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(54) **CHIMERIC VSV-G PROTEINS AS NUCLEIC ACID TRANSFER VEHICLES**

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(60) Provisional application No. 61/984,290, filed on Apr. 25, 2014.

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(57) **ABSTRACT**

The design and generation of a number of chimeric VSV-G (or VSV-G variants) proteins are used as transfer vehicles to enhance delivery of nucleic acids like plasmid DNA, single and double stranded DNA and RNA, and antisense oligonucleotides into human and animal cells. These chimeric VSV-G protein-nucleic acid transfer vehicles have widespread applications to deliver nucleic acids for exon skipping and gene delivery for gene replacement in human and animals.

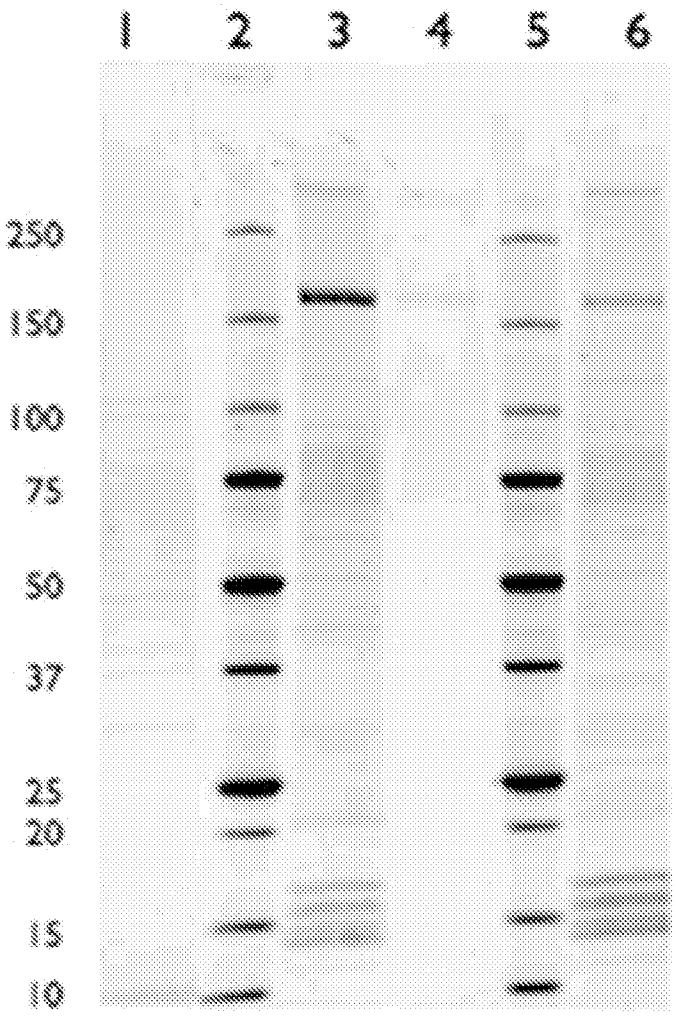



FIG. 1

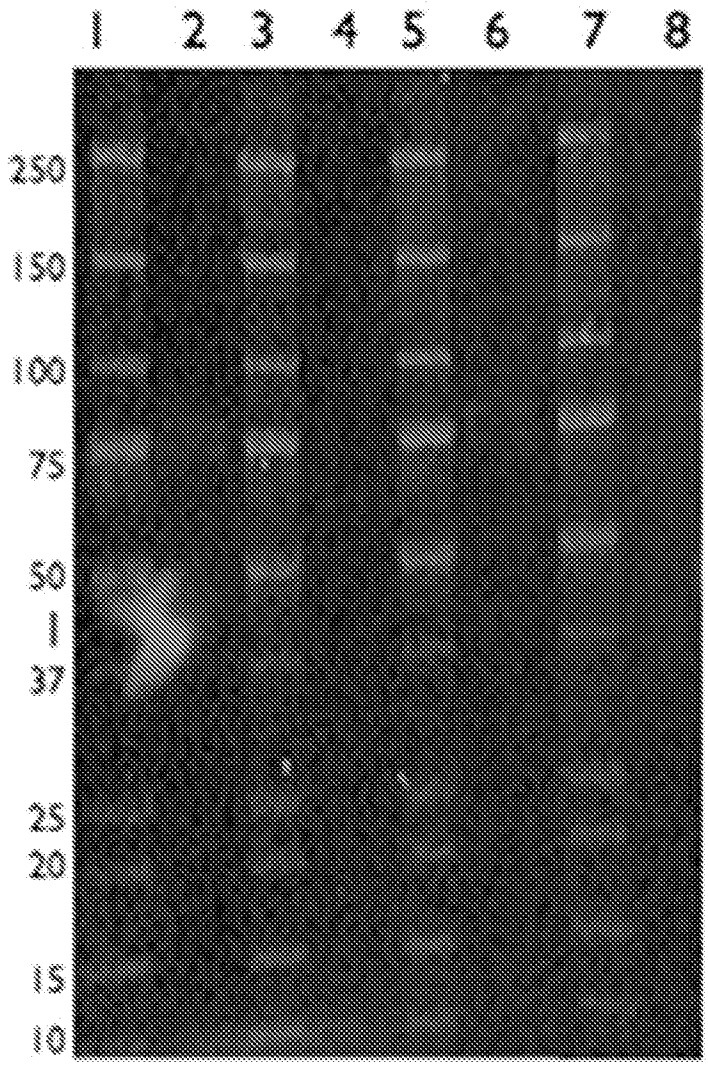



FIG. 2

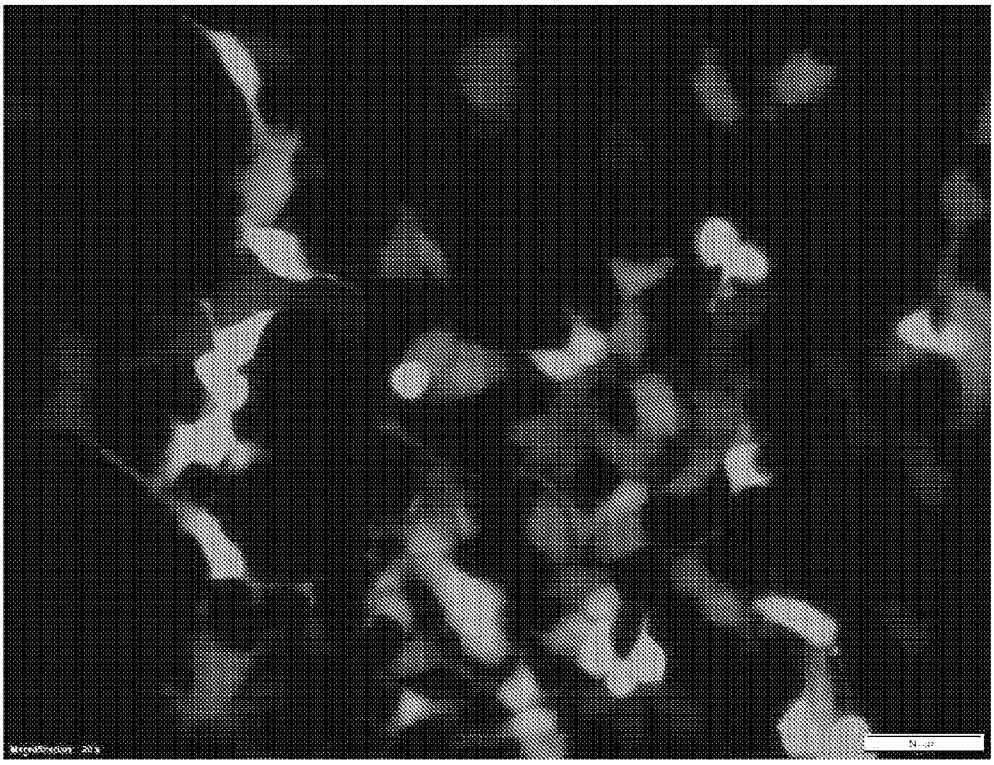


FIG. 3

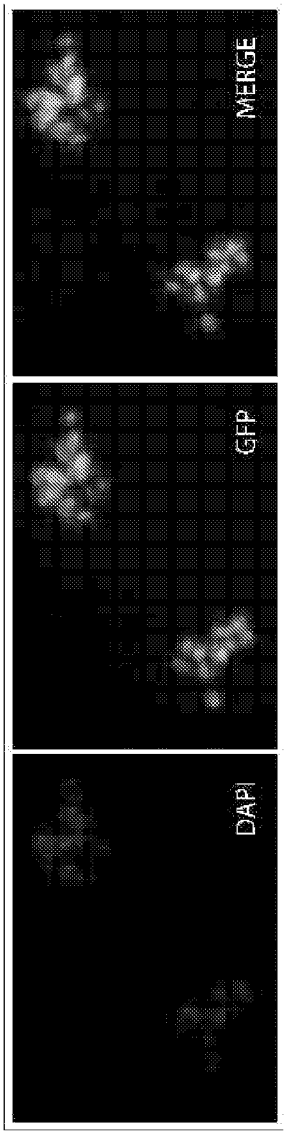



FIG. 4A

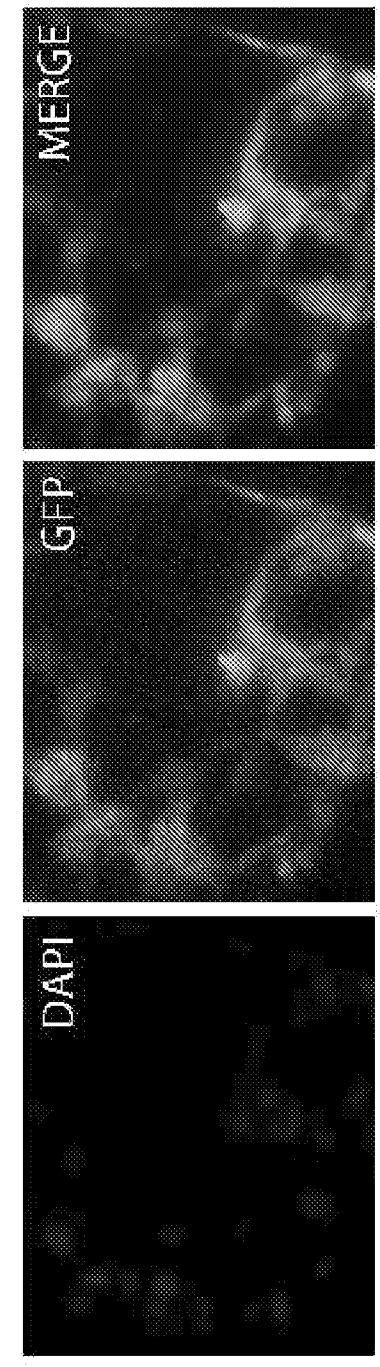



FIG. 4B

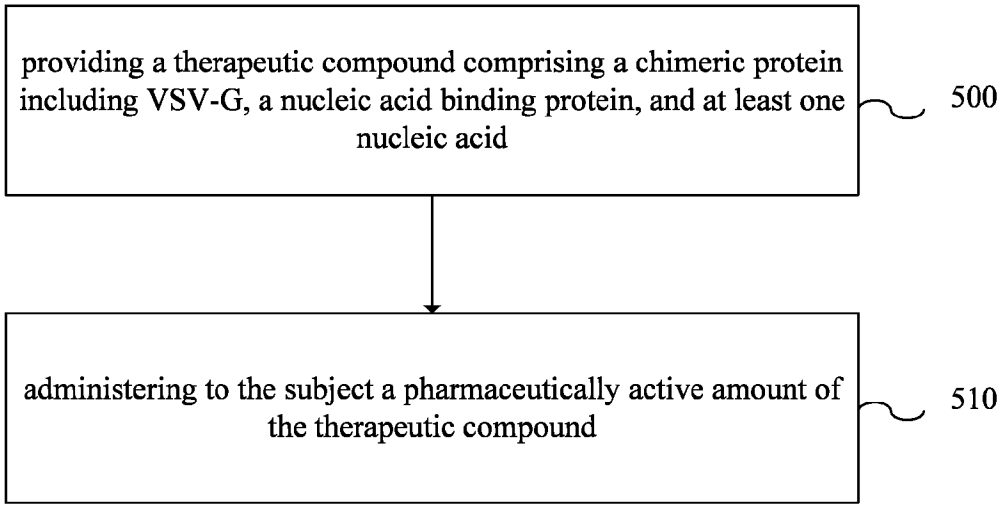

providing a therapeutic compound comprising a chimeric protein including VSV-G, a nucleic acid binding protein, and at least one nucleic acid
500
administering to the subject a pharmaceutically active amount of the therapeutic compound
510

FIG. 5

# CHIMERIC VSV-G PROTEINS AS NUCLEIC ACID TRANSFER VEHICLES

## CROSS-REFERENCE TO RELATED APPLICATIONS

**[0001]** This application claims the benefit of U.S. Provisional Patent No. 61/984,290, filed Apr. 25, 2014, which is incorporated by reference herein in its entirety.

## FIELD OF THE DISCLOSURE

**[0002]** What is disclosed is a chimeric or fusion protein including a membrane transport domain and a nucleic acid binding domain allowing targeted delivery of nucleic acids in humans and animals for the treatment of medical conditions.

## BACKGROUND OF THE DISCLOSURE

**[0003]** The vesicular stomatitis virus G glycoprotein (hereinafter referred to as "VSV-G") is widely used to pseudotype viral vectors due to its wide tropism and stability. These viral vectors facilitate gene transduction in human and animals. The VSV-G proteins, when not associated with any viral vectors, are also alone capable of forming complexes with naked plasmid DNA in cell free conditions which can be transfected to cells thereafter.

**[0004]** The fusogenic G glycoprotein of the vesicular stomatitis virus has proved to be a useful tool for viral-mediated gene delivery by acting as an envelope protein. Due to its wide tropism, VSV-G has been used as an efficient surrogate envelope protein to produce more stable and high titer pseudotyped murine leukemia virus (MLV)-based retrovirus and lentivirus-based vectors, all of which have been effectively used for gene therapy. The reason behind this pantropism of VSV remained elusive for a long period. Recently, it has been found that the VSV enters the cell through a highly ubiquitous low-density lipoprotein (LDL) receptor having wide distribution.

