



US009803006B2

(12) **United States Patent**
Zhou et al.

(10) **Patent No.:** **US 9,803,006 B2**
(45) **Date of Patent:** ***Oct. 31, 2017**

(54) **TARGETING OF HERPES SIMPLEX VIRUS TO SPECIFIC RECEPTORS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 76 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **14/589,581**

(22) Filed: **Jan. 5, 2015**

(65) **Prior Publication Data**

US 2016/0175370 A1 Jun. 23, 2016

Related U.S. Application Data

(63) Continuation of application No. 12/065,455, filed as application No. PCT/US2006/033865 on Aug. 30, 2006, now Pat. No. 8,927,251, which is a continuation of application No. 11/215,636, filed on Aug. 30, 2005, now Pat. No. 7,550,148, which is a continuation-in-part of application No. 10/530,774, filed as application No. PCT/US03/31598 on Oct. 6, 2003, now Pat. No. 7,501,126.

(60) Provisional application No. 60/416,716, filed on Oct. 7, 2002.

(51) **Int. Cl.**

C07K 14/00 (2006.01)
C07K 16/18 (2006.01)
A61K 47/48 (2006.01)
C07K 14/54 (2006.01)
A61K 38/20 (2006.01)
C12N 15/869 (2006.01)
C12N 15/86 (2006.01)
C12Q 1/70 (2006.01)
A61K 35/00 (2006.01)

(52) **U.S. Cl.**

CPC **C07K 16/18** (2013.01); **A61K 38/2086** (2013.01); **A61K 47/48269** (2013.01); **A61K 47/48376** (2013.01); **A61K 47/48776** (2013.01); **C07K 14/5437** (2013.01); **C12N 15/86** (2013.01); **C12N 15/8695** (2013.01); **A61K 35/00** (2013.01); **C12N 2710/16632** (2013.01); **C12N 2710/16643** (2013.01); **C12N 2710/16645** (2013.01); **C12N 2799/028** (2013.01); **C12N 2810/50** (2013.01); **C12N 2810/852** (2013.01); **C12Q 1/705** (2013.01)

(58) **Field of Classification Search**

None
See application file for complete search history.

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(57) **ABSTRACT**

The invention relates to engineered Herpes simplex virus (HSV) particles that are targeted to one or more specific binding pair members, such as receptors. Also, recombinant vectors for producing such HSV particles are provided. By reducing the affinity of HSV for its natural receptor(s) and increasing the affinity for a selected receptor, the HSV particles of the invention are useful for targeting cells that express the selected receptor, which itself may be a product of genetic engineering. The ability to selectively target cells renders the HSV particles, particularly useful in selectively diagnosing, treating, and imaging cells bearing the selected binding pair member, such as a receptor. The invention also provides for polynucleotide-based therapy to cells bearing the selected binding pair member such as a receptor.

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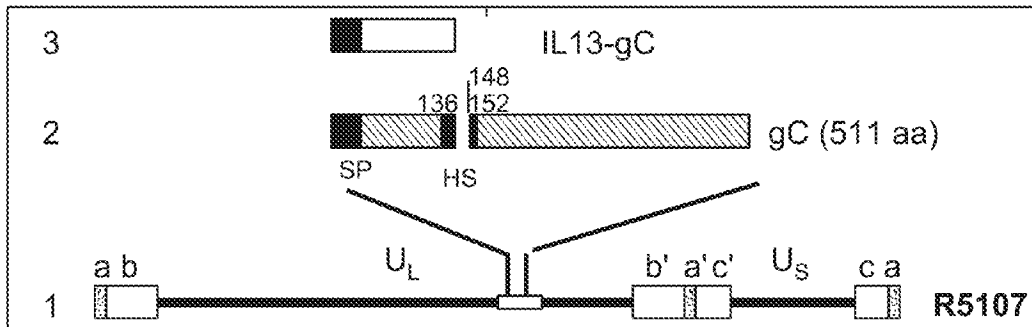


FIG. 1A

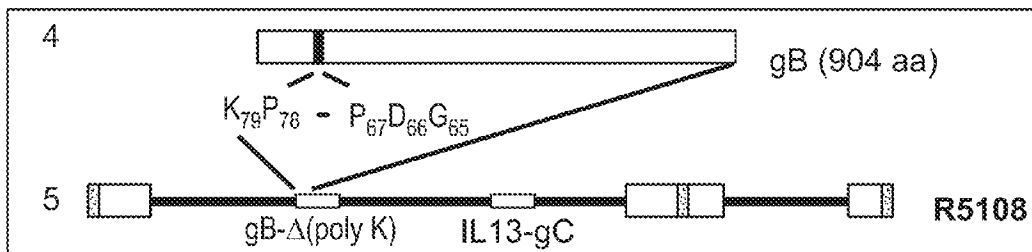


FIG. 1B

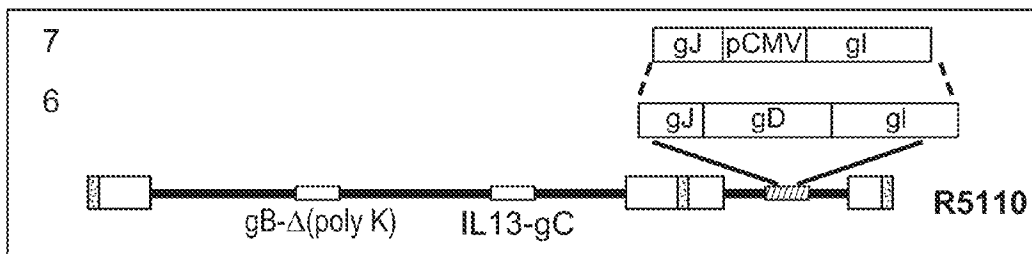


FIG. 1C

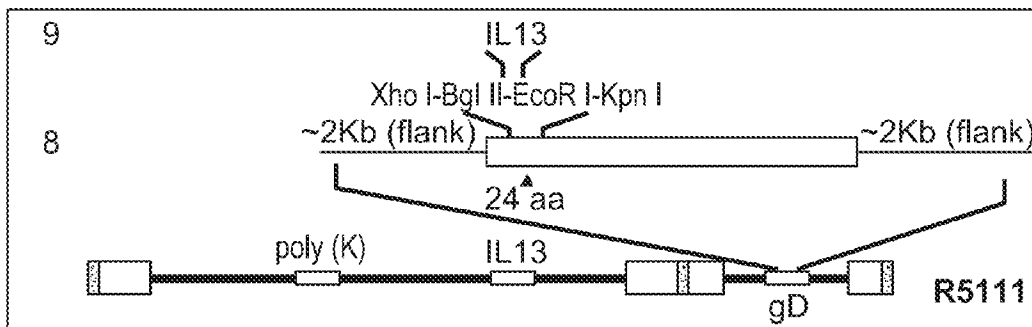


FIG. 1D

The amino terminal sequence of IL13-gC

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cttgggtcggggaggcagcatcgaacgcaacaccccccatacgggtgggtccgtgtppaggtcgtttttcagtpcc
pgtctcgtctttgpcaggggacggflagcctc.ATGGCGCTTTTGTGAAACCAAGGTCAATGCTCTCACTTCCCT
gC upstream ----- IL-13*
GGCGGCTTTGCGCTTCCCAAGGCTCTGTGCTCCCTCTACAGCTCTCAAGGTAGCTCAATTGAGGAGCTGGTCA
CATCACCCACAGAACCA GAAAGGCTCCGCTCTGCAATGSCAGCATGGTATGGAGCATCAACTTGACAGCTGGC
TGTACTGTGCAAGCTC CTGGAAATCCCTGATCAACGTGTCAAGCTGCAETGSCATGCAAGAGACCCAGAGGAT
CTGAGCGGATTC TGC CCGCACAAAGGCTCTCAGCTGGGCACTTTCAGCTTGCATGTCCGAGACACCAAAA
CGAGGTGGCCCAAGTTTGTAAAAGAATCTGCTCTTACATTTAAAGAAACTTTTTCGGGAGGGACGGTTGAA
GCACCCGCATGGAGTTCCTCCGCTCCAGATAAGCGTACTCCATGGGTCCGCTCCCGCCAAATCGCTCCGGC
----- gC downstream

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FIG. 2A

The sequence of the gB_{Δpoly(K)} domain

```

GGGTCTCTGGTGGCGTCCGGGGCTCCGAGTTCCCTCCGCAAGCCTGGGGTCCGGGGCCGCAACCCAGCCGGC
GAAAGGGGGACCTTGCCTCTCTGCGCTCCGCTCCCTCTGGCCCGCCCGCCCAAGGGGGATCTCAAAAGCCAAAG
AAAGATCTCAAAAGCCGAAAGCTCCAAAGCGCGCGCCCTCCGCGCCGACAAACGGGACCCCTCGCCCTCGGGCTA
CGCCACCTTGGCCGAGCACTTGGCGGACATCAAGGGCGAGAAACCCGATGCAAACTTTTACGTTGTCCCA
CCCCCAAGGGGCGCAAGGTTGCTCAGCTCCAGCAGCCCGCCCGCTCCCGCAACCCCGCCCGAGGGTCAAG

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FIG. 2B

The amino terminal sequence of IL13-gD

```

ATGGGGGGGGGCTGCGCGCCAGGTTGGGGGGCCGTGATTTTGTFTTGTCTCGTCAATAGTCCGGCTC
Signal peptide of gD→
CATGGGGTCCGCGCCAAATATGCTTGGGGGATGCTCTCTCAAGCTGGCCGACCCCAAT
CGCTTTCGCGCCAAAGACCTTCCGGTCCctegag*ATGGCGCTTTTGTGTTGACCACGSTCATY
24AA XhoI IL13→
GCTCTCACTTGCCTTGGCGGCTTTGCGCTCCCGAGGGCCCTGTGCTTCCCTCTACAGCCCTC
AGGAGCTCAATTGAGGAGCTGCTCAACATCAACCCAGAAACAGAGGGCTCCGCTCTGCAAT
GGCAGCATGGTTTGGAGCATCAACCTGACAGCTGGCATGTACTGTGCAAGCCCTGGAAATCC
CTGATCAACCTGTCAAGCTGCAAGTGCCTATCGAGAAAGACCCAGAGGATGCTGGGCGGATTC
TGGCCGCAAGGTTCTCAGCTGGGCAAGTTTCCAGCTTGCATGTCCGAGACACCAAAATC
GAGSTGGCCCAAGTTTGTAAAAGGACCTGCTCTTACATTTAAAGAAACTTTTTCGGGAGGGG
CGGTTCAACTGAAAC*ggtagcctGGAGCCAGCTGACCCGACCCCTCCGGGGGTCCCGCGCTG
←IL13 KpnI 75AA
TACCACATCCAGGCGGGCTACCGGACCCCTTCCAGCCCCCCAGCCCTCCCGATC

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FIG. 2C

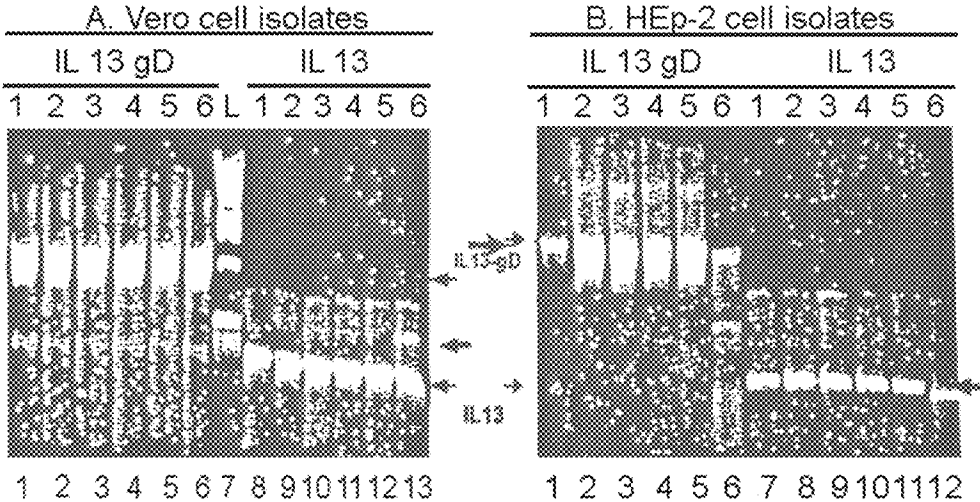


FIG. 3A

FIG. 3B

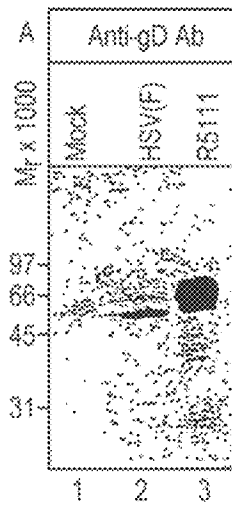


FIG. 4A

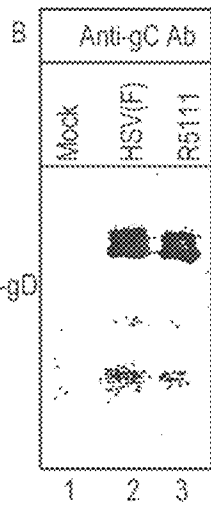


FIG. 4B

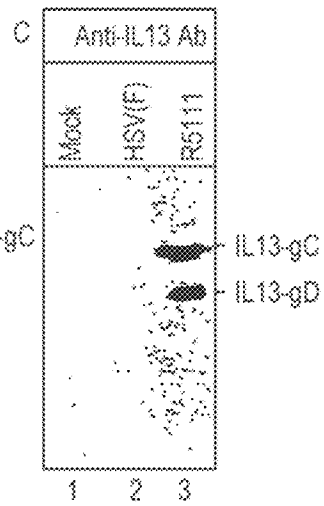


FIG. 4C

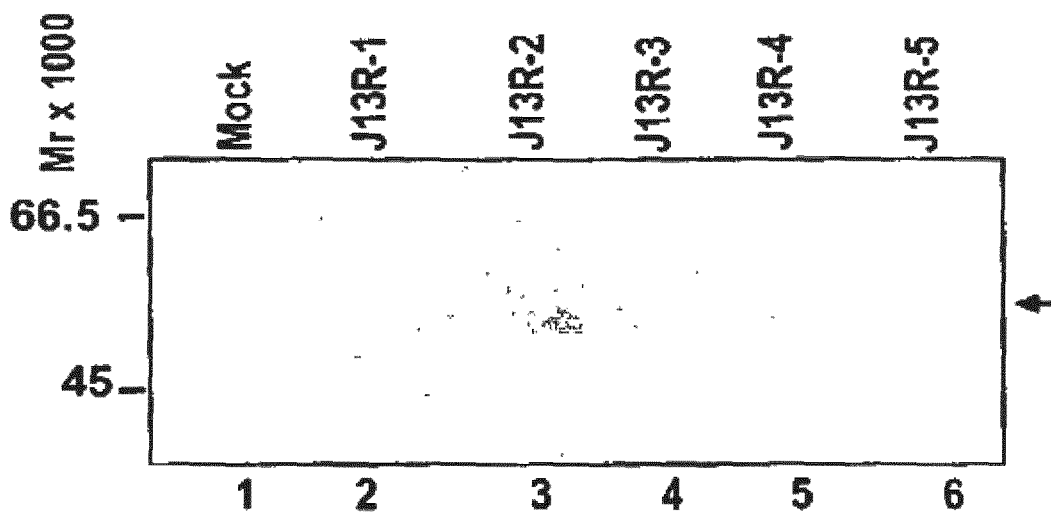
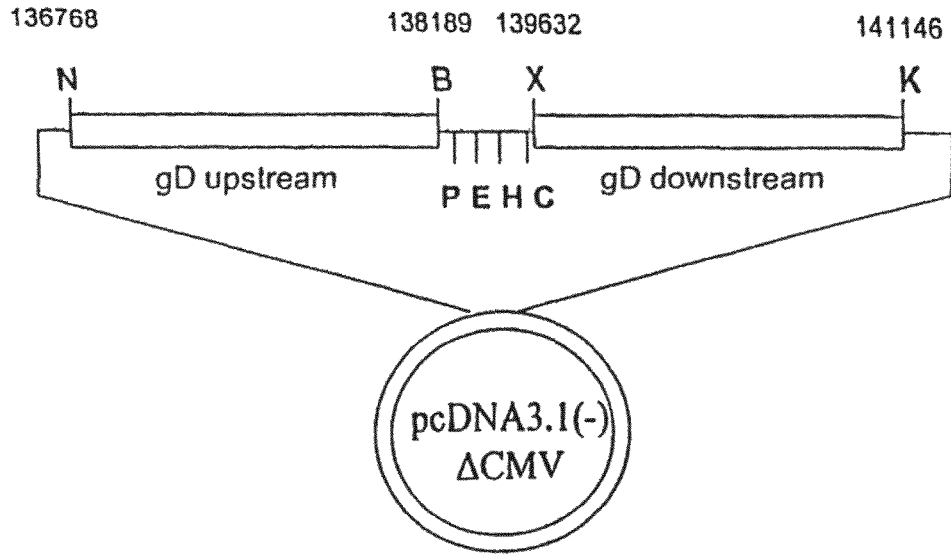


FIG. 5



pgD- in pcDNA3.1(-) with CMV promoter collapsed by NruI/NheI digestion. The fragment containing gD upstream at NotI/BamHI, and gD downstream at XhoI/KpnI in pBluescript II SK was excised by NotI/KpnI and ligated into pcDNA3.1(-) in which the CMV promoter had been collapsed. N, NotI, B, BamHI, P, PstI, E, EcoRI, H, HindIII, C, ClaI, X, XhoI, and K, KpnI.

FIG. 6

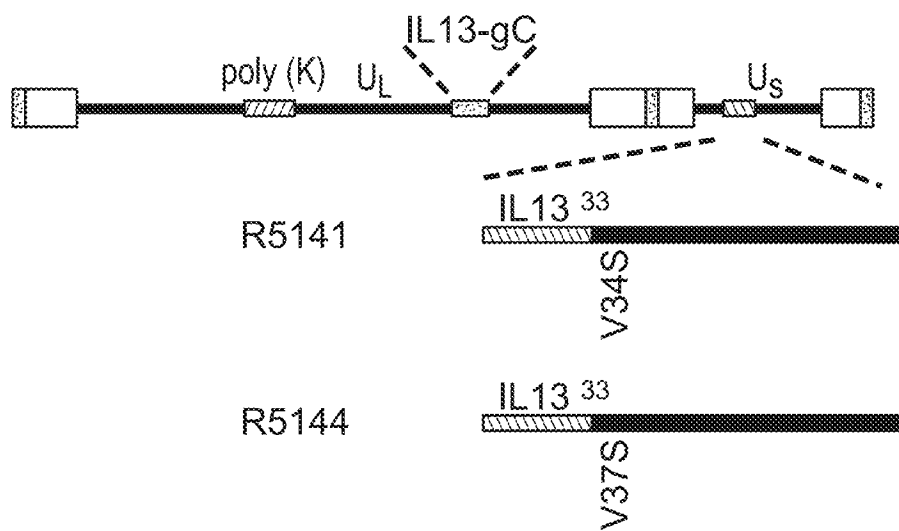


FIG. 7

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TARGETING OF HERPES SIMPLEX VIRUS TO SPECIFIC RECEPTORS

This application is a continuation-in-part application of U.S. Ser. No. 10/530,774, which is the US national phase of PCT/US03/31598 filed Oct. 6, 2003, which claims the priority benefit of U.S. Ser. No. 60/416,716, filed Oct. 7, 2002.

GOVERNMENT INTERESTS

The U.S. Government owns rights in the invention pursuant to National Cancer Institute grant number 1PO1 CA71933.

