH/E 67 TGTGTCCTCACCGACGTGCTTAATCAGTCGAAG 99
VH/E 100 CCAGTCACGTTGTTTTCTGTACGGCGTTGTCTTT 132
VH/E 133 CTCTTCGGTTCCATCGGCAACTTCTTGGTGATC 165
VH/E 166 TTCACCATCACCTGGCGACGTGGGATTCAATGT 198
VH/E 199 TCCGGCGATGTTTACTTTATCAACCTCGCGGCC 231
VH/E 232 GCCGATTTGCTTTTTCGTTTGTACACTACCTCTG 264
VH/E 265 TGGATGCAATACCTCCTAGATCACAACCTCCCTA 297
VH/E 298 GCCAGCGTGCCGTGTACGTTACTCACTGCCTGT 330
VH/E 331 TTCTACGTGGCTATGTTTGCCAGTTTGTGTTTT 363
VH/E 364 ATCACGGAGATTGCACTCGATCGCTACTACGCT 396
VH/E 397 ATTGTTTACATGAGATATCGGCCTGTAAAACAG 429
VH/E 430 GCCTGCCTTTTTCAGTATTTTTTTGGTGGATCTTT 462
VH/E 463 GCCGTGATCATCGCCATTCCACACTTTATGGTG 495
VH/E 496 GTGACCAAAAAAGACAATCAATGTATGACCGAC 528
VH/E 529 TACGACTACTTAGAGGTCAGTTACCCGATCATC 561
VH/E 562 CTCAACGTAGAACTCATGCTCGGTGCTTTTCGTG 594
VH/E 595 ATCCCGCTCAGTGTGATCAGCTACTGCTACTAC 627
VH/E 628 CGCATTTCAGAAATCGTTGCGGTGTCTCAGTCG 660
VH/E 661 CGCCACAAAGGCCGCAATTGTACGGGTACTTATA 693
VH/E 694 GCGGTCGTGCTTGTCTTTATCATCTTTTGGCTG 726
VH/E 727 CCGTACCACCTGACGCTGTTTGTGGACACGTTG 759
VH/E 760 AAAGTGCTCAAATGGATCTCCAGCAGCTGCGAG 782
VH/E 793 TTCGAAAAATCACTCAAGCGCGCGCTCATCTTG 825
VH/E 826 ACCGAGTCACTCGCCTTTTGTCACTGTTGTCTC 858
VH/E 859 AATCCGCTGCTGTACGTCTTCGTGGGCACCAAG 891
VH/E 892 TTTCCGGCAAGAACTGCACTGTCTGCTGGCCGAG 924
VH/E 925 TTTCCGCCAGCGACTGTTTTCCCGCGATGTATCC 957
VH/E 958 TGGTACCACAGCATGAGCTTTTCCGCGTCGGAGC 990
VH/E 991 TCGCCGAGCCGAAGAGAGACGTCTTCCGACACG 1023
VH/E 1024 CTGTCCGACGAGGCGTGTGCGCTCTCACAATT 1056
VH/E 1057 ATACCGTAA 1065

Fig. 1A

VHL/E	1	<u>MTPTTTTAE</u> <u>LTTEFDYDDEATPCVLT</u> <u>DV-LN</u> <u>QSK</u>	33
VHL/E	34	<u>PVT</u> <u>LF</u> <u>LYGVVFLFGS</u> <u>IGNFLVIFTITWRRRIQC</u>	66
VHL/E	67	SGDVYFINLAAADLLFVCTLPLWMQYLLDHNSL	99
VHL/E	100	ASVPCTLLTACFYVAMFASLCFITEIALDRYYA	132
VHL/E	133	IVYMRYPVKQACLFSLFWWIFAVIIAIPHFMV	165
VHL/E	166	VTKKDNQCMTDYDYLEVSYPIILNVELMLGAFV	198
VHL/E	199	IPLSVISYCYRISRIVAVSQSRHKGRIVRVLI	231
VHL/E	232	AVVLVFIIFWLPYHLTLFVDTLKLLKWISSSCE	264
VHL/E	265	FEKSLKRALILTESLAFCHCCLNPLLYVFGTK	297
VHL/E	298	FROELHCLLAEFRQRLFSRDVSWYHSMSFSRRS	330
VHL/E	331	SPSRRETSSDTLSDEACRVSQIIP	354