**[0005]** However, there are some limitations associated with the use of VSV-G. It is cytotoxic to producer cells, though the use of tetracycline-regulated promoters has helped to overcome this problem. In addition, serum inactivation of VSV-G pseudotyped viruses poses a problem and impedes their function to some extent in vivo. To overcome the latter problem, VSV-G mutants have been generated which are more thermostable as well as serum-resistant. VSV-G mutants harboring T230N+T368A or K66T+S162T+T230N+T368A mutations exhibited more resistance to serum inactivation and higher thermostability.

**[0006]** Apart from acting as a fusogenic envelope protein for many viral vectors, previous studies showed that purified soluble VSV-G itself can be inserted into lipid bilayers of liposomes and lipid vesicles in cell free system in vitro. Additionally, it has been shown that VSV-G can form a complex with naked plasmid DNA in the absence of any transfection reagent and can thereby enhance the transfection of naked plasmid DNA into cells. Sucrose gradient sedimentation analysis demonstrated that VSV-G associates with plasmid DNA and MLV gag-pol particles to form ternary complexes that co-sediment with high DNA transfecting activity. This transfection could be abolished by adding antibody for VSV-G.

**[0007]** In eukaryotic cells, heritable genetic material is packaged into structures known as chromatin consisting of DNA and protein. The basic repeating unit of chromatin is the nucleosome core, which consists of 147 base pairs of DNA wrapped in 1.7 left-handed superhelical turns around the surface of an octameric protein core formed by two molecules each of histones H2A, H2B, H3, and H4. Histones are highly basic proteins that bind very avidly and non-specifically to nucleic acids. Histones were among the first proteins studied due to their relative ease of isolation and all four histone proteins (H2A, H2B, H3, and H4) can be expressed in bacteria. This has allowed purifying and reconstituting of the histone proteins in cell free systems using well defined protocols. Though the native histone proteins undergo an extensive array of posttranslational modifications, recombinant histones do not undergo post-translational modifications and can be obtained in a highly pure form due to their high expression levels.

**[0008]** Single Strand DNA-Binding Proteins (hereinafter referred to as "SSBP") are ubiquitously expressed and involved in a variety of DNA metabolic processes including replication, recombination, damage, and repair. SSBP-1 is a housekeeping gene involved in mitochondrial biogenesis. It is also a subunit of a single-stranded DNA (ssDNA)-binding complex involved in the maintenance of genome stability.

**[0009]** Ribonuclease III (hereinafter referred to as "RNase III") is an enzyme that is expressed in most of the cells and is involved in the processing of pre-rRNA. It has a catalytic domain and an RNA binding domain that is located in the C-terminal end of the enzyme. Inhibition of human RNase III resulted in cell death suggesting a very important role of this enzyme.

**[0010]** Gene therapy and exon skipping have served as a means of gene transduction or gene manipulation respectively in humans during the past two decades. Gene therapy and exon skipping were initially developed as therapeutic strategies focused to address detrimental monogenetic diseases for which there were no available options for treatment, e.g. primary immunodeficiency. These approaches later found widespread application in curing neurodegenerative diseases, cancer, metabolic disorders, and more.

**[0011]** Gene therapy involves delivery of genes of interest cloned in viral vectors which are capable of producing viruses when transduced in human cells. Despite the continuous improvement of retroviral and lentiviral gene transfer systems for gene delivery during the last many years, there remain severe limitations preventing the development of efficient and safe clinical applications for these systems. These limitations include: their inability to target infection to cells of interest, inefficient transduction, propensity of viral vectors to get incorporated in human genome and create mutations, elicited high immune responses, inability to be administered intravenously or subcutaneously, and intramuscular administration that only leads to local delivery of the gene. Owing to these limitations, no gene therapy based medication has been approved by FDA for use in humans, though there have been many clinical trials during the past two decades and also many ongoing clinical trials.

**[0012]** Exon skipping is a therapeutic strategy where antisense oligonucleotides (AO) are delivered in humans to modulate splicing of genes resulting in mRNA that either produces functional proteins or blocks their production. AOs are short nucleic acid sequences designed to selectively bind to specific mRNA or pre-mRNA sequences. Despite the very convincing underlying principle behind this strategy, only one AO has been approved by the FDA (Vitravene™, an

intraocular injection to inhibit cytomegalovirus retinitis in immunocompromised patients; Isis Pharmaceuticals, Carlsbad, Calif.), and this drug is no longer marketed. There are certain limitations associated with the use of AOs including difficulty in achieving pharmacologically significant concentrations in cells due to biological barriers like endothelial and basement membrane, cell membrane, and sequestration by phagolysosomes.

**[0013]** Further discussion on the subjects of gene transfer and delivery may be found in U.S. Pat. No. 7,531,647 ("Lentiviral Vectors for Site-Specific Gene Insertion"); U.S. Pat. No. 8,158,827 ("Transfection Reagents"); and U.S. Pat. No. 8,652,460 ("Gene Delivery System and Method of Use") and U.S. patent application Ser. No. 14/635,012 ("Chimeric Dystrophin-VSV-G Protein to Treat Dystrophinopathies". The disclosures of each of U.S. Pat. Nos. 7,531,647, 8,158,827 and 8,652,460 and U.S. application Ser. No. 14/635,012 are incorporated by reference herein in their entireties.

**[0014]** The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects and advantages of the invention will be apparent from the description and drawings, and from the claims.

## BRIEF SUMMARY OF THE INVENTION

**[0015]** Disclosed herein is a chimeric protein incorporating a transport domain and a nucleic acid binding domain and methods of utilizing those chimeric proteins for targeted delivery of therapeutic nucleic acids.

**[0016]** In some embodiments, the present disclosure is directed to a chimeric protein comprising VSV-G and a nucleic acid binding protein. In some embodiments, the nucleic acid binding protein is a histone. In some embodiments, the histone is selected from the group consisting of: H2A, H2B, H3, and H4. In some embodiments, the histone is tagged with VSV-G at the C-terminus. In some embodiments, histone is tagged with VSV-G at the N-terminus.

**[0017]** In some embodiments, the chimeric protein comprises SEQ. ID NO.: 1, SEQ. ID NO.: 2, SEQ. ID NO.: 3, SEQ. ID NO.: 4, SEQ. ID NO.: 5, SEQ. ID NO.: 6, SEQ. ID NO.: 7, or SEQ. ID NO.: 8, and pharmacologically acceptable equivalents thereof. In some embodiments, the chimeric protein comprises SEQ. ID NO.: 15, SEQ. ID NO.: 16, SEQ. ID NO.: 17, SEQ. ID NO.: 18, SEQ. ID NO.: 19, SEQ. ID NO.: 20, SEQ. ID NO.: 21, or SEQ. ID NO.: 22, and pharmacologically acceptable equivalents thereof. In some embodiments, the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 1, SEQ. ID NO.: 2, SEQ. ID NO.: 3, SEQ. ID NO.: 4, SEQ. ID NO.: 5, SEQ. ID NO.: 6, SEQ. ID NO.: 7, or SEQ. ID NO.: 8. In some embodiments, the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 15, SEQ. ID NO.: 16, SEQ. ID NO.: 17, SEQ. ID NO.: 18, SEQ. ID NO.: 19, SEQ. ID NO.: 20, SEQ. ID NO.: 21, or SEQ. ID NO.: 22.

**[0018]** In some embodiments, the nucleic acid binding protein is SSBP-1. In some embodiments, SSBP-1 is tagged with VSV-G at the C-terminus. In some embodiments, SSBP-1 is tagged with VSV-G at the N-terminus. In some embodiments, the chimeric protein comprises SEQ. ID NO.: 9 or SEQ. ID NO.: 10, and pharmacologically acceptable equivalents thereof. In some embodiments, the chimeric protein comprises SEQ. ID NO.: 23 or SEQ. ID NO.: 24, and pharmacologically acceptable equivalents thereof. In some embodiments, the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 9 or SEQ. ID NO.: 10. In some embodiments, the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 23 or SEQ. ID NO.: 24.

**[0019]** In some embodiments, the nucleic acid binding protein is RNase III. In some embodiments, RNase III is tagged with VSV-G at the C-terminus. In some embodiments, RNase III is tagged with VSV-G at the N-terminus. In some embodiments, the chimeric protein comprises SEQ. ID NO.: 11, SEQ. ID NO.: 12, or SEQ. ID NO.: 13, and pharmacologically acceptable equivalents thereof. In some embodiments, wherein the chimeric protein comprises SEQ. ID NO.: 14, SEQ. ID NO.: 25, or SEQ. ID NO.: 26, and pharmacologically acceptable equivalents thereof. In some embodiments, wherein the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 11, SEQ. ID NO.: 12, or SEQ. ID NO.: 13. In some embodiments, wherein the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 14, SEQ. ID NO.: 25, or SEQ. ID NO.: 26.

**[0020]** In some embodiments, the present disclosure is directed to a method of treating a medical condition in a subject comprising the steps of providing a therapeutic compound comprising a chimeric protein including VSV-G, a nucleic acid binding protein, and at least one nucleic acid, and administering to said subject a pharmaceutically active amount of said therapeutic compound. In some embodiments, the present disclosure is directed to a therapeutic compound comprising a chimeric protein as described herein.

## BRIEF DESCRIPTION OF THE DRAWINGS

**[0021]** The subject matter that is regarded as the invention is particularly pointed out and distinctly claimed in the claims at the conclusion of the specification. The foregoing and other objects, features, and advantages of the invention will be apparent from the following detailed description taken in conjunction with the accompanying drawings.

**[0022]** FIG. **1** portrays chimeric VSV-G H2A protein fractions purified by SDS-PAGE analysis.

**[0023]** FIG. **2** portrays western blot analysis of the proteins in the purified fractions from SDS-PAGE analysis as seen in FIG. **1**.

**[0024]** FIG. **3** portrays expression of GFP:HEK 293 cells transfected with eGFPN1 plasmid.

**[0025]** FIG. **4**A portrays GFP-including plasmid eGFPN1 transfected in HEK293 cells using purified VSV-G-H2A protein.

**[0026]** FIG. **4**B portrays GFP-including plasmid eGFPN1 transfected in NIH 3T3 cells using purified VSV-G-H2A protein.

**[0027]** FIG. **5** portrays a method of treating a medical condition using a chimeric protein such as that isolated in FIG. **1**.

## DETAILED DESCRIPTION

**[0028]** In some embodiments, the present disclosure is directed to a number of chimeric VSV-G (or VSV-G variants) proteins comprising VSV-G and at least one nucleic acid binding protein. In some embodiments, these proteins are used as transfer vehicles to enhance delivery of nucleic acids like plasmid DNA, single and double stranded DNA and RNA, and antisense oligonucleotides into human and animal cells.

**[0029]** VSV-G cloned in expression plasmids, when transfected in cells, form sedimetable vesicles in the absence of any viral components. The chimeric proteins described here efficiently complex with nucleic acids in cell free systems and can be used as an effective means for delivering AOs and genes of interest in human and animal cells. This approach mitigates a number of risks and issues that are associated with gene therapy and exon skipping, i.e. there is no risk of toxicity related to viral production or risk of viral genome incorporation and possible mutations arising as a result. Since the VSV-G proteins enter into cells via the LDL receptors which are almost ubiquitously expressed, the transduction efficiency of the chimeric VSV-G-nucleic acid transfer vehicle is higher than that achieved by exon-skipping. The chimeric VSV-G-nucleic acid transfer vehicle consistent with some embodiments of the present disclosure can also replace the current mechanism of gene therapy. As this proposed chimeric VSV-G-nucleic acid transfer vehicle does not rely on virus production, it has fewer side effects and can be administered subcutaneously. This system can be used for gene replacement and can have wide application to cure many disorders arising from genetic mutations.

**[0030]** In some embodiments, wild-type VSV-G is used in the chimeric protein. In some embodiments, VSV-G variants are used in the chimeric protein. In some embodiments, the VSV-G variants include the thermostable and serum resistant mutants of VSV-G, e.g. S162T, T230N, T368A, or combined mutants T230N+T368A or K66T +S162T+ T230N+T368A. In some embodiments, variant VSV-G has at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with wild-type VSV-G. As used in the following embodiments, the term "VSV-G" refers to both wild-type VSV-G and VSV-G variants.

**[0031]** In some embodiments, the chimeric protein of the present disclosure has at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with the combined sequence of VSV-G +nucleic acid binding protein, with the nucleic acid binding protein tagged with VSV-G at the C-terminus. In some embodiments, chimeric protein has at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with the combined sequence of VSV-G+ nucleic acid binding protein, with the nucleic acid binding protein tagged with VSV-G at the N-terminus. In some embodiments, the chimeric protein comprises a nucleotide sequence that has at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with at least one of SEQ. ID NO.: 1, SEQ. ID NO.: 3, SEQ. ID NO.: 5, SEQ. ID NO.: 7, SEQ. ID NO.: 9, SEQ. ID NO.: 11, SEQ. ID NO.: 13, SEQ. ID NO.: 15, SEQ. ID NO.: 17, SEQ. ID NO.: 19, SEQ. ID NO.: 21, SEQ. ID NO.: 23, or SEQ. ID NO.: 25. In some embodiments, the chimeric protein comprises an amino acid sequence that has at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with at least one of SEQ. ID NO.: 2, SEQ. ID NO.: 4, SEQ. ID NO.: 6, SEQ. ID NO.: 8, SEQ. ID NO.: 10, SEQ. ID NO.: 12, SEQ. ID NO.: 14, SEQ. ID NO.: 16, SEQ. ID NO.: 18, SEQ. ID NO.: 20, SEQ. ID NO.: 22, SEQ. ID NO.: 24, or SEQ. ID NO.: 26. In some embodiments, any suitable mutations, substitutions, additions, and deletions may be made to the chimeric protein so long as the pharmacological activity of the resulting variant chimeric protein is retained.

**[0032]** In some embodiments, the nucleic acid binding protein is selected from the group consisting of H2A histone, H2B histone, H3 histone, H4 histone, SSBP-1, RNase III, and combinations thereof.

**[0033]** SEQ. ID NO: 1 is a nucleotide sequence of an H2A histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0034]** SEQ. ID NO: 2 is an amino acid sequence of an H2A histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0035]** SEQ. ID NO: 3 is a nucleotide sequence of an H2B histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0036]** SEQ. ID NO: 4 is an amino acid sequence of an H2B histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0037]** SEQ. ID NO: 5 is a nucleotide sequence of an H3 histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0038]** SEQ. ID NO: 6 is an amino acid sequence of an H3 histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0039]** SEQ. ID NO: 7 is a nucleotide sequence of an H4 histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0040]** SEQ. ID NO: 8 is an amino acid sequence of an H4 histone-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0041]** SEQ. ID NO: 9 is a nucleotide sequence of an SSBP-1-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0042]** SEQ. ID NO: 10 is an amino acid sequence of an SSBP-1-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0043]** SEQ. ID NO: 11 is a nucleotide sequence of an RNase III-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0044]** SEQ. ID NO: 12 is an amino acid sequence of an RNase III-VSV-G chimeric protein, with VSV-G at the C-terminus, consistent with some embodiments of the present disclosure.