BACKGROUND OF THE INVENTION

A steady rate of healthcare advances has led to continuing improvement in the health and quality of life for humans and animals. Nevertheless, a variety of diseases, disorders, and conditions have largely eluded the best efforts at prevention or treatment. Chief among these maladies is the loss of cell-cycle control that frequently results in the undesirable cell proliferation characteristic of cancer in its many forms, such as malignant glioma. Malignant gliomas are devastating brain tumors that afflict animals such as humans. The average life span after diagnosis is less than one year and few patients have been reported to survive five years. Furthermore, none of the conventional anti-cancer therapies has been successful in significantly prolonging the lifespan of patients with this disease. In recent years there have been numerous attempts to use genetically engineered herpes simplex viruses (HSV) as oncolytic agents to treat malignant gliomas. Because wild-type viruses are highly virulent, the viruses used in preclinical evaluations and in phase-I clinical studies have been thoroughly attenuated. While several deletion mutants have been tested, the mutants that reached clinical trials lacked the γ_1 34.5 gene encoding infected cell protein 34.5 (ICP34.5) and optionally, the U_L 39 gene encoding the large subunit of ribonucleotide reductase.

These attenuated HSV viruses, however, have been imperfectly engineered as oncolytic agents. One advantage of these mutant viruses is that they have a significantly reduced capacity to replicate in normal, non-dividing cells in vivo. Viral ribonucleotide reductase is an essential gene for viral replication in resting cells and, hence, the U_L 39 mutant virus is dysfunctional in the normal environment of the central nervous system (Simard et al. 1995). The major function of ICP34.5 is to preclude the shutoff of protein synthesis caused by activation of protein kinase R in infected cells. Once activated, this enzyme phosphorylates the a subunit of translation initiation factor 2 (eIF2 α), resulting in complete cessation of translation. Mutants lacking the γ_1 34.5 genes are highly attenuated because the lytic life cycle is completely blocked in an interferon⁺ cellular background. In contrast, γ_1 34.5 mutants are nearly as virulent as wild-type virus in mice lacking interferon receptor. Although mutants deleted in both γ_1 34.5 and U_L 39 are not significantly more attenuated than those lacking the γ_1 34.5 genes, such mutants do provide added insurance in the form of a reduced risk of reversion.

A significant disadvantage of these mutant HSV viruses is their poor replication, even in dividing cells. In experimental animal systems, the mutant viruses do not exhibit sustained lytic life cycles, with the loss of a potentially amplified response to a given therapeutic dose of the virus that would be expected upon re-infection of tumor cells by the multi-

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plied viral progeny. Consequently, maximum killing of tumor cells requires high doses of virus. Given the poor growth of these mutant HSV viruses, even in dividing cells, production of virus pools large enough to yield efficacious inocula of $>10^9$ plaque forming units (PFU) has remained a major obstacle. Moreover, indiscriminate binding of virus to non-tumor cells further diminishes the effectiveness of HSV virus dosages because mis-targeted viral particles do not contribute to the desired beneficial therapeutic effect of tumor cell destruction. One approach to overcoming these obstacles is to achieve a more thorough understanding of the HSV lytic life cycle and thereby facilitate the development of HSV mutants tailored for use as targeted therapeutic agents, such as targeted oncolytic agents.

HSV enters host cells using a two-step mechanism. The first step of entry is HSV attachment to the cell surface. This step is initiated by glycoproteins B and C (gB and gC), which project from the viral envelope, attaching to heparan sulfate proteoglycans on host cell surfaces. The gB and gC domains interacting with heparan sulfate have been mapped at the sequence level (Laquerre et al. 1998). Following this initial attachment, viral glycoprotein D (gD) interacts with one of several receptors. Of these gD receptors, two are particularly important for entry (Spear et al, 2000). One receptor, designated HveA (formerly, HveM), is a member of the family of receptors for tumor necrosis proteins. A second receptor, designated Nectin-1 (HveC), is a member of the nectin family of proteins, structurally related to the immunoglobulin superfamily, which serve as intercellular connectors (Campadelli-Fiume et al. 2000). The second step of HSV entry into a cell is fusion of the viral envelope with the plasma membrane of the cell. To effect fusion, gD, when bound to its receptor, recruits glycoproteins B, H and L, which results in fusion of the envelope with the plasma membrane.

Additional understanding of HSV infection has come from recent studies that have lent significance to an old observation that gD interacts with the cation-independent mannose 6 phosphate receptor, contributing to the accumulation of HSV in endosomes. Endocytosis of viral particles results in particle degradation by lysosomal enzymes, but the cells succumb as a consequence of the degradation of cellular DNA by lysosomal DNase. HSV gD blocks this apoptotic pathway to cell death through its interaction with the mannose 6 phosphate receptor. Thus, gD interacts with HveA, nectins, the mannose 6 phosphate receptor, and at least one of the complex of viral glycoproteins involved in the fusion of HSV with the plasma membrane.

In an attempt to target HSV-1 infection to specific cells, a recombinant HSV having a chimeric protein comprising gC and erythropoietin (EPO) on its surface was constructed. Although the recombinant virus bound to cells expressing EPO receptor and endocytosis of the virus occurred, successful infection of these EPO-receptor expressing cells did not occur.

Accordingly, a need continues to exist in the art for viral therapeutic agents exhibiting improved targeting capacities while retaining sufficient capacity to infect to be therapeutically useful. Ideally, suitable viruses would be therapeutic agents, such as oncolytic agents, themselves as well as providing a targeting vehicle or vector for the controlled delivery of polynucleotide coding regions useful as therapeutic agents. Another need in the art is for targeted agents useful in diagnostic applications as, e.g., imaging agents or targeted vehicles for imaging agents.

SUMMARY

The invention satisfies the aforementioned need in the art by providing viral forms suitable for use as therapeutic and

diagnostic agents themselves, as well as providing a ready vehicle for the delivery of therapeutic or diagnostic polynucleotide coding regions to cells. These viral forms are modified viruses of the Herpesviridae family of viruses, and are preferably derived from herpes simplex virus type 1 or type 2. The invention provides a method of making virus particles with a novel ligand (or binding pair member), and making said particles totally dependent on a receptor of the ligand (or binding pair member) for entry into targeted cells.

Disclosed herein are methods to modify the surface of, e.g., an HSV virus particle in a manner that targets the virus to a specific receptor present on the surface of a cell of choice, typically a cell in need of therapy or a cell whose presence provides information of diagnostic value. The invention provides viral particles, e.g., HSV particles, having a reduced affinity for their natural cell-surface receptor(s), and methods for producing and using such particles, which minimizes or eliminates the problem of reduced efficiency associated with the mis-targeting of therapeutic and diagnostic viruses. Additionally, the invention provides viral particles, e.g., HSV particles, that exhibit specific affinity for a cell surface component that is not a natural viral receptor and that is present solely or predominantly on a given target cell, as well as methods for producing and using such viruses. Modified viral particles (e.g., HSV) having increased affinity for a cell surface component associated with one or more target cells exhibit improved targeting capabilities relative to known viral particles. The modified HSV particles have reduced indiscriminate binding, thereby minimizing sequestration of viral dosages away from the target cells. The invention further provides modified viral particles, such as modified HSV particles, that have both a reduced affinity for natural viral receptors and an increased affinity for a cell surface component associated with a particular target cell(s), with the modified viral particle effectively recruiting that cell surface component for use as a viral receptor. Other benefits of the modified viruses are described herein and will be apparent to those of skill in the art upon review of this disclosure.

In one aspect, the invention provides a recombinant herpes simplex virus (HSV) particle having at least one protein on its surface, comprising: (a) an altered gD, wherein the alteration reduces binding of gD to one or more of its cellular receptors, said alteration comprising (i) a heterologous peptide ligand on the surface of the recombinant HSV particle forming a fusion protein with the altered gD; and (ii) an amino acid alteration; wherein said recombinant HSV particle preferentially binds to cells expressing a binding partner to said heterologous peptide ligand. In some embodiments, these particles preferentially bind to target cells (cell expressing a binding partner) in whole or part due to the greater frequency of the binding partner on the surface of the cell relative to any natural HSV binding proteins on the surface of that cell. In some embodiments, the recombinant HSV particle further comprises an altered viral surface protein, wherein the alteration reduces binding of the viral surface protein to a sulfated proteoglycan. Such recombinant herpes simplex virus (HSV) particles comprise a virus surface protein altered to reduce the wild-type level of binding of that protein to a sulfated proteoglycan on the surface of a cell and an altered gD. The altered gD exhibits a reduced binding to one or more of the natural cellular receptors for gD; the altered gD is also fused to a heterologous peptide ligand (or binding pair member) having a binding partner, e.g., a peptide ligand receptor, found on the surface of a cell. Stated in the alternative, this aspect of the invention provides a recombinant herpes simplex virus

(HSV) particle having at least one protein on its surface, comprising: (a) an altered viral surface protein, wherein the alteration reduces binding of the viral surface protein to a sulfated proteoglycan; and (b) an altered gD, wherein the alteration reduces binding of gD to one or more of its cellular receptors, the alteration comprising (i) a heterologous peptide ligand (or binding pair member) on the surface of the recombinant HSV particle forming a fusion protein with the altered gD; and (ii) an amino acid alteration; wherein the recombinant HSV particle preferentially binds to cells expressing a binding partner to the heterologous peptide ligand (or binding pair member).

The invention comprehends a recombinant HSV particle wherein the amino acid alteration is selected from the group consisting of an amino acid deletion, an amino acid substitution and an amino acid insertion. A preferred site for the amino acid alteration is amino acid position 34 of gD. Exemplary recombinant HSV particles according to the invention include HSV R5141 and HSV R5161, each described below.

Contemplated amino acid alterations include insertions or deletions of 1-10 amino acids, such as insertions or deletions of 1-5 amino acids. Exemplary insertions occur immediately upstream (N-terminal) or downstream (C-terminal) to amino acid position 34 of gD. Exemplary deletions include amino acid position 34 of gD. For alterations comprising amino acid substitutions, 1-10 amino acids are substituted, such as substitutions of 1-5 amino acids. Non-contiguous (dispersed) or contiguous amino acid substitutions are contemplated. In some embodiments, conservative amino acids known in the art are substituted. Exemplary amino acid substitutions include single amino acid substitutions for the Serine at position 34 of gD. Preferably, substitutions for Ser34 will be conservative as, for example, an amino acid substitution of V34S in gD.

The altered gD, moreover, reduces binding of the recombinant HSV particle to at least one HSV entry mediator (Hve) cell-surface protein, such as an Hve selected from the group consisting of HveA (formerly, HveM) and Nectin-1 (HveC). Further, the recombinant HSV particles of the invention include particles wherein the altered viral surface protein is selected from the group consisting of gB and gC. In some embodiments, the altered viral surface protein, preferably selected from the group of gB and gC, forms a fusion protein with a heterologous peptide ligand. In some embodiments, the binding partner is a cell surface receptor for the heterologous peptide ligand.

The preferential binding of the recombinant HSV particles of the invention results in a detectable variation in effective binding of the particle to the cells being compared. By "effective binding" is meant either sufficiently stable binding to permit detection of binding or binding sufficient to result in productive infection of the cell. In preferred embodiments, the preferential binding is such that the recombinant HSV particles bind only to one of the cell types being compared (e.g., cancer cells compared to healthy cells of the same type). Suitable cells include any hyperproliferative cell type, such as a cancer cell. A cancer cell, in turn, includes a tumor cell, e.g., a malignant glioma cell.

The invention comprehends recombinant HSV particles wherein the heterologous peptide ligand (or binding pair member) is any ligand (or binding pair member) for which a cell surface binding partner exists. Preferably, heterologous peptide ligands have specific cell surface binding partners, e.g., ligand receptors, that are preferentially exhibited on the surface of a target cell. More preferably, the cell surface binding partner is only exhibited on the surface of a

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target cell, when compared to the cells in an organism containing the target cell. Exemplary heterologous peptide ligands that include cytokines, such as IL13, and fragments, variants and derivatives thereof, provided that the ligand retains the capacity of binding to a cell-surface binding partner. An exemplary binding pair member contemplated as suitable for each aspect of the invention is a single-chain antibody, for which a binding partner would include an antigen thereof, or a fragment, derivative or variant thereof that retains the capacity to bind to the single-chain antibody.

Another aspect of the invention is drawn to the recombinant HSV particle described above, wherein a polynucleotide encoding the fusion protein is joined to a heterologous coding region for a leader sequence. In this context, "heterologous" means that the leader sequence is not found naturally associated with the upstream or 5' coding region participating in the fusion. Exemplary leader sequences include HSV leader sequences, e.g., an HSV gD leader sequence. In a related aspect, the invention provides the recombinant HSV particle described above, wherein a polynucleotide encoding the fusion protein is joined to a heterologous expression control element, such as a heterologous promoter (a promoter not naturally found in association with the polynucleotide coding region fused upstream or 5' in the fusion), a heterologous enhancer, or expression factor binding site known in the art.

Another aspect of the invention provides a pharmaceutical composition comprising a recombinant HSV particle described above and a pharmaceutically acceptable carrier, diluent, or excipient. Any pharmaceutical carrier, diluent or excipient known in the art is contemplated. A related aspect of the invention provides a kit comprising the pharmaceutical composition and a set of instructions for administering the composition to a subject in need. In each of these aspects of the invention, i.e., the pharmaceutical compositions and the kits, the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described in the context of describing the recombinant HSV particles are contemplated.

Yet another aspect of the invention provides a method of targeting a recombinant HSV particle to a cell comprising (a) identifying a binding pair member, such as a ligand for a ligand binding partner, exhibited on the surface of a target cell; and (b) creating an HSV particle as described herein, wherein the ligand or, more generally, the binding pair member, binds to the binding partner exhibited on the surface of the target cell. In some preferred embodiments of this aspect of the invention, the altered viral surface protein is selected from the group consisting of gB and gC. In some embodiments, the alteration to gD reduces binding of gD to at least one cellular receptor for gD selected from the group consisting of HveA and Nectin-1. In preferred embodiments, the altered gD has a conservative substitution at position 34 of gD, such as a V34S substitution. A second fusion protein, joining the ligand (or binding pair member) and either of gB or gC, is also contemplated in some embodiments. Suitable cells for targeting include any hyperproliferative cell, such as a cancer cell, including tumor cells (e.g., malignant glioma cells). Any of the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described above in the context of describing the recombinant HSV particles is suitable for use in the method.

Another aspect of the invention is drawn to a method of imaging a cell comprising: (a) contacting the cell with a recombinant HSV particle as described above, the recombinant HSV particle further comprising a coding region for a marker protein; and (b) detecting the presence of the

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marker protein. Any type of cell exhibiting a cell-surface binding partner for a ligand (or binding pair member) fusible to HSV gD is suitable for use in this aspect of the invention, such as a cancer cell. Using cancer cells as an example, the method is useful provided that the binding partner is present at a higher number on the cancer cell as compared to a non-cancerous cell of the same type. Any known marker protein is useful in this aspect of the invention, e.g., a marker protein selected from the group consisting of thymidine kinase, green fluorescent protein, and luciferase. In preferred embodiments, the altered gD exhibits an amino acid substitution of V34S. Any of the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described above in the context of describing the recombinant HSV particles is suitable for use in the method.

Another aspect of the invention provides a method of treating a cell-based disease comprising delivering a therapeutically effective amount of a recombinant HSV particle as described herein to a subject in need. A related aspect is the use of a recombinant HSV particle as described above in the preparation of a medicament for the treatment of a cell-based disease. A therapeutically effective amount of a recombinant HSV particle is that amount that produces the desired therapeutic effect, as would be understood and readily determinable by those of skill in the art. Any cell-based disease known or reasonably suspected to be amenable to treatment with a specifically targeted HSV is contemplated, e.g., a cell hyperproliferation disease such as cancer. Any of the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described above in the context of describing the recombinant HSV particles is suitable for use in the method.

In a related aspect, the invention provides a method of ameliorating a symptom associated with a disease comprising administering a therapeutically effective amount of a recombinant HSV particle described above to a subject in need. Another aspect is drawn to the use of a recombinant HSV particle as described above in the preparation of a medicament for ameliorating a symptom associated with a disease in a subject in need. Again, any disease known or reasonably suspected to have a symptom amenable to application of a specifically targeted HSV is contemplated, including any disease characterized by hyperproliferative cells, such as cancer. Any of the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described above in the context of describing the recombinant HSV particles is suitable for use in the method.

Another aspect of the invention is directed to a method of delivering a therapeutically useful peptide to a cell comprising: (a) inserting a therapeutically useful polynucleotide, such as an expression control element, an rDNA, or a coding region for a therapeutically useful peptide, into the DNA of a recombinant HSV particle as described above, thereby producing a recombinant HSV clone; and (b) delivering a therapeutically effective amount of the recombinant HSV clone to the cell. In a related aspect, the invention provides for the use of a recombinant HSV clone comprising a recombinant HSV particle according to claim 1 in the preparation of a medicament for delivering a therapeutically useful peptide to a cell comprising inserting a coding region for a therapeutically useful peptide into the DNA of the recombinant HSV particle, thereby producing the recombinant HSV clone. Each of the method and use comprehends delivery of the recombinant HSV clone in vivo, ex vivo, or in vitro. Any of the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described

above in the context of describing the recombinant HSV particles is suitable for use in the method or use.

Another aspect of the invention provides a method of killing a target cell, comprising contacting the target cell with a recombinant HSV particle as described above. A related aspect is the use of a recombinant HSV particle as described above in the preparation of a medicament for killing a target cell by contacting the target cell with the recombinant HSV particle. In preferred embodiments of either the method or the use, the recombinant HSV particle has an altered gD in which the V34S substitution is found. Any of the heterologous peptide ligands (or binding pair members) and cell-surface binding partners described above in the context of describing the recombinant HSV particles is suitable for use in the method or use.

In each of the above-described aspects of the invention, it is preferred that gD, or a portion thereof, maintains its membrane fusion properties, but has reduced capacity to bind HveA and/or Nectin-1.

Other features and advantages of the invention will be better understood by reference to the brief description of the drawing and the description of the illustrative embodiments that follow.

BRIEF DESCRIPTION OF THE DRAWING

FIG. 1. Schematic representation of the HSV-1 (F) genome and gene manipulations in glycoprotein C (gC) (FIG. 1A), glycoprotein B (gB) (FIG. 1B), and glycoprotein D (gD) (FIG. 1C). Line 1, sequence arrangement of the HSV-1 genome. The rectangular boxes represent the inverted repeat sequences ab and b'a' flanking the unique long (U_L) sequence, and inverted repeat c'a' and ca flanking the unique short (U_S) sequence. Line 2, sequence arrangement of domains of the glycoprotein C; the signal peptide (SP) domain and heparan sulfate (HS)-binding domain of gC are highlighted. Line 3, human IL13 with signal peptide that replaced the N-terminal segment of 148 amino acids of gC. Line 4, sequence arrangement of the poly-lysine domain of gB. Line 5, schematic representation of a recombinant HSV-1(F) genome, in which the N-terminal domain of gC was replaced with IL13 and the polylysine domain (from codon 68 to codon 77) of gB was deleted. Line 6, sequence arrangement of glycoprotein J (gJ), glycoprotein D (gD), and glycoprotein I (gI) in U_S . Line 7, replacement of gD with the immediate early promoter of CMV in order to enable the expression of gI. Line 8, schematic representation of recombinant HSV-1(F) genome, in which the N-terminal domain of gC was replaced with IL13, the poly-lysine domain of gB was deleted, and IL13 was inserted after amino acid 24 of gD (FIG. 1D). Line 9, a polylinker XhoI-BglII-EcoRI-KpnI was inserted after amino acid 24 of gD, with IL13 inserted into the XhoI and KpnI sites of gD.

FIG. 2. Amino acid sequence alignment of IL13-gC, IL13-gD junction sequence, and the HS binding domain of gB. FIG. 2A. The amino-terminal sequence of IL13-gC chimeric protein (SEQ ID NO:22). The sequences upstream and downstream of the HS binding site portion are shown. IL13 was inserted between the two restriction enzyme sites that are underlined. FIG. 2B. The domain of the gB open reading frame (i.e., ORF) from which the poly lysine [poly (K)] sequence was deleted (SEQ ID NO:23). The underlined sequences (codons 68-77) were not present in gB amplified from R5107. FIG. 2C. The amino-terminal sequence of IL13-gD (SEQ ID NO:24). The first underlined sequence identifies the gD signal peptide. IL13 (bracketed by arrows)

was inserted between residues 24 and 25 (underlined) of gD, between the XhoI and KpnI restriction enzyme sites.

