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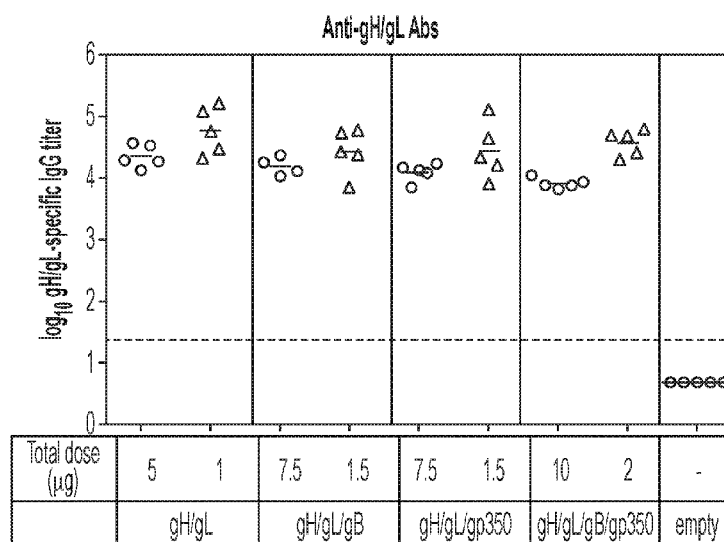


FIG. 7

(57) Abstract: The disclosure relates to EBV ribonucleic acid vaccines as well as methods of using the vaccines and compositions comprising the vaccines.

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EPSTEIN-BARR VIRUS VACCINES

BACKGROUND

Epstein-Barr virus (EBV), also referred to as human herpesvirus 4, is one of the most common human viruses worldwide. Ninety five percent of adults are infected with this virus. EBV spreads most commonly through bodily fluids, primarily saliva, and is the primary cause of infectious mononucleosis (“mono”) and other illnesses. Seventy five percent of college students (18-22 years) with primary EBV infection will develop mono. Symptoms of EBV can include fatigue, fever, inflamed throat, swollen lymph nodes in the neck, enlarged spleen, swollen liver, and rash. While many people are infected with EBV in childhood, childhood symptoms are not distinguished from other mild, brief childhood illnesses. Typically, only teenagers and adults exhibit symptoms characteristic of EBV infection, and although recover is about two to four weeks, some people may feel fatigued for several weeks or even months. Following an EBV infection, the virus becomes latent and, in some cases, may be reactivated. Those with weakened immune systems are more likely to develop symptoms if EBV is reactivated. Currently, there is no vaccine to prevent primary infection or disease.

SUMMARY

Provided herein, in some embodiments, are Epstein-Barr virus (EBV) ribonucleic acid (RNA) (e.g., mRNA) vaccines (e.g., combination vaccines) that elicit potent neutralizing antibodies and robust T cell responses, inhibit the production of viral immunomodulatory factors, and/or prevent viral latency. In some aspects, the EBV vaccines include a RNA having an open reading frame (ORF) encoding an EBV antigen, wherein intramuscular (IM) administration of a therapeutically effective amount of the vaccine to a subject induces in the subject a neutralizing antibody titer and/or a T cell immune response (e.g., a CD4+ and/or a CD8+ T cell immune response).

In some embodiments, the neutralizing antibody titer is at least 100 (e.g., at least 500, or at least 1000) NT₅₀ following, for example, a single dose (e.g., a single 10 µg - 200 µg dose) of an EBV RNA vaccine. In some embodiments, the neutralizing antibody titer is at least 100 (e.g., at least 500, or at least 1000) NT₅₀ following a booster (second) dose of an EBV RNA vaccine.

In some embodiments, the neutralizing antibody titer is sufficient to reduce EBV infection of B cells by at least 50% (e.g., by at least 60%, 70%, 80% or 90%), or relative to a neutralizing antibody titer of an unvaccinated control subject or relative to a neutralizing

antibody titer of a subject vaccinated with a live attenuated EBV vaccine, an inactivated EBV vaccine, or a protein subunit EBV vaccine.

In some embodiments, the neutralizing antibody titer is induced in the subject following fewer than three (one or two) doses of the vaccine.

5 In some embodiments, a single dose of an EBV RNA vaccine is of 10 µg-100 µg.

In some embodiments, the neutralizing antibody titer and/or a T cell immune response is sufficient to reduce the rate of symptomatic infectious mononucleosis relative to the neutralizing antibody titer of unvaccinated control subjects.

10 In some embodiments, the neutralizing antibody titer and/or a T cell immune response is sufficient to reduce the rate of asymptomatic EBV infection relative to the neutralizing antibody titer of unvaccinated control subjects.

In some embodiments, the neutralizing antibody titer and/or a T cell immune response is sufficient to prevent EBV latency the subject.

15 In some embodiments, the neutralizing antibody titer and/or a T cell immune response is sufficient to reduce chronic fatigue in the subject.

In some embodiments, the neutralizing antibody titer is sufficient to block fusion of EBV with epithelial cells and/or B cells of the subject.

20 In some embodiments, the neutralizing antibody titer is induced within 20 days following a single 10-100 µg of the vaccine. In some embodiments, the neutralizing antibody titer is induced within 40 days following a second 10-100 µg dose of the vaccine.

In some embodiments, the ability of a vaccine of the present disclosure to induce a neutralizing antibody response can be demonstrated by injecting animals, e.g., mice or non-human primates, with the vaccine and testing the ability of serum from the animal to neutralize the ability of the virus to infect human B cells.

25 In some embodiments, the T cell immune response comprises a CD4⁺ T cell immune response. In some embodiments, the T cell immune response comprises a CD8⁺ T cell immune response. In some embodiments, the T cell immune response comprises both a CD4⁺ T cell immune response and CD8⁺ T cell immune response.

30 In some embodiments, after vaccination, the EBV antigen is expressed on the surface of cells of the subject. In some embodiments, the ability of the vaccine to be expressed can be tested in a model system, e.g., a mouse or non-human primate model. In some embodiments, the ability of the vaccine to be expressed can be tested *in vitro*, e.g., using human cells.

In some embodiments, a single 2 µg dose of the vaccine induces in mice NT₅₀ neutralizing antibody titers of about 100. In some embodiments, a 2 µg booster dose of the vaccine induces in mice NT₅₀ neutralizing antibody titers of about 1000.

5 In some embodiments, the EBV vaccine comprises a RNA having an ORF encoding two EBV antigens, or two RNAs, each having an ORF encoding an EBV antigen.

10 In some embodiments, the vaccine comprises a RNA having an ORF encoding two (at least two) EBV antigens formulated in a lipid nanoparticle. In some embodiments, the vaccine comprises two (at least two) RNAs, each having an ORF encoding an EBV antigen, wherein the two RNAs are formulated in a single lipid nanoparticle. In some embodiments, the vaccine comprises two RNAs, each having an ORF encoding an EBV antigen, wherein the each RNAs is formulated in a separate lipid nanoparticle.

In some embodiments, the EBV vaccines further include at least one (e.g., 2, 3, 4, 5 or more) additional RNA having an ORF encoding at least one (e.g., 2, 3, 4, 5 or more) additional EBV antigen.

15 In some embodiments, the lipid nanoparticle comprises a molar ratio of 20-60% ionizable cationic lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid

In some embodiments, the EBV antigens are selected from the group consisting of: gp350, gH, gL, gB, gp42, LMP1, LMP2, EBNA1, and EBNA3.

20 In some embodiments, the EBV antigen is a gH-gL fusion, whereby gH is linked to gL through a linker, such as a GGGGS linker. In some embodiments, the GGGGS linker comprises three GGGGS motifs (SEQ ID NO: 224). In some embodiments, the GGGGS linker comprises four GGGGS motifs (SEQ ID NO: 225)). In some embodiments, the EBV RNA comprises the nucleotide sequence of SEQ ID NO: 218. In some embodiments, the EBV RNA comprises the nucleotide sequence of SEQ ID NO: 221.

25 In some embodiments, the EBV antigens include EBV gp350 antigen, EBV gH antigen, and EBV gL antigen. In some embodiments, the EBV antigens further include EBV gp42 antigen and/or gB antigen.

30 In some embodiments, the EBVgp350 antigen is a wild-type EBV gp350 antigen, a mutated EBV gp350 antigen, or a truncated EBV gp350 antigen.

In some embodiments, the EBV antigens are selected from the EBV antigens listed in the Sequence Listing.

In some embodiments, the EBV antigens (one or more EBV antigens) are fused to a scaffold moiety. In some embodiments, the scaffold moiety is selected from the group consisting

of: ferritin, encapsulin, lumazine synthase, hepatitis B surface antigen, and hepatitis B core antigen.

In some embodiments, the RNA comprises messenger RNA (mRNA).

In some embodiments, the RNA further comprises a 5' UTR. In some embodiments, the 5' UTR comprises a sequence identified by SEQ ID NO: 1 or SEQ ID NO: 104.

In some embodiments, the RNA further comprises a 3' UTR. In some embodiments, the 3' UTR comprises a sequence identified by SEQ ID NO: 3 or SEQ ID NO: 106.

In some embodiments, the EBV antigen is fused to a signal peptide. In some embodiments, the signal peptide is a bovine prolactin signal peptide, optionally comprising SEQ ID NO: 115.

In some embodiments, the RNA is unmodified.

In some embodiments, the RNA comprise at least one modified nucleotide. In some embodiments, at least 80% (e.g., 90% or 100%) of the uracil in the ORF comprise 1-methylpseudouridine modification.

Also provided herein, in some aspects, are methods that include administering to a subject an EBV vaccine of the present disclosure in a therapeutically effective amount to induce in the subject a neutralizing antibody titer and/or a T cell immune response.

In some embodiments, efficacy of the EBV vaccine is at least 80% (e.g., 85%, 90%, 95%, 98% or 100%) relative to unvaccinated control subjects.

In some embodiments, detectable levels of EBV antigen are produced in the serum of the subject at 1-72 hours post administration of the vaccine.

In some embodiments, a neutralizing antibody titer of at least 100 (e.g., at least 500 or at least 1000) NU/ml is produced in the serum of the subject at 1-72 hours post administration of the vaccine.

In some embodiments, the therapeutically effective amount is a total dose of 20 µg-200 µg (e.g., 50 µg-100 µg).

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1A shows data from a flow cytometry analysis of indel-free codon-optimized glycoprotein 350 (gp350) variant surface expression in HeLa cells using 72A1 antibody. FIGS. 1B and 1C are bar graphs showing percent gp350 variant expression (percent 72A1 positive) on the surface of HeLa cells transfected with 1 µg (FIG. 1B) or 0.5 µg (FIG. 1C) of mRNA.