**[0045]** SEQ. ID NO: 13 is a nucleotide sequence of a partial RNase III-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0046]** SEQ. ID NO: 14 is an amino acid sequence of a partial RNase III-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0047]** SEQ. ID NO: 15 is a nucleotide sequence of an H2A histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0048]** SEQ. ID NO: 16 is an amino acid sequence of an H2A histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0049]** SEQ. ID NO: 17 is a nucleotide sequence of an H2B histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0050]** SEQ. ID NO: 18 is an amino acid sequence of an H2B histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0051]** SEQ. ID NO: 19 is a nucleotide sequence of an H3 histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0052]** SEQ. ID NO: 20 is an amino acid sequence of an H3 histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0053]** SEQ. ID NO: 21 is a nucleotide sequence of an H4 histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0054]** SEQ. ID NO: 22 is an amino acid sequence of an H4 histone-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0055]** SEQ. ID NO: 23 is a nucleotide sequence of an SSBP-1-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0056]** SEQ. ID NO: 24 is an amino acid sequence of an SSBP-1-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0057]** SEQ. ID NO: 25 is a nucleotide sequence of an RNase III-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0058]** SEQ. ID NO: 26 is an amino acid sequence of an RNase III-VSV-G chimeric protein, with VSV-G at the N-terminus, consistent with some embodiments of the present disclosure.

**[0059]** In some embodiments, the present disclosure is directed to a therapeutic compound comprising a chimeric protein consistent with those described in the above-identified embodiments. In some embodiments, as shown in FIG. **5**, the present disclosure is directed to a method of treating a medical condition within a subject. In some embodiments, the method of treating a subject comprises the steps of providing **500** a therapeutic compound comprising a chimeric protein including VSV-G, a nucleic acid binding protein, and at least one nucleic acid, and administering **510** to the subject a pharmaceutically active amount of the therapeutic compound. In some embodiments, at least one nucleic acid is a therapeutic gene.

## EXAMPLE

**[0060]** The following example utilizes a VSV-G-H2A chimeric protein constructed from a human histone H2A protein tagged with VSV-G at the N-terminus. The VSV-G-H2A chimeric gene was synthesized using the propriety technology from Integrated DNA Technologies, Skokie, IL. The VSV-G-H2A gene was cloned in the mammalian expression vector pTT5 at EcoRI and NotI restriction enzyme sites. The plasmid was prepared and sequenced for confirmation.

**[0061]** HEK293T cells were passed to ~70% confluency a day prior to transfection (3× T75 flasks, ~$7.5\times10^6$ cells/flask). The following day, the cells in T75 flasks were transfected using Lipofectamine® 2000 (Life Technologies Corp., Carlsbad, Calif.) (per T75 flask: 3:1 ratio; 20 ug DNA; and 60 μL Lipofectamine® 2000). Flasks were incubated at 37° C. and 5% $CO_2$ overnight. 24 hours after transfection, the conditioned media was removed and replaced with fresh media (14 mL/flask). Cells were further incubated overnight. Conditioned media was harvested and replaced with fresh media (14 mL/flask) and again incubated overnight. Harvested media was then filtered using 0.45 μm filter and stored at −80° C. The following day, conditioned media was harvested again and filtered using 0.45 μm filter. Conditioned media was pooled with media from the previous day (~84 mL).

**[0062]** Conditioned media was centrifuged using the Optima® Ultra Centrifuge (with swinging bucket rotor SW32Ti) (Beckman Coulter, Inc., Brea, Calif.) at 25,000 rpm for 2 h at 4° C. (3 centrifuge tubes, ~28 mL/tube). Supernatant was removed and pellets were resuspended in 5 mL PBS per tube. 5 mL of 20% sucrose/PBS cushion plus 5 mL resuspended pellet was added to a new centrifuge tube. PBS was overlaid to fill the centrifuge tube. Samples were centrifuged at 25,000 rpm for 6 hours at 4° C. Supernatant was removed and each pellet was resuspended in 100 μL PBS (300 μL total volume). An additional 100 μL of PBS was added to each centrifuge tube to resuspend any remaining VSV-G-H2A protein (300 μL total volume). Protein concentration was measured by A660 Assay.

**[0063]** The chimeric VSV-G H2A protein fractions thus purified were run on polyacrylamide gels before transfer to nitrocellulose membranes. Proteins were run in 4-15% Bio-Rad TGX™ gel (BioRad Laboratories Inc., Hercules, Calif.) with BioRad Precision Plus Protein™ markers, at 300 V for 21 minutes and then stained with SYPRO®-Orange stain (Molecular Probes, Inc., Eugene, Oreg.), the results of which can be seen at FIG. **1**. The contents for each lane found in FIG. **1** are as follows: Lane 1: Negative Control—untransfected cells only; Lane 2: molecular weight marker; Lane 3: M20336-01 (20 μL load); Lane 4: M20336-01 (2 μL load); Lane 5: molecular weight marker; and Lane 6: M20336-02 (20 μL load). The HEK293 untransfected lane did not stain for any protein while rest of the lanes containing the fractions of purified VSV-G-H2A chimeric protein stained for proteins confirming the presence of purified proteins in the fractions.

**[0064]** After confirming the presence of the proteins in the purified fractions, proteins were run using the same conditions as described above and transferred to nitrocellulose membrane. The chimeric VSV-G-H2A protein was detected by probing with anti-VSV-G-primary antibody and anti-rabbit HRP secondary antibody. Proteins were transferred to nitrocellulose membrane using Bio-Rad Trans-Blot® Turbo™. Signal was detected using the SNAP id® system (Merck KGAA, Darmstadt, Del.) and SuperSignal® West Pico chemiluminescent substrate (Pierce Biotechnology, Inc., Rockford, Ill.), the results of which can be seen in the western blot shown in FIG. **2**. The contents for each lane found in FIG. **2** are as follows: Lane 1: molecular weight marker; Lane 2: M20336-01 (20 μL load); Lane 3: molecular weight marker; Lane 4: M20336-01 (2 μL load); Lane 5: molecular weight marker; Lane 6: M20336-02 (20 μL load); Lane 7: molecular weight marker; Lane 8: Negative Control—untransfected cells only. A band was detected specific to the size of VSV-G H2A chimeric protein at 75 kD in lanes 2 and 6 containing 204 load of protein. No bands were detected in lanes 4 and 8 with 2 μL load of purified protein fraction and non-transfected HEK293 protein fraction. Therefore, the presence of VSV-G-H2A chimeric protein in the purified fraction was confirmed.

**[0065]** In order to evaluate the capacity of the purified VSV-G-H2A chimeric protein to act as nucleic acid transfer vehicle, HEK293 cells and NIH 3T3 cells were transfected with green fluorescent protein (GFP) expressing plasmid eGFPN1 utilizing the VSV-G-H2A chimeric protein. Firstly, the eGFPN1 plasmid was transfected in HEK293 cells using ViaFect™ transfection reagent (Promega Corp., Madison, Wis.) to confirm that GFP was expressed properly. Successful GFP expression is shown in FIG. **3**.

**[0066]** To determine whether similar expression of GFP could be seen when VSV-G-H2A chimeric protein was used as a transfer vehicle, 2 μg of eGFPN1 plasmid was mixed with 3 μg of VSV-G H2A purified chimeric protein and overlaid in each of HEK293 and NIH 3T3 cells seeded on coverslips in 6-well plates. Cells were incubated for 48 hours before analysis. To detect whether GFP has expressed, the existing medium in the cells was aspirated, washed in Dulbecco's phosphate buffered saline (DPBS), and then fixed in 4% paraformaldehyde solution. Cells were washed again with DPBS a couple of times, stained with 4',6-diamidino-2-phenylindole (DAPI), and then mounted in appropriate mounting medium and viewed under a fluorescence microscope. The results of this procedure can be seen in FIGS. **4**A and **4**B, wherein DAPI staining depicts the nucleus and the green fluorescence depicts the GFP. Interestingly, the HEK293 and NIH 3T3 cells in which VSV-G-H2A purified chimeric protein was used as a transfer vehicle to transfect eGFPN1 plasmid expressed GFP. Therefore, it was concluded that VSV-G-H2A chimeric protein, as well as the other chimeric proteins disclosed in the present disclosure and functional equivalents thereof, are candidates for use as nucleic acid transfer vehicles as proposed by the present disclosure.

**[0067]** One or more embodiments of the present invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

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Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile Ile
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Asn Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn
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Ser His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys
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Trp Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr
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His Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser
225                 230                 235                 240

Ile Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro
                245                 250                 255

Gln Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val
            260                 265                 270

Gln Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp
        275                 280                 285

Val Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro
    290                 295                 300

Thr Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly
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Asn Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr
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Cys Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met
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Ala Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu
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Gly Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu
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Ile Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr
            420                 425                 430

Trp Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser
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Tyr Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile
    450                 455                 460

Asn Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile
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Ala Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr
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Thr Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu
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    530                 535                 540

Ser Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser
545                 550                 555                 560

Gln Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser
                565                 570                 575

Lys Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser
            580                 585                 590

Ser Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe
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Leu Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr
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Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Val Gln
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Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val
100 105 110

Ser Glu Gly Thr Lys Ala Val Thr Lys Tyr Thr Ser Ser Lys Lys Cys
115 120 125

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Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn Val Pro Ser
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Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile Glu Gln Thr
225                 230                 235                 240

Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln Ser Cys Gly
                245                 250                 255

Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln Val Thr Pro
            260                 265                 270

His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val Asp Ser Gln
        275                 280                 285

Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr Val His Asn
    290                 295                 300

Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu Cys Asp Ser
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Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp Gly Glu Leu
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            340                 345                 350

Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys Lys His Trp
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385                 390                 395                 400

Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile Gln Asp Val
                405                 410                 415

Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp Ser Lys Ile
            420                 425                 430

Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr Leu Ala Pro
        435                 440                 445

Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn Gly Thr Leu
    450                 455                 460

Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala Ala Pro Ile
465                 470                 475                 480

Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr Glu Arg Glu
                485                 490                 495

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Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu Tyr Met Ile
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Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser Lys Ala Gln
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Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys Asn Pro Ile
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35 40 45

Arg Glu Ile Arg Arg Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg Lys
50 55 60

Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Asn Thr
65 70 75 80

Asp Leu Arg Phe Gln Ser Ala Ala Val Gly Ala Leu Gln Glu Ala Ser
85 90 95

Glu Ala Tyr Leu Val Gly Leu Leu Glu Asp Thr Asn Leu Cys Ala Ile
100 105 110

His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Ile Gln Leu Ala Arg
115 120 125

Arg Ile Arg Gly Glu Arg Ala Lys Cys Leu Leu Tyr Leu Ala Phe Leu
130 135 140

Phe Ile Gly Val Asn Cys Lys Phe Thr Ile Val Phe Pro His Asn Gln
145 150 155 160

Lys Gly Asn Trp Lys Asn Val Pro Ser Asn Tyr His Tyr Cys Pro Ser
165 170 175

Ser Ser Asp Leu Asn Trp His Asn Asp Leu Ile Gly Thr Ala Leu Gln
180 185 190

Val Lys Met Pro Lys Ser His Lys Ala Ile Gln Ala Asp Gly Trp Met
195 200 205

Cys His Ala Ser Lys Trp Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly
210 215 220

Pro Lys Tyr Ile Thr His Ser Ile Arg Ser Phe Thr Pro Ser Val Glu
225 230 235 240

Gln Cys Lys Glu Ser Ile Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn
245 250 255

Pro Gly Phe Pro Pro Gln Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala
260 265 270

Glu Ala Ala Ile Val Gln Val Thr Pro His His Val Leu Val Asp Glu

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        275                 280                 285

Tyr Thr Gly Glu Trp Val Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser
    290                 295                 300

Asn Asp Ile Cys Pro Thr Val His Asn Ser Thr Thr Trp His Ser Asp
305                 310                 315                 320

Tyr Lys Val Lys Gly Leu Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile
                325                 330                 335

Thr Phe Phe Ser Glu Asp Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly
            340                 345                 350

Thr Gly Phe Arg Ser Asn Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala
        355                 360                 365

Cys Lys Met Gln Tyr Cys Lys His Trp Gly Val Arg Leu Pro Ser Gly
    370                 375                 380

Val Trp Phe Glu Met Ala Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe
385                 390                 395                 400

Pro Glu Cys Pro Glu Gly Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser
                405                 410                 415

Val Asp Val Ser Leu Ile Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser
            420                 425                 430

Leu Cys Gln Glu Thr Trp Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser
        435                 440                 445

Pro Val Asp Leu Ser Tyr Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro
    450                 455                 460

Val Phe Thr Ile Ile Asn Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr
465                 470                 475                 480

Ile Arg Val Asp Ile Ala Ala Pro Ile Leu Ser Arg Met Val Gly Met
                485                 490                 495

Ile Ser Gly Thr Thr Thr Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro
            500                 505                 510

Tyr Glu Asp Val Glu Ile Gly Pro Asn Gly Val Leu Arg Thr Ser Leu
        515                 520                 525

Gly Tyr Lys Phe Pro Leu Tyr Met Ile Gly His Gly Met Leu Asp Ser
    530                 535                 540

Asp Leu His Leu Ser Ser Lys Ala Gln Val Phe Glu His Pro His Ile
545                 550                 555                 560

Gln Asp Ala Ala Ser Gln Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly
                565                 570                 575

Asp Thr Gly Leu Ser Lys Asn Pro Ile Glu Phe Val Glu Gly Trp Phe
            580                 585                 590

Ser Ser Trp Lys Ser Ser Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu
        595                 600                 605

Ile Ile Gly Leu Phe Leu Val Leu Arg Val Gly Ile Tyr Leu Cys Ile
    610                 615                 620

Lys Leu Lys His Thr Lys Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met
625                 630                 635                 640

Asn Arg Leu Gly Lys
                645


<210> SEQ ID NO 7
<211> LENGTH: 1842
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: H4 VSV-G Chimeric Protein Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1842)