Fig. 1B

human US28 1	M T P T T	5
rhesus US28.1 1	M	1
rhesus US28.2 1	M T N A	4
rhesus US28.3 1	M T N T	4
rhesus US28.4 1		0
rhesus US28.5 1	M T T T T M S A T T N S S T T P Q A S S T T M T T K T S T P G N	32
human US28 6	- - - - T T A E L T T	12
rhesus US28.1 2		1
rhesus US28.2 5		4
rhesus US28.3 5		4
rhesus US28.4 1		0
rhesus US28.5 3	T T T G T T S T L T T I S T T S N A T S I T S N L S T T G N Q T	64
human US28 13		12
rhesus US28.1 2		4
rhesus US28.2 5		8
rhesus US28.3 5		7
rhesus US28.4 1		15
rhesus US28.5 5	A T T N A T T F S S T L T T S T N I S S T F S T V S T V A S N A	96
human US28 13		12
rhesus US28.1 5	S C N	8
rhesus US28.2 7	C H	9
rhesus US28.3 8	T C H	11
rhesus US28.4 6		21
rhesus US28.5 7	T C N S T I T T N I T T A F T T A A N T T A S S L T S I V T S L	128
human US28 13		37
rhesus US28.1 9	N V T L N A S A	23
rhesus US28.2 10	N E S L A S Y G	24
rhesus US28.3 12	N G T F E T F K	25
rhesus US28.4 22		21
rhesus US28.5 29	A T T I E T T S F D Y D E S A E A C N L T D I V H T T R S V T V	160
human US28 38	F L Y G V V F L E G S I G N F	68
rhesus US28.1 24	A M Y S L V I C G L V G N E L E C I V L V K - K R K L R Y S S	54
rhesus US28.2 25	T L Y S I A G I C G V T G N L E L L V L F T - R R I H W F A N	55
rhesus US28.3 27	S A Y T V L V I G L L G N I V L L S V L V V - K R K L K F P N	57
rhesus US28.4 22	- Y T C V F L E G I L G H F Y L Y W K N F R R T N S F S	51
rhesus US28.5 31	T F Y T I F E L G L L G N F - L V L M T I I W N R R I S F M V	191
human US28 69	D V Y F I N L A A A D L L F V C T L P L W M Q Y L L D H N S L A	100
rhesus US28.1 55	D V Y F F H A S M A D L V S T V M L P L W L H Y V L N F A Q L S	86
rhesus US28.2 56	D I Y Y L N M I F T D F L V F I T L P A W V Y Y L L N Y T Q L S	87
rhesus US28.3 58	D I Y F F N A S L A D V F A M C M L P A W V N Y A L D S T Q L S	89
rhesus US28.4 52	D V L F R H L M I T E E V F T L T I P V W A Y H L T T H G N L P	83
rhesus US28.5 52	E I Y F V N L A I S D L M F V C T L P F W I M Y L L E H D V M S	223
human US28 101	S V P C T L L T A C F Y V A M E A S L C F I T E I A L D R Y Y A	132
rhesus US28.1 87	R G A C I S F S V T F Y V P L F V Q A W L L I S I A M E R - Y S	117
rhesus US28.2 88	H Y A C I A L S F V F Y V S I F I Q A D F M V A V A I E R - Y R	118
rhesus US28.3 90	K F S C I T F T F G F Y V S L F I Q A W M L I E V T L E R - Y G	120
rhesus US28.4 84	G S W C R S L T F V F Y L T V F A R A F F Y L L L I W D R - Y S	114
rhesus US28.5 84	H A S C V A M T A I F Y C A L E A S T V F E L L I V L D R C Y A	255