FIG. 3. Verification of R5111 viral DNA by PCR. Photographs of electrophoretically separated PCR products amplified directly from the plaques picked from Vero (FIG. 3A) and HEp-2 (FIG. 3B) cells. Viral DNAs were extracted as described in Example 1 and subjected to PCR with "IL13" primers from the IL13 ORF and IL13-gD primers, which bracketed IL13 and the gD ectodomain.

FIG. 4. Photograph of electrophoretically separated proteins from lysates of cells infected with R5111 reacted with antibody to gC, gD or IL13. HEp-2 cells grown in 25 cm² flasks were exposed to 10 PFU of HSV-1 or R5111 per cell. The cells were harvested 24 hours after infection, solubilized, subjected to electrophoresis in 10% denaturing polyacrylamide gels, electrically transferred onto a nitrocellulose sheet, and exposed to a monoclonal antibody against gD (FIG. 4A), gC (FIG. 4B) or IL13 (FIG. 4C), respectively. The protein bands corresponding to the gC, IL13-gC fusion protein, gD and the IL13-gD fusion protein are indicated. IL13-gC was the same size as native gC, as expected.

FIG. 5. HA-tagged IL13R α 2 expression from individual clones of stable transfectants of the J1.1 cell line. The individual clones were amplified as described in Example 1. Cells were harvested from 25 cm² flasks, solubilized, and subjected to electrophoresis in 12% denaturing polyacrylamide gels, electrically transferred onto a nitrocellulose sheet, and exposed to a polyclonal antibody to HA tag.

FIG. 6. Diagram of the pgD-vector.

FIG. 7. Schematic representation of the HSV-1 (F) genome and genetic structure of R5141 and R5144.

DETAILED DESCRIPTION

The invention provides benefits that will improve the health and well-being of animals such as man by providing a targeted approach to the treatment of a variety of conditions and diseases that currently impair health, resulting in significant economic burdens using conventional treatments. In providing modified viral particles having controllable targeting capacities, the diagnostic and therapeutic benefit of the viruses themselves can be delivered with greater precision to particular cells. Additionally, these viral particles can be used as targeting vehicles for the delivery of a wide variety of therapeutic and diagnostic biomolecules, such as polynucleotides encoding therapeutic or diagnostic peptides.

Beyond the modified viral particles, the invention provides methods for making such therapeutic and diagnostic agents as well as methods for using the agents to diagnose or treat a variety of diseases and conditions, such as tumorigenic disease (e.g., gliomas). To facilitate understanding of the invention and all of its aspects, illustrative embodiments are described below. The descriptions of these illustrative embodiments are not meant to limit the invention to the embodiments disclosed herein. In light of the description, one of skill in the art will understand that many changes and modifications can be made to the illustrative embodiments and still remain within the invention. The illustrative embodiments are disclosed using as an exemplary virus a member of the Herpesviridae family of viruses, herpes simplex virus (HSV).

As noted above, HSV-1 and HSV-2 are members of the family of viruses known as the Herpesviridae, whose structures are well known in the art. The targeting methods of the invention are applicable to any member of the Herpesviridae and are not limited to the exemplary embodiments described in the examples. Furthermore, a large number of recombi-

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nant HSV viruses are known in the art. Such viruses may contain one or more heterologous genes. Also, such viruses may contain one or more mutated HSV genes, for example, mutations that render the virus replication-deficient or affect the virulence of the virus in one or more cell types.

Examples of recombinant HSV containing a heterologous gene and methods of making and using such viruses are described in U.S. Pat. No. 5,599,691 (incorporated herein by reference in its entirety). Preferred heterologous genes include genes encoding marker proteins. Marker proteins, such as green fluorescent protein, luciferase, and beta-galactosidase, allow detection of cells expressing the protein. In other embodiments, the heterologous gene encodes an enzyme that activates a prodrug thereby killing adjacent uninfected cells. In yet other embodiments, the heterologous gene encodes a protein that affects the immune response, such as interleukin 12 (IL-12). Such proteins that activate the immune response against a tumor are particularly useful.

In one aspect, the invention relates to altering the surface of an HSV particle to target the virus to a specific receptor. By creating a fusion protein comprising a portion of gD and a ligand (or binding pair member), the virus is targeted to a cell having a cell surface receptor that binds the ligand (or binding pair member). In preferred embodiments, one or more HSV surface proteins, such as gB (SEQ ID NOs:27 and 28), gC (SEQ ID NOs:29 and 30), or gD (SEQ ID NOs:25 and 26), are altered to reduce binding to natural HSV receptors.

“Alterations” of the surface of an HSV particle or HSV surface protein include insertions, deletions, and/or substitutions of one or more amino acid residues. One type of alteration is an insertion, which involves the incorporation of one or more amino acids into a known peptide, polypeptide or protein structure. For ease of exposition, alterations will be further described using a protein exemplar. Insertions may be located at either or both termini of the protein, or may be positioned within internal regions of known proteins, which yield proteins such as fusion proteins and proteins having amino acid tags or labels.

Another type of alteration is a deletion, wherein one or more amino acid residues in a protein are removed. Deletions can be effected at one or both termini of the protein, or with removal of one or more residues within the amino acid sequence. Deletion alterations, therefore, include all fragments of a protein described herein.

Yet another type of alteration is a substitution, which includes proteins wherein one or more amino acid residues are removed and replaced with alternative residues. In one aspect, the substitutions are conservative in nature; however, the invention embraces substitutions that are also non-conservative. Conservative substitutions for this purpose may be defined as set out in Tables A or B, below.

Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table A as described in Lehninger, [Biochemistry, 2nd Edition; Worth Publishers, Inc. New York (1975), pp. 71-77] and set out immediately below.

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TABLE A

Conservative Substitutions I	
SIDE CHAIN CHARACTERISTIC	AMINO ACID
Non-polar (hydrophobic):	
A. Aliphatic	A L I V P
B. Aromatic	F W
C. Sulfur-containing	M
D. Borderline	G
Uncharged-polar:	
A. Hydroxyl	S T Y
B. Amides	N Q
C. Sulfhydryl	C
D. Borderline	G
Positively charged (basic)	K R H
Negatively charged (acidic)	D E

Alternative, exemplary conservative substitutions are set out in Table B, immediately below.

TABLE B

Conservative Substitutions II	
ORIGINAL RESIDUE	EXEMPLARY SUBSTITUTION
Ala (A)	Val, Leu, Ile
Arg (R)	Lys, Gln, Asn
Asn (N)	Gln, His, Lys, Arg
Asp (D)	Glu
Cys (C)	Ser
Gln (Q)	Asn
Glu (E)	Asp
His (H)	Asn, Gln, Lys, Arg
Ile (I)	Leu, Val, Met, Ala, Phe,
Leu (L)	Ile, Val, Met, Ala, Phe
Lys (K)	Arg, Gln, Asn
Met (M)	Leu, Phe, Ile
Phe (F)	Leu, Val, Ile, Ala
Pro (P)	thy
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser
Val (V)	Ile, Leu, Met, Phe, Ala

The binding site of HveA has been reported to be at the amino terminal domain of gD (Carfi A., et al., 2001). The precise binding sites of gD for Nectin 1 are not known, although it has previously been reported to involve gD amino acids 38 and 221 (Manoj S., et al., 2004; Zago A., et al., 2004; Connolly S A., 2005). Accordingly, in one aspect the invention relates to amino acid alterations in the N-terminal region of gD such that the ability of gD to bind HveA or Nectin1 is reduced or eliminated. A “natural receptor” as used herein is a cell surface molecule that interacts with wild-type HSV in the absence of human intervention. For example, gB and gC of HSV-1 interact with heparan sulfate proteoglycans in a natural infection. In preferred embodiments, gB and/or gC are altered to reduce or eliminate binding to heparan sulfate proteoglycans. As another example, gD is known to bind to several receptors, including HveA and Nectin-1, in a natural infection. In preferred embodiments, gD is altered to reduce or eliminate binding to HveA and/or Nectin-1.

Receptor-Ligands

As used herein, “receptor” and “ligand” refer to two members of a specific binding pair and, hence, are binding partners. A receptor is that member of the pair that is found localized on the surface of the cell; the ligand is the member

of the pair that is found on the surface of HSV. Thus, in certain embodiments, the “ligand” may actually be what the art recognizes as a receptor outside the context of the invention and the “receptor” may be its respective ligand. More generally, the invention comprehends an HSV exhibiting a member of a binding pair, or a fragment thereof that retains the capacity to specifically bind the other member of the binding pair, on its surface and the other member of that binding pair, or a fragment thereof that retains the capacity to specifically bind its partner, is present on the surface of a target cell.

One advantage of the invention is the ability to tailor HSV to target a specific receptor while maintaining infectivity of the virus. In an exemplary embodiment, an HSV particle contains a fusion protein comprising a portion of gD and the cytokine IL-13. Such a virus is able to infect cells expressing the receptor IL-13R α 2. Because IL-13R α 2 is expressed on the surface of cells of malignant gliomas, HSV containing the gD/IL-13 fusion protein are effectively targeted to such cells. Ligands that bind to receptors which are overexpressed or differentially expressed on either tumor cells or cells associated with tumor growth (e.g., neovasculature) are particularly preferred. Examples include the $\alpha_v\beta_3$ - $\alpha_v\beta_5$ integrins, which are overexpressed in tumor neovasculature; epidermal growth factor receptor (EGFR), which is overexpressed in head, neck, lung, colon, breast, and brain cancer cells; HER-2/Neu, which is overexpressed in breast cancer cells; MUC-1, which is overexpressed in breast, lung, and pancreas cancer cells; and prostate-specific membrane antigen, which is overexpressed in prostate cancer cells. In certain embodiments, the ligand is a single-chain antibody that binds to its cognate specific binding pair member, herein referred to as a receptor. Single-chain antibodies have been shown to be effective in targeting applications, as evidenced by their ability to target retroviruses to specific receptors.

Essentially any two binding pair members or partners may be used as receptor-ligands in the invention. However, it is contemplated that certain factors, such as the distance from the binding site on the receptor to the membrane, or the conformation of the ligand when fused to gD, may affect the efficiency of recombinant HSV fusion to the cell membrane. Therefore, screens for effective receptor-ligand pairs are contemplated, using no more than routine procedures known in the art. Additional screens, conventional in nature, may be used to optimize constructs. One routine method of screening is to follow the protocol provided in the example for candidate receptor/ligand pairs, using IL-13R/IL-13 as a control receptor/ligand pair.

Alternatively, one may use a membrane fusion assay as described in Turner et al., 1998, incorporated herein by reference in its entirety. In the Turner assay, cells transfected with construct(s) encoding gB, gH, gL, and the gD/ligand fusion protein, and cells expressing the receptor, are co-cultured and the cells are examined for membrane fusion. Membrane fusion between gD/ligand-expressing cells and receptor-expressing cells indicates that the candidate receptor-ligand pair (the ligand being a gD/ligand fusion protein) is functional. Constructs encoding functional gD/ligand proteins can then be used to create recombinant HSV that are targeted to cells expressing the receptor.

Cell Targeting

Evident from the preceding discussion, another aspect of the invention is the targeting of a recombinant HSV to a cell having a specific receptor on its surface. In preferred embodiments, a recombinant HSV is designed to comprise a ligand that interacts with a receptor known to be expressed

on a cell of interest. The cell of interest is then infected with recombinant HSV. Such targeting methods may be used for a variety of purposes.

In one aspect, a recombinant HSV is used to introduce a heterologous gene into a cell that expresses the receptor. In preferred embodiments, the cell is not infected by, or is poorly infected by, wild-type HSV. Thus, in certain embodiments, the invention provides a vector for transforming a cell of interest with a heterologous gene.

Further, a cell can be rendered a target of a recombinant HSV of the invention. The cell can be rendered a target by transforming the cell to express one member of a binding pair, e.g., a receptor capable of specifically binding a ligand expressed on a recombinant HSV. For example, as described in Example 2, the J1.1 cell line, which was resistant to infection by a recombinant HSV expressing an IL-13 ligand, was rendered susceptible to infection by transforming the cell line with a vector encoding IL12R α 2 to produce the cell line J13R.

Generally, the targeted HSV according to the invention exhibit one member of a binding pair, with the other member of that pair found on the surface of a target cell. In some embodiments of the invention, targeting is achieved with a ligand-receptor binding pair, with the ligand exhibited on the targeted HSV and the cognate receptor found on the surface of the target cell, as described above. Although the invention comprehends embodiments involving binding pairs that do not exhibit a ligand-receptor relationship (e.g., biotin-avidin) and embodiments in which the receptor is exhibited by the targeted HSV (the “receptor” defined above as a “ligand” using an alternative definition of “ligand”) while the cognate ligand is found on the target cell (the “ligand” defined above as a “receptor” using an alternative definition of “receptor”), embodiments in which the targeted HSV exhibits a ligand and the target cell presents the cognate receptor on its surface is used as an illustrative embodiment to reveal the versatility of the invention and to disclose the full scope thereof. For example, several ligands have been used for receptor-mediated polynucleotide transfer. Some ligands that have been characterized are asialoorosomucoid (ASOR) and transferrin (Wagner et al., Proc. Natl. Acad. Sci. USA, 87(9):3410-3414, 1990). A synthetic neoglycoprotein, which recognizes the same receptor as ASOR, has also been used in a polynucleotide delivery vehicle (Ferkol et al., FASEB J., 7:1081-1091, 1993; Perales et al., Proc. Natl. Acad. Sci., USA 91:4086-4090, 1994) and epidermal growth factor (EGF) has further been used to deliver polynucleotides to squamous carcinoma cells (Myers, EPO 0273085). Each of these specific approaches, and other approaches known in the art to achieve some selectivity in DNA delivery, or targeting, are amenable to use in the compositions and methods of the invention and are contemplated as embodiments of the invention.

For embodiments in which a targeted HSV harboring a coding region, e.g., a therapeutic coding region or gene, is delivered to a target cell, the nucleic acid encoding the therapeutic gene product may ultimately be positioned and expressed at different sites. In certain embodiments, the nucleic acid encoding the therapeutic polynucleotide may be stably integrated into the genome of the cell. This integration may place the gene in its native location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or episomes encode functions sufficient to permit maintenance and replication

independent of or in synchronization with the host cell cycle. How the expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed, as would be understood in the art.

It is envisioned that promoters subject to cell cycle regulation will be useful in the present invention. For example, in a bicistronic HSV vector designed to treat a disease, disorder or condition by killing a target cell, use of a strong CMV promoter to drive expression of a first gene, such as p16, that arrests a cell in the G1 phase is accompanied by expression of a second gene, such as p53, under the control of a promoter that is active in the G1 phase of the cell cycle, thus providing a dual-gene approach to ensure that the target cell undergoes apoptosis. Other promoters, such as those of various cyclins, PCNA, galectin-3, E2F1, p53, BRCA1, and, indeed, any suitable promoter or expression element known in the art, could be used.

In embodiments of the invention designed to treat diseases, disorders, or conditions associated with unwanted or excessive cell proliferation, such as cancer or restenosis, HSV is targeted to proliferating cells thereby killing the cells. Because HSV is lethal to infected cells, expression of a heterologous gene is not required. However, in embodiments wherein the lethality of HSV is attenuated, an HSV harboring a gene that is lethal to the infected cell or that prevents proliferation of the infected cell may be used to target a cell.

Alternatively, HSV targeted to specific surface markers can be used to visualize the distribution of tumor cells in tissues. This diagnostic tool had been unavailable because of the indiscriminate binding of HSV to cells. Modification of HSV by eliminating (ablating) or reducing the indiscriminate binding of HSV to heparan sulfate proteoglycans without deleteriously affecting the capacity of such HSV to replicate in both dividing and non-dividing cells makes possible the use of these modified viral forms to visualize the distribution of tumor cells.

In one preferred method for visualizing the distribution of tumor cells, radioactive visualization is achieved by viral thymidine kinase (TK)-dependent incorporation of a radioactive precursor. Methods of molecular imaging of gene expression are well known in the art. Methods often use highly sensitive detection techniques such as positron emission tomography (PET) or single-photon emission-computed tomography (SPECT). In one embodiment, TK expression is measured using a gancyclovir analog, such as 9-(3-[¹⁸F]fluoro-1-hydroxy-2-propoxy)methyl)guanine, as the tracer or marker (Vries et al., 2002). For a review of imaging TK gene expression using PET or SPECT, see Sharma et al., 2002 or Vries et al., 2002.

A second preferred imaging method is to fuse a non-critical tegument protein (e.g. U_s11, which is present in nearly 2000 copies per virus particle) to a marker protein, such as green fluorescent protein, which is capable of being visualized in vivo. Alternatively, a non-critical protein can be fused to a luciferase and the presence of the luciferase visualized with a luminescent or chromatic luciferase substrate. Although a marker protein can be fused to essentially any viral structural protein, preferred viral proteins include gC, gE, gI, gG, gJ, gK, gN, U_L11, U_L13, U_L14, U_L21, U_L41, U_L35, U_L45, U_L46, U_L47, U_L51, U_L55, U_L56, U_s10, and U_s11. The marker protein also may be fused to thymidine kinase (Soling et al., 2002).

Library Screening

As noted above, HSV comprising a gD/ligand fusion protein can bind and infect cells expressing a receptor to the

ligand. In one embodiment, a cell line expressing a receptor is used in screening for ligands of the receptor. cDNA from a cDNA library is cloned into a vector encoding a portion of gD to produce a gD/cDNA-encoded fusion protein. The resulting vectors are then screened for membrane fusion using the assay of Turner et al. described above or by creating recombinant HSV expressing the gD/cDNA-encoded fusion protein and screening the viruses for the ability to infect receptor-expressing cells. Such methods may be used, e.g., to identify a ligand to an orphan receptor.

In other embodiments, mutations in, or variants of, the receptor or ligand are screened to determine whether the mutants or variants maintain the ability to interact with the respective partner. Such methods may be useful in determining the specific residues important in receptor-ligand interaction.

Therapeutic Methods

Another aspect of the invention is the use of the targeted HSV in therapeutic methods. By altering the cell-binding and infectivity properties of the virus, many routes and methods of administration become viable. For example, non-targeted HSV will bind indiscriminately to a variety of cells. Because of this property, large virus numbers are used and intravenous administration is generally not effective. However, by targeting the virus, one may lower the viral load (i.e., quantity of virus), yet maintain or increase efficacy. Furthermore, the targeted HSV can be administered intravenously and produce therapeutic effects.

Therapeutic methods of the invention include those methods wherein an HSV is targeted to a receptor of a cell that contributes to, or is the basis of, a disease or disorder. These targeted HSV can either exploit the therapeutic properties of HSV itself (e.g., the lethality of HSV to infected cells) or the targeted HSV can serve as a vector for the targeted delivery of at least one therapeutic polynucleotide, such as an expressible polynucleotide comprising a coding region. For example, in methods wherein the targeted HSV contains one or more gene products that render the virus toxic to the cell or that prevent or inhibit cell proliferation, a preferred receptor is overexpressed or selectively expressed on harmful or undesirable cells, such as cancer cells. In other embodiments, the targeted HSV encodes a gene product that provides a desired function or activity in the targeted cell, e.g., when a cell has one or more genetic defects preventing the cell from functioning properly.

Additionally, it is contemplated that a therapeutic polynucleotide (e.g., gene or coding region) of a targeted HSV may be engineered to be under the expression control of a cell- or tissue-specific expression control element, e.g., a promoter. In such embodiments, the targeted HSV provide a further enhancement to the selective treatment of a suitable disorder, disease or condition. The targeted HSV is specific for a binding partner located on the surface of those cells for which treatment is intended, and expression of the therapeutic coding region or gene borne by the targeted HSV is limited to particular cells or tissues.