<400> SEQUENCE: 7

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aaagtgctgc gggataacat ccaaggcatc accaaaccgg ccattcggcg ccttgctagg 120

cgtggtgggg ttaagcgaat ttccggtttg atttatgagg agactcgtgg cgttctcaag 180

gtgtttctgg agaacgtgat ccgggacgcc gtgacctaca cggagcacgc caagcgcaag 240

actgtcactg ccatggatgt ggtttacgcg ctcaagcgtc aaggacgcac tctgtacggc 300

ttcggcggta agtgcctttt gtacttagct tttttattca tcggggtgaa ttgcaagttc 360

accatagttt ttccacacaa ccaaaaagga aactggaaaa atgttccttc caattaccat 420

tattgcccgt caagctcaga tttaaattgg cataatgact taataggcac agccttacaa 480

gtcaaaatgc ccaagagtca caaggctatt caagcagacg gttggatgtg tcatgcttcc 540

aaatgggtca ctacttgtga tttccgctgg tacggaccga agtatataac acattccatc 600

cgatccttca ctccatctgt agaacaatgc aaggaaagca ttgaacaaac gaaacaagga 660

acttggctga atccaggctt ccctcctcaa agttgtggat atgcaactgt gacggatgct 720

gaagcagcga ttgtccaggt gactcctcac catgtgcttg ttgatgaata cacaggagaa 780

tgggttgatt cacagttcat caacggaaaa tgcagcaatg acatatgccc cactgtccat 840

aactccacaa cctggcattc cgactataag gtcaaagggc tatgtgattc taacctcatt 900

tccacggaca tcaccttctt ctcagaggac ggagagctat catccctagg aaaggagggc 960

acagggttca gaagtaacta ctttgcttat gaaactggag acaaggcctg caaaatgcag 1020

tactgcaagc attggggagt cagactccca tcaggtgtct ggttcgagat ggctgataag 1080

gatctctttg ctgcagccag attccctgaa tgcccagaag ggtcaagtat ctctgctcca 1140

tctcagacct cagtggatgt aagtctcatt caggacgttg agaggatctt ggattattcc 1200

ctctgccaag aaacctggag caaaatcaga gcgggtcttc ccatctctcc agtggatctc 1260

agctatcttg ctcctaaaaa cccaggaacc ggtcctgtct ttaccataat caatggtacc 1320

ctaaaatact ttgagaccag atacatcaga gtcgatattg ctgctccaat cctctcaaga 1380

atggtcggaa tgatcagtgg aactaccaca gaaagggaac tgtgggatga ctgggctcca 1440

tatgaagacg tggaaattgg acccaatgga gttctgagga ccagtttagg atataagttt 1500

cctttatata tgattggaca tggtatgttg gactccgatc ttcatcttag ctcaaaggct 1560

caggtgtttg aacatcctca cattcaagac gctgcttcgc agcttcctga tgatgagact 1620

ttatttttttg gtgatactgg gctatccaaa aatccaatcg agtttgtaga aggttggttc 1680

agtagttgga agagctctat tgcctctttt ttctttatca tagggttaat cattggacta 1740

ttcttggttc tccgagttgg tatttatctt tgcattaaat taaagcacac caagaaaaga 1800

cagatttata cagacataga gatgaaccga cttggaaagt aa 1842

<210> SEQ ID NO 8
<211> LENGTH: 613
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: H4 VSV-G Chimeric Protein Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(613)

<400> SEQUENCE: 8

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Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala
1               5                   10                  15

Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
            20                  25                  30

Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
        35                  40                  45

Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Val Phe Leu Glu
    50                  55                  60

Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Lys Arg Lys
65                  70                  75                  80

Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg
                85                  90                  95

Thr Leu Tyr Gly Phe Gly Gly Lys Cys Leu Leu Tyr Leu Ala Phe Leu
            100                 105                 110

Phe Ile Gly Val Asn Cys Lys Phe Thr Ile Val Phe Pro His Asn Gln
        115                 120                 125

Lys Gly Asn Trp Lys Asn Val Pro Ser Asn Tyr His Tyr Cys Pro Ser
    130                 135                 140

Ser Ser Asp Leu Asn Trp His Asn Asp Leu Ile Gly Thr Ala Leu Gln
145                 150                 155                 160

Val Lys Met Pro Lys Ser His Lys Ala Ile Gln Ala Asp Gly Trp Met
                165                 170                 175

Cys His Ala Ser Lys Trp Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly
            180                 185                 190

Pro Lys Tyr Ile Thr His Ser Ile Arg Ser Phe Thr Pro Ser Val Glu
        195                 200                 205

Gln Cys Lys Glu Ser Ile Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn
    210                 215                 220

Pro Gly Phe Pro Pro Gln Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala
225                 230                 235                 240

Glu Ala Ala Ile Val Gln Val Thr Pro His His Val Leu Val Asp Glu
                245                 250                 255

Tyr Thr Gly Glu Trp Val Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser
            260                 265                 270

Asn Asp Ile Cys Pro Thr Val His Asn Ser Thr Thr Trp His Ser Asp
        275                 280                 285

Tyr Lys Val Lys Gly Leu Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile
    290                 295                 300

Thr Phe Phe Ser Glu Asp Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly
305                 310                 315                 320

Thr Gly Phe Arg Ser Asn Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala
                325                 330                 335

Cys Lys Met Gln Tyr Cys Lys His Trp Gly Val Arg Leu Pro Ser Gly
            340                 345                 350

Val Trp Phe Glu Met Ala Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe
        355                 360                 365
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Pro Glu Cys Pro Glu Gly Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser
    370                 375                 380

Val Asp Val Ser Leu Ile Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser
385                 390                 395                 400

Leu Cys Gln Glu Thr Trp Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser
                405                 410                 415

Pro Val Asp Leu Ser Tyr Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro
            420                 425                 430

Val Phe Thr Ile Ile Asn Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr
        435                 440                 445

Ile Arg Val Asp Ile Ala Ala Pro Ile Leu Ser Arg Met Val Gly Met
    450                 455                 460

Ile Ser Gly Thr Thr Thr Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro
465                 470                 475                 480

Tyr Glu Asp Val Glu Ile Gly Pro Asn Gly Val Leu Arg Thr Ser Leu
                485                 490                 495

Gly Tyr Lys Phe Pro Leu Tyr Met Ile Gly His Gly Met Leu Asp Ser
            500                 505                 510

Asp Leu His Leu Ser Ser Lys Ala Gln Val Phe Glu His Pro His Ile
        515                 520                 525

Gln Asp Ala Ala Ser Gln Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly
    530                 535                 540

Asp Thr Gly Leu Ser Lys Asn Pro Ile Glu Phe Val Glu Gly Trp Phe
545                 550                 555                 560

Ser Ser Trp Lys Ser Ser Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu
                565                 570                 575

Ile Ile Gly Leu Phe Leu Val Leu Arg Val Gly Ile Tyr Leu Cys Ile
            580                 585                 590

Lys Leu Lys His Thr Lys Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met
        595                 600                 605

Asn Arg Leu Gly Lys
    610
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<210> SEQ ID NO 9
<211> LENGTH: 1977
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SSBP-1 VSV-G Chimeric Protein Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1977)

<400> SEQUENCE: 9

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atgtttcgaa gacctgtatt acaggtactt cgtcagtttg taagacatga gtccgaaaca     60

actaccagtt tggttcttga aagatccctg aatcgtgtgc acttacttgg gcgagtgggt    120

caggaccctg tcttgagaca ggtggaagga aaaaatccag tcacaatatt ttctctagca    180

actaatgaga tgtggcgatc aggggatagt gaagtttacc aactgggtga tgtcagtcaa    240

aagacaacat ggcacagaat atcagtattc cggccaggcc tcagagacgt ggcatatcaa    300

tatgtgaaaa aggggtctcg aatttatttg gaagggaaaa tagactatgg tgaatacatg    360

gataaaaata atgtgaggcg acaagcaaca acaatcatag ctgataatat tatatttctg    420
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agtgaccaga cgaaagagaa ggagaagtgc cttttgtact tagcttttt attcatcggg 480

gtgaattgca agttcaccat agtttttcca cacaaccaaa aaggaaactg gaaaaatgtt 540

ccttccaatt accattattg cccgtcaagc tcagatttaa attggcataa tgacttaata 600

ggcacagcct tacaagtcaa aatgcccaag agtcacaagg ctattcaagc agacggttgg 660

atgtgtcatg cttccaaatg ggtcactact tgtgatttcc gctggtacgg accgaagtat 720

ataacacatt ccatccgatc cttcactcca tctgtagaac aatgcaagga aagcattgaa 780

caaacgaaac aaggaacttg gctgaatcca ggcttccctc ctcaaagttg tggatatgca 840

actgtgacgg atgctgaagc agcgattgtc caggtgactc ctcaccatgt gcttgttgat 900

gaatacacag gagaatgggt tgattcacag ttcatcaacg gaaaatgcag caatgacata 960

tgccccactg tccataactc cacaacctgg cattccgact ataaggtcaa agggctatgt 1020

gattctaacc tcatttccac ggacatcacc ttcttctcag aggacggaga gctatcatcc 1080

ctaggaaagg agggcacagg gttcagaagt aactactttg cttatgaaac tggagacaag 1140

gcctgcaaaa tgcagtactg caagcattgg ggagtcagac tcccatcagg tgtctggttc 1200

gagatggctg ataaggatct ctttgctgca gccagattcc ctgaatgccc agaagggtca 1260

agtatctctg ctccatctca gacctcagtg gatgtaagtc tcattcagga cgttgagagg 1320

atcttggatt attccctctg ccaagaaacc tggagcaaaa tcagagcggg tcttcccatc 1380

tctccagtgg atctcagcta tcttgctcct aaaaacccag gaaccggtcc tgtctttacc 1440

ataatcaatg gtaccctaaa atactttgag accagataca tcagagtcga tattgctgct 1500

ccaatcctct caagaatggt cggaatgatc agtggaacta ccacagaaag ggaactgtgg 1560

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cttagctcaa aggctcaggt gtttgaacat cctcacattc aagacgctgc ttcgcagctt 1740

cctgatgatg agactttatt ttttggtgat actgggctat ccaaaaatcc aatcgagttt 1800

gtagaaggtt ggttcagtag ttggaagagc tctattgcct ctttttttctt tatcataggg 1860

ttaatcattg gactattctt ggttctccga gttggtattt atctttgcat taaattaaag 1920

cacaccaaga aaagacagat ttatacagac atagagatga accgacttgg aaagtaa 1977

<210> SEQ ID NO 10
<211> LENGTH: 658
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SSBP-1 VSV-G Chimeric Protein Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(658)

<400> SEQUENCE: 10

Met Phe Arg Arg Pro Val Leu Gln Val Leu Arg Gln Phe Val Arg His
1 5 10 15

Glu Ser Glu Thr Thr Thr Ser Leu Val Leu Glu Arg Ser Leu Asn Arg
20 25 30

Val His Leu Leu Gly Arg Val Gly Gln Asp Pro Val Leu Arg Gln Val
35 40 45

Glu Gly Lys Asn Pro Val Thr Ile Phe Ser Leu Ala Thr Asn Glu Met

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    50                  55                  60

Trp Arg Ser Gly Asp Ser Glu Val Tyr Gln Leu Gly Asp Val Ser Gln
65                  70                  75                  80

Lys Thr Thr Trp His Arg Ile Ser Val Phe Arg Pro Gly Leu Arg Asp
                85                  90                  95

Val Ala Tyr Gln Tyr Val Lys Lys Gly Ser Arg Ile Tyr Leu Glu Gly
            100                 105                 110

Lys Ile Asp Tyr Gly Glu Tyr Met Asp Lys Asn Asn Val Arg Arg Gln
        115                 120                 125

Ala Thr Thr Ile Ile Ala Asp Asn Ile Ile Phe Leu Ser Asp Gln Thr
    130                 135                 140

Lys Glu Lys Glu Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly
145                 150                 155                 160

Val Asn Cys Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn
                165                 170                 175

Trp Lys Asn Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp
            180                 185                 190

Leu Asn Trp His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met
        195                 200                 205

Pro Lys Ser His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala
    210                 215                 220

Ser Lys Trp Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr
225                 230                 235                 240

Ile Thr His Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys
                245                 250                 255

Glu Ser Ile Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe
            260                 265                 270

Pro Pro Gln Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala
        275                 280                 285

Ile Val Gln Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly
    290                 295                 300

Glu Trp Val Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile
305                 310                 315                 320

Cys Pro Thr Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val
                325                 330                 335

Lys Gly Leu Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe
            340                 345                 350

Ser Glu Asp Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe
        355                 360                 365

Arg Ser Asn Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met
    370                 375                 380

Gln Tyr Cys Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe
385                 390                 395                 400

Glu Met Ala Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys
                405                 410                 415

Pro Glu Gly Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val
            420                 425                 430

Ser Leu Ile Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln
        435                 440                 445

Glu Thr Trp Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp
    450                 455                 460
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Leu Ser Tyr Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr
465                 470                 475                 480

Ile Ile Asn Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val
                485                 490                 495

Asp Ile Ala Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly
            500                 505                 510

Thr Thr Thr Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp
        515                 520                 525

Val Glu Ile Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys
    530                 535                 540

Phe Pro Leu Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His
545                 550                 555                 560

Leu Ser Ser Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala
                565                 570                 575

Ala Ser Gln Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly
            580                 585                 590

Leu Ser Lys Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp
        595                 600                 605

Lys Ser Ser Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly
    610                 615                 620

Leu Phe Leu Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys
625                 630                 635                 640

His Thr Lys Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu
                645                 650                 655

Gly Lys
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<210> SEQ ID NO 11
<211> LENGTH: 5655
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: RNase III VSV-G Chimeric Protein with VSV-G at C-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(5655)