FIG. 2A shows data from a flow cytometry analysis of expression of gp350 mRNA having one of two different 5' untranslated region (UTR) sequences (compare UTR A and UTR

B). FIG. 2B is a bar graph showing percent gp350 expression on the surface of HeLa cells transfected with 0.5 µg of a gp350 mRNA having one of the two different 5' UTR sequences.

FIG. 3 is a graph showing the geometric mean (with 95% confidence interval) of neutralizing antibody titers produced in Balb/c mice following intramuscular (IM) vaccination with mRNA encoding EBV gp350 variants formulated in a lipid nanoparticle. A 2 µg dose was administered on Day 1 and then again on Day 21. Mice were bled on Day 21 and Day 43. NT₅₀ titers represent the reciprocal serum dilutions to block 50% viral entry. All gp350 variants exhibited comparable neutralizing titers.

FIG. 4A shows data from a flow cytometry analysis of surface expression of the indicated EBV antigens (EBV gp42) and EBV antigen complexes (EBV gH/gL/gp42 with indicated 5' UTR, or EBV gH/gp42) in HeLa cells using 2D4 antibody. FIG. 4B is a bar graph showing percent antigen expression (percent 2D4 positive) on the surface of HeLa cells transfected with 0.25 µg of the mRNA 24 hours post transfection.

FIG. 5 is a graph showing the geometric mean (with 95% confidence interval) of neutralizing antibody titers produced in Balb/c mice following IM vaccination with mRNA encoding indicated EBV antigens (EBV gp350) and EBV antigen complexes (EBV gH/gL/gp42 or gH/gL/gp42/gp350) formulated in a lipid nanoparticle. Various indicated doses were administered on Day 1 and then again on Day 29. Mice were bled on Day 28 and Day 57. NT₅₀ titers represent the reciprocal serum dilutions to block 50% viral entry. These data show that gp350 and gH/gL/gp42 elicit comparable B cell neutralizing titers. There is no interference observed by combining all of the mRNAs in one LNP vaccine.

FIG. 6A shows data from a flow cytometry analysis of surface expression of EBV gH antigen and EBV gH/gL antigen complex in HeLa cells using 2A8 antibody, or surface expression of EBV gH/gL antigen complex in HeLa cells using 2D4 antibody. FIG. 6B is a bar graph showing percent gH/gL expression on the surface of HeLa cells transfected with 0.25 µg of a gH mRNA and a gL mRNA, having one of the two different 5' UTR sequences, 24 hours post transfection.

FIG. 7 is a graph showing gH/gL-specific binding antibody titers (log₁₀) produced in Balb/c mice following IM vaccination with mRNA encoding indicated EBV antigen complexes (EBV gH/gL, EBV gH/gL/gB, EBV gH/gL/gp350, or EBV gH/gL/gB/gp350) formulated in a lipid nanoparticle. Various indicated doses were administered.

FIG. 8 is a graph showing gB-specific binding antibody titers (log₁₀) produced in Balb/c mice following IM vaccination with mRNA encoding indicated EBV antigen (EBV gB) or EBV

antigen complexes (EBV gH/gL/gB, EBV gB/gp350, or EBV gH/gL/gB/gp350) formulated in a lipid nanoparticle. Various indicated doses were administered.

FIG. 9 is a graph showing gp350-specific binding antibody titers ($\log_{10}$) produced in Balb/c mice following IM vaccination with mRNA encoding indicated EBV antigen (EBV gp350) or EBV antigen complexes (EBV gH/gL/gp350, EBV gB/gp350, or EBV gH/gL/gB/gp350) formulated in a lipid nanoparticle. Various indicated doses were administered.

FIGS. 10A-10D show antigen-specific CD8 T cell responses to various EBV latent genes in Balb/c mice following IM vaccination with mRNA encoding either LMP1, LMP2, EBNA1 (EBAN1d1-400), EBNA3A alone or a combination (combo) of LMP1, LMP2, EBNA1, EBNA3A and gp350.

FIGS. 11A-11D show antigen-specific CD4 T cell responses to various EBV latent genes in Balb/c mice following IM vaccination with mRNA encoding either LMP1, LMP2, EBNA1 (EBAN1d1-400), EBNA3A alone or a combination (combo) of LMP1, LMP2, EBNA1, EBNA3A and gp350.

FIG. 12 shows schematics of EBV gp350 variants of the present disclosure.

FIGS. 13A-13B show data from a flow cytometry analysis for surface expression in HeLa cells transfected with mRNA encoding either a linked glycoprotein L (gL) and glycoprotein H (gH) construct (gL-gH Linker A or gL-gH Linker B) or individual gH and gL that are co-transfected using 2A8 antibody. FIG. 13B is a bar graph showing percent gL-gH expression (percent 2A8 positive and percent CL40 positive) on the surface of the HeLa cells transfected with the indicated mRNA. Mean fluorescence intensity (MFI) is also shown.

FIG. 14 shows EBNA1-specific polyclonal CD4 and CD8 T cell responses (e.g., IFN γ , TNF α , and IL-2 secretion) in Balb/c mice following IM vaccination with various mRNAs encoding EBV antigens (LMP2, EBNA1, gH, gL, and gp350, with UTR1 or UTR2) or mRNA encoding EBNA1 antigen alone.

FIG. 15 shows LMP2-specific polyclonal CD4 and CD8 T cell responses (e.g., IFN γ , TNF α , and IL-2 secretion) in Balb/c mice following IM vaccination with mRNAs encoding various EBV antigens (LMP2, EBNA1, gH, gL, and gp350, with UTR1 or UTR2) or mRNA encoding LMP2 antigen alone.

FIG. 16 shows a schematic of the experimental protocol (top) and graphs of the resulting gp350-specific IgG titers (bottom left) and gH/gL-specific IgG titers (bottom right) in immune sera of non human primates (NHPs) vaccinated with a combination EBV mRNA vaccine (gp350, gH, gL, LMP2, and EBNA1) or control.

FIG. 17 is a graph showing the neutralizing titers against EBV infection of Raji B cells in immune sera of NHPs vaccinated with the indicated doses and constructs or the neutralizing titers present in EBV+ human sera.

FIG. 18 is a graph showing the gp350-specific IgG titers following cell transfection with EBV vaccine constructs generated using different downstream purification processes.

FIG. 19 is a graph showing the gH/gL-specific IgG titers following cell transfection with EBV vaccine constructs generated using different downstream purification processes.

DETAILED DESCRIPTION

The Epstein-Barr virus (EBV) is a double-stranded DNA γ -herpesvirus that infects B cells and epithelial cells, causing infectious mononucleosis, and that has been linked to malignancies, such as Burkitt's lymphoma, Hodgkin's lymphoma, and nasopharyngeal carcinoma, in both cell types *in vivo*. Nearly 95% of the population is infected by EBV by adulthood and carries EBV DNA throughout life. EBV is maintained in a latent state in infected B lymphocytes, with periodic reactivation of lytic replication.

EBV, widespread in all human populations, can be isolated *in vitro* via its ability to transform resting human B cells into permanent lymphoblastoid cell lines (LCLs) expressing the virus-coded antigens EBNA1, 2, 3A, 3B, 3C, and LP and the latent membrane proteins (LMPs) 1, 2A, and 2B. EBV isolates can be categorized as type 1 or type 2 on the basis of marked allelic polymorphisms within the EBNA2, 3A, 3B, and 3C genes and into distinct strains on the basis of more-subtle sequence variations within the EBNA1, EBNA2, and LMP1 genes and certain lytic cycle genes.

EBV has three glycoproteins, glycoprotein B (gB), gH, and gL, that form the core membrane fusion machinery mediating viral entry into a cell. The gH and gL proteins associate to form a heterodimeric complex, which is necessary for efficient membrane fusion and is also implicated in direct binding to epithelial cell receptors required for viral entry. EBV uses different pathways for the infection of epithelial cells and B lymphocytes. For both cell types, the minimal viral glycoprotein components that mediate membrane fusion have been identified. As with other herpesviruses, EBV uses the core viral entry glycoproteins, glycoprotein B (gB) and the gH/gL complex. For the infection of B lymphocytes, EBV requires an additional protein, gp42, which binds to host HLA class II molecules, triggering the membrane fusion step. gp42 has multiple functional sites for interaction with gH/gL, HLA class II, and potentially, another unknown binding ligand that could be engaged through a large surface-exposed hydrophobic pocket. The gp42 protein binds to the gH/gL complex with nanomolar affinity through its N-

terminal region, and this interaction can be recapitulated with a synthetic peptide of ~35 aa residues. EBV glycoprotein-mediated membrane fusion with epithelial cells does not require gp42 but only gB and gH/gL. Recent observations indicate that EBV gH/gL engages integrins $\alpha v\beta 6$ and/or $\alpha v\beta 8$ on epithelial cells to trigger membrane fusion and entry.

5 The EBV gp350 glycoprotein encoded by BLLF1 is important for efficient EBV infection of resting B cells. Gp350 is the most abundant viral protein in the viral envelope. This large protein is heavily glycosylated and localizes to various subcellular compartments (cytoplasm, endoplasmic reticulum, Golgi, and plasma membrane) of replicating cells. EBV binds to primary B cells through its interaction with CD21, the complement receptor 2 (CR2) via
10 gp350. Several gp350 domains appear to be involved in the formation of a stable complex with CD21, one of which has been identified as the receptor-binding site (amino acids [aa] 142 to 161). This glycan-free domain is also recognized by the neutralizing gp350-specific antibody 72A.

15 The present disclosure is not limited by a particular strain of EBV. The strain of EBV used in a vaccine may be any strain of EBV.

 The present disclosure provides RNA (e.g., mRNA) vaccines against EBV infection – vaccines that elicit potent neutralizing antibodies and robust T cell responses against EBV antigens, inhibit the production of viral immunomodulatory factors, and/or prevent viral latency.

20 In some embodiments, vaccines disclosed herein are used therapeutically, i.e., following infection with EBV (to treat the infection). In some embodiments, the vaccines of the present disclosure can be used to prevent or reduce the frequency of Hodgkin's lymphoma, Burkitt's lymphoma, gastric carcinoma, nasopharyngeal carcinoma, post-transplant lymphoproliferative disease, diffuse B cell lymphoma, and/or NK/T cell lymphoma.