As HSV has been engineered to overcome the barriers to vector-based therapies, the choice of recombinant polynucleotide to be inserted into the vector has widened to the point where a wide variety of diseases, disorders and conditions are amenable to treatment with targeted HSV. A number of diseases are amenable to polynucleotide-based therapy using HSV (see, e.g., Kennedy, et al., *Brain*. 120, 1245-1259, 1997, incorporated by reference herein in its entirety). Though most attention has focused on cancers, there has been success in treating Parkinson's disease by expressing tyrosine hydroxylase in striatal cells, thus restor-

ing L-dopa-induced nerve repair following axotomy of the superior cervical ganglion. Injection of a vector expressing nerve growth factor resulted in restored levels of tyrosine hydroxylase. More generally, HSV can now be used in polynucleotide-based therapy to replace missing or defective coding regions in the target cells. In the event of an inherited single-gene disorder (such as Lesch-Nyhan syndrome) where the complete DNA sequence, cause, and effect of the disorder are known, a single polynucleotide replacement mediated by targeted HSV is appropriate and contemplated. Another strategy amenable to the use of targeted HSV is the enhancement of endogenous expression levels of a gene product, e.g., a growth factor or enzyme. Yet another strategy for using targeted HSV is HSV-directed enzyme pro-drug therapy. The delivery of a drug-sensitivity gene would be beneficial in the treatment of, e.g., a malignant brain tumor, making the tumor more susceptible to conventional anti-cancer agents.

In other embodiments, the targeted HSV of the invention provide for vector-mediated delivery of anti-sense oligodeoxyribonucleotides (oligonucleotides). The oligonucleotides, short segments of DNA (e.g., 2-100 nucleotides in length), are delivered to target cells and therein bind to complementary mRNA, thus blocking the expression of specific genes within the target cells. The encoded protein fail to be synthesized, as the mRNA is not be recognized by the translational components of the cell. In preferred embodiments, a deleterious gene is targeted.

In yet other embodiments, targeted HSV are used to deliver polynucleotides, e.g., DNAs encoding gene products, that can recruit or enhance an immune system response, thereby bringing a subject's or patient's own immune system to bear in the treatment of a disease, disorder or condition known in the art to be amenable to immune system activity. For example, an increase in cellular antigen expression of tumor cells, mediated by delivery of an expressible coding region for the antigen by a targeted HSV, would enhance the immune response and increase the susceptibility of such tumor cells to host cytotoxic immunity.

In some embodiments, a targeted HSV composition of the invention is delivered to a patient at or around the site of a tumor, which is a very efficient method for counteracting clinical disease. Alternatively, systemic delivery of targeted HSV compositions may be appropriate in other circumstances, for example, where extensive metastasis has occurred, or where inaccessible tumors are encountered.

It is contemplated that in certain embodiments of the invention a protein that acts as an angiogenesis inhibitor is targeted to a tumor. Also, an angiogenesis inhibitor agent may be administered in combination with a targeted HSV of the invention. These agents include, for example, Marimastat (British Biotech, Annapolis Md.; indicated for non-small cell lung, small cell lung and breast cancers); AG3340 (Agouron, LaJolla, Calif.; for glioblastoma multiforme); COL-3 (Collagenex, Newtown Pa.; for brain tumors); Neovastat (Aeterna, Quebec, Canada; for kidney and non-small cell lung cancer) BMS-275291 (Bristol-Myers Squibb, Wallingford Conn.; for metastatic non-small cell lung cancer); Thalidomide (Celgen; for melanoma, head and neck cancer, ovarian, and metastatic prostate cancers; Kaposi's sarcoma; recurrent or metastatic colorectal cancer (with adjuvants); gynecologic sarcomas, liver cancer; multiple myeloma; CLL, recurrent or progressive brain cancer, multiple myeloma, and non-small cell lung, nonmetastatic prostate, refractory multiple myeloma, and renal cancer); Squalamine (Magainin Pharmaceuticals Plymouth Meeting,

PA; non-small cell lung cancer and ovarian cancer); Endostatin (EntreMed, Rockville, Md.; for solid tumors); SU5416 (Sugen, San Francisco, Calif.; recurrent head and neck, advanced solid tumors, stage IIIB or IV breast cancer; recurrent or progressive brain (pediatric) cancer; ovarian cancer, AML (acute myeloid leukemia); glioma, advanced malignancies, advanced colorectal cancer, von-Hippel Lindau disease, advanced soft tissue cancer; prostate cancer, colorectal cancer, metastatic melanoma, multiple myeloma, malignant mesothelioma: metastatic renal, advanced or recurrent head and neck cancer, metastatic colorectal cancer); SU6668 (Sugen San Francisco, Calif.; advanced tumors); interferon- α ; Anti-VEGF antibody (National Cancer Institute, Bethesda Md.; Genentech San Francisco, Calif., for refractory solid tumors; metastatic renal cell cancer, in untreated advanced colorectal cancer; EMD121974 (Merck KGaA, Darmstadt, Germany, for HIV-related Kaposi's sarcoma, and progressive or recurrent Anaplastic Glioma); Interleukin 12 (Genetics Institute, Cambridge, Mass., for Kaposi's sarcoma) and IM862 (Cytran, Kirkland, Wash., for ovarian cancer, untreated metastatic cancers of colon and rectal origin, and Kaposi's sarcoma). The parenthetical information following the agents indicates the cancers against which the agents are being used in these trials. It is contemplated that any of these disorders may be treated with the targeted HSV compositions of the invention, either alone or in combination with the agents listed.

In order to prepare a therapeutic composition for clinical use, it will be necessary to prepare the therapeutic composition as a pharmaceutical composition, i.e., in a form appropriate for in vivo applications. Generally, this will entail preparing compositions that are essentially free of pyrogens, as well as other impurities that could be harmful to humans or other vertebrates.

Generally, appropriate salts and buffers are included to render delivery vectors stable and to allow for uptake by target cells. Aqueous compositions of the invention comprise an effective amount of the targeted HSV, dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium. Such compositions also are referred to as inocula. The phrase "pharmaceutically acceptable" or "pharmacologically acceptable" refer to molecular entities and compositions that do not produce adverse, allergic, or other untoward reactions when administered to an animal or a human. As used herein, "pharmaceutically acceptable carriers" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like. The use of such media and agents for pharmaceutically active substances is well known in the art. Unless a conventional medium or agent is incompatible with either the vectors of the invention or the intended subject receiving treatment, its use in therapeutic compositions is contemplated. Supplementary active or inert ingredients also can be incorporated into the compositions.

The active compositions of the invention include standard pharmaceutical preparations. Administration of these compositions according to the invention is by any known route, provided that the target tissue is accessible via that route. The pharmaceutical compositions may be introduced into the subject by any conventional method, e.g., by intravenous, intradermal, intramuscular, intramammary, intraperitoneal, intrathecal, retrobulbar, intravesicular, intrapulmonary (e.g., term release); sublingual, nasal, anal, vaginal, or transdermal delivery, or by surgical implantation at a par-

ticular site. The treatment may consist of a single dose or a plurality of doses over a period of time.

Upon formulation, solutions are administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. Appropriate dosages may be ascertained through the use of established routine assays. As studies are conducted, further information will emerge regarding optimal dosage levels and duration of treatment for specific diseases, disorders, and conditions.

In preferred embodiments, the unit dose may be calculated in terms of the dose of viral particles being administered. Viral doses are defined as a particular number of virus particles or plaque forming units (pfu). Particular unit doses include 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} or 10^{14} pfu. Particle doses may be somewhat higher (10- to 100-fold) due to the presence of infection-defective particles, which is determinable by routine assays known in the art.

The pharmaceutical compositions and treatment methods of the invention are useful in the fields of human medicine and veterinary medicine. Thus, the subject to be treated may be a vertebrate, e.g., a mammal, preferably human. For veterinary purposes, subjects include, for example, farm animals such as cows, sheep, pigs, horses and goats, companion animals such as dogs and cats, exotic and/or zoo animals, laboratory animals including mice, rats, rabbits, guinea pigs and hamsters; and poultry such as chickens, turkey, ducks and geese.

In some embodiments of the invention, it is contemplated that the targeted HSV is administered in conjunction with chemo- or radiotherapeutic intervention, immunotherapy, or with any other therapy conventionally employed in the treatment of cancer.

To kill cells, inhibit cell growth, inhibit metastasis, inhibit angiogenesis or otherwise reverse or reduce malignant phenotypes using the methods and compositions of the invention, one contacts a "target" cell, a tumor, or its vasculature with a targeted HSV composition and at least one other agent. The components of these compositions are provided in a combined amount effective to kill or inhibit proliferation of cancer cells. This process may involve contacting the cells with the targeted HSV composition and the agent(s) or factor(s) at the same time. This may be achieved by contacting the subject organism, or cell of interest, with a single composition or pharmacological formulation that includes both agents, or by contacting the cell with two distinct compositions or formulations, at the same or different times, wherein one composition includes a targeted HSV composition of the invention and the other composition includes the second agent.

Another aspect of the invention provides diagnostic methods that involve imaging a tumor or diseased tissue using a targeted HSV. Such methods are useful in diagnosing a patient with a disease, disorder, or condition that is indicated by the presence of a receptor on the surface of a cell. Diagnostic imaging methods are discussed above.

Kits

Kits according to the invention may include recombinant viruses of the invention or may include vectors for producing such recombinant viruses. A vector for producing a recombinant virus of the invention may encode the gD/ligand fusion protein or may be designed to facilitate cloning of a ligand to produce a gD/ligand fusion protein (e.g., a vector containing a multiple cloning site within the gD coding region that facilitates in-frame insertions).

Other components that can be included in a kit of the invention include a receptor-expressing cell line (useful as a

control), a nucleic acid molecule for expressing the receptor in a particular cell type, and instructions for using the kit to effect diagnostic analyses or therapeutic treatments. In certain embodiments, a therapeutic kit will further contain a component for bringing about a therapeutic effect, such as a prodrug or a toxic compound. In other embodiments, a diagnostic kit will contain a compound useful in imaging methods, such as a chromophore or fluorophore, or an antibody for detecting infected cells.

Having provided a general description of the various aspects of the invention, the following disclosure provides examples illustrative of the invention, wherein Example 1 describes construction of a targeted HSV, Example 2 illustrates the construction of a cell line expressing a targeted HSV, and Example 3 describes the controlled infection of a desired cell by a targeted HSV.

Example 1

Construction of HSV Targeting Vector R5111

A targeted HSV was constructed to target the recombinant virus to cells of malignant gliomas. The target for entry of the virus into such cells is the IL13R α 2 receptor known to be present in malignant gliomas. Unlike the more prevalent IL13 α R1 receptor, the IL13R α 2 receptor has a shorter cytoplasmic domain and does not interact with IL4, of which IL13 is a close relative. In general, the construction of the targeted HSV involved mutagenizing gB and gC to preclude their interaction with heparan sulfate. Also, IL13 was inserted into gD at amino acid 24 thereby disrupting the gD binding site for HveA. The resulting IL13-gD chimeric virus can use IL13R α 2 for entry into cells carrying that receptor.

More specifically, the targeted HSV R5111 was constructed in several steps depicted in the four panels of FIG. 1 and detailed below.

(i) Substitution of Amino Terminal Domain of gC with IL13 Fused to the Signal Sequence of gC.

FIG. 1A, lines 1-3 schematically depicts a cDNA consisting of the IL13 coding sequence fused at its amino terminus to its signal sequence. The complete cDNA of IL13, with the N-terminal signal peptide coding region, was amplified using the PCR primer elongation method. The primers were as follows:

pIL13F1,

(SEQ ID NO: 1)
CATTGCTCTCACTTGCCTTGGCGGCTTTGCCTCCCCAGGCCCTGTGC
CTCCCTCTACAGC;

pIL13F2,

(SEQ ID NO: 2)
GCAGCTAGCCTCATGGCGCTTTTGTGACCACGGTCATTGCTCTCAC
TTGCCTTGGCGGC;

and pIL13REcoRI,

(SEQ ID NO: 3)
GAGCTCGGATCCTGAATTCAACCGTCCCTC.

First-round PCR used pIL13F1 and pIL13REcoRI as primers, with pRB5830 (containing the IL13 coding region) as the template. The PCR reaction mixture was then diluted 10-fold and 1 μ l of the diluted reaction mixture was used as template for the second round of PCR amplifications with pIL13F2 and pIL13REcoRI as the primer set. The PCR

product was gel-purified, digested with NheI/EcoRI, and ligated into pBluescript II KS(+) at XbaI/EcoRI sites to generate pRB5832. To construct the transfer plasmid pRB5835, a 4.8-kbp HindIII/SacI fragment containing the HSV-1 gC coding region was released from cosmid pBC1007 and inserted into pBluescript II KS(+) to generate pRB5833. pRB5833 was cleaved with NheI and EcoRI and the N-terminal 148 residues of gC were replaced with the gC-signal/IL13 chimeric sequence (pRB5834). The insert in pRB5834 was released by XhoI/SacI digestion and ligated into pKO5Y at the same sites to generate pRB5835.

The recombinant virus R5107 (FIG. 1A, line 1) carrying the IL13-gC chimera was generated with the aid of the BAC-HSV system. RR1 competent cells that harbored bacterial artificial chromosome (BAC)-HSV bacmids were transformed with the transfer plasmid pRB5835 by electroporation. After incubation for 1 hour at 30° C. in LB broth, the transformed bacteria were plated on pre-warmed Zeocine (Zeo) plus chloramphenicol (Cm) (20 µg/ml of each) plates and incubated overnight at 43° C. for integration. The next day, six colonies were picked and each was separately diluted in 1 ml LB. Five pi of the diluted bacteria were then plated on Cm/10% sucrose (Suc) plates, and incubated at 30° C. overnight. To further confirm the loss of the replacement vector, 24 Cm/Suc-resistant colonies (four colonies from each plate) were restreaked in duplicate on Cm LB and Zeo LB plates, respectively. The Suc^r/Cm^r/Zeo^r colonies were further screened by PCR (95° C., 4 minutes for cycle 1; then 35 cycles of 94° C., 1 minute; 60° C., 1 minute; and 72° C., 1 minute). The primers were:

pgC-F,

(SEQ ID NO: 4)
GACACGGGCTACCTCACTATCGAGGGC;

from nt 96158 to 96185 in HSV-1 strain 17),
and pgC-R,

(SEQ ID NO: 5)
GGTGATGTTTCGTCAGGACCTCCTTAGGTC;

from nt 96859 to 96830 in HSV-1 strain 17).

The DNA fragment amplified from PCR-positive clones (FIG. 2B) was sequenced to further confirm the integration of IL13 in the correct open reading frame (ORF) of gC. To verify the viability of the recombinant (R5607), the recombinant BAC-HSV DNA was prepared as described elsewhere (Ye et al., 2000) and transfected into rabbit skin cells by Lipofectamine reagent (Life Technologies, Grand Island, N.Y.). The resultant virus, R5607, was stored at -80° C.

(ii) Deletion of the Polylysine Track from gB, FIG. 1 Panel B.

To make a transfer plasmid for the deletion of the gB heparan sulfate binding domain (polylysine), a 4.76 kbp BstEII fragment (from nt 53164 to 57923 of HSV-1) containing the U₂27 (gB) ORF released from cosmid BC1014 was blunt-ended and cloned into pBluescript II KS (+) at a SmaI site to generate pRB5846. To construct pRB5847, from which the 10-amino-acid polylysine domain of gB was deleted, two fragments flanking the polylysine domain were amplified by PCR from pRB5846. The primer sets were: pgB1BamHI:

(SEQ ID NO: 6)
GTTCTTCTTCGGTTTCGGATCCCCCG;

pgB2BspEI:

(SEQ ID NO: 7)
CGGCATTTCCGGAATAACGCCCACTC;

and pgB3BamHI:

(SEQ ID NO: 8)
CAGAAAACCGGATCCCCCAAGCCGCC;

pgB4BsiWI:

(SEQ ID NO: 9)
GCCAACACAAACTCGTCGTACGGGTAC.

PCR amplified fragments were then cut with BspEI/BamHI, or BsiWI/BamHI and ligated into pRB5846, which had the 1.2 kbp BsiWI/BspEI fragment already deleted. To generate the transfer plasmid pRB5848, the 4.76 kbp insert in pRB5847 was released by XbaI/EcoRV digestion and ligated into pKO5Y at the sites of XbaI and ScaI. Recombinant HSV-1 virus R5108 is based on R5107 with the additional deletion of the gB heparan sulfate binding domain. It was made by the same procedure as BAC-R5607, except that the transfer plasmid pRB5848 was used instead of BAC-HSV wild-type and pRB5835. The sequence of the mutant gB was verified by sequencing the entire ORF.

(iii) Deletion of gD (FIG. 1 Panel C, Lines 6 and 7).

The coding sequence of gD was replaced with the human cytomegalovirus immediate early promoter to enable the expression of glycoprotein I. A 0.65 kbp fragment containing the promoter was released from pRB5836 by ClaI digestion and inserted into pgD⁻ (FIG. 6), a plasmid obtained from G. Campadelli-Fiume. This plasmid, containing the flanking sequences of gD but lacking the gD ORF, had been cut with ClaI to generate pRB5849. pRB5849 was then cut with NotI and PmeI and ligated into pKO5Y at the NotI and ScaI sites to generate the transfer plasmid pRB5850. Recombinant HSV-1 virus R5110 is based on R5608 with the additional deletion of gD. It was made by the same procedure as BAC-R5607 except that transfer plasmid pRB5850 was used instead of BAC-HSV wild-type and pRB5835. The recombinant BAC-HSV DNA was prepared as described in (Ye et al., 2000). The mutant virus was designated R5110.

(iv) Construction of the R5111 Mutant Carrying the IL-13-gD Chimeric Gene (FIG. 1 Panel D).

Plasmid pRB123 carries a 6,584 bp BamHI J fragment containing the gD coding region and flanking sequences in the BamHI site of pBR322. To construct the IL-13-gD chimeric plasmid, pRB123 was digested with AflIII and HpaI to release two fragments of 7.6 kb and 3.2 kb. The 3.2 kb fragment was further digested with FspI to release 2.5 kb and 0.7 kb fragments that contain the amino-terminal 661 bp of the gD ORF. A polylinker sequence containing the restriction sites XhoI-BglIII-EcoRI-KpnI was inserted into the 0.7 kb fragment downstream of the 24th codon of gD by two PCR reactions using a first forward primer,

(SEQ ID NO: 10)
5' - CAGTTATCCTTAAGGTCTCTTTTGTGTGGTG - 3' ,

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and a first reverse primer,

(SEQ ID NO: 11)
5' - CCGGAATTCGGAGATCTTCCCTCGAGGACCGGAAGGTCT
TTGCCGCGAAAG - 3' ,

and a second forward primer,

(SEQ ID NO: 12)
5' CCGGAATTCGGGGTACCCTGGACCAGCTGACCGACCCCT
CGG - 3' ,

and a second reverse primer,

(SEQ ID NO: 13)
5' - CGGGGGATGCGCAGCGGGAGGGCGTACTTAC - 3' ,

respectively. After digestion of the two PCR products by EcoRI, they were ligated and amplified by PCR again to obtain the desired DNA fragment containing the polylinker insertion.

IL13 was amplified by PCR with the forward primer,

(SEQ ID NO: 14)
5' - CCGCTCGAGATGGCGCTTTTGTGACCACGG - 3' ,

and the reverse primer,

(SEQ ID NO: 15)
5' - GGGGTACCGTTGAACCGTCCCTCGCGAAA - 3' ,

and then inserted into the XhoI and KpnI sites of the 0.7 kb fragment described above. This new fragment with the IL13 insertion was then ligated with the 2.5 kb and 7.6 kb fragments (see above) to generate the IL13-gD chimeric transfer plasmid, pRB13-24.

R5111 was generated by co-transfection of transfer plasmid pRB13-24 and the R5110 viral DNA into U87 glioma cells. The progeny of the transfection was plated at a high dilution on Vero and HEp-2 cell cultures to yield individual, well-spaced plaques. From each of the infected cell cultures, six single plaques were picked, frozen-thawed, sonicated, and then replated on fresh cultures of Vero or HEp-2 cells (depending on the origin of the plaque) for preparation of virus stocks and to prepare viral DNA for sequencing.

Viral DNA Extraction.