FIG. 2 (Page 1 of 2)

human US28.133	I V Y M R Y R P V K Q - - - - - A C L F S I F W W I F A W I	157
rhesus US28.118	N L V W M A P I S V K - - - T A F K H C I G T - - - W I V S A F	143
rhesus US28.219	S L V K N K P L S V K - - - K A S V S C A C I - - - W I V S A F	144
rhesus US28.321	S L V W I A P I T R N - - - K A I A N C V L F - - - W I V S F	146
rhesus US28.415	V I I C R H P L P V N L N Y S Q V I G - - - L S V W - - - L V A V	141
rhesus US28.556	I L L G T E K A N R R L L R N A V S G C M L M - - - W G L C F I	284
human US28.158	I A I P H F M V V T K - K D N Q C - M T D Y D Y - L E V S Y P I	186
rhesus US28.144	V A S P Y Y A Y R N S - E H E C I L G N Y T W H I N E P L H T	175
rhesus US28.245	Y S S P Y Y M F R S Q H E T N S C I L G N Y T W H M N S P E R T	176
rhesus US28.347	L A A P Y Y S F R N E S E H Q C I M R N Y T W S V G E T W H I	178
rhesus US28.442	L S A S P F S I F N G - S V K Q C - L G N M G - S I P S E S S A	170
rhesus US28.555	L A L P H F I F M K K - G T N V C - V A E Y E P G I N N F Y V I	314
human US28.187	I L N V E L M L G A F V I P S V I S Y C Y Y R I S R I V A V S	218
rhesus US28.176	C M D V V I V W T F L A P V L V I I A S V K M - R R I T W G	206
rhesus US28.277	T M D A S I N I W S F V P A V T T L I A R R I Y V - C T S G	207
rhesus US28.379	A L D F L I T E I M P V T I V L A L S E K M A R W S T F G	210
rhesus US28.471	V L N L E V H L C S F W L P L I M S A N C Y Y Q A K R R A S P D	202
rhesus US28.515	F I N T E V N L C T V L P A A A I I Y W Y I K L T K A L K T H	346
human US28.219	Q S - R H K G R I V R V L I A V V I F E F W L P Y H L T L F	249
rhesus US28.307	N T - R L N E K N S D I L T I V M M T V F F W G P F N I V L V	237
rhesus US28.208	N K - K M N A R A S G L L E A M V I S M L F E G G I F N L N I F	238
rhesus US28.311	Y R - N I T S R T S L I I I I I I I I I I I I I I I I I I I	241
rhesus US28.403	Q - L H E L Y R C S L I T T I T T Y A I V W F P E H L A L E	232
rhesus US28.547	E R L R H R L T S L N I V L A N C V A F W L P Y N L M L M	378
human US28.250	V D T L K I - L K W I S S S C E F E R S I K R A L I L T E S L A	280
rhesus US28.338	I D N I L Q R Y Y D T - T N C D V E K I K H I M A M I S E A I V	268
rhesus US28.239	R D - I V S D T S E D N K D C T Y L K Q E H F I M V G V A L V	269
rhesus US28.342	I E N V A G Q I Y H I Q P D C W Y L Q L R H L C S L M T E T L V	273
rhesus US28.433	I D A L I S - I S H V E P S S A L H W A - S I V V T C K S F T	261
rhesus US28.579	M Y S L V H - M Q - L P W E C S S E K I L R R S L I T E S I A	408
human US28.281	F C H C C L N P L L Y V F V G T K F R Q E L H C L L A E F R O R	312
rhesus US28.369	Y F R G I T A P I I Y V G I S G R F R E E I Y S L F R R O B Y N	300
rhesus US28.270	Y G R A I F N P F M Y M C V S T R L R Q E I K C L F M R I P Y E	301
rhesus US28.374	F L R S V F N P Y I Y M I S Y K R Q Q V R S L L K R T Q Y D	305
rhesus US28.462	F V Y A G I S P L V Y F T C C P T V R R E L L M S L R P F F T	292
rhesus US28.509	L S H C C L N P L I Y L L F G P R C S E E C H L L R C C F T R	440
human US28.313	I F S R D V S W - - Y H S M S F S R R S S S F S R R E T S S D T L	342
rhesus US28.301	D L D P D A N - - - - - Q F M I E L T S Q G R S E N R N A R O S	327
rhesus US28.302	T L D A E H A - - - - - K L M V N L K N R N A N V P D P K - - -	325
rhesus US28.306	A L D T T Q L - - - - - A E T M O L K A K G V P V S D P A - - -	329
rhesus US28.303	- - - - - M I S S K T E R G Y A P I K T O P L N I P D E P I	317
rhesus US28.541	L - C P H R S W S S I R A E T V S I S L S H S Q V S A S S E D E	471
human US28.343	S D E V C R V S O I I P	354
rhesus US28.328	E S N V P O P E E C F W	339
rhesus US28.228	- - - - - P R E Y E S V L	333
rhesus US28.330	- - - - - P H D C E C E L	337
rhesus US28.418	D N K S P H L L N - - E	327
rhesus US28.572	D N D V H D E L O F L I	483