25 The EBV RNA vaccines described herein are superior to current vaccines in several ways. For example, the lipid nanoparticle (LNP) delivery system used herein increases the efficacy of RNA vaccines in comparison to other formulations, including a protamine-based approach described in the literature. The use of this LNP delivery system enables the effective delivery of chemically-modified RNA vaccines or unmodified RNA vaccines, without requiring additional adjuvant to produce a therapeutic result (e.g., production neutralizing antibody titer
30 and/or a T cell response). In some embodiments, the EBV RNA vaccines disclosed herein are superior to conventional vaccines by a factor of at least 10 fold, 20, fold, 40, fold, 50 fold, 100 fold, 500 fold, or 1,000 fold when administered intramuscularly (IM) or intradermally (ID). These results can be achieved even when significantly lower doses of the RNA (e.g., mRNA) are administered in comparison with RNA doses used in other classes of lipid based formulations.

The LNP used in the studies described herein has been used previously to deliver siRNA in various animal models as well as in humans. In view of the observations made in association with the siRNA delivery of LNP formulations, the fact that LNP is useful in vaccines is quite surprising, particularly when immunity to an antigen has been hard to generate, as in the case of EBV. It has been observed that therapeutic delivery of siRNA formulated in LNP causes an undesirable inflammatory response associated with a transient IgM response, typically leading to a reduction in antigen production and a compromised immune response. In contrast to the findings observed with siRNA, the LNP-mRNA formulations of the present disclosure are demonstrated herein to generate enhanced IgG levels, sufficient for prophylactic and therapeutic methods rather than transient IgM responses.

Exemplary Epstein-Barr Virus (EBV) Antigens

Antigens are proteins capable of inducing an immune response (e.g., causing an immune system to produce antibodies against the antigens). Herein, use of the term antigen encompasses immunogenic proteins and immunogenic fragments (an immunogenic fragment that induces (or is capable of inducing) an immune response to EBV), unless otherwise stated. It should be understood that the term “protein” encompasses peptides and the term “antigen” encompasses antigenic fragments.

A number of different antigens are associated with EBV. EBV vaccines, as provided herein, comprise at least one (one or more) ribonucleic acid (RNA, e.g., mRNA) having an open reading frame encoding at least one EBV antigen. Non-limiting examples of EBV antigens are provided below.

Exemplary EBV antigens are provided in the Sequence Listing elsewhere herein. For example, the antigens may be encoded by (thus the RNA may comprise or consist of) any one of sequences set forth in SEQ ID NO: 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, and/or 210. In some embodiments, the aforementioned sequences may further comprise a 5' cap (e.g., 7mG(5')ppp(5')NlmpNp), a polyA tail, or a 5' cap and a polyA tail.

It should be understood that the EBV vaccines of the present disclosure may comprise any of the RNA open reading frames (ORFs), or encode any of the protein ORFs, described herein, with or without a signal sequence. It should also be understood that the EBV vaccines of

the present disclosure may include any 5' untranslated region (UTR) and/or any 3' UTR. Exemplary UTR sequences are provided in the Sequence Listing (e.g., SEQ ID NOs: 1, 3, 104 and 106; however, other UTR sequences (e.g., of the prior art) may be used or exchanged for any of the UTR sequences described herein. UTRs may also be omitted from the vaccine constructs provided herein.

EBV entry into B cells is initiated by attachment of glycoprotein gp350 to the complement receptor type 2 (CR2). A complex of three glycoproteins, gH, gL, and gp42, is subsequently required for penetration. gp42 binds to HLA class II, which functions as an entry mediator or co-receptor and, by analogy with other herpesviruses, gH is then thought to be involved virus-cell fusion. Entry of virus into epithelial cells is different. It can be initiated by attachment by an unknown glycoprotein in the absence of CR2. There is no interaction between gp42 and HLA class II and instead a distinct complex of only the two glycoproteins gH and gL interacts with a novel entry mediator.

EBV gH-gL complex includes of three glycoproteins, gp85, the gH homolog, which is the product of the BXLF2 open reading frame (ORF); gp25, the gL homolog, which is the product of the BKRF2 ORF; and gp42, which is the product of the BZLF2 ORF. The complex behaves in many respects like its counterparts in other herpesviruses. Glycoprotein gH is dependent on gL for authentic processing and transport, and the complex as a whole has been implicated as important to the ability of virus to fuse with the cell membrane and penetrate into the cytoplasm

The gp350 glycoprotein encoded by BLLF1 is important for efficient Epstein-Barr virus (EBV) infection of resting B cells.

The major EBV glycoprotein gp350 mediates docking of EBV on B cells by binding receptor type 2 (CR2) (Nemerow et al., *J of Virol.* (61):1416-1420 (1987); Szakonyi et al., *Nat Struct Mol Biol.* (13): 996-1001 (2006)). Due to alternative splicing, *BLLF1* encodes gp350 and gp220, which are glycosylated and are approximately 350 and 220 kilodaltons in molecular weight, respectively (Beisel et al., *J Virol.* (54):665-674 (1985); Hummel et al., *J Virol.* (49):413-417 (1984)). In some embodiments, the EBV gp350 antigen comprises the sequence identified by SEQ ID NO: 81, 204, 185, 182, 207, or 208.

After EBV docking, EBV fuses with the plasma membrane of the host cell using a complex of glycoproteins. The core EBV membrane fusion machinery for entry into B cells and epithelial cells includes glycoprotein B (gB), glycoprotein H (gH) and glycoprotein L (gL) (Hutt-Fletcher et al., *J Virol.* (81): 7825-7832 (2007)).

gB is a single pass type 1 membrane protein also referred to as gp110 and is encoded by the *BALF4* open reading frame (ORF) (Herrold *et al.*, *J of Virol.* (70):2049-2054 (1996); Haan *et al.*, *Virology* (290): 106-114 (2001)); McShane *et al.*, *Proc Natl Acad Sci USA.* (101): 17474-17479 (2004)). In some embodiments, the EBV gB antigen comprises the sequence identified by SEQ ID NO: 209.

gH (also referred to as gp85) is a type 1 transmembrane protein encoded by the open reading frame (ORF) of the *BXLF2* gene (Heineman *et al.*, *J Virol.* (62):1101–1107 (1988)); Oba *et al.*, *J Virol.* (62):1108–1114 (1988)). In some embodiments, the EBV gH antigen comprises the sequence identified by SEQ ID NO: 187.

gL (also referred to as gp25) and encoded by *BKRF2* ORF is required for proper folding and localization of gH (Li *et al.*, *J Virol.* (69): 3987- 3994 (1995); Yaswen *et al.*, *Virology.* (195): 387-396 (1993)). Therefore, gH and gL often functions as a complex to mediate viral fusion and this complex has been crystallized (Matsurra *et al.*, *Proc Natl Acad Sci USA.* (107):22641–2264 (2010)). In some embodiments, the EBV gL antigen comprises the sequence identified by SEQ ID NO: 188.

In addition to the core membrane fusion machinery, EBV entry into B cells requires gp42, which is encoded by a *BZLF2* ORF (Kirschner *et al.*, *J. Virol.* (80):9444-54 (2006); Wang *et al.*, *J. Virol.*, (72):5552–5558 (1998); Silva *et al.*, *J. Virol.* (78): 5946–5956 (2004); Li *et al.* *J. Virol.*, (69):3987–3994 (1995). EBV gp42 mediates viral fusion with B cells by binding MHC class II molecules (Mullen *et al.*, *Molecular Cell.* (9):375-385 (2002); Haan *et al.* *J Virol.* (74): 2451-4 (2000)). In some embodiments, the EBV gp42 antigen comprises the sequence identified by SEQ ID NO: 189.

Latent membrane protein 1 (LMP1) is a six transmembrane domain protein that promotes immortalization of resting B cells and helps protect EBV-infected B cells from apoptosis (Hennessy *et al.*, *Proc Natl. Acad. Sci USA.* (81): 7207-11 (1984); Kaye *et al.*, *Proc Natl Acad Sci USA.* (90): 9150-9154 (1993); Henderson *et al.*, *Cell* (65): 1107-1115 (1991)). A number of signaling pathways may be activated by LMP1, including tumor necrosis factor receptor family signaling and DNA synthesis (Peng *et al.* *Oncogene.* (7): 1775 -1782; Masialos *et al.*, *Cell.* (80):389-399 (1995); Li *et al.*, *J Biomed Sci.* (10):490-504 (2003)). Furthermore, LMP1 signaling can upregulate expression of the anti-apoptosis Bcl-2 oncogene in B cells (Rowe *et al.*, *J Virol.* (68):5602-12 (1994)). In some embodiments, the EBV LMP1 antigen comprises the sequence identified by SEQ ID NO: 179.

Similar to LMP1, Latent membrane protein 2 (LMP2) is an EBV-encoded transmembrane protein that is often expressed in latently infected cells. There are two isoforms

of LMP2 (LMP2A and LMP2B) (Laux *et al.*, *EMBO J.* (7):769-74 (1988); Longnecker *et al.*, *J Virol.* (64):2319-26 (1990)). LMP2A is implicated in maintaining EBV latency. For example, LMP2A can exclude B-cell receptor (BCR) from lipid rafts to prevent lytic induction (Dykstra *et al.*, *Immunity.* (14):57-67 (2001)). LMP2A can also activate the phosphatidylinositol 3-kinase (PI3-K)/Akt pathway to promote cell survival (Scholle *et al.*, *J Virol.* (74): 10681-10689 (2000); Swart *et al.* *J Virol.* (74): 10838-10845 (2000); Fukuda *et al.*, *J. Virol.* (78): 1697-16705 (2004)). LMP2B protein generally lacks 119 amino-terminal amino acids compared to LMP2A and is implicated in epithelial cell spreading and motility (Allen *et al.*, *J Virol.* (79):1789-1802 (2005)). In some embodiments, the EBV LMP2 antigen comprises the sequence identified by SEQ ID NO: 181.

Epstein-Barr nuclear antigens (EBNAs) that help establish latent infection include EBNA1, EBNA2, EBNA3A and EBNA3C. EBNA1 encoded by *BKRF1* promotes viral DNA replication, episomal maintenance and episomal partitioning (Rawlins *et al.*, *Cell* (42): 859-68 (1985); (Hung *et al.*, *Proc Natl Acad Sciences USA* (98): 1865-1870 (2001)). In particular, EBNA1 can bind family of repeats and dyad symmetry elements of the latent origin oriP. In some embodiments, the EBV EBNA1 antigen comprises the sequence identified by SEQ ID NO: 178.