<400> SEQUENCE: 11

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ctgcttcacc ctcagcagcc tcctgtgcaa tatcaatatg aacctccaag tgccccttcc    180

accactttct caaactctcc agcccccaat tttctccctc cacgaccaga ctttgtaccc    240

ttcccccccac ccatgcctcc gtcagcgcaa ggccctcttc ccccctgccc aatcaggccg    300

cctttcccca accaccagat gaggcacccc ttcccagttc ctccttgttt tcctcccatg    360

ccaccaccaa tgccttgtcc taataacccc ccagtccctg gggcacctcc tggacaaggc    420

actttccccct tcatgatgcc ccctccctcc atgcctcatc ccccgccccc tccagtcatg    480

ccgcagcagg ttaattatca gtaccctccg ggctattctc accacaactt cccacctccc    540

agttttaata gtttccagaa caaccctagt tctttcctgc ccagtgctaa taacagcagt    600

agtcctcatt tcagacatct ccctccatac ccactcccaa aggctcccag tgagagaagg    660

tccccagaaa ggctgaaaca ctatgatgac cacaggcacc gagatcacag tcatgggcga    720
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ggtgagaggc atcggtccct ggatcggcgg gagcgaggcc gcagtcccga caggagaaga 780

caagacagcc ggtacagatc tgattatgac cgagggagaa caccatctcg ccaccgcagc 840

tacgaacgga gcagagagcg agaacgggag agacacaggc atcgagacaa ccgaagatca 900

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aagagagctc gttgggagga agaaaaagac cgttggagtg acaaccagag ttctggcaaa 1140

gacaagaact atacctcaat caaggaaaaa gagcccgagg agaccatgcc tgacaagaat 1200

gaggaggaag aagaagaact tcttaagcct gtgtggattc gatgcactca ttcagaaaac 1260

tactactcca gtgaccccat ggatcaggtg ggagattcta cagtggttgg aacgagtagg 1320

cttcgtgact tatatgacaa atttgaggag gagttgggga gcaggcaaga aaaggccaaa 1380

gctgctcggc ctccgtggga acctccaaag acgaagctcg atgaagattt agagagttcc 1440

agtgaatccg agtgtgagtc tgatgaggac agcacctgtt ctagcagctc agactctgaa 1500

gtttttgacg ttattgcaga aatcaaacgc aaaaaggccc accctgaccg acttcatgat 1560

gaactttggt acaacgatcc aggccagatg aatgatggac cactctgcaa atgcagcgca 1620

aaggcaagac gcacaggaat taggcacagc atttatcctg gagaagaggc catcaagccc 1680

tgtcgtccta tgaccaacaa tgctggcaga cttttccact accggatcac agtctccccg 1740

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gactggaatc ttaaaggtcc tttgtttgaa gacagccctc cctgctgccc aagatttcat 2040

ttcatgccac gttttgtaag atttcttcca gatggaggaa aggaagtgct gtccatgcac 2100

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aatatgcttc agtgggagga gctggagtgg cagaaatatg cagaagaatg caaaggcatg 2220

attgttacca accctgggac gaaaccaagc tctgtccgta tcgatcaact ggatcgtgaa 2280

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cgccacctcc tagcaaatag tcccaaagtc aaacaaactg acaaacagaa gctggcacag 2460

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gagctaagta gccaaggatt ctggaaaact ggcatccgtt ctgatgtctg tcagcatgca 2580

atgatgctac ctgttctgac ccatcatatc cgctaccacc aatgcctaat gcatttggac 2640

aagttgatag gatatacttt ccaagatcgt tgtctgttgc agctggccat gactcatcca 2700

agtcatcatt taaattttgg aatgaatcct gatcatgcca ggaattcatt atctaactgt 2760

ggaattcggc agcccaaata cggagacaga aaagttcatc acatgcacat gcggaagaaa 2820

gggattaaca ccttgataaa tatcatgtca cgccttggcc aagatgaccc aactccctcg 2880

aggattaacc acaatgaacg gttggaattc ctgggtgatg ctgttgttga atttctgacc 2940

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aagcagttat ttggacgctt gctctttaat gatccggacc tgcgcgaagt ctggctcaat 3240

tatcctctcc acccactcca actacaagag ccaaatactg atcgacaact tattgaaact 3300

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aagcggttca tcgaacggaa gtacagacaa gagttaaaag aaatgaggtg ggaaagagag 4080

catcaagaga gagagccaga tgagactgaa gacatcaaga aaaagtgcct tttgtactta 4140

gctttttttat tcatcggggt gaattgcaag ttcaccatag tttttccaca caaccaaaaa 4200

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<210> SEQ ID NO 12
<211> LENGTH: 1884
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: RNase III VSV-G Chimeric Protein with VSV-G at C-terminal Amino Acid Sequence

<400> SEQUENCE: 12

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Gly Cys Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro
20 25 30

Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro
35 40 45

Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
50 55 60

Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro
65 70 75 80

Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
85 90 95

Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro
100 105 110

Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
115 120 125

Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
130 135 140

Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Pro Val Met
145 150 155 160

Pro Gln Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn
165 170 175

Phe Pro Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe
180 185 190

Leu Pro Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro
195 200 205

Pro Tyr Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg
210 215 220

Leu Lys His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg
225 230 235 240

Gly Glu Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro
245 250 255

Asp Arg Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly
260 265 270

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Arg Thr Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu
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Arg Glu Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu
    290                 295                 300

Arg Ser Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu
305                 310                 315                 320

Ser Val Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu
                325                 330                 335

Ile Ile Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn
            340                 345                 350

His Arg Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu
        355                 360                 365

Lys Asp Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr
    370                 375                 380

Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
385                 390                 395                 400

Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
                405                 410                 415

His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
            420                 425                 430

Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
        435                 440                 445

Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
    450                 455                 460

Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
465                 470                 475                 480

Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
                485                 490                 495

Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
            500                 505                 510

Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
        515                 520                 525

Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
    530                 535                 540

Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
545                 550                 555                 560

Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
                565                 570                 575

Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile
            580                 585                 590

Glu Tyr Asp Asp His Glu Tyr Ile Phe Glu Gly Phe Ser Met Phe Ala
        595                 600                 605

His Ala Pro Leu Thr Asn Ile Pro Leu Cys Lys Val Ile Arg Phe Asn
    610                 615                 620

Ile Asp Tyr Thr Ile His Phe Ile Glu Glu Met Met Pro Glu Asn Phe
625                 630                 635                 640

Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile
                645                 650                 655

Leu Glu Leu Tyr Asp Trp Asn Leu Lys Gly Pro Leu Phe Glu Asp Ser
            660                 665                 670
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Pro Pro Cys Cys Pro Arg Phe His Phe Met Pro Arg Phe Val Arg Phe
        675                 680                 685

Leu Pro Asp Gly Gly Lys Glu Val Leu Ser Met His Gln Ile Leu Leu
    690                 695                 700

Tyr Leu Leu Arg Cys Ser Lys Ala Leu Val Pro Glu Glu Glu Ile Ala
705                 710                 715                 720

Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu
                725                 730                 735

Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
            740                 745                 750

Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr
        755                 760                 765

Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr
    770                 775                 780

Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu
785                 790                 795                 800

Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln
                805                 810                 815

Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn
            820                 825                 830

Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp
        835                 840                 845

Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
    850                 855                 860

Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
865                 870                 875                 880

Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
                885                 890                 895

Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His
            900                 905                 910

Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly
        915                 920                 925

Asp Arg Lys Val His His Met His Met Arg Lys Lys Gly Ile Asn Thr
    930                 935                 940

Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser
945                 950                 955                 960

Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val
                965                 970                 975

Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
            980                 985                 990

Glu Gly Gly Leu Ala Thr Tyr Arg  Thr Ala Ile Val Gln  Asn Gln His
        995                 1000                1005

Leu Ala  Met Leu Ala Lys Lys  Leu Glu Leu Asp Pro  Phe Met Leu
    1010                1015                1020

Tyr Ala  His Gly Pro Asp Leu  Cys Arg Glu Ser Asp  Leu Arg His
    1025                1030                1035

Ala Met  Ala Asn Cys Phe Glu  Ala Leu Ile Gly Ala  Val Tyr Leu
    1040                1045                1050

Glu Gly  Ser Leu Glu Glu Ala  Lys Gln Leu Phe Gly  Arg Leu Leu
    1055                1060                1065

Phe Asn  Asp Pro Asp Leu Arg  Glu Val Trp Leu Asn  Tyr Pro Leu
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    1070                1075                1080

His Pro  Leu Gln Leu Gln Glu  Pro Asn Thr Asp Arg  Gln Leu Ile
    1085                1090                1095

Glu Thr  Ser Pro Val Leu Gln  Lys Leu Thr Glu Phe  Glu Glu Ala
    1100                1105                1110

Ile Gly  Val Ile Phe Thr His  Val Arg Leu Leu Ala  Arg Ala Phe
    1115                1120                1125

Thr Leu  Arg Thr Val Gly Phe  Asn His Leu Thr Leu  Gly His Asn
    1130                1135                1140

Gln Arg  Met Glu Phe Leu Gly  Asp Ser Ile Met Gln  Leu Val Ala
    1145                1150                1155

Thr Glu  Tyr Leu Phe Ile His  Phe Pro Asp His His  Glu Gly His
    1160                1165                1170

Leu Thr  Leu Leu Arg Ser Ser  Leu Val Asn Asn Arg  Thr Gln Ala
    1175                1180                1185

Lys Val  Ala Glu Glu Leu Gly  Met Gln Glu Tyr Ala  Ile Thr Asn
    1190                1195                1200

Asp Lys  Thr Lys Arg Pro Val  Ala Leu Arg Thr Lys  Thr Leu Ala
    1205                1210                1215

Asp Leu  Leu Glu Ser Phe Ile  Ala Ala Leu Tyr Thr  Asp Lys Asp
    1220                1225                1230

Leu Glu  Tyr Val His Thr Phe  Met Asn Val Cys Phe  Phe Pro Arg
    1235                1240                1245

Leu Lys  Glu Phe Ile Leu Asn  Gln Asp Trp Asn Asp  Pro Lys Ser
    1250                1255                1260

Gln Leu  Gln Gln Cys Cys Leu  Thr Leu Arg Thr Glu  Gly Lys Glu
    1265                1270                1275

Pro Asp  Ile Pro Leu Tyr Lys  Thr Leu Gln Thr Val  Gly Pro Ser
    1280                1285                1290

His Ala  Arg Thr Tyr Thr Val  Ala Val Tyr Phe Lys  Gly Glu Arg
    1295                1300                1305

Ile Gly  Cys Gly Lys Gly Pro  Ser Ile Gln Gln Ala  Glu Met Gly
    1310                1315                1320

Ala Ala  Met Asp Ala Leu Glu  Lys Tyr Asn Phe Pro  Gln Met Ala
    1325                1330                1335

His Gln  Lys Arg Phe Ile Glu  Arg Lys Tyr Arg Gln  Glu Leu Lys
    1340                1345                1350

Glu Met  Arg Trp Glu Arg Glu  His Gln Glu Arg Glu  Pro Asp Glu
    1355                1360                1365

Thr Glu  Asp Ile Lys Lys Lys  Cys Leu Leu Tyr Leu  Ala Phe Leu
    1370                1375                1380

Phe Ile  Gly Val Asn Cys Lys  Phe Thr Ile Val Phe  Pro His Asn
    1385                1390                1395

Gln Lys  Gly Asn Trp Lys Asn  Val Pro Ser Asn Tyr  His Tyr Cys
    1400                1405                1410

Pro Ser  Ser Ser Asp Leu Asn  Trp His Asn Asp Leu  Ile Gly Thr
    1415                1420                1425

Ala Leu  Gln Val Lys Met Pro  Lys Ser His Lys Ala  Ile Gln Ala
    1430                1435                1440

Asp Gly  Trp Met Cys His Ala  Ser Lys Trp Val Thr  Thr Cys Asp
    1445                1450                1455
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Phe Arg  Trp Tyr Gly Pro Lys  Tyr Ile Thr His Ser  Ile Arg Ser
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Phe Thr  Pro Ser Val Glu Gln  Cys Lys Glu Ser Ile  Glu Gln Thr
    1475                 1480                 1485

Lys Gln  Gly Thr Trp Leu Asn  Pro Gly Phe Pro Pro  Gln Ser Cys
    1490                 1495                 1500

Gly Tyr  Ala Thr Val Thr Asp  Ala Glu Ala Ala Ile  Val Gln Val
    1505                 1510                 1515

Thr Pro  His His Val Leu Val  Asp Glu Tyr Thr Gly  Glu Trp Val
    1520                 1525                 1530

Asp Ser  Gln Phe Ile Asn Gly  Lys Cys Ser Asn Asp  Ile Cys Pro
    1535                 1540                 1545

Thr Val  His Asn Ser Thr Thr  Trp His Ser Asp Tyr  Lys Val Lys
    1550                 1555                 1560

Gly Leu  Cys Asp Ser Asn Leu  Ile Ser Thr Asp Ile  Thr Phe Phe
    1565                 1570                 1575

Ser Glu  Asp Gly Glu Leu Ser  Ser Leu Gly Lys Glu  Gly Thr Gly
    1580                 1585                 1590

Phe Arg  Ser Asn Tyr Phe Ala  Tyr Glu Thr Gly Asp  Lys Ala Cys
    1595                 1600                 1605

Lys Met  Gln Tyr Cys Lys His  Trp Gly Val Arg Leu  Pro Ser Gly
    1610                 1615                 1620

Val Trp  Phe Glu Met Ala Asp  Lys Asp Leu Phe Ala  Ala Ala Arg
    1625                 1630                 1635

Phe Pro  Glu Cys Pro Glu Gly  Ser Ser Ile Ser Ala  Pro Ser Gln
    1640                 1645                 1650

Thr Ser  Val Asp Val Ser Leu  Ile Gln Asp Val Glu  Arg Ile Leu
    1655                 1660                 1665

Asp Tyr  Ser Leu Cys Gln Glu  Thr Trp Ser Lys Ile  Arg Ala Gly
    1670                 1675                 1680

Leu Pro  Ile Ser Pro Val Asp  Leu Ser Tyr Leu Ala  Pro Lys Asn
    1685                 1690                 1695

Pro Gly  Thr Gly Pro Val Phe  Thr Ile Ile Asn Gly  Thr Leu Lys
    1700                 1705                 1710

Tyr Phe  Glu Thr Arg Tyr Ile  Arg Val Asp Ile Ala  Ala Pro Ile
    1715                 1720                 1725

Leu Ser  Arg Met Val Gly Met  Ile Ser Gly Thr Thr  Thr Glu Arg
    1730                 1735                 1740

Glu Leu  Trp Asp Asp Trp Ala  Pro Tyr Glu Asp Val  Glu Ile Gly
    1745                 1750                 1755

Pro Asn  Gly Val Leu Arg Thr  Ser Leu Gly Tyr Lys  Phe Pro Leu
    1760                 1765                 1770

Tyr Met  Ile Gly His Gly Met  Leu Asp Ser Asp Leu  His Leu Ser
    1775                 1780                 1785

Ser Lys  Ala Gln Val Phe Glu  His Pro His Ile Gln  Asp Ala Ala
    1790                 1795                 1800