FIG. 2 (Page 2 of 2)

Species	Accession	Position	Sequence	Start	End
human	UL78	1	M S P S V E E T T S V T E S I M F A I V S F K H M G P F E G Y	31	
rhesus	UL78	1	- -	0	
human	UL78	32	S M S A D R A A S D L L I G M F G S V S L V N L E T T I G C L	62	
rhesus	UL78	1	- M I T E R V L A G I L A G M T A A G S L V I L L A V V - - M	28	
human	UL78	63	W V L R V T R P - - P V S V M I F T W N L V L S Q F F S I L A	91	
rhesus	UL78	29	W L N M L D R A G M P M A V G H Y T G N L V L T Q V I C I F S	59	
human	UL78	92	T M L S K G I M L R G A L N L S L C R L V L F V D D V G L Y S	122	
rhesus	UL78	60	- M L A S K I V G M T S A A N M G F C G I M V F L E D T G L Y	89	
human	UL78	123	T A L F I L L I L D R L S A I S Y G R D L W H H E - T R E N	152	
rhesus	UL78	90	V T S L L F M F M I L D R M A A F L N G R L F W R Q Q T I K Q	120	
human	UL78	153	A G V A L Y A V A F A W L S I V A A V P T A A T G S L D Y R	183	
rhesus	UL78	121	N L S T S V Y I L I F C W V L G M A A A V P S A A V A A P N S	151	
human	UL78	184	W L G C Q I P I Q Y A A V D L T I K M W F L L G A P M I A V L	214	
rhesus	UL78	152	R W E R C E I P V S Y A A I D M I V K L W F V L L A P V V L I	182	
human	UL78	215	A N V V E L A Y S D R R D H V W S Y V G R V C T F Y V T C L M	245	
rhesus	UL78	183	M A V I I Q S S Y H R R E R I W Y Y A R R V F M F Y T A C E	213	
human	UL78	246	L F V P Y Y C F R V - - - - - L R G V - L Q P A S A A G T G	269	
rhesus	UL78	214	V M M V P Y Y F V R V M L S D F A L V D I K T K T A N S D G C	244	
human	UL78	270	F G I M D Y V E L A T R T L L T M R L G I L P L F I A F F S	300	
rhesus	UL78	245	D S T F L D Y L N M F T H V I Y S F K L V V F A L F I V L F C	275	
human	UL78	301	R E P T K D L D D S F D Y L V E R C Q Q S C H G H F V R R L V	331	
rhesus	UL78	276	S I N P M E T L E E C L E R A D A E R Q S R S E A S O G E R R	306	
human	UL78	332	Q A L K R A M Y S V E L A V C Y F S T S V R D V A E A V K K S	362	
rhesus	UL78	307	L P I N T C C I K L I E L I K Q Y V S T L S K A T R D N S G E	337	
human	UL78	363	S S R C Y A D A T S A A V V V T T T T S E K A T L V E H A E G	393	
rhesus	UL78	338	R A N L P E N A E D I G T T G S D Q L P T E V T V T P N S S A	368	
human	UL78	394	M A S E M C P G T T I D V S A E S S S V L C T D G E N T V A S	424	
rhesus	UL78	369	V F S T G G T V S P V	379	
human	UL78	425	D A T V T A L	431	