There are three members of the EBNA3 family: EBNA3A, EBNA3B and EBNA3C. EBNA3s regulate transcription by binding RBPJ, which is a transcriptional regulator in the Notch signaling pathway (Zhao *et al.*, *J Virol.* (70):4228–4236 (1996); Robertson *et al.*, *J Virol.* (69):3108–3116 (1995); Robertson *et al.* *J Virol.* (70):3068–3074 (1996)). In particular, EBNA3A and EBNA3C have been shown to be required for EBV-mediated transformation of B cells (Tomkinson *et al.* *J Virol.* (67):2014-25 (1993)). In some embodiments, the EBV EBNA3A antigen comprises the sequence identified by SEQ ID NO: 177.

Nucleic Acids

The EBV vaccines of the present disclosure comprise at least one (one or more) ribonucleic acid (RNA) having an open reading frame encoding at least one EBV antigen. In some embodiments, the RNA is a messenger RNA (mRNA) having an open reading frame encoding at least one EBV antigen. In some embodiments, the RNA (e.g., mRNA) further comprises a (at least one) 5' UTR, 3' UTR, a polyA tail and/or a 5' cap.

Nucleic acids comprise a polymer of nucleotides (nucleotide monomers), also referred to as polynucleotides. Nucleic acids may be or may include, for example, deoxyribonucleic acids (DNAs), ribonucleic acids (RNAs), threose nucleic acids (TNAs), glycol nucleic acids (GNAs),

peptide nucleic acids (PNAs), locked nucleic acids (LNAs, including LNA having a β -D-ribo configuration, α -LNA having an α -L-ribo configuration (a diastereomer of LNA), 2'-amino-LNA having a 2'-amino functionalization, and 2'-amino- α -LNA having a 2'-amino functionalization), ethylene nucleic acids (ENA), cyclohexenyl nucleic acids (CeNA) and/or chimeras and/or combinations thereof.

Messenger RNA (mRNA) is any ribonucleic acid that encodes a (at least one) protein (a naturally-occurring, non-naturally-occurring, or modified polymer of amino acids) and can be translated to produce the encoded protein *in vitro*, *in vivo*, *in situ* or *ex vivo*. The skilled artisan will appreciate that, except where otherwise noted, nucleic acid sequences set forth in the instant application may recite "T"s in a representative DNA sequence but where the sequence represents RNA (e.g., mRNA), the "T"s would be substituted for "U"s. Thus, any of the DNAs disclosed and identified by a particular sequence identification number herein also disclose the corresponding RNA (e.g., mRNA) sequence complementary to the DNA, where each "T" of the DNA sequence is substituted with "U."

An open reading frame (ORF) is a continuous stretch of DNA or RNA beginning with a start codon (e.g., methionine (ATG or AUG)) and ending with a stop codon (e.g., TAA, TAG or TGA, or UAA, UAG or UGA). An ORF typically encodes a protein. It will be understood that the sequences disclosed herein may further comprise additional elements, e.g., 5' and 3' UTRs, but that those elements, unlike the ORF, need not necessarily be present in a vaccine of the present disclosure.

Variants

In some embodiments, an RNA of the present disclosure encodes an EBV antigen variant. Antigen or other polypeptide variants refers to molecules that differ in their amino acid sequence from a wild-type, native or reference sequence. The antigen/polypeptide variants may possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence, as compared to a native or reference sequence. Ordinarily, variants possess at least 50% identity to a wild-type, native or reference sequence. In some embodiments, variants share at least 80%, or at least 90% identity with a wild-type, native or reference sequence.

Variant antigens/polypeptides encoded by nucleic acids of the disclosure may contain amino acid changes that confer any of a number of desirable properties, e.g., that enhance their immunogenicity, enhance their expression, and/or improve their stability or PK/PD properties in a subject. Variant antigens/polypeptides can be made using routine mutagenesis techniques and assayed as appropriate to determine whether they possess the desired property. Assays to

determine expression levels and immunogenicity are well known in the art and exemplary such assays are set forth in the Examples section. Similarly, PK/PD properties of a protein variant can be measured using art recognized techniques, e.g., by determining expression of antigens in a vaccinated subject over time and/or by looking at the durability of the induced immune response.

- 5 The stability of protein(s) encoded by a variant nucleic acid may be measured by assaying thermal stability or stability upon urea denaturation or may be measured using *in silico* prediction. Methods for such experiments and *in silico* determinations are known in the art.

In some embodiments, an EBV vaccine comprises an mRNA ORF having a nucleotide sequence identified by any one of the sequences provided herein (see e.g., Sequence Listing), or
10 having a nucleotide sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a nucleotide sequence identified by any one of the sequence provided herein.

The term “identity” refers to a relationship between the sequences of two or more polypeptides (e.g. antigens) or polynucleotides (nucleic acids), as determined by comparing the
15 sequences. Identity also refers to the degree of sequence relatedness between or among sequences as determined by the number of matches between strings of two or more amino acid residues or nucleic acid residues. Identity measures the percent of identical matches between the smaller of two or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (e.g., “algorithms”). Identity of related antigens or
20 nucleic acids can be readily calculated by known methods. “Percent (%) identity” as it applies to polypeptide or polynucleotide sequences is defined as the percentage of residues (amino acid residues or nucleic acid residues) in the candidate amino acid or nucleic acid sequence that are identical with the residues in the amino acid sequence or nucleic acid sequence of a second sequence after aligning the sequences and introducing gaps, if necessary, to achieve the
25 maximum percent identity. Methods and computer programs for the alignment are well known in the art. It is understood that identity depends on a calculation of percent identity but may differ in value due to gaps and penalties introduced in the calculation. Generally, variants of a particular polynucleotide or polypeptide (e.g., antigen) have at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% but less
30 than 100% sequence identity to that particular reference polynucleotide or polypeptide as determined by sequence alignment programs and parameters described herein and known to those skilled in the art. Such tools for alignment include those of the BLAST suite (Stephen F. Altschul, *et al* (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402). Another popular local alignment technique

is based on the Smith-Waterman algorithm (Smith, T.F. & Waterman, M.S. (1981) "Identification of common molecular subsequences." *J. Mol. Biol.* 147:195-197). A general global alignment technique based on dynamic programming is the Needleman-Wunsch algorithm (Needleman, S.B. & Wunsch, C.D. (1970) "A general method applicable to the search for similarities in the amino acid sequences of two proteins." *J. Mol. Biol.* 48:443-453). More recently a Fast Optimal Global Sequence Alignment Algorithm (FOGSAA) has been developed that purportedly produces global alignment of nucleotide and protein sequences faster than other optimal global alignment methods, including the Needleman-Wunsch algorithm.

As such, polynucleotides encoding peptides or polypeptides containing substitutions, insertions and/or additions, deletions and covalent modifications with respect to reference sequences, in particular the polypeptide (e.g., antigen) sequences disclosed herein, are included within the scope of this disclosure. For example, sequence tags or amino acids, such as one or more lysines, can be added to peptide sequences (e.g., at the N-terminal or C-terminal ends). Sequence tags can be used for peptide detection, purification or localization. Lysines can be used to increase peptide solubility or to allow for biotinylation. Alternatively, amino acid residues located at the carboxy and amino terminal regions of the amino acid sequence of a peptide or protein may optionally be deleted providing for truncated sequences. Certain amino acids (e.g., C-terminal or N-terminal residues) may alternatively be deleted depending on the use of the sequence, as for example, expression of the sequence as part of a larger sequence which is soluble, or linked to a solid support. In some embodiments, sequences for (or encoding) signal sequences, termination sequences, transmembrane domains, linkers, multimerization domains (such as, e.g., foldon regions) and the like may be substituted with alternative sequences that achieve the same or a similar function. In some embodiments, cavities in the core of proteins can be filled to improve stability, e.g., by introducing larger amino acids. In other embodiments, buried hydrogen bond networks may be replaced with hydrophobic residues to improve stability. In yet other embodiments, glycosylation sites may be removed and replaced with appropriate residues. Such sequences are readily identifiable to one of skill in the art. It should also be understood that some of the sequences provided herein contain sequence tags or terminal peptide sequences (e.g., at the N-terminal or C-terminal ends) that may be deleted, for example, prior to use in the preparation of an RNA (e.g., mRNA) vaccine.

As recognized by those skilled in the art, protein fragments, functional protein domains, and homologous proteins are also considered to be within the scope of EBV antigens of interest. For example, provided herein is any protein fragment (meaning a polypeptide sequence at least one amino acid residue shorter than a reference antigen sequence but otherwise identical) of a

reference protein, provided that the fragment is immunogenic and confers a protective immune response to the EBV pathogen. In addition to variants that are identical to the reference protein but are truncated, in some embodiments, an antigen includes 2, 3, 4, 5, 6, 7, 8, 9, 10, or more mutations, as shown in any of the sequences provided or referenced herein. Antigens/antigenic polypeptides can range in length from about 4, 6, or 8 amino acids to full length proteins.

Stabilizing Elements

Naturally-occurring eukaryotic mRNA molecules can contain stabilizing elements, including, but not limited to untranslated regions (UTR) at their 5'-end (5' UTR) and/or at their 3'-end (3' UTR), in addition to other structural features, such as a 5'-cap structure or a 3'-poly(A) tail. Both the 5' UTR and the 3' UTR are typically transcribed from the genomic DNA and are elements of the premature mRNA. Characteristic structural features of mature mRNA, such as the 5'-cap and the 3'-poly(A) tail are usually added to the transcribed (premature) mRNA during mRNA processing.

In some embodiments, a vaccine includes at least one RNA polynucleotide having an open reading frame encoding at least one antigenic polypeptide having at least one modification, at least one 5' terminal cap, and is formulated within a lipid nanoparticle. 5'-capping of polynucleotides may be completed concomitantly during the in vitro-transcription reaction using the following chemical RNA cap analogs to generate the 5'-guanosine cap structure according to manufacturer protocols: 3'-O-Me-m7G(5')ppp(5') G [the ARCA cap]; G(5')ppp(5')A; G(5')ppp(5')G; m7G(5')ppp(5')A; m7G(5')ppp(5')G (New England BioLabs, Ipswich, MA). 5'-capping of modified RNA may be completed post-transcriptionally using a Vaccinia Virus Capping Enzyme to generate the "Cap 0" structure: m7G(5')ppp(5')G (New England BioLabs, Ipswich, MA). Cap 1 structure may be generated using both Vaccinia Virus Capping Enzyme and a 2'-O methyl-transferase to generate: m7G(5')ppp(5')G-2'-O-methyl. Cap 2 structure may be generated from the Cap 1 structure followed by the 2'-O-methylation of the 5'-antepenultimate nucleotide using a 2'-O methyl-transferase. Cap 3 structure may be generated from the Cap 2 structure followed by the 2'-O-methylation of the 5'-preantepenultimate nucleotide using a 2'-O methyl-transferase. Enzymes may be derived from a recombinant source.