Infected cells were removed from each of the 25 cm² flasks exposed to individual plaque isolates, rinsed, and resuspended in 500 µl of Lyse-O-Lot (150 mM NaCl, 10 mM Tris, 1.5 mM MgCl₂ in the presence of 0.1% of NP40). Nuclei were removed by low-speed centrifugation. To the supernatant fluid were added sodium dodecyl sulfate (SDS) to 0.2%, EDTA to 5 mM and β-ME to 50 mM. The solution was then extracted twice with phenol/chloroform. Viral DNA was finally precipitated by ethanol, resuspended, and the IL13 ORF and IL13-gD chimeric reading frame were amplified by PCR with two sets of primers. The first set, designed to amplify IL13, consisted of: a forward primer,

(SEQ ID NO: 16)
5' - CCGCTCGAGATGGCGCTTTTGTGACCACGG - 3' ,

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and a reverse primer,

(SEQ ID NO: 17)
5' - GGGGTACCGTTGAACCGTCCCTCGCGAAA - 3' ,

which will amplify the IL13 ORF. The second set, designed to amplify the IL13-gD junction, consisted of a forward junction primer,

(SEQ ID NO: 18)
5' - CCGCTCGAGATGGCGCTTTTGTGACCACGG - 3' ,

and a reverse junction primer,

(SEQ ID NO: 19)
5' - AACTGCAGGTTGTTGGGGTGGCCGGGG - 3' .

All 12 IL13-gD PCR products were sequenced to determine whether the gD sequence contained deletions or substitutions.

Verification of the Structure of R5111

The construction of the R5111 virus is depicted in FIG. 1. The design involved replacement of the HveA binding site with the IL13 ligand to enable the recombinant virus to bind the IL13α2 receptor on cell surfaces and to delete the sequences reported to bind to heparan sulfate. Verification of the structure of R5111 was done as follows:

(i) The replacement of the amino-terminal domain of gC with IL13 and the disruption of the heparan sulfate binding site was initially verified by sequencing gC from recombinant R5107 (FIG. 2 A).

(ii) The deletion of codons 68-77 of gB was verified by sequencing the gB ORF amplified by PCR from recombinant R5108 (FIG. 2 B). The nucleotide and amino acid sequences of gB with the polylysine track deleted are set out in SEQ ID NOS.:35 and 36, respectively.

(iii) The presence of chimeric IL13-gD in R5111 was verified by PCR, as illustrated in FIG. 3, and by sequencing the entire IL13-gD coding region, amplified by PCR, as shown in FIG. 2. The nucleotide and amino acid sequences of gD with the IL13 integration are set out in SEQ ID NOS.:39 and 40, respectively. The R5111 recombinant was initially isolated from transfected U87 cells and grown in parallel in Vero cells and HEp-2 cells. To determine whether the virus grown in Vero cells or HEp-2 cells differed with respect to amino acid sequence, six plaques each from Vero or HEp-2 cultures containing well-separated plaques were picked. In this series of verification experiments, two sets of primers were used to confirm the presence of the IL13 insert in gD and to verify the presence of a junction between IL13 and gD. In a second round of verifications, the 12 clones of gD were sequenced to determine whether the isolates obtained from the viruses passaged in Vero cells or in HEp-2 cells differed in amino acid sequence. No differences were found. Furthermore, except for the inserted IL13 sequence, no differences were found between the sequence of HSV-1(F) gD and those of the cloned IL-13-gD chimeric genes (FIG. 2 C).

(iv) In denaturing polyacrylamide gels, IL13 migrated as a protein with an apparent Mr of 15-17,000. In the recombinant R5111, IL13 replaced 148 amino acids of gC. FIG. 4B shows an immunoblot of electrophoretically separated proteins from a lysate of R5111 mutant-infected cells exposed to an antibody to gC. As illus-

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trated in that figure, the anti-gC antibody reacted with proteins present in lysates of HSV-1(F) and with proteins from R5111 lysates, exhibiting similar electrophoretic mobilities. In contrast, an antibody to IL13 reacted with a band of similar mobility in R5111 lysates (FIG. 4C, lane 3) but not in lysates of HSV-1(F) (FIG. 4 C, lane 2). The IL13-gD fusion protein in the R5111 mutant virus was verified by reacting the cell lysates with gD and IL13 antibody. Comparison of wild-type gD and the chimeric IL13-gD chimeric protein (FIG. 4 A, lane 3), showed that, as expected, IL13-gD migrated more slowly than the wild-type gD (FIG. 4 A, lane 2). The faster migrating band of gD did not react with the antibody to IL13 (FIG. 4C, lane 2).

Example 2

Construction of a Cell Line Expressing the IL13 Receptor (IL13R α 2)

A rigorous test of the ability of R5111 to utilize the IL13R α 2 protein as a receptor for entry required construction of a cell line expressing IL13R α 2 (nucleotides 126-1265 of SEQ ID NO.:33; SEQ ID NO:34) in the absence of other HSV-1 entry receptors. The J1.1 cell line was selected for this construction. In essence, this cell line lacks the receptors necessary for the entry of virus into cells and the cell line is not susceptible to infection by wild-type virus. The construction of a plasmid encoding a IL13R α 2 protein fused at its carboxyl terminus to a HA tag, transfection of J1.1 cells with the plasmid encoding the tagged IL13R α 2 protein, and selection of the cell line expressing the protein is described below.

To test for the production of IL13R α 2 protein, five clones of the selected cells were harvested, solubilized, subjected to electrophoresis in denaturing polyacrylamide gels and tested for expression of the protein.

Construction of J13R, a Cell Line Stably Expressing IL13R α 2 Receptor.

The IL13 α 2 coding region was tagged with an HA tag at its 3' end (the carboxyl terminus of the encoded polypeptide) by PCR with forward primer,

(SEQ ID NO: 20)
5' - AAGATTTGGGC - TAGCATGGCTTTTCGTTGC - 3' ,

and reverse primer,

(SEQ ID NO: 21)
5' - TCCCTCGAAGCTTCAAGCATAATCTGGCACATCATATGTA
TCACAGAA - AAA - 3' .

NheI and HindIII restriction digests were used to create compatible ends. The DNA fragment was then inserted into pcDNA 3.1 (zeo) vector (Invitrogen; Carlsbad, Calif.) to generate transfer plasmid pRB13-R2. All of the constructs were sequenced to insure fidelity.

J1.1, a derivative of BHK thymidine kinase⁻ cells which lack both HveA and nectin 1 receptors, was obtained from Dr. G. Campadelli-Fiume, University of Bologna, Italy. J1.1 cells, stably transfected with pRB 13-R2 using a Lipofectamine kit (Gibco-BRL), were selected on the basis of their resistance to zeocin (Invitrogen). Zeocin-resistant clones were amplified and screened for IL13R α 2 expression by immunoblotting with anti-HA polyclonal antibody. Lysates of parental and transformed cells formed by solubilized in SDS were each electrophoretically separated in a

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denaturing gel (50 μ g/lane), transferred to a nitrocellulose sheet, and probed with antibody against HA (Santa Cruz Biotechnology). The protein bands were visualized by an enhanced chemiluminescent detection (ECL) system (Pierce, Rockford, Ill.) according to the instructions of the manufacturer. One (J13R-2) was selected for testing the ability of R5111 to use the IL13R α 2 receptor.

As shown in FIG. 5, all clones expressed a protein band reactive with the anti-HA antibody. The apparent size of the protein was consistent with the reported size of IL13R α 2. Of 5 J13R-positive clones, J13R-2 (FIG. 5, lane 3) was selected and designated J13R.

Example 3

Infection by the HSV Targeting Vector R5111

SK-N-SH, HEP-2, Vero, and U87 cells were obtained from American Type Culture Collection (Rockville, Md.) and maintained in Dulbecco's modification of Eagle's Minimal Essential Medium (DMEM) supplemented with 10% fetal bovine serum. Replicate cultures of SK-N-SH, HEP-2, Vero, U87, J1.1, and J13R were exposed to 0.01 PFU of R5111 virus per cell. After 24 hours of incubation, the cells were harvested and viral yields were titered on Vero cells.

Immunoblotting Electrophoretically Separated Proteins.

The indicated cells were mock-infected or exposed to 10 PFU of recombinant or wild-type HSV-1(F) per cell. The cells were harvested at 24 hours after infection, disrupted in SDS disruption buffer, boiled, cleared by centrifugation and electrophoretically separated on a 10% denaturing polyacrylamide gel. After transfer to a nitrocellulose membrane, the isolated proteins were reacted with antibodies as indicated using known and conventional techniques. Monoclonal antibodies against gD- (clone H170), gC- and HA-specific polyclonal antisera were purchased from the Goodwin Institute, Plantation, Fla. Polyclonal antibodies against IL13 were purchased from Santa Cruz Biotechnology.

The results shown in Table 1 were as follows: R5111 replicated to within a 10-fold range in HEP-2, Vero, U87, and J13R cells. The titer obtained from J1.1 cells was approximately 10⁵-fold lower than that obtained from all other cell lines. To test whether the J13R cell line had acquired a receptor for wild-type HSV-1 (HSV-1(F)), J1.1 and J13R cells were also exposed to the wild-type virus. The results, also shown in Table 1, indicate that the cells remain resistant to the wild-type virus. It was known that HEP-2 cells express the nectin receptor but not the HveA receptor. The results show that the targeted HSV containing an IL13-gD fusion can target (i.e., bind and infect) cells expressing a particular receptor (IL13R α 2) approximately as well as wild-type HSV targets cells expressing the HveA receptor. The results indicate that R5111 can use IL13R α 2 as a receptor for entry in a cell line lacking all other HSV-1 receptors.

TABLE 1

Replication of R5111 in various cell lines		
Virus	Cell Line*	Yield**
R5111	Vero	11 \times 10 ⁷
	HEP-2	1.2 \times 10 ⁷
	SK-N-SH	17 \times 10 ⁷
	U87	27 \times 10 ⁷
	J1.1	2 \times 10 ²
	J13R	11 \times 10 ⁷

TABLE 1-continued

Replication of R5111 in various cell lines		
Virus	Cell Line*	Yield**
HSV-1(F)	J1.1	6×10^3
	J13R	4×10^3

*cell lines derived from human brain tumors.

**The cells were exposed to 0.01 PFU of R5111 or HSV-1(F) per cell and harvested 24 hours after infection. Progeny virus were titered on Vero cells.

This disclosure contains an exemplary description of the construction and properties of a recombinant HSV virus, R5111. In R5111, the heparan sulfate binding sites on the surface of the viral particle were ablated to preclude or at least reduce the attachment of virus to non-targeted cells. Attachment even in the absence of fusogenic activity may lead to endocytosis, degradation of the virus particle, and to potential damage to the cell by lysosomal enzymes (Zhou et al. 2002; Zhou et al. 2000). At the same time, a copy of IL13 was inserted into gC to enhance binding of virus particles to the IL13R α 2 receptor. The major restructuring of the viral genome, consisted of insertion of IL13 at amino acid 24 of gD. Available data indicate that this modification ablates the gD binding site for the HveA receptor (Carfi et al. 2001). The data obtained using R5111 indicate that the virus retains the capacity to interact with the Nectin receptor. Nonetheless, the R5111-targeted HSV was able to infect and replicate in J13R cells but not in the parental, J1.1, cells.

Example 4

Construction of HSV Targeting Vector R5141 and R5144

A therapeutic herpes simplex virus 1 (HSV-1) capable of infecting and replicating solely in cells harboring the IL13R α 2 receptor was constructed using recombinant DNA techniques. As disclosed above, construction of R5111, which expresses IL13 on its surface and lacks the binding sites for heparin sulfate, allowed R5111 to infect 3-13R cells as well as cells exhibiting the natural receptors for HSV-1. Thus, the involvement of fusogenic glycoproteins of R5111—a key step in viral entry—is independent of the receptor with which gD interacts.

The binding site of HveA has been reported to be at the amino terminal domain of gD (Carfi A., et al., 2001). The precise binding sites of gD for Nectin 1 are not known, although it has previously been reported to involve gD amino acids 38 and 221 (Manoj S., et al., 2004; Zago A., et al., 2004; Connolly S A., 2005). The general assumption within the field is that the HveA and Nectin 1 sites do not overlap and that each independently promotes the same structural alteration of gD to enable entry of the virus into cells. However, it is possible that the surface structure of HveA and Nectin 1 at their binding sites may be similar even though the Hve1 and Nectin1 amino acid sequences are not identical.

Based in part on the foregoing information, viruses capable of productive replication solely in targeted cells were designed as shown in FIG. 7. Using standard molecular biological cloning techniques known in the art, recombinant virus R5141 was constructed by inserting IL13 in the place of gD residues 1-32. In addition, the valine residue at position 34 was substituted with serine ("V34S") (SEQ ID NOs.:41 and 42, respectively). Similarly, recombinant virus R5144 was constructed by inserting IL13 in the place of gD residues 1-32, and the valine at position 37 was substituted with serine ("V37S") (SEQ ID NOs.:43 and 44, respectively).

One of skill would appreciate that a variety of re-targeted SHV, both HSV-1 and HSV-2, could be constructed and assessed using routine techniques in view of the disclosures herein. In particular, substituting a binding domain of a binding partner for the N-terminal region of gD, e.g., for amino acids 1-32 of gD, would be within the skill in the art. Further alteration of the gD fusion, e.g., by amino acid substitution, whether conservative substitution or not, would also be within the skill in the art. Of course, additions or deletions to gD fusions would also be within the skill in the art and assessing the targeting capacities of such constructs would involve routine experimentation in view of the teachings herein.

Example 5

Infection by the HSV Targeting Vectors R5141 and R5144

The capacities of the recombinant viruses described in Example 4 to productively replicate solely in targeted cells were assessed using the cell lines which express either HveA (J-HveA) alone (relative to the group of HveA, Nectin1, and IL13R α 2), Nectin1 (J-Nectin1) alone, or IL13R α 2 (J-13R) alone. For cell infection, the procedure set forth in Example 3 was repeated using recombinant virus R5141 and recombinant virus R5144.

The replication of R5141 and R5144 in J-Nectin-, J-HveA-, and J-13R-specific cells are summarized in Table 2. R5141 and R5144 do not productively interact with either native gD receptors, HveA or Nectin1. Significantly, however, R5141 interacts with, and replicates in IL13R α 2 for productive entry into cells.

TABLE 2

Replication of R5141 and R5144 in J-Nectin, J-HveA and J-13R cells.			
	HSV-1 (F)	R5141	R5144
J-Nectin	4×10^8	7×10^1	5×10^1
J-HveA	3×10^8	4×10^1	3×10^2
J-13R	3×10^1	5×10^6	7×10^2

Thus, recombinant virus R5141 is capable of productive replication solely in targeted cells and this result opens the way for development of therapeutic viruses targeting cells exhibiting the IL13R α 2 receptor, such as malignant gliomas and other human tumors exhibiting IL13R α 2. It is expected that other mutations (i.e., those that abolish binding of Nectin and those that have a similar effect on HveA) will yield viruses that enter solely via non-natural HSV receptors.

Example 6

HSV Targeting Vector R5161

An HSV targeting vector designated HSV R5161 has a structure analogous to the structure of HSV R5141, and HSV R5161 was constructed in the manner described in Example 4, above, with the exception that HSV R5161 contains the sequence encoding the HSV gD leader sequence, whereas HSV R5141 contains the sequence encoding the IL-13 leader sequence. In particular, HSV R5161 encodes an IL-13-gD fusion protein in which IL-13 sequence replaces the sequence encoding gD amino acids 1-32, with a V34S substitution in the gD moiety of the fusion protein, as described above in the context of describing HSV R5141.

The relative capacities of recombinant viruses HSV R5141 and HSV R5161 to productively replicate in targeted cells were measured in the J-13R cell line, which expresses IL13R α 2, but not HveA or Nectin1. HSV R5161 was expressed at a level 10-fold higher than the expression level of HSV R5141 in J-13R cells.

It is expected that in the majority of embodiments of the invention, relatively high levels of expression will be advantageous in ensuring that targeted cells are efficiently contacted by the re-targeted HSV. In re-targeting the HSV, the invention provides an approach to controlling the virulence of the virus in a manner that minimizes undesirable pathogenicity, i.e., pathogenicity towards non-targeted cells. In addition, the virulence of any re-targeted HSV can be further attenuated using known approaches to virulence control that do not interfere with the re-targeting, such as by mutating the γ _{134.5} gene(s). In those embodiments in which it is desirable to have relatively high expression levels of the re-targeted HSV, it is preferred that the leader sequence of gD be used. Alternative leader sequences, such as leaders from other HSV genes, are contemplated. Moreover, expression control elements (e.g., promoters, enhancers, expression factor binding sites) can be engineered to achieve desired expression levels of the fusion protein using ordinary levels of skill and techniques known in the art.

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<400> SEQUENCE: 24

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```

atgggggggg ctgccgcag gttgggggcc gtgattttgt ttgtcgcat agtcggcctc 60
catgggggtcc gcgcaaaata tgccttggcg gatgcctctc tcaagctggc cgaccccaat 120
cgctttcgcc gcaaagacct tccggtcctc gagatggcgc ttttgttgac cacggtcatt 180
gtctcactt gccttggcgg ctttgccctc ccaggccctg tgcctcccct ctacagccct 240
cagggagctc attgaggagc tggtaacat caccagaac cagaaggctc cgctctgcaa 300
tggcagcatg gtttgagca tcaacctgac agctggcatg tactgtgcag ccttgaatc 360
cctgatcaac gtgtcaggct gcagtgccat cgagaagacc cagaggatgc tgggcggtt 420
ctgcccgcac aagggtctcag ctgggcagtt ttccagcttg catgtccgag acacaaaaat 480
cgaggtggcc cagttttaa aggacctgct cttacattta aagaaacttt ttcgcgaggg 540
acggttcaac tgaacggta ccttgacca gctgaccgac cctccggggg tccggcgcgt 600
gtaccacatc caggcgggcc taccggacce gttccagccc ccagcctcc cgatc 655

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<210> SEQ ID NO 25
<211> LENGTH: 1185
<212> TYPE: DNA
<213> ORGANISM: Herpes Simplex Virus-1

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<400> SEQUENCE: 25

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atgggggggg ctgccgcag gttgggggcc gtgattttgt ttgtcgcat agtgggcctc 60
catgggggtcc gcgcaaaata tgccttggcg gatgcctctc tcaagctggc cgaccccaat 120
cgctttcgcg gcaaagacct tccggtcccg gaccggctga ccgaccctcc gggggtccgg 180
cgcgtgtacc acatccaggc gggcctaccg gaccggctcc agccccccag cctcccgatc 240
acggtttact acgccgtggt ggagcgcgcc tgccgcagcg tgctcctaaa cgcaccgtcg 300
gaggcccccc agattgtccg cggggcctcc gaagacgtcc ggaacaacc ctacaacctg 360
accatcgctt ggtttcggat gggaggcaac tgtctatccc ccatcacggc catggagtac 420
accgaatgct cctacaacaa gtctctgggg gctgtcccca tccgaacgca gccccgctgg 480
aactactatg acagcttcag cgccgtcagc gaggataacc tggggttcct gatgcaagcc 540
cccgcgtttg agaccgcggc cacgtacctg cggctcgtga agataaacga ctggacggag 600
attacacagt ttatcctgga gcaccgagcc aagggtcctc gtaagtagc ccttccgctg 660
cgcaccccc cgtagcctg cctctcccc caggcctacc agcagggggg gacgggtggc 720
agcatcggga tgetgcccc cttcatcccc gagaaccagc gcaccgtcgc cgtatacagc 780
ttgaagatcg ccgggtggca cgggcccagg gcccataca cgagcaccct gctgcccccg 840
gagctgtccg agacccccaa cgccacgcag ccagaactcg ccccggaaga ccccgaggat 900

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tcggccctct tggaggacc cgtgggggacg gtggtgccc aaatcccacc aaactggcac   960
ataccgtcga tccaggagc cgcgacgect taccatcccc cggccacccc gaacaacatg   1020
ggcctgatcg ccggcgcggt gggcggcagt ctctggtag ccctggatcat ttgcggaatt   1080
gtgtactgga tgcgccgocg cactcaaaaa gcccctaaagc gcatacgect ccccacatc   1140
cgggaagacg accagccgtc ctcgcaccag cccttgtttt actag                       1185