FIG. 3

H UL33	1	M		1
HUL33splice	1	M	DTIIHNSM	9
RhUL33	1	M		1
RhUL33splice	1	M	AVTLRGGSPINFKLMIVSHHNNHGFHEIRLFQ	32
H UL33	2			1
HUL33splice	10	HNNPP	HINDTCNM	23
RhUL33	2			1
RhUL33splice	33	RSAIRPGGLWKPFFTTETETNSILHINTTCNV		64
H UL33	2	TGPLFAIRTTTEAVLNTEFEVGGPLNA		33
HUL33splice	24	TGPLFAIRTTTEAVLNTEFEVGGPLNA		56
RhUL33	2			1
RhUL33splice	66	TDISLIYAAKILGEALVNSALALEGTPINAVV		96
H UL33	34	QLLTNRVLGYSTPTIYMTNLYSTNFLTETVLP		66
HUL33splice	56	QLLTNRVLGYSTPTIYMTNLYSTNFLTETVLP		87
RhUL33	2			16
RhUL33splice	97	QLLANRVHGYSTPTIYMTNLYSANFLTETVLP		128
H UL33	66	IVLSNQWLLPAGVASCKFLSVIYYSSCTVGF		97
HUL33splice	66	IVLSNQWLLPAGVASCKFLSVIYYSSCTVGF		119
RhUL33	17	IVLSNQWLLPASAVTCKFLSLLYYSSCSVGF		48
RhUL33splice	129	IVLSNQWLLPASAVTCKFLSLLYYSSCSVGF		160
H UL33	96	ATVAAIAADRYRVLHKRRAAROSYRSTYMLL		129
HUL33splice	120	ATVAAIAADRYRVLHKRRAAROSYRSTYMLL		151
RhUL33	49	ATVAAIAADRYRVLHKRRAAROSYRSTYMLV		80
RhUL33splice	161	ATVAAIAADRYRVLHKRRAAROSYRSTYMLV		192
H UL33	130	ETWLAGLIFSVPAAVYTTVVMHHDANDTNNGN		161
HUL33splice	152	ETWLAGLIFSVPAAVYTTVVMHHDANDTNNGN		183
RhUL33	81	ETWLAGLIFCATPGGVYTTIVAHRRDGE		110
RhUL33splice	183	ETWLAGLIFCATPGGVYTTIVAHRRDGE		222
H UL33	162	GHATCVLYFVAEEVHTVLLSWKVLLLMVWGAA		193
HUL33splice	184	GHATCVLYFVAEEVHTVLLSWKVLLLMVWGAA		216
RhUL33	111	GHNTCIMHFAYDEVYVLMVWKLTLMLVWGAV		141
RhUL33splice	223	GHNTCIMHFAYDEVYVLMVWKLTLMLVWGAV		253
H UL33	194	PVIMMTWIFYAFFYSTVORTSKKSSRTLTFFVS		226
HUL33splice	216	PVIMMTWIFYAFFYSTVORTSKKSSRTLTFFVS		247
RhUL33	142	PVIMMSWIFYAFFYSTVORTSKKQQRRTLTKEFK		172
RhUL33splice	254	PVIMMSWIFYAFFYSTVORTSKKQQRRTLTKEFK		284
H UL33	226	VLLLSSEVALQTPYVSIMIFNSYATTAWPMQCE		257
HUL33splice	248	VLLLSSEVALQTPYVSIMIFNSYATTAWPMQCE		279
RhUL33	173	VLLLSSEVALQTPYVSIMIFNTYATVGWPMQCA		204
RhUL33splice	285	VLLLSSEVALQTPYVSIMIFNTYATVGWPMQCA		316
H UL33	258	HLTLRRTIGTLARVVPPLHCLINPILYALLGH		288
HUL33splice	280	HLTLRRTIGTLARVVPPLHCLINPILYALLGH		311
RhUL33	205	DLTIRRRVINTEFSRLVPNLHCMVNPILYALMGN		236
RhUL33splice	317	DLTIRRRVINTEFSRLVPNLHCMVNPILYALMGN		348
H UL33	290	DFLQRMRCQFRGQLLDRRAFLRSQNNORATAE		321
HUL33splice	312	DFLQRMRCQFRGQLLDRRAFLRSQNNORATAE		343
RhUL33	237	DFVSKVVGQCERGEILTNRRTFLRSKQDARNSD		268
RhUL33splice	349	DFVSKVVGQCERGEILTNRRTFLRSKQDARNSD		380
H UL33	322	TNLAAGNNSQSVATSLDTNISKNNVNOHAKRSVS		363
HUL33splice	344	TNLAAGNNSQSVATSLDTNISKNNVNOHAKRSVS		375
RhUL33	269	VPTIVSQQP-ATPTIIVNKPEN-NPHVKRGVS		297
RhUL33splice	381	VPTIVSQQP-ATPTIIVNKPEN-NPHVKRGVS		408
H UL33	364	FNFPSTWTKGGQKTA-SNDISTKI:PHRLSQSHH		386
HUL33splice	376	FNFPSTWTKGGQKTA-SNDISTKI:PHRLSQSHH		407
RhUL33	296	FSVSASSIELAAAKKAKEDKA- - - -KRLSMSHO		324
RhUL33splice	410	FSVSASSIELAAAKKAKEDKA- - - -KRLSMSHO		436
H UL33	386	NLSGV		390
HUL33splice	406	NLSGV		412
RhUL33	325	NLRIT		329
RhUL33splice	457	NLRIT		441