The 3'-poly(A) tail is typically a stretch of adenine nucleotides added to the 3'-end of the transcribed mRNA. It can, in some instances, comprise up to about 400 adenine nucleotides. In some embodiments, the length of the 3'-poly(A) tail may be an essential element with respect to the stability of the individual mRNA.

In some embodiments, EBV RNA vaccines may include one or more stabilizing elements. Stabilizing elements may include for instance a histone stem-loop. A stem-loop binding protein (SLBP), a 32 kDa protein has been identified. It is associated with the histone stem-loop at the 3'-end of the histone messages in both the nucleus and the cytoplasm. Its expression level is regulated by the cell cycle; it peaks during the S-phase, when histone mRNA levels are also elevated. The protein has been shown to be essential for efficient 3'-end processing of histone pre-mRNA by the U7 snRNP. SLBP continues to be associated with the stem-loop after processing, and then stimulates the translation of mature histone mRNAs into histone proteins in the cytoplasm. The RNA binding domain of SLBP is conserved through metazoa and protozoa; its binding to the histone stem-loop depends on the structure of the loop. The minimum binding site includes at least three nucleotides 5' and two nucleotides 3' relative to the stem-loop.

In some embodiments, EBV RNA vaccines include a coding region, at least one histone stem-loop, and optionally, a poly(A) sequence or polyadenylation signal. The poly(A) sequence or polyadenylation signal generally should enhance the expression level of the encoded protein. The encoded protein, in some embodiments, is not a histone protein, a reporter protein (*e.g.* Luciferase, GFP, EGFP, β -Galactosidase, EGFP), or a marker or selection protein (*e.g.* alpha-Globin, Galactokinase and Xanthine:guanine phosphoribosyl transferase (GPT)).

In some embodiments, the combination of a poly(A) sequence or polyadenylation signal and at least one histone stem-loop, even though both represent alternative mechanisms in nature, acts synergistically to increase the protein expression beyond the level observed with either of the individual elements. The synergistic effect of the combination of poly(A) and at least one histone stem-loop does not depend on the order of the elements or the length of the poly(A) sequence.

In some embodiments, EBV RNA vaccines do not comprise a histone downstream element (HDE). "Histone downstream element" (HDE) includes a purine-rich polynucleotide stretch of approximately 15 to 20 nucleotides 3' of naturally occurring stem-loops, representing the binding site for the U7 snRNA, which is involved in processing of histone pre-mRNA into mature histone mRNA. In some embodiments, the nucleic acid does not include an intron.

In some embodiments, EBV RNA vaccines may or may not contain an enhancer and/or promoter sequence, which may be modified or unmodified or which may be activated or inactivated. In some embodiments, the histone stem-loop is generally derived from histone genes, and includes an intramolecular base pairing of two neighbored partially or entirely reverse complementary sequences separated by a spacer, consisting of a short sequence, which

forms the loop of the structure. The unpaired loop region is typically unable to base pair with either of the stem loop elements. It occurs more often in RNA, as is a key component of many RNA secondary structures, but may be present in single-stranded DNA as well. Stability of the stem-loop structure generally depends on the length, number of mismatches or bulges, and base composition of the paired region. In some embodiments, wobble base pairing (non-Watson-Crick base pairing) may result. In some embodiments, the at least one histone stem-loop sequence comprises a length of 15 to 45 nucleotides.

In some embodiments, EBV RNA vaccines may have one or more AU-rich sequences removed. These sequences, sometimes referred to as AURES are destabilizing sequences found in the 3'UTR. The AURES may be removed from the RNA vaccines. Alternatively the AURES may remain in the RNA vaccine.

Signal Peptides

In some embodiments, an EBV vaccine comprises a RNA having an ORF that encodes a signal peptide fused to the EBV antigen. Signal peptides, comprising the N-terminal 15-60 amino acids of proteins, are typically needed for the translocation across the membrane on the secretory pathway and, thus, universally control the entry of most proteins both in eukaryotes and prokaryotes to the secretory pathway. In eukaryotes, the signal peptide of a nascent precursor protein (pre-protein) directs the ribosome to the rough endoplasmic reticulum (ER) membrane and initiates the transport of the growing peptide chain across it for processing. ER processing produces mature proteins, wherein the signal peptide is cleaved from precursor proteins, typically by a ER-resident signal peptidase of the host cell, or they remain uncleaved and function as a membrane anchor. A signal peptide may also facilitate the targeting of the protein to the cell membrane.

A signal peptide may have a length of 15-60 amino acids. For example, a signal peptide may have a length of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, or 60 amino acids. In some embodiments, a signal peptide has a length of 20-60, 25-60, 30-60, 35-60, 40-60, 45-60, 50-60, 55-60, 15-55, 20-55, 25-55, 30-55, 35-55, 40-55, 45-55, 50-55, 15-50, 20-50, 25-50, 30-50, 35-50, 40-50, 45-50, 15-45, 20-45, 25-45, 30-45, 35-45, 40-45, 15-40, 20-40, 25-40, 30-40, 35-40, 15-35, 20-35, 25-35, 30-35, 15-30, 20-30, 25-30, 15-25, 20-25, or 15-20 amino acids.

Signal peptides from heterologous genes (which regulate expression of genes other than EBV antigens in nature) are known in the art and can be tested for desired properties and then

incorporated into a nucleic acid of the disclosure. In some embodiments, the signal peptide is a bovine prolactin signal peptide. For example, the bovine prolactin signal peptide may comprise sequence MDSKGSSQKGSRLLLL VVSNLLLPQGVVG (SEQ ID NO: 115). Other signal peptide sequences may also be used. For example, the signal peptide may comprise one of the following sequences: MDWTWILFLVAAATRVHS (SEQ ID NO: 116); METPAQLLFLLLLWLPDTTG (SEQ ID NO: 117); MLGSNSGQRVVFTILLLLVAPAYS (SEQ ID NO: 118); MKCLLYLAFLFIGVNCA (SEQ ID NO: 119); MWLVSLAIVTACAGA (SEQ ID NO: 120).

10 Fusion Proteins

In some embodiments, an EBV RNA vaccine of the present disclosure includes an RNA encoding an antigenic fusion protein. Thus, the encoded antigen or antigens may include two or more proteins (e.g., protein and/or protein fragment) joined together. Alternatively, the protein to which a protein antigen is fused does not promote a strong immune response to itself, but rather to the EBV antigen. Antigenic fusion proteins, in some embodiments, retain the functional property from each original protein.

Scaffold Moieties

The RNA (e.g., mRNA) vaccines as provided herein, in some embodiments, encode fusion proteins which comprise EBV antigens linked to scaffold moieties. In some embodiments, such scaffold moieties impart desired properties to an antigen encoded by a nucleic acid of the disclosure. For example scaffold proteins may improve the immunogenicity of an antigen, e.g., by altering the structure of the antigen, altering the uptake and processing of the antigen, and/or causing the antigen to bind to a binding partner.

In some embodiments, the scaffold moiety is protein that can self-assemble into protein nanoparticles that are highly symmetric, stable, and structurally organized, with diameters of 10–150 nm, a highly suitable size range for optimal interactions with various cells of the immune system. In some embodiments, viral proteins or virus-like particles can be used to form stable nanoparticle structures. Examples of such viral proteins are known in the art. For example, in some embodiments, the scaffold moiety is a hepatitis B surface antigen (HBsAg). HBsAg forms spherical particles with an average diameter of ~22 nm and which lacked nucleic acid and hence are non-infectious (Lopez-Sagaseta, J. et al. *Computational and Structural Biotechnology Journal* 14 (2016) 58–68). In some embodiments, the scaffold moiety is a hepatitis B core antigen (HBcAg) self-assembles into particles of 24–31 nm diameter, which resembled the viral

cores obtained from HBV-infected human liver. HBcAg produced in self-assembles into two classes of differently sized nanoparticles of 300 Å and 360 Å diameter, corresponding to 180 or 240 protomers. In some embodiments an EBV antigen is fused to HBsAG or HBcAG to facilitate self-assembly of nanoparticles displaying the EBV antigen.

5 In another embodiment, bacterial protein platforms may be used. Non-limiting examples of these self-assembling proteins include ferritin, lumazine and encapsulin.

Ferritin is a protein whose main function is intracellular iron storage. Ferritin is made of 24 subunits, each composed of a four-alpha-helix bundle, that self-assemble in a quaternary structure with octahedral symmetry (Cho K.J. et al. *J Mol Biol.* 2009;390:83–98). Several high-
10 resolution structures of ferritin have been determined, confirming that *Helicobacter pylori* ferritin is made of 24 identical protomers, whereas in animals, there are ferritin light and heavy chains that can assemble alone or combine with different ratios into particles of 24 subunits (Granier T. et al. *J Biol Inorg Chem.* 2003;8:105–111; Lawson D.M. et al. *Nature.* 1991;349:541–544). Ferritin self-assembles into nanoparticles with robust thermal and chemical
15 stability. Thus, the ferritin nanoparticle is well-suited to carry and expose antigens.

Lumazine synthase (LS) is also well-suited as a nanoparticle platform for antigen display. LS, which is responsible for the penultimate catalytic step in the biosynthesis of riboflavin, is an enzyme present in a broad variety of organisms, including archaea, bacteria, fungi, plants, and eubacteria (Weber S.E. *Flavins and Flavoproteins. Methods and Protocols,*
20 Series: Methods in Molecular Biology. 2014). The LS monomer is 150 amino acids long, and consists of beta-sheets along with tandem alpha-helices flanking its sides. A number of different quaternary structures have been reported for LS, illustrating its morphological versatility: from homopentamers up to symmetrical assemblies of 12 pentamers forming capsids of 150 Å diameter. Even LS cages of more than 100 subunits have been described (Zhang X. et al. *J Mol*
25 *Biol.* 2006;362:753–770).

Encapsulin, a novel protein cage nanoparticle isolated from thermophile *Thermotoga maritima*, may also be used as a platform to present antigens on the surface of self-assembling nanoparticles. Encapsulin is assembled from 60 copies of identical 31 kDa monomers having a thin and icosahedral T = 1 symmetric cage structure with interior and exterior diameters of 20
30 and 24 nm, respectively (Sutter M. et al. *Nat Struct Mol Biol.* 2008, 15: 939-947). Although the exact function of encapsulin in *T. maritima* is not clearly understood yet, its crystal structure has been recently solved and its function was postulated as a cellular compartment that encapsulates proteins such as DyP (Dye decolorizing peroxidase) and Flp (Ferritin like protein), which are involved in oxidative stress responses (Rahmanpour R. et al. *FEBS J.* 2013, 280: 2097-2104).