Ser Gln  Leu Pro Asp Asp Glu  Thr Leu Phe Phe Gly  Asp Thr Gly
    1805                 1810                 1815

Leu Ser  Lys Asn Pro Ile Glu  Phe Val Glu Gly Trp  Phe Ser Ser
    1820                 1825                 1830
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Trp Lys  Ser Ser Ile Ala Ser  Phe Phe Phe Ile Ile  Gly Leu Ile
    1835                 1840                 1845

Ile Gly  Leu Phe Leu Val Leu  Arg Val Gly Ile Tyr  Leu Cys Ile
    1850                 1855                 1860

Lys Leu  Lys His Thr Lys Lys  Arg Gln Ile Tyr Thr  Asp Ile Glu
    1865                 1870                 1875

Met Asn  Arg Leu Gly Lys
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<210> SEQ ID NO 13
<211> LENGTH: 3501
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Partial RNase III VSV-G Chimeric Protein with VSV-G at N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3501)

<400> SEQUENCE: 13

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ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa    180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg    240

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ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg    360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca    420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt    480

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acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg    600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg    660

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acagtgggcc catcccatgc ccgaacctac actgtggctg tttatttcaa gggagaaaga 3300

ataggctgtg ggaaaggacc aagtattcag caagcggaaa tgggagcagc aatggatgcg 3360

cttgaaaaat ataattttcc ccagatggcc catcagaagc ggttcatcga acggaagtac 3420

agacaagagt taaaagaaat gaggtgggaa agagagcatc aagagagaga gccagatgag 3480

actgaagaca tcaagaaata a 3501

<210> SEQ ID NO 14
<211> LENGTH: 1166
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Partial RNase III VSV-G Chimeric Protein with
VSV-G at N-terminal Amino Acid Sequence

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<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(1166)

<400> SEQUENCE: 14

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            20                  25                  30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
        35                  40                  45

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
    50                  55                  60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65                  70                  75                  80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
                85                  90                  95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
        115                 120                 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
    130                 135                 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145                 150                 155                 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
                165                 170                 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
            180                 185                 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
        195                 200                 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
    210                 215                 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225                 230                 235                 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
                245                 250                 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
            260                 265                 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
        275                 280                 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
    290                 295                 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
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    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430

Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
        435                 440                 445

Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Ala
            500                 505                 510

Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu
        515                 520                 525

Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
    530                 535                 540

Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr
545                 550                 555                 560

Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr
                565                 570                 575

Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu
            580                 585                 590

Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln
        595                 600                 605

Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn
    610                 615                 620

Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp
625                 630                 635                 640

Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
                645                 650                 655

Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
            660                 665                 670

Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
        675                 680                 685

Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His
    690                 695                 700

Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly
705                 710                 715                 720

Asp Arg Lys Val His His Met His Met Arg Lys Lys Gly Ile Asn Thr
                725                 730                 735

Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser
            740                 745                 750

Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val
        755                 760                 765

Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
    770                 775                 780
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Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
785                 790                 795                 800

Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
                805                 810                 815

Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
            820                 825                 830

Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu Glu Gly Ser
        835                 840                 845

Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe Asn Asp Pro
    850                 855                 860

Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro Leu Gln Leu
865                 870                 875                 880

Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser Pro Val Leu
                885                 890                 895

Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His
            900                 905                 910

Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn
        915                 920                 925

His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser
    930                 935                 940

Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp
945                 950                 955                 960

His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn
                965                 970                 975

Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala
            980                 985                 990

Ile Thr Asn Asp Lys Thr Lys Arg  Pro Val Ala Leu Arg  Thr Lys Thr
        995                 1000                1005

Leu Ala  Asp Leu Leu Glu Ser  Phe Ile Ala Ala Leu  Tyr Thr Asp
    1010                1015                1020

Lys Asp  Leu Glu Tyr Val His  Thr Phe Met Asn Val  Cys Phe Phe
    1025                1030                1035

Pro Arg  Leu Lys Glu Phe Ile  Leu Asn Gln Asp Trp  Asn Asp Pro
    1040                1045                1050

Lys Ser  Gln Leu Gln Gln Cys  Cys Leu Thr Leu Arg  Thr Glu Gly
    1055                1060                1065

Lys Glu  Pro Asp Ile Pro Leu  Tyr Lys Thr Leu Gln  Thr Val Gly
    1070                1075                1080

Pro Ser  His Ala Arg Thr Tyr  Thr Val Ala Val Tyr  Phe Lys Gly
    1085                1090                1095

Glu Arg  Ile Gly Cys Gly Lys  Gly Pro Ser Ile Gln  Gln Ala Glu
    1100                1105                1110

Met Gly  Ala Ala Met Asp Ala  Leu Glu Lys Tyr Asn  Phe Pro Gln
    1115                1120                1125

Met Ala  His Gln Lys Arg Phe  Ile Glu Arg Lys Tyr  Arg Gln Glu
    1130                1135                1140

Leu Lys  Glu Met Arg Trp Glu  Arg Glu His Gln Glu  Arg Glu Pro
    1145                1150                1155

Asp Glu  Thr Glu Asp Ile Lys  Lys
    1160                1165
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<210> SEQ ID NO 15
<211> LENGTH: 1923
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H2A Chimeric Protein with VSV-G at the
N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1923)

<400> SEQUENCE: 15

atgaagtgcc ttttgtactt agctttttta ttcatcgggg tgaattgcaa gttcaccata 60

gtttttccac acaaccaaaa aggaaactgg aaaaatgttc cttccaatta ccattattgc 120

ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa 180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg 240

gtcactactt gtgatttccg ctggtacgga ccgaagtata taacacattc catccgatcc 300

ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg 360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca 420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt 480

gattcacagt tcatcaacgg aaaatgcagc aatgacatat gccccactgt ccataactcc 540

acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg 600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg 660

ttcagaagta actactttgc ttatgaaact ggagacaagg cctgcaaaat gcagtactgc 720

aagcattggg gagtcagact cccatcaggt gtctggttcg agatggctga taaggatctc 780

tttgctgcag ccagattccc tgaatgccca gaagggtcaa gtatctctgc tccatctcag 840

acctcagtgg atgtaagtct cattcaggac gttgagagga tcttggatta ttccctctgc 900

caagaaacct ggagcaaaat cagagcgggt cttcccatct ctccagtgga tctcagctat 960

cttgctccta aaaacccagg aaccggtcct gtctttacca taatcaatgg taccctaaaa 1020

tactttgaga ccagatacat cagagtcgat attgctgctc caatcctctc aagaatggtc 1080

ggaatgatca gtggaactac cacagaaagg gaactgtggg atgactgggc tccatatgaa 1140

gacgtggaaa ttggacccaa tggagttctg aggaccagtt taggatataa gtttccttta 1200

tatatgattg gacatggtat gttggactcc gatcttcatc ttagctcaaa ggctcaggtg 1260

tttgaacatc ctcacattca agacgctgct tcgcagcttc ctgatgatga gactttattt 1320

tttggtgata ctgggctatc caaaaatcca atcgagtttg tagaaggttg gttcagtagt 1380

tggaagagct ctattgcctc ttttttcttt atcatagggt taatcattgg actattcttg 1440

gttctccgag ttggtattta tctttgcatt aaattaaagc acaccaagaa aagacagatt 1500

tatacagaca tagagatgaa ccgacttgga aagtctggac gtggaaagca aggcggcaaa 1560

gctcgggcaa aagctaaaac gcgttcttcc agggccggtc ttcagtttcc agttggccgt 1620

gtgcaccgcc tcctccgcaa aggcaactac tccgaacgag tcggggccgg cgctccagtg 1680

tacctggcag cggtgctgga atatctgacg gccgagatct tagagctagc tggcaacgcg 1740

gctcgcgaca ataagaagac ccgcatcatc ccgcgccacc tgcagctagc catccgcaac 1800

gacgaggagc taaataagct tctaggtcgc gtgaccatcg cgcagggcgg tgtcctgccc 1860

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aacatccagg ccgtattgct gcctaagaag acggagagcc accataaggc caagggcaag 1920

tga 1923

<210> SEQ ID NO 16
<211> LENGTH: 640
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H2A Chimeric Protein with VSV-G at the N-terminal Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(640)

<400> SEQUENCE: 16

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
20 25 30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
35 40 45

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
50 55 60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65 70 75 80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
85 90 95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
115 120 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
130 135 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145 150 155 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
165 170 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
180 185 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
195 200 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
210 215 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225 230 235 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
245 250 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
260 265 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
275 280 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
290 295 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr

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305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430

Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
        435                 440                 445

Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Ser
            500                 505                 510

Gly Arg Gly Lys Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys Thr Arg
        515                 520                 525

Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His Arg Leu
    530                 535                 540

Leu Arg Lys Gly Asn Tyr Ser Glu Arg Val Gly Ala Gly Ala Pro Val
545                 550                 555                 560

Tyr Leu Ala Ala Val Leu Glu Tyr Leu Thr Ala Glu Ile Leu Glu Leu
                565                 570                 575

Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile Ile Pro Arg
            580                 585                 590

His Leu Gln Leu Ala Ile Arg Asn Asp Glu Glu Leu Asn Lys Leu Leu
        595                 600                 605

Gly Arg Val Thr Ile Ala Gln Gly Gly Val Leu Pro Asn Ile Gln Ala
    610                 615                 620

Val Leu Leu Pro Lys Lys Thr Glu Ser His His Lys Ala Lys Gly Lys
625                 630                 635                 640


<210> SEQ ID NO 17
<211> LENGTH: 1911
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H2B Chimeric Protein with VSV-G at the
      N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1911)

<400> SEQUENCE: 17
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atgaagtgcc ttttgtactt agctttttta ttcatcgggg tgaattgcaa gttcaccata 60

gtttttccac acaaccaaaa aggaaactgg aaaaatgttc cttccaatta ccattattgc 120

ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa 180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg 240

gtcactactt gtgatttccg ctggtacgga ccgaagtata taacacattc catccgatcc 300

ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg 360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca 420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt 480

gattcacagt tcatcaacgg aaaatgcagc aatgacatat gccccactgt ccataactcc 540

acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg 600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg 660

ttcagaagta actactttgc ttatgaaact ggagacaagg cctgcaaaat gcagtactgc 720

aagcattggg gagtcagact cccatcaggt gtctggttcg agatggctga taaggatctc 780

tttgctgcag ccagattccc tgaatgccca gaagggtcaa gtatctctgc tccatctcag 840

acctcagtgg atgtaagtct cattcaggac gttgagagga tcttggatta ttcctctgc 900

caagaaacct ggagcaaaat cagagcgggt cttcccatct ctccagtgga tctcagctat 960

cttgctccta aaaacccagg aaccggtcct gtctttacca taatcaatgg taccctaaaa 1020

tactttgaga ccagatacat cagagtcgat attgctgctc caatcctctc aagaatggtc 1080

ggaatgatca gtggaactac cacagaaagg gaactgtggg atgactgggc tccatatgaa 1140

gacgtggaaa ttggacccaa tggagttctg aggaccagtt taggatataa gtttccttta 1200

tatatgattg gacatggtat gttggactcc gatcttcatc ttagctcaaa ggctcaggtg 1260

tttgaacatc ctcacattca agacgctgct tcgcagcttc ctgatgatga gactttattt 1320

tttggtgata ctgggctatc caaaaatcca atcgagtttg tagaaggttg gttcagtagt 1380

tggaagagct ctattgcctc ttttttcttt atcatagggt taatcattgg actattcttg 1440

gttctccgag ttggtattta tctttgcatt aaattaaagc acaccaagaa aagacagatt 1500

tatacagaca tagagatgaa ccgacttgga aagccagacc cgtccaaatc ggctcctgcg 1560

cccaagaagg gttctaaaaa ggctgtcacc aaggcacaga agaaggacgg caagaagcgc 1620

aagcgcggcc gcaaggagag ctattctatc tacgtgtaca aggtgctgaa gcaggtgcac 1680

cccgacaccg gcatctcgtc caaggccatg ggcatcatga actccttcgt caatgacatc 1740

ttcgagcgca tcgccagcga ggcctcccgc ctggcacact acaacaagcg ctccaccatc 1800

acgtcccgcg aagtgcagac ggccgttcgc ctgctgctgc ccggcgagct ggccaagcac 1860

gccgtgtccg agggcaccaa ggctgtcacc aagtacacca gctccaagtg a 1911

<210> SEQ ID NO 18
<211> LENGTH: 636
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H2B Chimeric Protein with VSV-G at the
N-terminal Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(636)