FIG. 4

Binding of Fractalkine to HCMV Virions

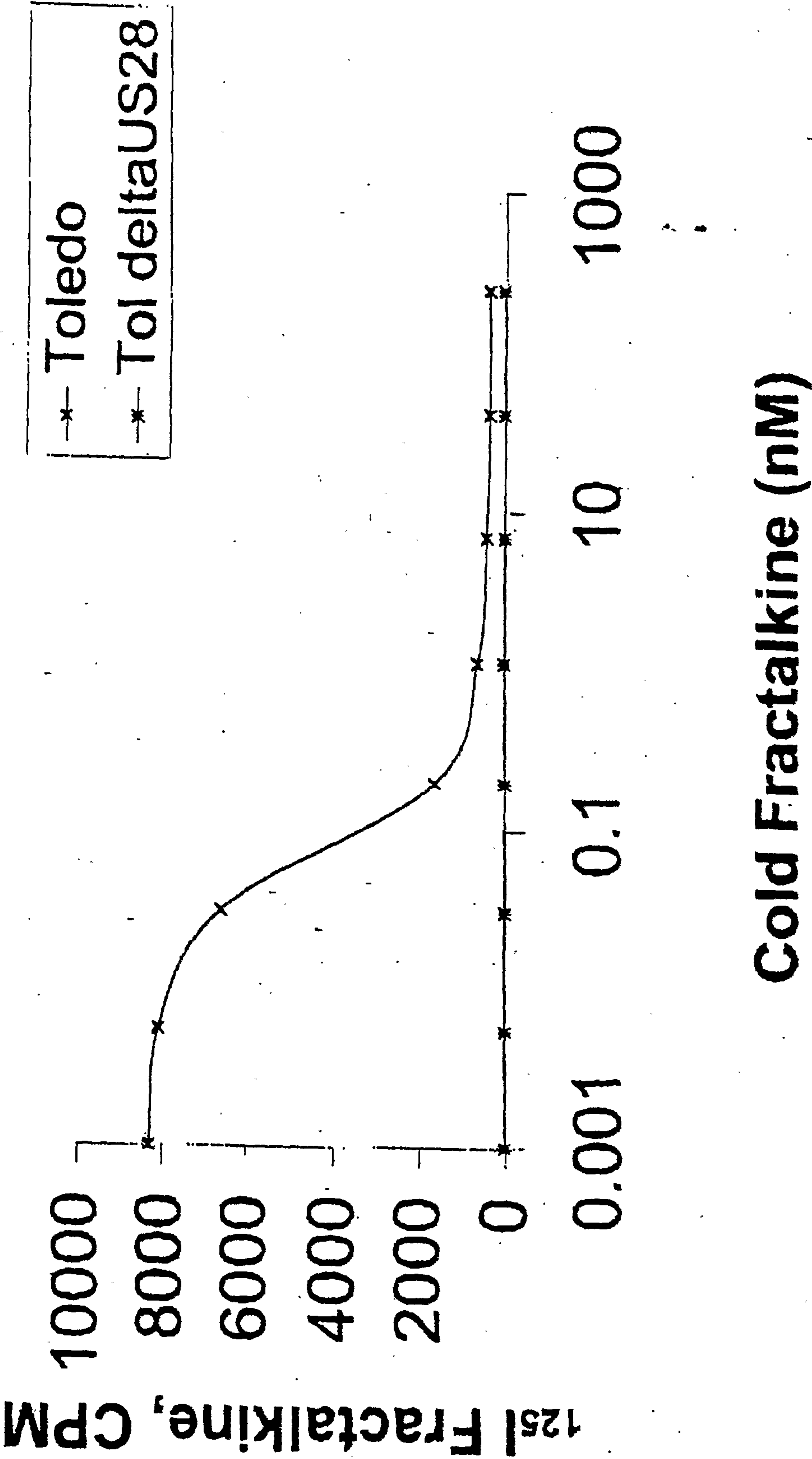