Linkers and Cleavable Peptides

In some embodiments, the mRNAs of the disclosure encode more than one polypeptide, referred to herein as fusion proteins. In some embodiments, the mRNA further encodes a linker located between at least one or each domain of the fusion protein. The linker can be, for example, a cleavable linker or protease-sensitive linker. In some embodiments, the linker is selected from the group consisting of F2A linker, P2A linker, T2A linker, E2A linker, and combinations thereof. This family of self-cleaving peptide linkers, referred to as 2A peptides, has been described in the art (see for example, Kim, J.H. et al. (2011) *PLoS ONE* 6:e18556). In some embodiments, the linker is an F2A linker. In some embodiments, the linker is a GGGG linker or a GGGGS linker, for example, including one or more (e.g., 1, 2, 3, 4, or more) repeat GGGG (SEQ ID NO: 226) or GGGGS (SEQ ID NO: 227) sequences (e.g., GGGGS GGGGS GGGGS (SEQ ID NO: 224) and/or GGGGS GGGGS GGGGS GGGGS (SEQ ID NO: 225)). In some embodiments, the fusion protein contains three domains with intervening linkers, having the structure: domain-linker-domain-linker-domain.

Cleavable linkers known in the art may be used in connection with the disclosure. Exemplary such linkers include: F2A linkers, T2A linkers, P2A linkers, E2A linkers (See, e.g., WO2017/127750). The skilled artisan will appreciate that other art-recognized linkers may be suitable for use in the constructs of the disclosure (e.g., encoded by the nucleic acids of the disclosure). The skilled artisan will likewise appreciate that other polycistronic constructs (mRNA encoding more than one antigen/polypeptide separately within the same molecule) may be suitable for use as provided herein.

Sequence Optimization

In some embodiments, an ORF encoding an antigen of the disclosure is codon optimized. Codon optimization methods are known in the art. For example, an ORF of any one or more of the sequences provided herein may be codon optimized. Codon optimization, in some embodiments, may be used to match codon frequencies in target and host organisms to ensure proper folding; bias GC content to increase mRNA stability or reduce secondary structures; minimize tandem repeat codons or base runs that may impair gene construction or expression; customize transcriptional and translational control regions; insert or remove protein trafficking sequences; remove/add post translation modification sites in encoded protein (e.g., glycosylation sites); add, remove or shuffle protein domains; insert or delete restriction sites; modify ribosome binding sites and mRNA degradation sites; adjust translational rates to allow the various domains of the protein to fold properly; or reduce or eliminate problem secondary structures

within the polynucleotide. Codon optimization tools, algorithms and services are known in the art – non-limiting examples include services from GeneArt (Life Technologies), DNA2.0 (Menlo Park CA) and/or proprietary methods. In some embodiments, the open reading frame (ORF) sequence is optimized using optimization algorithms.

5 In some embodiments, a codon optimized sequence shares less than 95% sequence identity to a naturally-occurring or wild-type sequence ORF (*e.g.*, a naturally-occurring or wild-type mRNA sequence encoding an EBV antigen). In some embodiments, a codon optimized sequence shares less than 90% sequence identity to a naturally-occurring or wild-type sequence (*e.g.*, a naturally-occurring or wild-type mRNA sequence encoding an EBV antigen). In some
10 embodiments, a codon optimized sequence shares less than 85% sequence identity to a naturally-occurring or wild-type sequence (*e.g.*, a naturally-occurring or wild-type mRNA sequence encoding an EBV antigen). In some embodiments, a codon optimized sequence shares less than 80% sequence identity to a naturally-occurring or wild-type mRNA sequence encoding an EBV antigen). In some embodiments, a codon
15 optimized sequence shares less than 75% sequence identity to a naturally-occurring or wild-type sequence (*e.g.*, a naturally-occurring or wild-type mRNA sequence encoding an EBV antigen).

In some embodiments, a codon optimized sequence shares between 65% and 85% (*e.g.*, between about 67% and about 85% or between about 67% and about 80%) sequence identity to a naturally-occurring or wild-type sequence (*e.g.*, a naturally-occurring or wild-type mRNA
20 sequence encoding an EBV antigen). In some embodiments, a codon optimized sequence shares between 65% and 75% or about 80% sequence identity to a naturally-occurring or wild-type sequence (*e.g.*, a naturally-occurring or wild-type mRNA sequence encoding an EBV antigen).

In some embodiments, a codon-optimized sequence encodes an antigen that is as immunogenic as, or more immunogenic than (*e.g.*, at least 10%, at least 20%, at least 30%, at
25 least 40%, at least 50%, at least 100%, or at least 200% more), than an EBV antigen encoded by a non-codon-optimized sequence.

When transfected into mammalian host cells, the modified mRNAs have a stability of between 12-18 hours, or greater than 18 hours, *e.g.*, 24, 36, 48, 60, 72, or greater than 72 hours and are capable of being expressed by the mammalian host cells.

30 In some embodiments, a codon optimized RNA may be one in which the levels of G/C are enhanced. The G/C-content of nucleic acid molecules (*e.g.*, mRNA) may influence the stability of the RNA. RNA having an increased amount of guanine (G) and/or cytosine (C) residues may be functionally more stable than RNA containing a large amount of adenine (A) and thymine (T) or uracil (U) nucleotides. As an example, WO02/098443 discloses a

pharmaceutical composition containing an mRNA stabilized by sequence modifications in the translated region. Due to the degeneracy of the genetic code, the modifications work by substituting existing codons for those that promote greater RNA stability without changing the resulting amino acid. The approach is limited to coding regions of the RNA.

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Chemically Unmodified Nucleotides

In some embodiments, at least one RNA (e.g., mRNA) of an EBV vaccines of the present disclosure is not chemically modified and comprises the standard ribonucleotides consisting of adenosine, guanosine, cytosine and uridine. In some embodiments, nucleotides and nucleosides of the present disclosure comprise standard nucleoside residues such as those present in transcribed RNA (e.g. A, G, C, or U). In some embodiments, nucleotides and nucleosides of the present disclosure comprise standard deoxyribonucleosides such as those present in DNA (e.g. dA, dG, dC, or dT).

Chemical Modifications

EBV RNA vaccines of the present disclosure comprise, in some embodiments, at least one nucleic acid (e.g., RNA) having an open reading frame encoding at least one EBV antigen, wherein the nucleic acid comprises nucleotides and/or nucleosides that can be standard (unmodified) or modified as is known in the art. In some embodiments, nucleotides and nucleosides of the present disclosure comprise modified nucleotides or nucleosides. Such modified nucleotides and nucleosides can be naturally-occurring modified nucleotides and nucleosides or non-naturally occurring modified nucleotides and nucleosides. Such modifications can include those at the sugar, backbone, or nucleobase portion of the nucleotide and/or nucleoside as are recognized in the art.

In some embodiments, a naturally-occurring modified nucleotide or nucleotide of the disclosure is one as is generally known or recognized in the art. Non-limiting examples of such naturally occurring modified nucleotides and nucleotides can be found, inter alia, in the widely recognized MODOMICS database.

In some embodiments, a non-naturally occurring modified nucleotide or nucleoside of the disclosure is one as is generally known or recognized in the art. Non-limiting examples of such non-naturally occurring modified nucleotides and nucleosides can be found, inter alia, in published US application Nos. PCT/US2012/058519; PCT/US2013/075177; PCT/US2014/058897; PCT/US2014/058891; PCT/US2014/070413; PCT/US2015/36773;

PCT/US2015/36759; PCT/US2015/36771; or PCT/IB2017/051367 all of which are incorporated by reference herein.

Hence, nucleic acids of the disclosure (*e.g.*, DNA nucleic acids and RNA nucleic acids, such as mRNA nucleic acids) can comprise standard nucleotides and nucleosides, naturally-occurring nucleotides and nucleosides, non-naturally-occurring nucleotides and nucleosides, or any combination thereof.

Nucleic acids of the disclosure (*e.g.*, DNA nucleic acids and RNA nucleic acids, such as mRNA nucleic acids), in some embodiments, comprise various (more than one) different types of standard and/or modified nucleotides and nucleosides. In some embodiments, a particular region of a nucleic acid contains one, two or more (optionally different) types of standard and/or modified nucleotides and nucleosides.

In some embodiments, a modified RNA nucleic acid (*e.g.*, a modified mRNA nucleic acid), introduced to a cell or organism, exhibits reduced degradation in the cell or organism, respectively, relative to an unmodified nucleic acid comprising standard nucleotides and nucleosides.

In some embodiments, a modified RNA nucleic acid (*e.g.*, a modified mRNA nucleic acid), introduced into a cell or organism, may exhibit reduced immunogenicity in the cell or organism, respectively (*e.g.*, a reduced innate response) relative to an unmodified nucleic acid comprising standard nucleotides and nucleosides.

Nucleic acids (*e.g.*, RNA nucleic acids, such as mRNA nucleic acids), in some embodiments, comprise non-natural modified nucleotides that are introduced during synthesis or post-synthesis of the nucleic acids to achieve desired functions or properties. The modifications may be present on internucleotide linkages, purine or pyrimidine bases, or sugars. The modification may be introduced with chemical synthesis or with a polymerase enzyme at the terminal of a chain or anywhere else in the chain. Any of the regions of a nucleic acid may be chemically modified.

The present disclosure provides for modified nucleosides and nucleotides of a nucleic acid (*e.g.*, RNA nucleic acids, such as mRNA nucleic acids). A “nucleoside” refers to a compound containing a sugar molecule (*e.g.*, a pentose or ribose) or a derivative thereof in combination with an organic base (*e.g.*, a purine or pyrimidine) or a derivative thereof (also referred to herein as “nucleobase”). A “nucleotide” refers to a nucleoside, including a phosphate group. Modified nucleotides may be synthesized by any useful method, such as, for example, chemically, enzymatically, or recombinantly, to include one or more modified or non-natural nucleosides. Nucleic acids can comprise a region or regions of linked nucleosides. Such regions

may have variable backbone linkages. The linkages can be standard phosphodiester linkages, in which case the nucleic acids would comprise regions of nucleotides.