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<210> SEQ ID NO 26

<211> LENGTH: 394

<212> TYPE: PRT

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 26

```

Met Gly Gly Ala Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
 1          5          10          15
Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
 20          25          30
Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35          40          45
Val Pro Asp Arg Leu Thr Asp Pro Pro Gly Val Arg Arg Val Tyr His
 50          55          60
Ile Gln Ala Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile
 65          70          75          80
Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
 85          90          95
Asn Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp
 100         105         110
Val Arg Lys Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly
 115         120         125
Gly Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser
 130         135         140
Tyr Asn Lys Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp
 145         150         155         160
Asn Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
 165         170         175
Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
 180         185         190
Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
 195         200         205
Arg Ala Lys Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
 210         215         220
Ser Ala Cys Leu Ser Pro Gln Ala Tyr Gln Gln Gly Val Thr Val Asp
 225         230         235         240
Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
 245         250         255
Ala Val Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Ala Pro
 260         265         270
Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro Asn Ala
 275         280         285
Thr Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
 290         295         300
Glu Asp Pro Val Gly Thr Val Val Pro Gln Ile Pro Pro Asn Trp His
 305         310         315         320

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Ile Pro Ser Ile Gln Asp Ala Ala Thr Pro Tyr His Pro Pro Ala Thr
 325 330 335

Pro Asn Asn Met Gly Leu Ile Ala Gly Ala Val Gly Gly Ser Leu Leu
 340 345 350

Val Ala Leu Val Ile Cys Gly Ile Val Tyr Trp Met Arg Arg Arg Thr
 355 360 365

Gln Lys Ala Pro Lys Arg Ile Arg Leu Pro His Ile Arg Glu Asp Asp
 370 375 380

Gln Pro Ser Ser His Gln Pro Leu Phe Tyr
 385 390

<210> SEQ ID NO 27
 <211> LENGTH: 2715
 <212> TYPE: DNA
 <213> ORGANISM: Herpes Simplex Virus-1
 <400> SEQUENCE: 27

```

atgcgccagg gcgccccgc gcgggggcgc cgggtggtcg tcgtatgggc gctcctgggg      60
ttgacgctgg gggctcctggt ggcgtcggcg getccgagtt cccccggcac gectgggggtc      120
gcggcccgca cccaggcggc gaacgggggc cctgccactc cggcgccgcc cgcccctggc      180
gccccccaa cgggggaccc gaaaccgaag aagaacagaa aaccgaaacc cccaaagccg      240
cgcgcccccg cgcgcgacaa cgcgacgctc gcccggggcc acgccaccct gcgcgagcac      300
ctgctgggaca tcaaggcggga gaacaccgat gcaaactttt acgtgtgccc accccccacg      360
ggcgccacgg tgggtcagtt cgagcagccg cgcctgctgc cgaccgggcc cgagggtcag      420
aactacacgg agggcatcgc ggtggtcttc aaggagaaca tcgccccgta caagtcaag      480
gccaccatgt actacaaaga cgtcacctgt tcgcaggtgt ggttcggcca ccgctactcc      540
cagtttatgg ggatcttga ggaccgcgcc cccgtcccct tcgaggaggt gatcgacaag      600
atcaacgcca agggggctgt tcggtccacg gccaaagtac tgcgcaaaa cctggagacc      660
accgcgttcc accgggacga ccacgagacc gacatggagc tgaaccggc caacgcccgc      720
accgcacga gccggggctg gcacaccacc gacctcaagt acaaccctc gccgggtggag      780
gcggtccacc ggtacgggac gacggtaaac tgcctcgtcg aggaggtgga cgcgctcgc      840
gtgtaccctg acgacgagtt tgtggtggcg actggcgact ttgtgtacat gtccccgttt      900
tacggctacc gggagggggtc gcacaccgaa cacaccagct acgccgccga ccgcttcaag      960
caggtcgacg gcttctacgc gcgcgacctc accaccaagg cccggggccac ggcgcccacc      1020
accggaaacc tgctcacgac ccccaagttc accgtggcct gggactgggt gccaaagcgc      1080
ccgtcggctc gcaccatgac caagtggcag gaggtggacg agatgctgcg ctccgagtac      1140
ggcggctcct tccgattctc ttcgacgcc atatccacca ccttcaccac caacctgacc      1200
gagtaccctg tctcgcgctg ggacctgggg gactgcatcg gcaaggacgc ccgcaacgcc      1260
atggaccgca tcttcgcccc caggtacaac gcgacgcaca tcaaggtggg ccagcccgag      1320
tactacctgg ccaatggggg ctttctgac gcgtaccagc cccttctcag caaacgctc      1380
gaggagctgt acgtgcggga acacctccgc gagcagagcc gcaagcccc aaaccccacg      1440
ccccgccgc cggggggccg cgccaacgcg tccgtggagc gcatcaagac cacctctccc      1500
atcgagttcg ccaggctgca gtttacgtac aaccacatac agcgcctatg caacgatatg      1560
ttgggccgcg ttgccatcgc gtgggtgcgag ctgcagaatc acgagctgac cctgtggaac      1620
gaggcccgca agctgaaccc caacgccatc gcctcggcca ccgtgggccg gccgggtgagc      1680
    
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gcgcggatgc tcggcgacgt gatggccgtc tccacgtgcg tgccggtcgc cgcggacaac 1740
gtgatcgtcc aaaactcgat gcgcatcagc tcgcggcccg gggcctgcta cagccgcccc 1800
ctggtcagct ttcggtacga agaccaggc cegttggtcg aggggcagct gggggagAAC 1860
aacgagctgc ggctgacgcg cgatgcgatc gagccgtgca ccgtgggaca ccggcgctac 1920
ttcaccttcg gtgggggcta cgtgtacttc gaggagtacg cgtactccca ccagctgagc 1980
cgcgccgaca tcaccaccgt cagcaccttc atcgacctca acatcaccat gctggaggat 2040
cacgagtttg tccccctgga ggtgtacacc cgccaagaga tcaaggacag cggcctgctg 2100
gactacacgg aggtccagcg ccgcaaccag ctgcacgacc tgcgcttcgc cgacatcgac 2160
acggctatcc acgccgacgc caacgccgcc atgtttgctg gcctgggctg gttcttcgag 2220
gggatgggcg acctggggcg cgcggtcggc aaggtggtga tgggcatcgt gggcgcgctg 2280
gtatcggcgg tgtegggctg gtcctccttc atgtccaacc cctttggggc gctggccctg 2340
ggtctgtttg tcctggcccg cctggcggcg gcctctctcg cctttcgcta cgtcatcgcg 2400
ctgcagagca accccatgaa ggccctgtac ccgctaacca ccaaggagct caagaacccc 2460
accaaccccg acgcgtcccg ggagggcgag gagggcggcg actttgacga ggccaagcta 2520
gccgagggccc gggagatgat acgggtacatg gccctggtgt ctgccatgga gcgcacggaa 2580
cacaaggcca agaagaaggg cagcagcgcg ctgctcagcg ccaaggtcac cgacatggtc 2640
atgcgcaagc gcccaacac caactacacc caagttccca acaagacggg tgacgccgac 2700
gaggacgacc tgtga 2715

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<210> SEQ ID NO 28

<211> LENGTH: 904

<212> TYPE: PRT

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 28

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

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Pro Phe Glu Glu Val Ile Asp Lys Ile Asn Ala Lys Gly Val Cys Arg
 195 200 205
 Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu Glu Thr Thr Ala Phe His
 210 215 220
 Arg Asp Asp His Glu Thr Asp Met Glu Leu Lys Pro Ala Asn Ala Ala
 225 230 235 240
 Thr Arg Thr Ser Arg Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro
 245 250 255
 Ser Arg Val Glu Ala Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile
 260 265 270
 Val Glu Glu Val Asp Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val
 275 280 285
 Leu Ala Thr Gly Asp Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg
 290 295 300
 Glu Gly Ser His Thr Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys
 305 310 315 320
 Gln Val Asp Gly Phe Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala
 325 330 335
 Thr Ala Pro Thr Thr Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val
 340 345 350
 Ala Trp Asp Trp Val Pro Lys Arg Pro Ser Val Cys Thr Met Thr Lys
 355 360 365
 Trp Gln Glu Val Asp Glu Met Leu Arg Ser Glu Tyr Gly Gly Ser Phe
 370 375 380
 Arg Phe Ser Ser Asp Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr
 385 390 395 400
 Glu Tyr Pro Leu Ser Arg Val Asp Leu Gly Asp Cys Ile Gly Lys Asp
 405 410 415
 Ala Arg Asp Ala Met Asp Arg Ile Phe Ala Arg Arg Tyr Asn Ala Thr
 420 425 430
 His Ile Lys Val Gly Gln Pro Gln Tyr Tyr Leu Ala Asn Gly Gly Phe
 435 440 445
 Leu Ile Ala Tyr Gln Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr
 450 455 460
 Val Arg Glu His Leu Arg Glu Gln Ser Arg Lys Pro Pro Asn Pro Thr
 465 470 475 480
 Pro Pro Pro Pro Gly Ala Ser Ala Asn Ala Ser Val Glu Arg Ile Lys
 485 490 495
 Thr Thr Ser Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His
 500 505 510
 Ile Gln Arg His Val Asn Asp Met Leu Gly Arg Val Ala Ile Ala Trp
 515 520 525
 Cys Glu Leu Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys
 530 535 540
 Leu Asn Pro Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser
 545 550 555 560
 Ala Arg Met Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val
 565 570 575
 Ala Ala Asp Asn Val Ile Val Gln Asn Ser Met Arg Ile Ser Ser Arg
 580 585 590
 Pro Gly Ala Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp
 595 600 605

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Gln Gly Pro Leu Val Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg
 610 615 620

Leu Thr Arg Asp Ala Ile Glu Pro Cys Thr Val Gly His Arg Arg Tyr
 625 630 635 640

Phe Thr Phe Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser
 645 650 655

His Gln Leu Ser Arg Ala Asp Ile Thr Thr Val Ser Thr Phe Ile Asp
 660 665 670

Leu Asn Ile Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val
 675 680 685

Tyr Thr Arg His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu
 690 695 700

Val Gln Arg Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp
 705 710 715 720

Thr Val Ile His Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Gly
 725 730 735

Ala Phe Phe Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val
 740 745 750

Val Met Gly Ile Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser
 755 760 765

Ser Phe Met Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val
 770 775 780

Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala Phe Arg Tyr Val Met Arg
 785 790 795 800

Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu
 805 810 815

Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser Gly Glu Gly Glu Glu Gly
 820 825 830

Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
 835 840 845

Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Lys
 850 855 860

Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala Lys Val Thr Asp Met Val
 865 870 875 880

Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr Gln Val Pro Asn Lys Asp
 885 890 895

Gly Asp Ala Asp Glu Asp Asp Leu
 900

<210> SEQ ID NO 29
 <211> LENGTH: 1800
 <212> TYPE: DNA
 <213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 29

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agggcgcttg gtcgggagggc cgcacgaac gcacaccccc atccgggtgtg ccgtgtggag      60
gtcgttttca tgcccgttct cgtttgtgct ggaacgctag ccggtccctc gggaggggga      120
ggcgtcgggc atggccccgg ggcgggtggg ccttgccgtg gtccctgtgga gcctgtttgtg      180
gctcgggggag ggggtggccg ggggctcgga aactgectcc accgggcccc cgatcaccgc      240
gggagcgggtg acgaacgcga gcgaggcccc cacatcgggg tccccgggt cagccgccag      300
cccggaagtc acccccacat cgaccccaaa cccaacaat gtcacacaaa acaaaaccac      360
ccccaccgag ccggccagcc cccaacaac cccaagccc acctccacgc ccaaaagccc      420
    
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ccccacgtcc acccccgacc ccaaaccxaa gaacaacacc acccccgcca agtcggggccg 480
ccccactaaa cccccgggc ccgtgtggtg cgaccgccc gaccattgg cccggtacgg 540
ctcgtgggtg cagatccgat gccggttttg gaattocacc cgeatggagt tccgcctcca 600
gatatggcgt tactccatgg gtcctgcccc cccaatcgct ccggtcccc acctagagga 660
ggtcctgacg aacatcaccg ccccaccccg gggactcctg gtgtacgaca gcgcccccaa 720
cctgacggac ccccacgtgc tetgggcgga gggggccggc ccggggcggc accctccgtt 780
gtattctgtc accggggcgc tgccgaacca gcggctgatt atcggcgagg tgacgcccgc 840
gaccacagga atgtattact tggcctgggg ccggatggac agcccgcacg agtacgggac 900
gtgggtgcgc gtcgcatgt tccgcccccc gtctctgacc ctccagcccc acgcggtgat 960
ggagggtcag ccgttcaagg cgacgtgac gcccgcccgc tactaccgcg gtaaccccg 1020
ggagtttgtc tggttcgagg acgaccgcca ggtgtttaac ccgggccaga tcgacacgca 1080
gacgcacgag cacccecgag ggttcaccac agtctctacc gtgacctccg aggctgtcgg 1140
cggccaggtc ccccccgga ccttcaoctg ccagatgacg tggcaccgcg actccgtgac 1200
gttctcgcga cgcaatgcca ccgggtggc cctggtgctg ccgcccga ccatcaccat 1260
ggaatttggg gtcggcatg tggctgac gcccggtgc gtccccgagg gcgtgacgtt 1320
tgcttggttc ctgggggacg acccctcacc gccggctaag tcggccgta cggccagga 1380
gtcgtgacg cacccegggc tggctacggt ccggtcacc ctgcccattt cgtacgacta 1440
cagcgagtac atctgtcggg tgaccggata tccggccggg attcccgttc tagagacca 1500
cggcagtcac cagccccac ccagggacc caccgagcgg caggtgatcg aggcgatcga 1560
gtgggtgggg attggaatcg gggttctcgc gccgggggtc ctggtcgtaa cgcaatcgt 1620
gtacgtcgtc cgcacatcac agtcgcccga gcgtcatcgg cggtaacgag agaccccc 1680
gttacctttt taatatctat atagtttgg cccccctcta tcccgccac cgctggggcg 1740
tataaagcgc ccaccctctc ttccctcagg tcctccttgg tcgatcccga acgacacag 1800

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<210> SEQ ID NO 30

<211> LENGTH: 511

<212> TYPE: PRT

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 30

```

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

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130			135			140									
Arg	Phe	Arg	Asn	Ser	Thr	Arg	Met	Glu	Phe	Arg	Leu	Gln	Ile	Trp	Arg
145				150				155							160
Tyr	Ser	Met	Gly	Pro	Ser	Pro	Pro	Ile	Ala	Pro	Ala	Pro	Asp	Leu	Glu
			165					170						175	
Glu	Val	Leu	Thr	Asn	Ile	Thr	Ala	Pro	Pro	Gly	Gly	Leu	Leu	Val	Tyr
			180					185						190	
Asp	Ser	Ala	Pro	Asn	Leu	Thr	Asp	Pro	His	Val	Leu	Trp	Ala	Glu	Gly
		195					200					205			
Ala	Gly	Pro	Gly	Ala	Asp	Pro	Pro	Leu	Tyr	Ser	Val	Thr	Gly	Pro	Leu
	210				215						220				
Pro	Thr	Gln	Arg	Leu	Ile	Ile	Gly	Glu	Val	Thr	Pro	Ala	Thr	Gln	Gly
225				230						235					240
Met	Tyr	Tyr	Leu	Ala	Trp	Gly	Arg	Met	Asp	Ser	Pro	His	Glu	Tyr	Gly
			245					250						255	
Thr	Trp	Val	Arg	Val	Arg	Met	Phe	Arg	Pro	Pro	Ser	Leu	Thr	Leu	Gln
			260					265						270	
Pro	His	Ala	Val	Met	Glu	Gly	Gln	Pro	Phe	Lys	Ala	Thr	Cys	Thr	Ala
		275					280						285		
Ala	Ala	Tyr	Tyr	Pro	Arg	Asn	Pro	Val	Glu	Phe	Asp	Trp	Phe	Glu	Asp
	290				295						300				
Asp	Arg	Gln	Val	Phe	Asn	Pro	Gly	Gln	Ile	Asp	Thr	Gln	Thr	His	Glu
305					310					315					320
His	Pro	Asp	Gly	Phe	Thr	Thr	Val	Ser	Thr	Val	Thr	Ser	Glu	Ala	Val
			325					330						335	
Gly	Gly	Gln	Val	Pro	Pro	Arg	Thr	Phe	Thr	Cys	Gln	Met	Thr	Trp	His
			340					345					350		
Arg	Asp	Ser	Val	Thr	Phe	Ser	Arg	Arg	Asn	Ala	Thr	Gly	Leu	Ala	Leu
		355					360						365		
Val	Leu	Pro	Arg	Pro	Thr	Ile	Thr	Met	Glu	Phe	Gly	Val	Arg	His	Val
	370				375						380				
Val	Cys	Thr	Ala	Gly	Cys	Val	Pro	Glu	Gly	Val	Thr	Phe	Ala	Trp	Phe
385				390						395					400
Leu	Gly	Asp	Asp	Pro	Ser	Pro	Ala	Ala	Lys	Ser	Ala	Val	Thr	Ala	Gln
			405					410						415	
Glu	Ser	Cys	Asp	His	Pro	Gly	Leu	Ala	Thr	Val	Arg	Ser	Thr	Leu	Pro
			420					425						430	
Ile	Ser	Tyr	Asp	Tyr	Ser	Glu	Tyr	Ile	Cys	Arg	Leu	Thr	Gly	Tyr	Pro
		435					440						445		
Ala	Gly	Ile	Pro	Val	Leu	Glu	His	His	Gly	Ser	His	Gln	Pro	Pro	Pro
	450				455						460				
Arg	Asp	Pro	Thr	Glu	Arg	Gln	Val	Ile	Glu	Ala	Ile	Glu	Trp	Val	Gly
465				470						475					480
Ile	Gly	Ile	Gly	Val	Leu	Ala	Ala	Gly	Val	Leu	Val	Val	Thr	Ala	Ile
			485					490						495	
Val	Tyr	Val	Val	Arg	Thr	Ser	Gln	Ser	Arg	Gln	Arg	His	Arg	Arg	
			500					505						510	

<210> SEQ ID NO 31

<211> LENGTH: 1282

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

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aagccacca gcctatgcat ccgctcctca atcctctcct gttggcactg ggcctcatgg    60
cgcttttggt gaccacggtc attgctctca ctgctctgg cggtttggcc tccccaggcc    120
ctgtgcctcc ctctacagcc ctcagggagc tcattgagga gctgggtcaac atcaccaga    180
accagaaggc tccgctctgc aatggcagca tggatggag catcaacctg acagctggca    240
tgtactgtgc agccttgaa tcctgatca acgtgtcagg ctgcagtgcc atcgagaaga    300
cccagaggat gctgagcgga ttctgccgc acaaggcttc agctgggcag tttccagct    360
tgcatgtccg agacacaaa atcgaggtgg cccagtttgt aaaggacctg ctcttacatt    420
taaagaaact ttttcgagag ggacagttca actgaaactt cgaaagcatc attatttgca    480
gagacaggac ctgactattg aagttgcaga ttcatttttc tttctgatgt caaaaatgtc    540
ttgggtaggc ggggaaggagg gttagggagg ggtaaaattc cttagcttag acctcagcct    600
gtgctgcccg tcttcagcct agccgacctc agccttcccc ttgccagggg ctcagcctgg    660
tgggectcct ctgtccaggg cctgagctc ggtggaccca gggatgacat gtcctacac    720
ccctcccctg ccctagagca cactgtagca ttacagtggg tgccccctt gccagacatg    780
tgggtgggaca gggaccact tcacacacag gcaactgagg cagacagcag ctcaggcaca    840
cttctctctg gtctatttta ttattgtgtg ttatttaaat gagtgtgttt gtcaccgtt    900
gggattgggg aagactgtgg ctgctagcac ttggagccaa gggttcagag actcagggcc    960
ccagactaa agcagtggac accaggagtc cctggtaata agtactgtgt acagaattct   1020
gtacctcac tggggctctg gggcctcgga gctctatccg aggcagggtc aggagagggg   1080
cagaacagcc gctcctgtct gccagccagc agccagctct cagccaacga gtaatttatt   1140
gtttttcctt gtatttaaat attaaatag ttagcaaaga gttaatatat agaagggtag   1200
cttgaacact gggggagggg acattgaaca agttgtttca ttgactatca aactgaagcc   1260
agaaataaag ttggtgacag at                                             1282

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<210> SEQ ID NO 32

<211> LENGTH: 146

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