FIG. 5

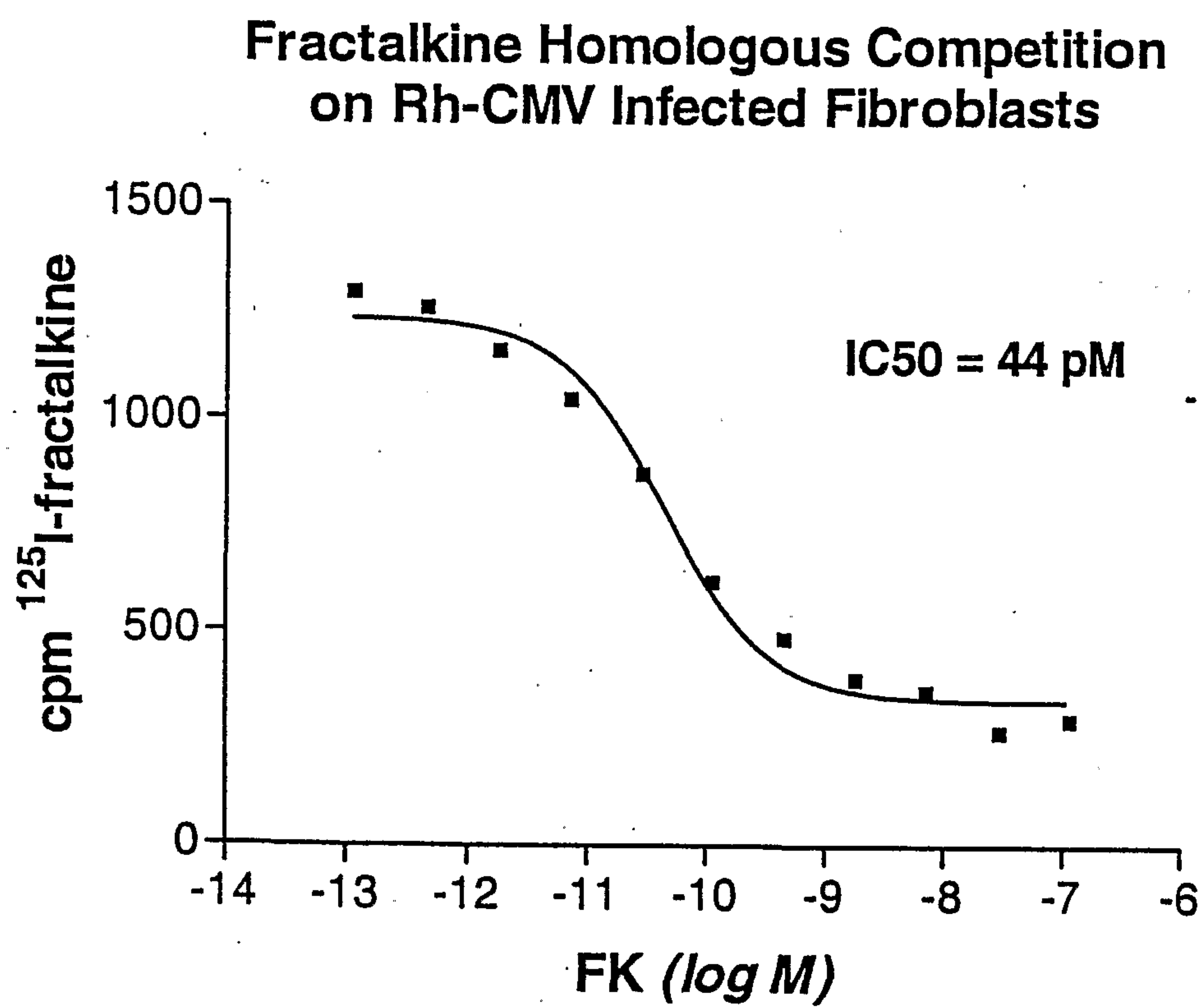


FIG. 6