Modified nucleotide base pairing encompasses not only the standard adenosine-thymine, adenosine-uracil, or guanosine-cytosine base pairs, but also base pairs formed between
5 nucleotides and/or modified nucleotides comprising non-standard or modified bases, wherein the arrangement of hydrogen bond donors and hydrogen bond acceptors permits hydrogen bonding between a non-standard base and a standard base or between two complementary non-standard base structures, such as, for example, in those nucleic acids having at least one chemical modification. One example of such non-standard base pairing is the base pairing between the
10 modified nucleotide inosine and adenine, cytosine or uracil. Any combination of base/sugar or linker may be incorporated into nucleic acids of the present disclosure.

In some embodiments, modified nucleobases in nucleic acids (*e.g.*, RNA nucleic acids, such as mRNA nucleic acids) comprise 1-methyl-pseudouridine (m1 ψ), 1-ethyl-pseudouridine (e1 ψ), 5-methoxy-uridine (mo5U), 5-methyl-cytidine (m5C), and/or pseudouridine (ψ). In some
15 embodiments, modified nucleobases in nucleic acids (*e.g.*, RNA nucleic acids, such as mRNA nucleic acids) comprise 5-methoxymethyl uridine, 5-methylthio uridine, 1-methoxymethyl pseudouridine, 5-methyl cytidine, and/or 5-methoxy cytidine. In some embodiments, the polyribonucleotide includes a combination of at least two (*e.g.*, 2, 3, 4 or more) of any of the aforementioned modified nucleobases, including but not limited to chemical modifications.

20 In some embodiments, a RNA nucleic acid of the disclosure comprises 1-methyl-pseudouridine (m1 ψ) substitutions at one or more or all uridine positions of the nucleic acid.

In some embodiments, a RNA nucleic acid of the disclosure comprises 1-methyl-pseudouridine (m1 ψ) substitutions at one or more or all uridine positions of the nucleic acid and 5-methyl cytidine substitutions at one or more or all cytidine positions of the nucleic acid.

25 In some embodiments, a RNA nucleic acid of the disclosure comprises pseudouridine (ψ) substitutions at one or more or all uridine positions of the nucleic acid.

In some embodiments, a RNA nucleic acid of the disclosure comprises pseudouridine (ψ) substitutions at one or more or all uridine positions of the nucleic acid and 5-methyl cytidine substitutions at one or more or all cytidine positions of the nucleic acid..

30 In some embodiments, a RNA nucleic acid of the disclosure comprises uridine at one or more or all uridine positions of the nucleic acid.

In some embodiments, nucleic acids (*e.g.*, RNA nucleic acids, such as mRNA nucleic acids) are uniformly modified (*e.g.*, fully modified, modified throughout the entire sequence) for a particular modification. For example, a nucleic acid can be uniformly modified with 1-methyl-

pseudouridine, meaning that all uridine residues in the mRNA sequence are replaced with 1-methyl-pseudouridine. Similarly, a nucleic acid can be uniformly modified for any type of nucleoside residue present in the sequence by replacement with a modified residue such as those set forth above.

5 The nucleic acids of the present disclosure may be partially or fully modified along the entire length of the molecule. For example, one or more or all or a given type of nucleotide (*e.g.*, purine or pyrimidine, or any one or more or all of A, G, U, C) may be uniformly modified in a nucleic acid of the disclosure, or in a predetermined sequence region thereof (*e.g.*, in the mRNA including or excluding the polyA tail). In some embodiments, all nucleotides X in a nucleic acid
10 of the present disclosure (or in a sequence region thereof) are modified nucleotides, wherein X may be any one of nucleotides A, G, U, C, or any one of the combinations A+G, A+U, A+C, G+U, G+C, U+C, A+G+U, A+G+C, G+U+C or A+G+C.

 The nucleic acid may contain from about 1% to about 100% modified nucleotides (either in relation to overall nucleotide content, or in relation to one or more types of nucleotide, *i.e.*,
15 any one or more of A, G, U or C) or any intervening percentage (*e.g.*, from 1% to 20%, from 1% to 25%, from 1% to 50%, from 1% to 60%, from 1% to 70%, from 1% to 80%, from 1% to 90%, from 1% to 95%, from 10% to 20%, from 10% to 25%, from 10% to 50%, from 10% to 60%, from 10% to 70%, from 10% to 80%, from 10% to 90%, from 10% to 95%, from 10% to 100%, from 20% to 25%, from 20% to 50%, from 20% to 60%, from 20% to 70%, from 20% to 80%,
20 from 20% to 90%, from 20% to 95%, from 20% to 100%, from 50% to 60%, from 50% to 70%, from 50% to 80%, from 50% to 90%, from 50% to 95%, from 50% to 100%, from 70% to 80%, from 70% to 90%, from 70% to 95%, from 70% to 100%, from 80% to 90%, from 80% to 95%, from 80% to 100%, from 90% to 95%, from 90% to 100%, and from 95% to 100%). It will be understood that any remaining percentage is accounted for by the presence of unmodified A, G,
25 U, or C.

 The nucleic acids may contain at a minimum 1% and at maximum 100% modified nucleotides, or any intervening percentage, such as at least 5% modified nucleotides, at least 10% modified nucleotides, at least 25% modified nucleotides, at least 50% modified nucleotides, at least 80% modified nucleotides, or at least 90% modified nucleotides. For example, the
30 nucleic acids may contain a modified pyrimidine such as a modified uracil or cytosine. In some embodiments, at least 5%, at least 10%, at least 25%, at least 50%, at least 80%, at least 90% or 100% of the uracil in the nucleic acid is replaced with a modified uracil (*e.g.*, a 5-substituted uracil). The modified uracil can be replaced by a compound having a single unique structure, or can be replaced by a plurality of compounds having different structures (*e.g.*, 2, 3, 4 or more

unique structures). In some embodiments, at least 5%, at least 10%, at least 25%, at least 50%, at least 80%, at least 90% or 100% of the cytosine in the nucleic acid is replaced with a modified cytosine (e.g., a 5-substituted cytosine). The modified cytosine can be replaced by a compound having a single unique structure, or can be replaced by a plurality of compounds having different structures (e.g., 2, 3, 4 or more unique structures).

Untranslated Regions (UTRs)

The nucleic acids of the present disclosure may comprise one or more regions or parts which act or function as an untranslated region. Where nucleic acids are designed to encode at least one antigen of interest, the nucleic acid may comprise one or more of these untranslated regions (UTRs). Wild-type untranslated regions of a nucleic acid are transcribed but not translated. In mRNA, the 5' UTR starts at the transcription start site and continues to the start codon but does not include the start codon; whereas, the 3' UTR starts immediately following the stop codon and continues until the transcriptional termination signal. There is growing body of evidence about the regulatory roles played by the UTRs in terms of stability of the nucleic acid molecule and translation. The regulatory features of a UTR can be incorporated into the polynucleotides of the present disclosure to, among other things, enhance the stability of the molecule. The specific features can also be incorporated to ensure controlled down-regulation of the transcript in case they are misdirected to undesired organs sites. A variety of 5'UTR and 3'UTR sequences are known and available in the art.

A 5' UTR is region of an mRNA that is directly upstream (5') from the start codon (the first codon of an mRNA transcript translated by a ribosome). A 5' UTR does not encode a protein (is non-coding). Natural 5'UTRs have features that play roles in translation initiation. They harbor signatures like Kozak sequences which are commonly known to be involved in the process by which the ribosome initiates translation of many genes. Kozak sequences have the consensus CCR(A/G)CCAUGG (SEQ ID NO: 121), where R is a purine (adenine or guanine) three bases upstream of the start codon (AUG), which is followed by another 'G'. 5'UTR also have been known to form secondary structures which are involved in elongation factor binding.

In some embodiments of the disclosure, a 5' UTR is a heterologous UTR, i.e., is a UTR found in nature associated with a different ORF. In another embodiment, a 5' UTR is a synthetic UTR, i.e., does not occur in nature. Synthetic UTRs include UTRs that have been mutated to improve their properties, e.g., which increase gene expression as well as those which are completely synthetic. Exemplary 5' UTRs include *Xenopus* or human derived α -globin or β -globin (8278063; 9012219), human cytochrome b-245 a polypeptide, and hydroxysteroid (17b)

dehydrogenase, and Tobacco etch virus (US8278063, 9012219). CMV immediate-early 1 (IE1) gene (US20140206753, WO2013/185069), the sequence GGGAUCCUACC (SEQ ID NO: 122) (WO2014/144196) may also be used. In another embodiment, 5' UTR of a TOP gene is a 5' UTR of a TOP gene lacking the 5' TOP motif (the oligopyrimidine tract) (e.g., WO2015/101414, WO2015/101415, WO2015/062738, WO2015/024667, WO2015/024668; 5' UTR element derived from ribosomal protein Large 32 (L32) gene (WO2015/101414, WO2015/101415, WO2015/062738), 5' UTR element derived from the 5'UTR of an hydroxysteroid (17- β) dehydrogenase 4 gene (HSD17B4) (WO2015/024667), or a 5' UTR element derived from the 5' UTR of ATP5A1 (WO2015/024667) can be used. In some embodiments, an internal ribosome entry site (IRES) is used instead of a 5' UTR.

In some embodiments, a 5' UTR of the present disclosure comprises a sequence selected from SEQ ID NO: 1 and SEQ ID NO: 104.

A 3' UTR is region of an mRNA that is directly downstream (3') from the stop codon (the codon of an mRNA transcript that signals a termination of translation). A 3' UTR does not encode a protein (is non-coding). Natural or wild type 3' UTRs are known to have stretches of adenosines and uridines embedded in them. These AU rich signatures are particularly prevalent in genes with high rates of turnover. Based on their sequence features and functional properties, the AU rich elements (AREs) can be separated into three classes (Chen et al, 1995): Class I AREs contain several dispersed copies of an AUUUA motif within U-rich regions. C-Myc and MyoD contain class I AREs. Class II AREs possess two or more overlapping UUAUUUA(U/A)(U/A) (SEQ ID NO: 123) nonamers. Molecules containing this type of AREs include GM-CSF and TNF- α . Class III AREs are less well defined. These U rich regions do not contain an AUUUA motif. c-Jun and Myogenin are two well-studied examples of this class. Most proteins binding to the AREs are known to destabilize the messenger, whereas members of the ELAV family, most notably HuR, have been documented to increase the stability of mRNA. HuR binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3' UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message *in vivo*.