```

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

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-continued

Phe Asn
145

<210> SEQ ID NO 33
 <211> LENGTH: 1376
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

```

gtaagaacac tctcgtgagt ctaacggtct tccggatgaa ggctatttga agtcgccata    60
acctggtcag aagtgtgctt gtcggcgggg agagaggcaa tatcaagggt ttaaatctcg    120
gagaaatggc tttcgtttgc ttggctatcg gatgcttata tacctttctg ataagcacia    180
catttggctg tacttcatct tcagacaccg agataaaagt taaccctcct caggattttg    240
agatagtggg tcccggtatc ttaggttata tctatttga atggcaaccc ccaactgtctc    300
tggatcattt taaggaatgc acagtgggat atgaactaaa ataccgaaac attggtagtg    360
aaacatggaa gaccatcatt actaagaatc tacattacaa agatgggttt gatcttaaca    420
agggcattga agcgaagata cacacgcttt taccatggca atgcacaaat ggatcagaag    480
ttcaaagttc ctgggcagaa actacttatt ggatatcacc acaaggaatt ccagaaacta    540
aagttcagga tatggattgc gtatattaca attggcaata tttactctgt tcttggaaac    600
ctggcatagg tgtacttctt gataccaatt acaacttggt ttactggtat gagggcttgg    660
atcatgcatt acagtgtggt gattacatca aggctgatgg acaaaatata ggatgcagat    720
ttccctatth ggaggcatca gactataaag atttctatat ttgtgttaat ggatcatcag    780
agaacaagcc tatcagatcc agttatttca cttttcagct tcaaaatata gttaaacctt    840
tgccgccagt ctatcttact tttactcggg agagttcatg tgaaattaag ctgaaatgga    900
gcataccttt gggacctatt ccagcaaggt gttttgatta tgaaattgag atcagagaag    960
atgatactac cttggtgact gctacagttg aaaatgaaac atacaccttg aaaacaacia   1020
atgaaacccg acaattatgc tttgtagtaa gaagcaaagt gaatatttat tgctcagatg   1080
acggaatttg gagtgagtgg agtgataaac aatgctggga aggtgaagac ctatcgaaga   1140
aaactttgct acgtttctgg ctaccatttg gtttcatctt aatattagtt atatttgtaa   1200
ccggtctgct tttgcgtaag ccaaacacct acccaaaaat gattccagaa tttttctgtg   1260
atacatgaag actttccata tcaagagaca tggatttgac tcaacagttt ccagtcatgg   1320
ccaaatgttc aatatgagtc tcaataaact gaatttttct tgcgaatggt gaaaaa     1376

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<210> SEQ ID NO 34
 <211> LENGTH: 380
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

```

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

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Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

<210> SEQ ID NO 35
 <211> LENGTH: 2685
 <212> TYPE: DNA
 <213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 35

atgcgccagg gcgccccgc gcgggggcgc cggtggttcg tcgtatgggc gctcttgggg 60
 ttgacgctgg gggctcctggt ggcgtcggeg gctccgagtt cccccggcac gcctggggtc 120
 ggggccgcga cccaggcggc gaacgggggc cctgccaactc cggcgccgcc cgcccctggc 180
 gcccccccaa cgggggaccc gccaaagccg ccgcgccccg ccggcgacaa cgcgaccgtc 240
 gccgcgggcc acgccacct gcgcgagcac ctgcgggaca tcaaggcggga gaacaccgat 300
 gcaaactttt acgtgtgccc accccccacg ggcgccacgg tgggtgcagtt cgagcagccg 360
 cgccgctgcc cgaccggcc cgagggtcag aactacacgg agggcatcgc ggtggtcttc 420

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aaggagaaca	tcgccccgta	caagttcaag	gccaccatgt	actacaaaga	cgtcaccggt	480
tcgcaggtgt	ggttcggcca	ccgctactcc	cagtttatgg	ggatctttga	ggaccgcgcc	540
cccgtcccct	tcgaggaggt	gatcgacaag	atcaacgcca	agggggtctg	tcggtccacg	600
gccaaagtag	tgcgcaacaa	cctggagacc	accgcgtttc	accgggacga	ccacgagacc	660
gacatggagc	tgaaacccgc	caacgcgcg	acccgcacga	gccggggctg	gcacaccacc	720
gacctcaagt	acaacccctc	gcgggtggag	gcgttccacc	ggtacgggac	gacggtaaac	780
tgcacgtcg	aggaggtgga	cgcgcgctcg	gtgtaccctg	acgacgagtt	tgtgttgccg	840
actggcgact	ttgtgtacat	gtccccgttt	tacggctacc	gggaggggtc	gcacaccgaa	900
cacaccagct	acgcccgcga	ccgcttcaag	caggtcgacg	gcttctacgc	gcgcgacctc	960
accaccaagg	cccggggccac	ggcgccgacc	acccggaacc	tgctcacgac	ccccaaagttc	1020
accgtggcct	gggactgggt	gccaaagcgc	ccgtcggctc	gcacatgac	caagtggcag	1080
gaggtggacg	agatgctgcg	ctccgagtag	ggcggtcctc	tccgattctc	ttccgacgcc	1140
atateccacca	ccttcaccac	caacctgacc	gagtagccgc	tctcgcgcgt	ggacctgggg	1200
gactgcatcg	gcaaggacgc	ccgcgacgcc	atggaccgca	tcttcgcccg	caggtacaa	1260
gcgacgcaca	tcaaggtggg	ccagccgcag	tactacctgg	ccaatggggg	ctttctgatc	1320
gcgtaccagc	cccttctcag	caacacgctc	gcggagctgt	acgtgcggga	acacctccgc	1380
gagcagagcc	gcaagccccc	aaaccccacg	cccccgccgc	ccggggccag	cgccaacgcg	1440
tccgtggagc	gcatcaagac	caacctctcc	atcgagttcg	ccaggctgca	gtttacgtac	1500
aaccacatac	agccccatgt	caacgatatg	ttgggcccgc	ttgccatcgc	gtggtgcgag	1560
ctgcagaatc	acgagctgac	cctgtggaac	gaggcccgca	agctgaacct	caacgccatc	1620
gcctcggcca	ccgtgggccc	gcgggtgagc	gcgcggatgc	tcggcgcagc	gatggccgctc	1680
tccacgtgcg	tgcgggtcgc	cgcggaaca	gtgatcgtcc	aaaactcgat	gcgcatcagc	1740
tcgcggcccg	gggcccgtca	cagcccgcgc	ctggtcagct	ttcggtaaca	agaccagggc	1800
ccgttggtcg	aggggcagct	gggggagaa	aacgagctgc	ggctgacgcg	cgatgcgatc	1860
gagccgtgca	ccgtgggaca	ccggcgctac	ttcaccttcg	gtgggggcta	cgtgtacttc	1920
gaggagtagc	cgtactccca	ccagctgagc	cgcccgaca	tcaccacctg	cagcaccttc	1980
atcgacctca	acatcaccat	gctggaggat	cacgagtttg	tccccctgga	ggtgtacacc	2040
cgccacgaga	tcaaggacag	cgccctgctg	gactacacgg	aggtccagcg	ccgcaaccag	2100
ctgcacgacc	tgcgcttcgc	cgacatcgac	acggtcatcc	acgcccagc	caacgcgcgc	2160
atggttgccg	gcctgggccc	gttcttcgag	gggatgggcg	acctggggcg	cgcggtccgc	2220
aaggtggtga	tgggcatcgt	gggcggcgtg	gtatcgcccg	tgctgggctg	gtctctcttc	2280
atgtccaacc	cctttggggc	gctggccgtg	ggtctgttgg	tcctggcccg	cctggcggcg	2340
gccttcttcg	cctttcgcta	cgctcatgcg	ctgcagagca	accccatgaa	ggccctgtac	2400
ccgctaacca	ccaaggagct	caagaacccc	accaaccccg	acgcgtccgg	ggagggcgag	2460
gagggcggcg	actttgacga	ggccaagcta	gccgaggccc	gggagatgat	acggtacatg	2520
gccctggtgt	ctgccatgga	gcgcacggaa	cacaaggcca	agaagaaggg	cacgagcgcg	2580
ctgctcagcg	ccaaggtcac	cgacatggtc	atcgcaagc	gcccaaacac	caactacacc	2640
caagttccca	acaagacgg	tgacgcccgc	gaggacgacc	tgtga		2685

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<211> LENGTH: 894

<212> TYPE: PRT

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 36

Met Arg Gln Gly Ala Pro Ala Arg Gly Arg Arg Trp Phe Val Val Trp
 1 5 10 15

Ala Leu Leu Gly Leu Thr Leu Gly Val Leu Val Ala Ser Ala Ala Pro
 20 25 30

Ser Ser Pro Gly Thr Pro Gly Val Ala Ala Ala Thr Gln Ala Ala Asn
 35 40 45

Gly Gly Pro Ala Thr Pro Ala Pro Pro Ala Pro Gly Ala Pro Pro Thr
 50 55 60

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

Ala Ala Gly His Ala Thr Leu Arg Glu His Leu Arg Asp Ile Lys Ala
 85 90 95

Glu Asn Thr Asp Ala Asn Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala
 100 105 110

Thr Val Val Gln Phe Glu Gln Pro Arg Arg Cys Pro Thr Arg Pro Glu
 115 120 125

Gly Gln Asn Tyr Thr Glu Gly Ile Ala Val Val Phe Lys Glu Asn Ile
 130 135 140

Ala Pro Tyr Lys Phe Lys Ala Thr Met Tyr Tyr Lys Asp Val Thr Val
 145 150 155 160

Ser Gln Val Trp Phe Gly His Arg Tyr Ser Gln Phe Met Gly Ile Phe
 165 170 175

Glu Asp Arg Ala Pro Val Pro Phe Glu Glu Val Ile Asp Lys Ile Asn
 180 185 190

Ala Lys Gly Val Cys Arg Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu
 195 200 205

Glu Thr Thr Ala Phe His Arg Asp Asp His Glu Thr Asp Met Glu Leu
 210 215 220

Lys Pro Ala Asn Ala Ala Thr Arg Thr Ser Arg Gly Trp His Thr Thr
 225 230 235 240

Asp Leu Lys Tyr Asn Pro Ser Arg Val Glu Ala Phe His Arg Tyr Gly
 245 250 255

Thr Thr Val Asn Cys Ile Val Glu Glu Val Asp Ala Arg Ser Val Tyr
 260 265 270

Pro Tyr Asp Glu Phe Val Leu Ala Thr Gly Asp Phe Val Tyr Met Ser
 275 280 285

Pro Phe Tyr Gly Tyr Arg Glu Gly Ser His Thr Glu His Thr Ser Tyr
 290 295 300

Ala Ala Asp Arg Phe Lys Gln Val Asp Gly Phe Tyr Ala Arg Asp Leu
 305 310 315 320

Thr Thr Lys Ala Arg Ala Thr Ala Pro Thr Thr Arg Asn Leu Leu Thr
 325 330 335

Thr Pro Lys Phe Thr Val Ala Trp Asp Trp Val Pro Lys Arg Pro Ser
 340 345 350

Val Cys Thr Met Thr Lys Trp Gln Glu Val Asp Glu Met Leu Arg Ser
 355 360 365

Glu Tyr Gly Gly Ser Phe Arg Phe Ser Ser Asp Ala Ile Ser Thr Thr
 370 375 380

Phe Thr Thr Asn Leu Thr Glu Tyr Pro Leu Ser Arg Val Asp Leu Gly

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385	390	395	400
Asp Cys Ile Gly Lys Asp Ala Arg Asp Ala Met Asp Arg Ile Phe Ala	405	410	415
Arg Arg Tyr Asn Ala Thr His Ile Lys Val Gly Gln Pro Gln Tyr Tyr	420	425	430
Leu Ala Asn Gly Gly Phe Leu Ile Ala Tyr Gln Pro Leu Leu Ser Asn	435	440	445
Thr Leu Ala Glu Leu Tyr Val Arg Glu His Leu Arg Glu Gln Ser Arg	450	455	460
Lys Pro Pro Asn Pro Thr Pro Pro Pro Pro Gly Ala Ser Ala Asn Ala	465	470	475
Ser Val Glu Arg Ile Lys Thr Thr Ser Ser Ile Glu Phe Ala Arg Leu	485	490	495
Gln Phe Thr Tyr Asn His Ile Gln Arg His Val Asn Asp Met Leu Gly	500	505	510
Arg Val Ala Ile Ala Trp Cys Glu Leu Gln Asn His Glu Leu Thr Leu	515	520	525
Trp Asn Glu Ala Arg Lys Leu Asn Pro Asn Ala Ile Ala Ser Ala Thr	530	535	540
Val Gly Arg Arg Val Ser Ala Arg Met Leu Gly Asp Val Met Ala Val	545	550	555
Ser Thr Cys Val Pro Val Ala Ala Asp Asn Val Ile Val Gln Asn Ser	565	570	575
Met Arg Ile Ser Ser Arg Pro Gly Ala Cys Tyr Ser Arg Pro Leu Val	580	585	590
Ser Phe Arg Tyr Glu Asp Gln Gly Pro Leu Val Glu Gly Gln Leu Gly	595	600	605
Glu Asn Asn Glu Leu Arg Leu Thr Arg Asp Ala Ile Glu Pro Cys Thr	610	615	620
Val Gly His Arg Arg Tyr Phe Thr Phe Gly Gly Gly Tyr Val Tyr Phe	625	630	635
Glu Glu Tyr Ala Tyr Ser His Gln Leu Ser Arg Ala Asp Ile Thr Thr	645	650	655
Val Ser Thr Phe Ile Asp Leu Asn Ile Thr Met Leu Glu Asp His Glu	660	665	670
Phe Val Pro Leu Glu Val Tyr Thr Arg His Glu Ile Lys Asp Ser Gly	675	680	685
Leu Leu Asp Tyr Thr Glu Val Gln Arg Arg Asn Gln Leu His Asp Leu	690	695	700
Arg Phe Ala Asp Ile Asp Thr Val Ile His Ala Asp Ala Asn Ala Ala	705	710	715
Met Phe Ala Gly Leu Gly Ala Phe Phe Glu Gly Met Gly Asp Leu Gly	725	730	735
Arg Ala Val Gly Lys Val Val Met Gly Ile Val Gly Gly Val Val Ser	740	745	750
Ala Val Ser Gly Val Ser Ser Phe Met Ser Asn Pro Phe Gly Ala Leu	755	760	765
Ala Val Gly Leu Leu Val Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala	770	775	780
Phe Arg Tyr Val Met Arg Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr	785	790	795
Pro Leu Thr Thr Lys Glu Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser	805	810	815

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Gly Glu Gly Glu Glu Gly Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu
 820 825 830

Ala Arg Glu Met Ile Arg Tyr Met Ala Leu Val Ser Ala Met Glu Arg
 835 840 845

Thr Glu His Lys Ala Lys Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala
 850 855 860

Lys Val Thr Asp Met Val Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr
 865 870 875 880

Gln Val Pro Asn Lys Asp Gly Asp Ala Asp Glu Asp Asp Leu
 885 890

<210> SEQ ID NO 37

<211> LENGTH: 1626

<212> TYPE: DNA

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 37

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atggcgcttt tgttgaccac ggtcattgct ctcacttgcc ttggcggcct tgcctcccca    60
ggccctgtgc ctccctctac agccctcagg gagctcattg aggagctggt caacatcacc    120
cagaaccaga aggtccgct ctgcaatgac agcatggtat ggagcatcaa cctgacagct    180
ggcatgtact gtgcagccct ggaatccctg atcaacgtgt caggctgcag tgccatcgag    240
aagaccacga ggatgctgag cggattctgc ccgcacaagg tctcagctgg gcagttttcc    300
agcttgcatg tccgagacac caaaatcgag gtggcccagt ttgtaaagga cctgctetta    360
catttaaaga aactttttcg cgagggacag ttcaacgaat tccaccgccg tggagtccg    420
cctccagata tggcgttact ccatgggtcc gtccccccca atcgctccgg ctcccacct    480
agaggaggtc ctgacgaaca tcaccgcccc acccggggga ctctggtgt acgacagcgc    540
ccccaacctg acggaccccc acgtgctctg ggcggagggg gccggcccgg gcgcccaccc    600
tccgttgtat tctgtcaccg ggcgctgcc gaccacagcg ctgattatcg gcgaggtgac    660
gcccgcgacc cagggaaatg attacttggc ctggggccgg atggacagcc cgcacagta    720
cgggacgtgg gtgcgcgtcc gcatgttccg cccccctct ctgaccctcc agccccacgc    780
ggtgatggag ggtcagccgt tcaaggcgac gtgcacggcc gccgcctact acccgcgtaa    840
ccccgtggag tttgtctggt tcgaggacga ccgccaggtg ttttaaccgg gccagatcga    900
cacgcagacg cacgagcacc ccgacggggt caccacagtc tctaccgtga cctccgaggc    960
tgtcggcggc caggctcccc ccgaggacct cacctgccag atgacgtggc accgcgactc   1020
cgtgacgttc tcgcgacgca atgccaccgg gctggccctg gtgtgcccgc ggccaacct   1080
caccatggaa tttggggtcc ggcattggtt ctgcaaggcc gctgctgccc ccgagggcgt   1140
gacgtttgcc tggttctctg gggacgaccc ctcaaccgcg gctaagtccg ccggttacggc   1200
ccaggagtgc tgcgaccacc ccgggctggc tacggtccgg tccaccctgc ccatttcgta   1260
cgactacagc gagtacatct gtcggttgac cggatatccg gccgggattc ccgttctaga   1320
gcaccacggc agtcaccagc cccaccccag ggaccccacc gageggcagg tgatcgaggc   1380
gatcgagtgg gtggggattg gaatcggggt tctcgcggcg ggggtcctgg tcgtaacggc   1440
aatcgtgtac gtcgtccgca catcacagtc gcggcagcgt catcggcggg aacgcgagac   1500
cccccgta cctttttaat atctatatag tttggtcccc cctctatccc gcccccgct   1560
gggcgctata aagccgccac cctctcttcc ctcaggteat ccttggtcga tcccgaacga   1620
cacacg                                           1626

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<210> SEQ ID NO 38
 <211> LENGTH: 497
 <212> TYPE: PRT
 <213> ORGANISM: Herpes Simplex Virus-1