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<400> SEQUENCE: 18

```
Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1               5                  10                  15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
            20                  25                  30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
        35                  40                  45

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
    50                  55                  60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65                  70                  75                  80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
                85                  90                  95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
        115                 120                 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
    130                 135                 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145                 150                 155                 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
                165                 170                 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
            180                 185                 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
        195                 200                 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
    210                 215                 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225                 230                 235                 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
                245                 250                 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
            260                 265                 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
        275                 280                 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
    290                 295                 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400
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Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430

Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
        435                 440                 445

Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Pro
            500                 505                 510

Asp Pro Ser Lys Ser Ala Pro Ala Pro Lys Lys Gly Ser Lys Lys Ala
        515                 520                 525

Val Thr Lys Ala Gln Lys Lys Asp Gly Lys Lys Arg Lys Arg Gly Arg
    530                 535                 540

Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln Val His
545                 550                 555                 560

Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn Ser Phe
                565                 570                 575

Val Asn Asp Ile Phe Glu Arg Ile Ala Ser Glu Ala Ser Arg Leu Ala
            580                 585                 590

His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Val Gln Thr Ala
        595                 600                 605

Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val Ser Glu
    610                 615                 620

Gly Thr Lys Ala Val Thr Lys Tyr Thr Ser Ser Lys
625                 630                 635


<210> SEQ ID NO 19
<211> LENGTH: 1938
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H3 Chimeric Protein with VSV-G at the
      N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1938)

<400> SEQUENCE: 19

atgaagtgcc ttttgtactt agctttttta ttcatcgggg tgaattgcaa gttcaccata     60

gtttttccac acaaccaaaa aggaaactgg aaaaatgttc cttccaatta ccattattgc    120

ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa    180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg    240

gtcactactt gtgatttccg ctggtacgga ccgaagtata taacacattc catccgatcc    300

ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg    360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca    420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt    480
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gattcacagt tcatcaacgg aaaatgcagc aatgacatat gccccactgt ccataactcc 540

acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg 600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg 660

ttcagaagta actactttgc ttatgaaact ggagacaagg cctgcaaaat gcagtactgc 720

aagcattggg gagtcagact cccatcaggt gtctggttcg agatggctga taaggatctc 780

tttgctgcag ccagattccc tgaatgccca gaagggtcaa gtatctctgc tccatctcag 840

acctcagtgg atgtaagtct cattcaggac gttgagagga tcttggatta ttcctctgc 900

caagaaacct ggagcaaaat cagagcgggt cttcccatct ctccagtgga tctcagctat 960

cttgctccta aaaacccagg aaccggtcct gtctttacca taatcaatgg taccctaaaa 1020

tactttgaga ccagatacat cagagtcgat attgctgctc caatcctctc aagaatggtc 1080

ggaatgatca gtggaactac cacagaaagg gaactgtggg atgactgggc tccatatgaa 1140

gacgtggaaa ttggacccaa tggagttctg aggaccagtt taggatataa gtttccttta 1200

tatatgattg gacatggtat gttggactcc gatcttcatc ttagctcaaa ggctcaggtg 1260

tttgaacatc ctcacattca agacgctgct tcgcagcttc ctgatgatga gactttattt 1320

tttggtgata ctgggctatc caaaaatcca atcgagtttg tagaaggttg gttcagtagt 1380

tggaagagct ctattgcctc ttttttcttt atcatagggt taatcattgg actattcttg 1440

gttctccgag ttggtattta tctttgcatt aaattaaagc acaccaagaa aagacagatt 1500

tatacagaca tagagatgaa ccgacttgga aaggcccgaa ccaagcagac tgctcgtaaa 1560

tccaccggtg ggaaagcccc ccgcaaacag ctggccacga aagctgccag gaaaagcacc 1620

ccctctacct gcggggtgaa gcctcatcgc tacaggcctg ggaccgtggc gcttcgagag 1680

attcgtcgtt atcagaagtc gaccgagctg ctcatccgga agctgccctt ccagaggttg 1740

gtgagggaga tcgcgcagga tttcaacact gacctgaggt ttcagagcgc agccgtcggt 1800

gcgctgcagg aggctagcga agcgtacctg gtgggtctgt tggaagatac taacctgtgt 1860

gccatccacg ctaagagagt caccatcatg cccaaagaca tccagttggc tcgccggata 1920

cggggagaga gagcttaa 1938

<210> SEQ ID NO 20
<211> LENGTH: 645
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H3 Chimeric Protein with VSV-G at the N-terminal Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(645)

<400> SEQUENCE: 20

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
20 25 30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
35 40 45

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
50 55 60

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His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65                  70                  75                  80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
                85                  90                  95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
        115                 120                 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
    130                 135                 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145                 150                 155                 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
                165                 170                 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
            180                 185                 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
        195                 200                 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
    210                 215                 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225                 230                 235                 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
                245                 250                 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
            260                 265                 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
        275                 280                 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
    290                 295                 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430

Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
        435                 440                 445

Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
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465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Ala
            500                 505                 510

Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro Arg
        515                 520                 525

Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Thr Pro Ser Thr Cys
    530                 535                 540

Gly Val Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala Leu Arg Glu
545                 550                 555                 560

Ile Arg Arg Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg Lys Leu Pro
                565                 570                 575

Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Asn Thr Asp Leu
            580                 585                 590

Arg Phe Gln Ser Ala Ala Val Gly Ala Leu Gln Glu Ala Ser Glu Ala
        595                 600                 605

Tyr Leu Val Gly Leu Leu Glu Asp Thr Asn Leu Cys Ala Ile His Ala
    610                 615                 620

Lys Arg Val Thr Ile Met Pro Lys Asp Ile Gln Leu Ala Arg Arg Ile
625                 630                 635                 640

Arg Gly Glu Arg Ala
                645


<210> SEQ ID NO 21
<211> LENGTH: 1842
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H4 Chimeric Protein with VSV-G at the
      N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1842)

<400> SEQUENCE: 21

atgaagtgcc ttttgtactt agctttttta ttcatcgggg tgaattgcaa gttcaccata     60

gtttttccac acaaccaaaa aggaaactgg aaaaatgttc cttccaatta ccattattgc    120

ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa    180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg    240

gtcactactt gtgatttccg ctggtacgga ccgaagtata taacacattc catccgatcc    300

ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg    360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca    420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt    480

gattcacagt tcatcaacgg aaaatgcagc aatgacatat gccccactgt ccataactcc    540

acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg    600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg    660

ttcagaagta actactttgc ttatgaaact ggagacaagg cctgcaaaat gcagtactgc    720

aagcattggg gagtcagact cccatcaggt gtctggttcg agatggctga taaggatctc    780

tttgctgcag ccagattccc tgaatgccca gaagggtcaa gtatctctgc tccatctcag    840
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acctcagtgg atgtaagtct cattcaggac gttgagagga tcttggatta ttccctctgc    900

caagaaacct ggagcaaaat cagagcgggt cttcccatct ctccagtgga tctcagctat    960

cttgctccta aaaacccagg aaccggtcct gtctttacca taatcaatgg taccctaaaa   1020

tactttgaga ccagatacat cagagtcgat attgctgctc caatcctctc aagaatggtc   1080

ggaatgatca gtggaactac cacagaaagg gaactgtggg atgactgggc tccatatgaa   1140

gacgtggaaa ttggacccaa tggagttctg aggaccagtt taggatataa gtttccttta   1200

tatatgattg gacatggtat gttggactcc gatcttcatc ttagctcaaa ggctcaggtg   1260

tttgaacatc ctcacattca agacgctgct tcgcagcttc ctgatgatga gactttattt   1320

tttggtgata ctgggctatc caaaaatcca atcgagtttg tagaaggttg gttcagtagt   1380

tggaagagct ctattgcctc ttttttcttt atcatagggt taatcattgg actattcttg   1440

gttctccgag ttggtattta tctttgcatt aaattaaagc acaccaagaa aagacagatt   1500

tatacagaca tagagatgaa ccgacttgga aagtctggtc gcggcaaagg cggtaaaggt   1560

ttgggtaagg gaggtgccaa gcgtcaccga aaagtgctgc gggataacat ccaaggcatc   1620

accaaaccgg ccattcggcg ccttgctagg cgtggtgggg ttaagcgaat ttccggtttg   1680

atttatgagg agactcgtgg cgttctcaag gtgtttctgg agaacgtgat ccgggacgcc   1740

gtgacctaca cggagcacgc caagcgcaag actgtcactg ccatggatgt ggtttacgcg   1800

ctcaagcgtc aaggacgcac tctgtacggc ttcggcggtt aa                      1842
```

<210> SEQ ID NO 22
<211> LENGTH: 613
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G H4 Chimeric Protein with VSV-G at the N-terminal Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(613)

<400> SEQUENCE: 22

```
Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1               5                   10                  15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
            20                  25                  30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
        35                  40                  45

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
    50                  55                  60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65                  70                  75                  80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
                85                  90                  95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
        115                 120                 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
    130                 135                 140
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Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145                 150                 155                 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
                165                 170                 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
            180                 185                 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
        195                 200                 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
    210                 215                 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225                 230                 235                 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
                245                 250                 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
            260                 265                 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
        275                 280                 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
    290                 295                 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430

Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
        435                 440                 445

Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Ser
            500                 505                 510

Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg
        515                 520                 525

His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala
    530                 535                 540

Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu
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545                 550                 555                 560

Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Val Phe Leu Glu Asn Val
                565                 570                 575

Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Lys Arg Lys Thr Val
            580                 585                 590

Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg Thr Leu
        595                 600                 605

Tyr Gly Phe Gly Gly
    610
```

<210> SEQ ID NO 23
<211> LENGTH: 1977
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G SSBP-1 Chimeric Protein with VSV-G at the N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1977)

<400> SEQUENCE: 23

```
atgaagtgcc ttttgtactt agctttttta ttcatcgggg tgaattgcaa gttcaccata     60

gtttttccac acaaccaaaa aggaaactgg aaaaatgttc cttccaatta ccattattgc    120

ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa    180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg    240

gtcactactt gtgatttccg ctggtacgga ccgaagtata taacacattc catccgatcc    300

ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg    360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca    420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt    480

gattcacagt tcatcaacgg aaaatgcagc aatgacatat gccccactgt ccataactcc    540

acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg    600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg    660

ttcagaagta actactttgc ttatgaaact ggagacaagg cctgcaaaat gcagtactgc    720

aagcattggg gagtcagact cccatcaggt gtctggttcg agatggctga taaggatctc    780

tttgctgcag ccagattccc tgaatgccca gaagggtcaa gtatctctgc tccatctcag    840

acctcagtgg atgtaagtct cattcaggac gttgagagga tcttggatta ttccctctgc    900

caagaaacct ggagcaaaat cagagcgggt cttcccatct ctccagtgga tctcagctat    960

cttgctccta aaaacccagg aaccggtcct gtctttacca taatcaatgg taccctaaaa   1020

tactttgaga ccagatacat cagagtcgat attgctgctc caatcctctc aagaatggtc   1080

ggaatgatca gtggaactac cacagaaagg gaactgtggg atgactgggc tccatatgaa   1140

gacgtggaaa ttggacccaa tggagttctg aggaccagtt taggatataa gtttccttta   1200

tatatgattg gacatggtat gttggactcc gatcttcatc ttagctcaaa ggctcaggtg   1260

tttgaacatc ctcacattca agacgctgct tcgcagcttc ctgatgatga gactttattt   1320

tttggtgata ctgggctatc caaaaatcca atcgagtttg tagaaggttg gttcagtagt   1380

tggaagagct ctattgcctc ttttttcttt atcatagggt taatcattgg actattcttg   1440
```

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gttctccgag ttggtattta tctttgcatt aaattaaagc acaccaagaa aagacagatt 1500

tatacagaca tagagatgaa ccgacttgga aagtttcgaa gacctgtatt acaggtactt 1560

cgtcagtttg taagacatga gtccgaaaca actaccagtt tggttcttga aagatccctg 1620

aatcgtgtgc acttacttgg gcgagtgggt caggaccctg tcttgagaca ggtggaagga 1680

aaaaatccag tcacaatatt ttctctagca actaatgaga tgtggcgatc aggggatagt 1740

gaagtttacc aactgggtga tgtcagtcaa aagacaacat ggcacagaat atcagtattc 1800

cggccaggcc tcagagacgt ggcatatcaa tatgtgaaaa aggggtctcg aatttatttg 1860

gaagggaaaa tagactatgg tgaatacatg gataaaaata atgtgaggcg acaagcaaca 1920

acaatcatag ctgataatat tatatttctg agtgaccaga cgaaagagaa ggagtag 1977

<210> SEQ ID NO 24
<211> LENGTH: 658
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VSV-G SSBP-1 Chimeric Protein with VSV-G at the N-terminal Amino Acid Sequence
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(658)

<400> SEQUENCE: 24

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
20 25 30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
35 40 45

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
50 55 60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65 70 75 80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
85 90 95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
115 120 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
130 135 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145 150 155 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
165 170 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
180 185 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
195 200 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
210 215 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225 230 235 240

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Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
                245                 250                 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
            260                 265                 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
        275                 280                 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
    290                 295                 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430

Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
        435                 440                 445

Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Phe
            500                 505                 510

Arg Arg Pro Val Leu Gln Val Leu Arg Gln Phe Val Arg His Glu Ser
        515                 520                 525

Glu Thr Thr Thr Ser Leu Val Leu Glu Arg Ser Leu Asn Arg Val His
    530                 535                 540

Leu Leu Gly Arg Val Gly Gln Asp Pro Val Leu Arg Gln Val Glu Gly
545                 550                 555                 560

Lys Asn Pro Val Thr Ile Phe Ser Leu Ala Thr Asn Glu Met Trp Arg
                565                 570                 575

Ser Gly Asp Ser Glu Val Tyr Gln Leu Gly Asp Val Ser Gln Lys Thr
            580                 585                 590

Thr Trp His Arg Ile Ser Val Phe Arg Pro Gly Leu Arg Asp Val Ala
        595                 600                 605

Tyr Gln Tyr Val Lys Lys Gly Ser Arg Ile Tyr Leu Glu Gly Lys Ile
    610                 615                 620