Sucrose Virions/CX3C binding

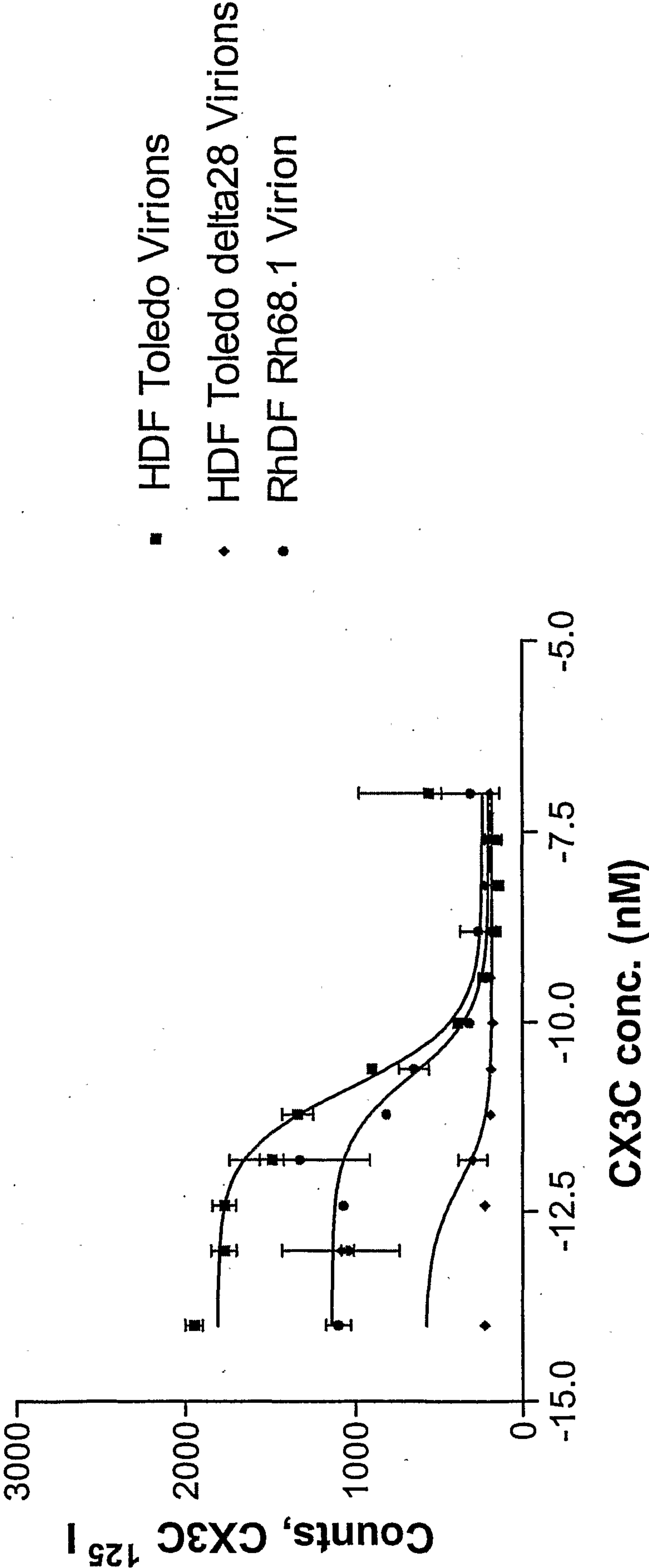


Fig. 7