 <400> SEQUENCE: 38

 Met Ala Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly
 1 5 10 15

 Phe Ala Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu
 20 25 30

 Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys
 35 40 45

 Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys
 50 55 60

 Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu
 65 70 75 80

 Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala
 85 90 95

 Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala
 100 105 110

 Gln Phe Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu
 115 120 125

 Gly Gln Phe Asn Glu Phe Ser Thr Arg Met Glu Phe Arg Leu Gln Ile
 130 135 140

 Trp Arg Tyr Ser Met Gly Pro Ser Pro Pro Ile Ala Pro Ala Pro Asp
 145 150 155 160

 Leu Glu Glu Val Leu Thr Asn Ile Thr Ala Pro Pro Gly Gly Leu Leu
 165 170 175

 Val Tyr Asp Ser Ala Pro Asn Leu Thr Asp Pro His Val Leu Trp Ala
 180 185 190

 Glu Gly Ala Gly Pro Gly Ala Asp Pro Pro Leu Tyr Ser Val Thr Gly
 195 200 205

 Pro Leu Pro Thr Gln Arg Leu Ile Ile Gly Glu Val Thr Pro Ala Thr
 210 215 220

 Gln Gly Met Tyr Tyr Leu Ala Trp Gly Arg Met Asp Ser Pro His Glu
 225 230 235 240

 Tyr Gly Thr Trp Val Arg Val Arg Met Phe Arg Pro Pro Ser Leu Thr
 245 250 255

 Leu Gln Pro His Ala Val Met Glu Gly Gln Pro Phe Lys Ala Thr Cys
 260 265 270

 Thr Ala Ala Ala Tyr Tyr Pro Arg Asn Pro Val Glu Phe Asp Trp Phe
 275 280 285

 Glu Asp Asp Arg Gln Val Phe Asn Pro Gly Gln Ile Asp Thr Gln Thr
 290 295 300

 His Glu His Pro Asp Gly Phe Thr Thr Val Ser Thr Val Thr Ser Glu
 305 310 315 320

 Ala Val Gly Gly Gln Val Pro Pro Arg Thr Phe Thr Cys Gln Met Thr
 325 330 335

 Trp His Arg Asp Ser Val Thr Phe Ser Arg Arg Asn Ala Thr Gly Leu
 340 345 350

 Ala Leu Val Leu Pro Arg Pro Thr Ile Thr Met Glu Phe Gly Val Arg
 355 360 365

 His Val Val Cys Thr Ala Gly Cys Val Pro Glu Gly Val Thr Phe Ala

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370			375			380									
Trp	Phe	Leu	Gly	Asp	Asp	Pro	Ser	Pro	Ala	Ala	Lys	Ser	Ala	Val	Thr
385					390					395					400
Ala	Gln	Glu	Ser	Cys	Asp	His	Pro	Gly	Leu	Ala	Thr	Val	Arg	Ser	Thr
				405					410						415
Leu	Pro	Ile	Ser	Tyr	Asp	Tyr	Ser	Glu	Tyr	Ile	Cys	Arg	Leu	Thr	Gly
			420					425					430		
Tyr	Pro	Ala	Gly	Ile	Pro	Val	Leu	Glu	His	His	Gly	Ser	His	Gln	Pro
		435					440					445			
Pro	Pro	Arg	Asp	Pro	Thr	Glu	Arg	Gln	Val	Ile	Glu	Ala	Ile	Glu	Trp
	450					455					460				
Val	Gly	Ile	Gly	Ile	Gly	Val	Leu	Ala	Ala	Gly	Val	Leu	Val	Val	Thr
465					470					475					480
Ala	Ile	Val	Tyr	Val	Val	Arg	Thr	Ser	Gln	Ser	Arg	Gln	Arg	His	Arg
				485					490						495

Arg

<210> SEQ ID NO 39

<211> LENGTH: 1593

<212> TYPE: DNA

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 39

```

atgggggggg ctgccgcccag gttggggggcc gtgattttgt ttgtcgtcat agtgggectc   60
catgggggtcc gcgcaaaata tgccctggcg gatgcctctc tcaagatggc cgacccaat   120
cgcttttcgcg gcaaaagacct tccggctctc gagatggcgc ttttggtgac cacggtcatt   180
gctctcactt gccttgggcg ctttgccctc ccaggccctg tgcctccctc tacagccctc   240
agggagctca ttgaggagct ggtcaacatc acccagaacc agaaggctcc gctctgcaat   300
ggcagcatgg tatggagcat caacctgaca gctggcatgt actgtgcagc cctggaatcc   360
ctgatcaacg tgtcaggctg cagtgccatc gagaagacct agaggatgct gagcggattc   420
tgcccgcaca aggtctcagc tgggcagttt tccagcttgc atgtccgaga caccaaaatc   480
gaggtggccc agtttgtaaa ggacctgctc ttacatttaa agaaactttt tcgcgagggg   540
cagttcaacg gtaccctgga ccggctgacc gaccctccgg gggtcggcg cgtgtaccac   600
atccaggcgg gcctaccgga cccgttcag cccccagcc tcccgatcac ggtttactac   660
gccgtggttg agcgcgctg ccgcagcgtg ctccctaaacg caccgtcgga ggccccccag   720
attgtccgcg gggcctccga agacgtccgg aaacaacct acaacctgac catcgcttgg   780
tttcggatgg gaggcaactg tgctatcccc atcaccgtca tggagtacac cgaatgctcc   840
tacaacaagt ctctgggggc ctgtcccac cgaacgcagc cccgctggaa ctactatgac   900
agcttcagcg ccgtcagcga ggataacctg gggttcctga tgcacgcccc cgcgtttgag   960
accgcccgca cgtacctgcg gctcgtgaag ataaacgact ggacggagat tacacagttt  1020
atcctggagc accgagccaa gggctcctgt aagtacgccc ttcgctgcg catccccccg  1080
tcagcctgcc tctcccccca ggccctaccag caggggggtga cgggtggacag catcgggatg  1140
ctgccccgct tcatccccga gaaccagcgc accgtcggcg tatacagctt gaagatcgcc  1200
gggtggcaag ggcccaaggc cccatacacg agcacctgc tgcccccgga gctgtccgag  1260
acccccaaag ccaacgcagc agaactcgcc ccggaagacc ccgaggattc ggccctcttg  1320
gaggaccgag tggggacggg ggtgccgcaa atcccacaa actggcacat accgtcgatc  1380

```

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caggacgccc cgacgcctta ccatccccc gccaccccga acaacatggg cctgatcgcc 1440
ggcgcggtgg gccgcagtct cctggttagcc ctggtcattt gcggaattgt gtactggatg 1500
cgccgcccga ctcaaaaagc cccaaagcgc atacgcctcc cccacatccg ggaagacgac 1560
cagccgtcct cgcaccagcc cttgttttac tag 1593

```

<210> SEQ ID NO 40

<211> LENGTH: 530

<212> TYPE: PRT

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 40

```

Met Gly Gly Ala Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
 1          5          10          15
Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
 20          25          30
Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35          40          45
Val Leu Glu Met Ala Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys
 50          55          60
Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu
 65          70          75          80
Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala
 85          90          95
Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly
 100         105         110
Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser
 115         120         125
Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys
 130         135         140
Val Ser Ala Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile
 145         150         155         160
Glu Val Ala Gln Phe Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu
 165         170         175
Phe Arg Glu Gly Gln Phe Asn Gly Thr Pro Asp Arg Leu Thr Asp Pro
 180         185         190
Pro Gly Val Arg Arg Val Tyr His Ile Gln Ala Gly Leu Pro Asp Pro
 195         200         205
Phe Gln Pro Pro Ser Leu Pro Ile Thr Val Tyr Tyr Ala Val Leu Glu
 210         215         220
Arg Ala Cys Arg Ser Val Leu Leu Asn Ala Pro Ser Glu Ala Pro Gln
 225         230         235         240
Ile Val Arg Gly Ala Ser Glu Asp Val Arg Lys Gln Pro Tyr Asn Leu
 245         250         255
Thr Ile Ala Trp Phe Arg Met Gly Gly Asn Cys Ala Ile Pro Ile Thr
 260         265         270
Val Met Glu Tyr Thr Glu Cys Ser Tyr Asn Lys Ser Leu Gly Ala Cys
 275         280         285
Pro Ile Arg Thr Gln Pro Arg Trp Asn Tyr Tyr Asp Ser Phe Ser Ala
 290         295         300
Val Ser Glu Asp Asn Leu Gly Phe Leu Met His Ala Pro Ala Phe Glu
 305         310         315         320
Thr Ala Gly Thr Tyr Leu Arg Leu Val Lys Ile Asn Asp Trp Thr Glu
 325         330         335

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Ile Thr Gln Phe Ile Leu Glu His Arg Ala Lys Gly Ser Cys Lys Tyr
 340 345 350

Ala Leu Pro Leu Arg Ile Pro Pro Ser Ala Cys Leu Ser Pro Gln Ala
 355 360 365

Tyr Gln Gln Gly Val Thr Val Asp Ser Ile Gly Met Leu Pro Arg Phe
 370 375 380

Ile Pro Glu Asn Gln Arg Thr Val Ala Val Tyr Ser Leu Lys Ile Ala
 385 390 395 400

Gly Trp His Gly Pro Lys Ala Pro Tyr Thr Ser Thr Leu Leu Pro Pro
 405 410 415

Glu Leu Ser Glu Thr Pro Asn Ala Thr Gln Pro Glu Leu Ala Pro Glu
 420 425 430

Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro Val Gly Thr Val Val
 435 440 445

Pro Gln Ile Pro Pro Asn Trp His Ile Pro Ser Ile Gln Asp Ala Ala
 450 455 460

Thr Pro Tyr His Pro Pro Ala Thr Pro Asn Asn Met Gly Leu Ile Ala
 465 470 475 480

Gly Ala Val Gly Gly Ser Leu Leu Val Ala Leu Val Ile Cys Gly Ile
 485 490 495

Val Tyr Trp Met Arg Arg Arg Thr Gln Lys Ala Pro Lys Arg Ile Arg
 500 505 510

Leu Pro His Ile Arg Glu Asp Asp Gln Pro Ser Ser His Gln Pro Leu
 515 520 525

Phe Tyr
 530

<210> SEQ ID NO 41
 <211> LENGTH: 1416
 <212> TYPE: DNA
 <213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 41

```

atggcgcttt tgttgaccac ggtcattgct ctcacttgcc ttggcggctt tgctcccca    60
ggcctgtgct ctcctctac agccctcagg gagctcattg aggagctggt caacatcacc    120
cagaaccaga aggctccgct ctgcaatggc agcatggtat ggagcatcaa cctgacagct    180
ggcatgtact gtgcagccct ggaatccctg atcaacgtgt caggctgcag tgccatcgag    240
aagaccacaga ggatgctgag cggattctgc ccgcacaagg tctcagctgg gcagttttcc    300
agcttgcatg tccgagacac caaaatcgag gtggcccagt ttgtaaagga cctgctctta    360
catttaaaga aactttttcg cgagggacag ttcaacggtta ccgggtcccg gcgcgtgtac    420
cacatccagg cgggcttacc ggacccttc cagccccca gcctcccgat cacggtttac    480
tacgccgtgt tggagcgcgc ctgccgcagc gtgctcctaa acgcaccgtc ggaggcccc    540
cagattgtcc gcggggcctc cgaagacgtc cggaaacaac cctacaacct gaccatcgct    600
tggtttcgga tggagggcaa ctgtgctatc cccatcacgg tcatggagta caccgaatgc    660
tcctacaaca agtctctggg ggctgtccc atccgaacgc agccccgctg gaactactat    720
gacagcttca gcgccgtcag cgaggataac ctgggggttc tgatgcacgc ccccgcttt    780
gagaccgccc gcacgtacct gcggctcgtg aagataaacg actggacgga gattacacag    840
tttatcctgg agcaccgagc caagggtccc tgtaagtaac cccttccgct gcgcatcccc    900
ccgtcagcct gcctctcccc ccaggcctac cagcaggggg tgacgggtgga cagcatcggg    960
    
```

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atgctgcccc gcttcatccc cgagaaccag cgcaccgtcg ccgatacag cttgaagatc 1020
gccgggtggc acggggcccaa ggcccatac acgagcaccg tgctgcccc ggagtggtcc 1080
gagaccccc acgccacgca gccagaactc gccccggaag accccgagga ttcggcctc 1140
ttggaggacc ccgtggggac ggtggtgccc caaatcccac caaactggca cataccgtcg 1200
atccaggacg ccgcgacgcc ttaccatccc ccggccaccg cgaacaacat gggcctgatc 1260
gccggcgcgg tggggcgag tctcctggta gccctggta tttgcggaat tgtgtactgg 1320
atgcgccgcc gactcaaaa agccccaaag cgcatacggc tccccacat ccgggaagac 1380
gaccagccgt cctcgacca gcccttgttt tactag 1416

```

<210> SEQ ID NO 42

<211> LENGTH: 471

<212> TYPE: PRT

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 42

```

Met Ala Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly
 1          5          10          15
Phe Ala Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu
 20          25          30
Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys
 35          40          45
Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys
 50          55          60
Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu
 65          70          75          80
Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala
 85          90          95
Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala
 100         105         110
Gln Phe Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu
 115         120         125
Gly Gln Phe Asn Gly Thr Gly Ser Arg Arg Val Tyr His Ile Gln Ala
 130         135         140
Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile Thr Val Tyr
 145         150         155         160
Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu Asn Ala Pro
 165         170         175
Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp Val Arg Lys
 180         185         190
Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly Gly Asn Cys
 195         200         205
Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser Tyr Asn Lys
 210         215         220
Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp Asn Tyr Tyr
 225         230         235         240
Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe Leu Met His
 245         250         255
Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu Val Lys Ile
 260         265         270
Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His Arg Ala Lys
 275         280         285
Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro Ser Ala Cys

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290			295			300									
Leu	Ser	Pro	Gln	Ala	Tyr	Gln	Gln	Gly	Val	Thr	Val	Asp	Ser	Ile	Gly
305					310					315					320
Met	Leu	Pro	Arg	Phe	Ile	Pro	Glu	Asn	Gln	Arg	Thr	Val	Ala	Val	Tyr
				325					330						335
Ser	Leu	Lys	Ile	Ala	Gly	Trp	His	Gly	Pro	Lys	Ala	Pro	Tyr	Thr	Ser
			340					345						350	
Thr	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Glu	Thr	Pro	Asn	Ala	Thr	Gln	Pro
		355					360					365			
Glu	Leu	Ala	Pro	Glu	Asp	Pro	Glu	Asp	Ser	Ala	Leu	Leu	Glu	Asp	Pro
	370					375					380				
Val	Gly	Thr	Val	Val	Pro	Gln	Ile	Pro	Pro	Asn	Trp	His	Ile	Pro	Ser
385					390					395					400
Ile	Gln	Asp	Ala	Ala	Thr	Pro	Tyr	His	Pro	Pro	Ala	Thr	Pro	Asn	Asn
				405					410						415
Met	Gly	Leu	Ile	Ala	Gly	Ala	Val	Gly	Gly	Ser	Leu	Leu	Val	Ala	Leu
			420					425						430	
Val	Ile	Cys	Gly	Ile	Val	Tyr	Trp	Met	Arg	Arg	Arg	Thr	Gln	Lys	Ala
		435					440					445			
Pro	Lys	Arg	Ile	Arg	Leu	Pro	His	Ile	Arg	Glu	Asp	Asp	Gln	Pro	Ser
	450					455						460			
Ser	His	Gln	Pro	Leu	Phe	Tyr									
465					470										

<210> SEQ ID NO 43

<211> LENGTH: 1416

<212> TYPE: DNA

<213> ORGANISM: Herpes Simplex Virus-1

<400> SEQUENCE: 43

```

atggcgcttt tgttgaccac ggtcattgct etcacttgcc ttggcggctt tgectcccca      60
ggccctgtgc ctcctctac agccctcagg gagctcattg aggagctggt caacatcacc      120
cagaaccaga aggctccgct ctgcaatggc agcatgggat ggagcatcaa cctgacagct      180
ggcatgtact gtgcagccct ggaatccctg atcaacgtgt caggctgcag tgccatcgag      240
aagaccaga g gatgctgag cggattctgc ccgcacaagg tctcagctgg gcagttttcc      300
agcttgcatg tccgagacac caaaatcgag gtggcccagt ttgtaaagga cctgctctta      360
catttaaaga aactttttcg cgagggacag ttcaacggta ccgggggtccg gcgctcgtac      420
cacatccagg cgggcctacc ggacccttc cagcccccca gcctcccgat cacggtttac      480
tacgccgtgt tggagcgcgc ctgccgcagc gtgctcctaa acgcaccgtc ggaggccccc      540
cagattgtcc gcggggcctc cgaagacgtc cggaaacaac cctacaacct gaccatcgct      600
tggtttcgga tgggaggcaa ctgtgctatc cccatcacgg tcatggagta caccgaatgc      660
tctacaaca agtctctggg ggccctgtccc atccgaacgc agccccgctg gaactactat      720
gacagcttca gcgcctcag cgaggataac ctgggggttc tgatgcacgc ccccgcttt      780
gagaccgccc gcacgtacct gcggtctgtg aagataaacg actggacgga gattacacag      840
tttatcctgg agcaccgagc caagggctcc tgtaagtacg cccttccgct gcgcateccc      900
ccgtcagcct gcctctcccc ccaggcctac cagcaggggg tgacgggtgga cagcatcggg      960
atgctgcccc gcttcatccc cgagaaccag cgcaccgtcg ccgtatacag cttgaagatc     1020
gccgggtggc acgggcccac ggccccatac acgagcaccg tgctgcccc ggagctgtcc     1080

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gagaccccc aacgcccacgca gccagaactc gccccggaag acccccaggga ttcggcctc 1140
ttggaggacc ccgtggggac ggtggtgccg caaatcccac caaactggca cataccgtcg 1200
atccaggacg ccgcgacgcc ttaccatccc ccggccaccc cgaacaacat gggcctgatc 1260
gccggcggcg tggggcggcag tctcctggta gccctggta tttggggaat tgtgtactgg 1320
atgcccgcgc gactcaaaa agcccaaaag cgcatacgcc tccccacat ccgggaagac 1380
gaccagccgt cctcgcacca gcccttggtt tactag 1416

```

```

<210> SEQ ID NO 44
<211> LENGTH: 471
<212> TYPE: PRT
<213> ORGANISM: Herpes Simplex Virus-1

```

```

<400> SEQUENCE: 44

```

```

Met Ala Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly
1      5      10     15
Phe Ala Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu
20     25     30
Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys
35     40     45
Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys
50     55     60
Ala Ala Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu
65     70     75     80
Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala
85     90     95
Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala
100    105   110
Gln Phe Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu
115    120   125
Gly Gln Phe Asn Gly Thr Gly Val Arg Arg Ser Tyr His Ile Gln Ala
130    135   140
Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile Thr Val Tyr
145    150   155   160
Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu Asn Ala Pro
165    170   175
Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp Val Arg Lys
180    185   190
Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly Gly Asn Cys
195    200   205
Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser Tyr Asn Lys
210    215   220
Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp Asn Tyr Tyr
225    230   235   240
Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe Leu Met His
245    250   255
Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu Val Lys Ile
260    265   270
Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His Arg Ala Lys
275    280   285
Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro Ser Ala Cys
290    295   300
Leu Ser Pro Gln Ala Tyr Gln Gln Gly Val Thr Val Asp Ser Ile Gly
305    310   315   320

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-continued

Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val Ala Val Tyr
 325 330 335

Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Ala Pro Tyr Thr Ser
 340 345 350

Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro Asn Ala Thr Gln Pro
 355 360 365

Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu Glu Asp Pro
 370 375 380

Val Gly Thr Val Val Pro Gln Ile Pro Pro Asn Trp His Ile Pro Ser
 385 390 395 400

Ile Gln Asp Ala Ala Thr Pro Tyr His Pro Pro Ala Thr Pro Asn Asn
 405 410 415

Met Gly Leu Ile Ala Gly Ala Val Gly Gly Ser Leu Leu Val Ala Leu
 420 425 430

Val Ile Cys Gly Ile Val Tyr Trp Met Arg Arg Arg Thr Gln Lys Ala
 435 440 445

Pro Lys Arg Ile Arg Leu Pro His Ile Arg Glu Asp Asp Gln Pro Ser
 450 455 460

Ser His Gln Pro Leu Phe Tyr
 465 470

The invention claimed is:

1. A method of targeting a recombinant HSV particle to a cell comprising

- (a) identifying a ligand for a ligand binding partner exhibited on the surface of a target cell; and
- (b) contacting the target cell with an HSV particle having at least one protein on its surface, comprising an altered gD, wherein the altered gD comprises an amino acid substitution at position 34, wherein the alteration reduces binding of gD to one or more of its cellular receptors, said alteration comprising
 - (i) a heterologous peptide ligand on the surface of the recombinant HSV particle forming a fusion protein with the altered gD; and
 - (ii) an amino acid alteration;

- 30 wherein said recombinant HSV particle preferentially binds to cells expressing a binding partner to said heterologous peptide ligand, and wherein the ligand binds to the binding partner exhibited on the surface of said target cell.
- 2. The method of claim 1, wherein the alteration to gD reduces binding of gD to at least one cellular receptor for gD selected from the group consisting of HveA and Nectin-1.
- 3. The method of claim 1, wherein the ligand forms a second fusion protein with gC.
- 4. The method of claim 3, wherein the ligand is a cytokine.
- 5. The method of claim 4, wherein the cytokine is IL13.
- 6. The method of claim 1, wherein the amino acid alteration is a V34S amino acid substitution.

* * * * *