Asp Tyr Gly Glu Tyr Met Asp Lys Asn Asn Val Arg Arg Gln Ala Thr
625                 630                 635                 640
```

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Thr Ile Ile Ala Asp Asn Ile Ile Phe Leu Ser Asp Gln Thr Lys Glu
645 650 655

Lys Glu

<210> SEQ ID NO 25
<211> LENGTH: 5655
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: RNase III VSV-G Chimeric Protein with VSV-G at N-terminal Nucleotide Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(5655)

<400> SEQUENCE: 25

atgaagtgcc ttttgtactt agctttttta ttcatcgggg tgaattgcaa gttcaccata 60

gtttttccac acaaccaaaa aggaaactgg aaaaatgttc cttccaatta ccattattgc 120

ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagcctt acaagtcaaa 180

atgcccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg 240

gtcactactt gtgatttccg ctggtacgga ccgaagtata taacacattc catccgatcc 300

ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg 360

ctgaatccag gcttccctcc tcaaagttgt ggatatgcaa ctgtgacgga tgctgaagca 420

gcgattgtcc aggtgactcc tcaccatgtg cttgttgatg aatacacagg agaatgggtt 480

gattcacagt tcatcaacgg aaaatgcagc aatgacatat gccccactgt ccataactcc 540

acaacctggc attccgacta taaggtcaaa gggctatgtg attctaacct catttccacg 600

gacatcacct tcttctcaga ggacggagag ctatcatccc taggaaagga gggcacaggg 660

ttcagaagta actactttgc ttatgaaact ggagacaagg cctgcaaaat gcagtactgc 720

aagcattggg gagtcagact cccatcaggt gtctggttcg agatggctga taaggatctc 780

tttgctgcag ccagattccc tgaatgccca gaagggtcaa gtatctctgc tccatctcag 840

acctcagtgg atgtaagtct cattcaggac gttgagagga tcttggatta ttccctctgc 900

caagaaacct ggagcaaaat cagagcgggt cttcccatct ctccagtgga tctcagctat 960

cttgctccta aaaacccagg aaccggtcct gtctttacca taatcaatgg taccctaaaa 1020

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20 25 30

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His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Lys Ser
    50                  55                  60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65                  70                  75                  80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr His
                85                  90                  95

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

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
        115                 120                 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Ala Ile Val Gln
    130                 135                 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145                 150                 155                 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Asp Ile Cys Pro Thr
                165                 170                 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
            180                 185                 190

Cys Asp Ser Asn Leu Ile Ser Thr Asp Ile Thr Phe Phe Ser Glu Asp
        195                 200                 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
    210                 215                 220

Tyr Phe Ala Tyr Glu Thr Gly Asp Lys Ala Cys Lys Met Gln Tyr Cys
225                 230                 235                 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
                245                 250                 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
            260                 265                 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
        275                 280                 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
    290                 295                 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305                 310                 315                 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Val Phe Thr Ile Ile Asn
                325                 330                 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
            340                 345                 350

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

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
    370                 375                 380

Gly Pro Asn Gly Val Leu Arg Thr Ser Leu Gly Tyr Lys Phe Pro Leu
385                 390                 395                 400

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
                405                 410                 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
            420                 425                 430
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Leu Pro Asp Asp Glu Thr Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
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Asn Pro Ile Glu Phe Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
    450                 455                 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465                 470                 475                 480

Val Leu Arg Val Gly Ile Tyr Leu Cys Ile Lys Leu Lys His Thr Lys
                485                 490                 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys Met
            500                 505                 510

Gln Gly Asn Thr Cys His Arg Met Ser Phe His Pro Gly Arg Gly Cys
        515                 520                 525

Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro Ser Phe
    530                 535                 540

Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro Val Gln
545                 550                 555                 560

Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser Asn Ser
                565                 570                 575

Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro Phe Pro
            580                 585                 590

Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys Pro Ile
        595                 600                 605

Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro Val Pro
    610                 615                 620

Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn Asn Pro
625                 630                 635                 640

Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe Met Met
                645                 650                 655

Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Pro Val Met Pro Gln
            660                 665                 670

Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn Phe Pro
        675                 680                 685

Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe Leu Pro
    690                 695                 700

Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro Pro Tyr
705                 710                 715                 720

Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg Leu Lys
                725                 730                 735

His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg Gly Glu
            740                 745                 750

Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro Asp Arg
        755                 760                 765

Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly Arg Thr
    770                 775                 780

Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu Arg Glu
785                 790                 795                 800

Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu Arg Ser
                805                 810                 815

Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu Ser Val
            820                 825                 830

Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu Ile Ile
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        835                 840                 845

Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn His Arg
    850                 855                 860

Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu Lys Asp
865                 870                 875                 880

Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr Thr Ser
                885                 890                 895

Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn Glu Glu
            900                 905                 910

Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr His Ser
        915                 920                 925

Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp Ser Thr
    930                 935                 940

Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe Glu Glu
945                 950                 955                 960

Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro Pro Trp
                965                 970                 975

Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser Ser Glu
            980                 985                 990

Ser Glu Cys Glu Ser Asp Glu Asp  Ser Thr Cys Ser Ser  Ser Ser Asp
        995                 1000                1005

Ser Glu  Val Phe Asp Val Ile  Ala Glu Ile Lys Arg  Lys Lys Ala
    1010                1015                1020

His Pro  Asp Arg Leu His Asp  Glu Leu Trp Tyr Asn  Asp Pro Gly
    1025                1030                1035

Gln Met  Asn Asp Gly Pro Leu  Cys Lys Cys Ser Ala  Lys Ala Arg
    1040                1045                1050

Arg Thr  Gly Ile Arg His Ser  Ile Tyr Pro Gly Glu  Glu Ala Ile
    1055                1060                1065

Lys Pro  Cys Arg Pro Met Thr  Asn Asn Ala Gly Arg  Leu Phe His
    1070                1075                1080

Tyr Arg  Ile Thr Val Ser Pro  Pro Thr Asn Phe Leu  Thr Asp Arg
    1085                1090                1095

Pro Thr  Val Ile Glu Tyr Asp  Asp His Glu Tyr Ile  Phe Glu Gly
    1100                1105                1110

Phe Ser  Met Phe Ala His Ala  Pro Leu Thr Asn Ile  Pro Leu Cys
    1115                1120                1125

Lys Val  Ile Arg Phe Asn Ile  Asp Tyr Thr Ile His  Phe Ile Glu
    1130                1135                1140

Glu Met  Met Pro Glu Asn Phe  Cys Val Lys Gly Leu  Glu Leu Phe
    1145                1150                1155

Ser Leu  Phe Leu Phe Arg Asp  Ile Leu Glu Leu Tyr  Asp Trp Asn
    1160                1165                1170

Leu Lys  Gly Pro Leu Phe Glu  Asp Ser Pro Pro Cys  Cys Pro Arg
    1175                1180                1185

Phe His  Phe Met Pro Arg Phe  Val Arg Phe Leu Pro  Asp Gly Gly
    1190                1195                1200

Lys Glu  Val Leu Ser Met His  Gln Ile Leu Leu Tyr  Leu Leu Arg
    1205                1210                1215

Cys Ser  Lys Ala Leu Val Pro  Glu Glu Glu Ile Ala  Asn Met Leu
    1220                1225                1230
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```
Gln Trp  Glu Glu Leu Glu Trp  Gln Lys Tyr Ala Glu  Glu Cys Lys
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Gly Met  Ile Val Thr Asn Pro  Gly Thr Lys Pro Ser  Ser Val Arg
    1250                1255                1260

Ile Asp  Gln Leu Asp Arg Glu  Gln Phe Asn Pro Asp  Val Ile Thr
    1265                1270                1275

Phe Pro  Ile Ile Val His Phe  Gly Ile Arg Pro Ala  Gln Leu Ser
    1280                1285                1290

Tyr Ala  Gly Asp Pro Gln Tyr  Gln Lys Leu Trp Lys  Ser Tyr Val
    1295                1300                1305

Lys Leu  Arg His Leu Leu Ala  Asn Ser Pro Lys Val  Lys Gln Thr
    1310                1315                1320

Asp Lys  Gln Lys Leu Ala Gln  Arg Glu Glu Ala Leu  Gln Lys Ile
    1325                1330                1335

Arg Gln  Lys Asn Thr Met Arg  Arg Glu Val Thr Val  Glu Leu Ser
    1340                1345                1350

Ser Gln  Gly Phe Trp Lys Thr  Gly Ile Arg Ser Asp  Val Cys Gln
    1355                1360                1365

His Ala  Met Met Leu Pro Val  Leu Thr His His Ile  Arg Tyr His
    1370                1375                1380

Gln Cys  Leu Met His Leu Asp  Lys Leu Ile Gly Tyr  Thr Phe Gln
    1385                1390                1395

Asp Arg  Cys Leu Leu Gln Leu  Ala Met Thr His Pro  Ser His His
    1400                1405                1410

Leu Asn  Phe Gly Met Asn Pro  Asp His Ala Arg Asn  Ser Leu Ser
    1415                1420                1425

Asn Cys  Gly Ile Arg Gln Pro  Lys Tyr Gly Asp Arg  Lys Val His
    1430                1435                1440

His Met  His Met Arg Lys Lys  Gly Ile Asn Thr Leu  Ile Asn Ile
    1445                1450                1455

Met Ser  Arg Leu Gly Gln Asp  Asp Pro Thr Pro Ser  Arg Ile Asn
    1460                1465                1470

His Asn  Glu Arg Leu Glu Phe  Leu Gly Asp Ala Val  Val Glu Phe
    1475                1480                1485

Leu Thr  Ser Val His Leu Tyr  Tyr Leu Phe Pro Ser  Leu Glu Glu
    1490                1495                1500

Gly Gly  Leu Ala Thr Tyr Arg  Thr Ala Ile Val Gln  Asn Gln His
    1505                1510                1515

Leu Ala  Met Leu Ala Lys Lys  Leu Glu Leu Asp Arg  Phe Met Leu
    1520                1525                1530

Tyr Ala  His Gly Pro Asp Leu  Cys Arg Glu Ser Asp  Leu Arg His
    1535                1540                1545

Ala Met  Ala Asn Cys Phe Glu  Ala Leu Ile Gly Ala  Val Tyr Leu
    1550                1555                1560

Glu Gly  Ser Leu Glu Glu Ala  Lys Gln Leu Phe Gly  Arg Leu Leu
    1565                1570                1575

Phe Asn  Asp Pro Asp Leu Arg  Glu Val Trp Leu Asn  Tyr Pro Leu
    1580                1585                1590

His Pro  Leu Gln Leu Gln Glu  Pro Asn Thr Asp Arg  Gln Leu Ile
    1595                1600                1605
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```
Glu Thr  Ser Pro Val Leu Gln  Lys Leu Thr Glu Phe  Glu Glu Ala
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Ile Gly  Val Ile Phe Thr His  Val Arg Leu Leu Ala  Arg Ala Phe
    1625                 1630                 1635

Thr Leu  Arg Thr Val Gly Phe  Asn His Leu Thr Leu  Gly His Asn
    1640                 1645                 1650

Gln Arg  Met Glu Phe Leu Gly  Asp Ser Ile Met Gln  Leu Val Ala
    1655                 1660                 1665

Thr Glu  Tyr Leu Phe Ile His  Phe Pro Asp His His  Glu Gly His
    1670                 1675                 1680

Leu Thr  Leu Leu Arg Ser Ser  Leu Val Asn Asn Arg  Thr Gln Ala
    1685                 1690                 1695

Lys Val  Ala Glu Glu Leu Gly  Met Gln Glu Tyr Ala  Ile Thr Asn
    1700                 1705                 1710

Asp Lys  Thr Lys Arg Pro Val  Ala Leu Arg Thr Lys  Thr Leu Ala
    1715                 1720                 1725

Asp Leu  Leu Glu Ser Phe Ile  Ala Ala Leu Tyr Ile  Asp Lys Asp
    1730                 1735                 1740

Leu Glu  Tyr Val His Thr Phe  Met Asn Val Cys Phe  Phe Pro Arg
    1745                 1750                 1755

Leu Lys  Glu Phe Ile Leu Asn  Gln Asp Trp Asn Asp  Pro Lys Ser
    1760                 1765                 1770

Gln Leu  Gln Gln Cys Cys Leu  Thr Leu Arg Thr Glu  Gly Lys Glu
    1775                 1780                 1785

Pro Asp  Ile Pro Leu Tyr Lys  Thr Leu Gln Thr Val  Gly Pro Ser
    1790                 1795                 1800

His Ala  Arg Thr Tyr Thr Val  Ala Val Tyr Phe Lys  Gly Glu Arg
    1805                 1810                 1815

Ile Gly  Cys Gly Lys Gly Pro  Ser Ile Gln Gln Ala  Glu Met Gly
    1820                 1825                 1830

Ala Ala  Met Asp Ala Leu Glu  Lys Tyr Asn Phe Pro  Gln Met Ala
    1835                 1840                 1845

His Gln  Lys Arg Phe Ile Glu  Arg Lys Tyr Arg Gln  Glu Leu Lys
    1850                 1855                 1860

Glu Met  Arg Trp Glu Arg Glu  His Gln Glu Arg Glu  Pro Asp Glu
    1865                 1870                 1875

Thr Glu  Asp Ile Lys Lys
    1880
```

What is claimed is:

**1**. A chimeric protein comprising VSV-G and a nucleic acid binding protein.

**2**. The chimeric protein according to claim **1**, wherein the nucleic acid binding protein is a histone.

**3**. The chimeric protein according to claim **2**, wherein the histone is selected from the group consisting of: H2A, H2B, H3, and H4.

**4**. The chimeric protein according to claim **2**, wherein the histone is tagged with VSV-G at the C-terminus.

**5**. The chimeric protein according to claim **2**, wherein the histone is tagged with VSV-G at the N-terminus.

**6**. The chimeric protein according to claim **4**, wherein the chimeric protein comprises SEQ. ID NO.: 1, SEQ. ID NO.: 2, SEQ. ID NO.: 3, SEQ. ID NO.: 4, SEQ. ID NO.: 5, SEQ. ID NO.: 6, SEQ. ID NO.: 7, or SEQ. ID NO.: 8, and pharmacologically acceptable equivalents thereof.

**7**. The chimeric protein according to claim **5**, wherein the chimeric protein comprises SEQ. ID NO.: 15, SEQ. ID NO.: 16, SEQ. ID NO.: 17, SEQ. ID NO.: 18, SEQ. ID NO.: 19, SEQ. ID NO.: 20, SEQ. ID NO.: 21, or SEQ. ID NO.: 22, and pharmacologically acceptable equivalents thereof.

**8**. The chimeric protein according to claim **4**, wherein the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 1, SEQ. ID NO.: 2, SEQ. ID NO.: 3, SEQ. ID NO.: 4, SEQ. ID NO.: 5, SEQ. ID NO.: 6, SEQ. ID NO.: 7, or SEQ. ID NO.: 8.

**9**. The chimeric protein according to claim **5**, wherein the chimeric protein includes a sequence having at least 90%, at

least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 15, SEQ. ID NO.: 16, SEQ. ID NO.:

17, SEQ. ID NO.: 18, SEQ. ID NO.: 19, SEQ. ID NO.: 20, SEQ. ID NO.: 21, or SEQ. ID NO.: 22.

**10**. The chimeric protein according to claim **1**, wherein the nucleic acid binding protein is SSBP-1.

**11**. The chimeric protein according to claim **10**, wherein SSBP-1 is tagged with VSV-G at the C-terminus.

**12**. The chimeric protein according to claim **10**, wherein SSBP-1 is tagged with VSV-G at the N-terminus.

**13**. The chimeric protein according to claim **11**, wherein the chimeric protein comprises SEQ. ID NO.: 9 or SEQ. ID NO.: 10, and pharmacologically acceptable equivalents thereof.

**14**. The chimeric protein according to claim **12**, wherein the chimeric protein comprises SEQ. ID NO.: 23 or SEQ. ID NO.: 24, and pharmacologically acceptable equivalents thereof.

**15**. The chimeric protein according to claim **11**, wherein the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 9 or SEQ. ID NO.: 10.

**16**. The chimeric protein according to claim **12**, wherein the chimeric protein includes a sequence having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with SEQ. ID NO.: 23 or SEQ. ID NO.: 24.

**17**. The chimeric protein according to claim **1**, wherein the nucleic acid binding protein is RNase III.

**18**. The chimeric protein according to claim **17**, wherein RNase III is tagged with VSV-G at the C-terminus.

**19**. The chimeric protein according to claim **17**, wherein RNase III is tagged with VSV-G at the N-terminus.

**20**. The chimeric protein according to claim **18**, wherein the chimeric protein comprises SEQ. ID NO.: 11, SEQ. ID NO.: 12, or SEQ. ID NO.: 13, and pharmacologically acceptable equivalents thereof.

* * * * *