Introduction, removal or modification of 3' UTR AU rich elements (AREs) can be used to modulate the stability of nucleic acids (e.g., RNA) of the disclosure. When engineering specific nucleic acids, one or more copies of an ARE can be introduced to make nucleic acids of the disclosure less stable and thereby curtail translation and decrease production of the resultant protein. Likewise, AREs can be identified and removed or mutated to increase the intracellular stability and thus increase translation and production of the resultant protein. Transfection

experiments can be conducted in relevant cell lines, using nucleic acids of the disclosure and protein production can be assayed at various time points post-transfection. For example, cells can be transfected with different ARE-engineering molecules and by using an ELISA kit to the relevant protein and assaying protein produced at 6 hour, 12 hour, 24 hour, 48 hour, and 7 days post-transfection.

3' UTRs may be heterologous or synthetic. With respect to 3' UTRs, globin UTRs, including Xenopus β -globin UTRs and human β -globin UTRs are known in the art (8278063, 9012219, US20110086907). A modified β -globin construct with enhanced stability in some cell types by cloning two sequential human β -globin 3'UTRs head to tail has been developed and is well known in the art (US2012/0195936, WO2014/071963). In addition α 2-globin, α 1-globin, UTRs and mutants thereof are also known in the art (WO2015/101415, WO2015/024667). Other 3' UTRs described in the mRNA constructs in the non-patent literature include CYBA (Ferizi et al., 2015) and albumin (Thess et al., 2015). Other exemplary 3' UTRs include that of bovine or human growth hormone (wild type or modified) (WO2013/185069, US20140206753, WO2014/152774), rabbit β globin and hepatitis B virus (HBV), α -globin 3' UTR and Viral VEEV 3' UTR sequences are also known in the art. In some embodiments, the sequence UUUGAAUU (WO2014/144196) is used. In some embodiments, 3' UTRs of human and mouse ribosomal protein are used. Other examples include rps9 3'UTR (WO2015/101414), FIG4 (WO2015/101415), and human albumin 7 (WO2015/101415).

In some embodiments, a 3' UTR of the present disclosure comprises a sequence selected from SEQ ID NO: 3 and SEQ ID NO: 106.

Those of ordinary skill in the art will understand that 5'UTRs that are heterologous or synthetic may be used with any desired 3' UTR sequence. For example, a heterologous 5'UTR may be used with a synthetic 3'UTR with a heterologous 3' UTR.

Non-UTR sequences may also be used as regions or subregions within a nucleic acid. For example, introns or portions of introns sequences may be incorporated into regions of nucleic acid of the disclosure. Incorporation of intronic sequences may increase protein production as well as nucleic acid levels.

Combinations of features may be included in flanking regions and may be contained within other features. For example, the ORF may be flanked by a 5' UTR which may contain a strong Kozak translational initiation signal and/or a 3' UTR which may include an oligo(dT) sequence for templated addition of a poly-A tail. 5' UTR may comprise a first polynucleotide fragment and a second polynucleotide fragment from the same and/or different genes such as the

5' UTRs described in US Patent Application Publication No.20100293625 and PCT/US2014/069155, herein incorporated by reference in its entirety.

It should be understood that any UTR from any gene may be incorporated into the regions of a nucleic acid. Furthermore, multiple wild-type UTRs of any known gene may be utilized. It is also within the scope of the present disclosure to provide artificial UTRs which are not variants of wild type regions. These UTRs or portions thereof may be placed in the same orientation as in the transcript from which they were selected or may be altered in orientation or location. Hence a 5' or 3' UTR may be inverted, shortened, lengthened, made with one or more other 5' UTRs or 3' UTRs. As used herein, the term "altered" as it relates to a UTR sequence, means that the UTR has been changed in some way in relation to a reference sequence. For example, a 3' UTR or 5' UTR may be altered relative to a wild-type or native UTR by the change in orientation or location as taught above or may be altered by the inclusion of additional nucleotides, deletion of nucleotides, swapping or transposition of nucleotides. Any of these changes producing an "altered" UTR (whether 3' or 5') comprise a variant UTR.

In some embodiments, a double, triple or quadruple UTR such as a 5' UTR or 3' UTR may be used. As used herein, a "double" UTR is one in which two copies of the same UTR are encoded either in series or substantially in series. For example, a double beta-globin 3' UTR may be used as described in US Patent publication 20100129877, the contents of which are incorporated herein by reference in its entirety.

It is also within the scope of the present disclosure to have patterned UTRs. As used herein "patterned UTRs" are those UTRs which reflect a repeating or alternating pattern, such as ABABAB or AABBAABBAABB or ABCABCABC or variants thereof repeated once, twice, or more than 3 times. In these patterns, each letter, A, B, or C represent a different UTR at the nucleotide level.

In some embodiments, flanking regions are selected from a family of transcripts whose proteins share a common function, structure, feature or property. For example, polypeptides of interest may belong to a family of proteins which are expressed in a particular cell, tissue or at some time during development. The UTRs from any of these genes may be swapped for any other UTR of the same or different family of proteins to create a new polynucleotide. As used herein, a "family of proteins" is used in the broadest sense to refer to a group of two or more polypeptides of interest which share at least one function, structure, feature, localization, origin, or expression pattern.

The untranslated region may also include translation enhancer elements (TEE). As a non-limiting example, the TEE may include those described in US Application No.20090226470, herein incorporated by reference in its entirety, and those known in the art.

5 In Vitro Transcription of RNA

cDNA encoding the polynucleotides described herein may be transcribed using an in vitro transcription (IVT) system. *In vitro* transcription of RNA is known in the art and is described in International Publication WO/2014/152027, which is incorporated by reference herein in its entirety.

10 In some embodiments, the RNA transcript is generated using a non-amplified, linearized DNA template in an *in vitro* transcription reaction to generate the RNA transcript. In some embodiments, the template DNA is isolated DNA. In some embodiments, the template DNA is cDNA. In some embodiments, the cDNA is formed by reverse transcription of a RNA polynucleotide, for example, but not limited to EBV RNA, *e.g.* EBV mRNA. In some
15 embodiments, cells, *e.g.*, bacterial cells, *e.g.*, *E. coli*, *e.g.*, DH-1 cells are transfected with the plasmid DNA template. In some embodiments, the transfected cells are cultured to replicate the plasmid DNA which is then isolated and purified. In some embodiments, the DNA template includes a RNA polymerase promoter, *e.g.*, a T7 promoter located 5' to and operably linked to the gene of interest.

20 In some embodiments, an *in vitro* transcription template encodes a 5' untranslated (UTR) region, contains an open reading frame, and encodes a 3' UTR and a polyA tail. The particular nucleic acid sequence composition and length of an *in vitro* transcription template will depend on the mRNA encoded by the template.

A “5' untranslated region” (UTR) refers to a region of an mRNA that is directly upstream
25 (*i.e.*, 5') from the start codon (*i.e.*, the first codon of an mRNA transcript translated by a ribosome) that does not encode a polypeptide. When RNA transcripts are being generated, the 5' UTR may comprise a promoter sequence. Such promoter sequences are known in the art. It should be understood that such promoter sequences will not be present in a vaccine of the disclosure.

30 A “3' untranslated region” (UTR) refers to a region of an mRNA that is directly downstream (*i.e.*, 3') from the stop codon (*i.e.*, the codon of an mRNA transcript that signals a termination of translation) that does not encode a polypeptide.

An “open reading frame” is a continuous stretch of DNA beginning with a start codon (*e.g.*, methionine (ATG)), and ending with a stop codon (*e.g.*, TAA, TAG or TGA) and encodes a polypeptide.

5 A “polyA tail” is a region of mRNA that is downstream, *e.g.*, directly downstream (*i.e.*, 3'), from the 3' UTR that contains multiple, consecutive adenosine monophosphates. A polyA tail may contain 10 to 300 adenosine monophosphates. For example, a polyA tail may contain 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290 or 300 adenosine monophosphates. In some
10 embodiments, a polyA tail contains 50 to 250 adenosine monophosphates. In a relevant biological setting (*e.g.*, in cells, *in vivo*) the poly(A) tail functions to protect mRNA from enzymatic degradation, *e.g.*, in the cytoplasm, and aids in transcription termination, and/or export of the mRNA from the nucleus and translation.

In some embodiments, a nucleic acid includes 200 to 3,000 nucleotides. For example, a nucleic acid may include 200 to 500, 200 to 1000, 200 to 1500, 200 to 3000, 500 to 1000, 500 to
15 1500, 500 to 2000, 500 to 3000, 1000 to 1500, 1000 to 2000, 1000 to 3000, 1500 to 3000, or 2000 to 3000 nucleotides).

An *in vitro* transcription system typically comprises a transcription buffer, nucleotide triphosphates (NTPs), an RNase inhibitor and a polymerase.

The NTPs may be manufactured in house, may be selected from a supplier, or may be
20 synthesized as described herein. The NTPs may be selected from, but are not limited to, those described herein including natural and unnatural (modified) NTPs.

Any number of RNA polymerases or variants may be used in the method of the present disclosure. The polymerase may be selected from, but is not limited to, a phage RNA polymerase, *e.g.*, a T7 RNA polymerase, a T3 RNA polymerase, a SP6 RNA polymerase, and/or
25 mutant polymerases such as, but not limited to, polymerases able to incorporate modified nucleic acids and/or modified nucleotides, including chemically modified nucleic acids and/or nucleotides. Some embodiments exclude the use of DNase.

In some embodiments, the RNA transcript is capped *via* enzymatic capping. In some
30 embodiments, the RNA comprises 5' terminal cap, for example, 7mG(5')ppp(5')NlmpNp.

Chemical Synthesis

Solid-phase chemical synthesis. Nucleic acids the present disclosure may be manufactured in whole or in part using solid phase techniques. Solid-phase chemical synthesis of nucleic acids is an automated method wherein molecules are immobilized on a solid support

and synthesized step by step in a reactant solution. Solid-phase synthesis is useful in site-specific introduction of chemical modifications in the nucleic acid sequences.

Liquid Phase Chemical Synthesis. The synthesis of nucleic acids of the present disclosure by the sequential addition of monomer building blocks may be carried out in a liquid phase.

5 *Combination of Synthetic Methods.* The synthetic methods discussed above each has its own advantages and limitations. Attempts have been conducted to combine these methods to overcome the limitations. Such combinations of methods are within the scope of the present disclosure. The use of solid-phase or liquid-phase chemical synthesis in combination with enzymatic ligation provides an efficient way to generate long chain nucleic acids that cannot be
10 obtained by chemical synthesis alone.

Ligation of Nucleic Acid Regions or Subregions

Assembling nucleic acids by a ligase may also be used. DNA or RNA ligases promote intermolecular ligation of the 5' and 3' ends of polynucleotide chains through the formation of a
15 phosphodiester bond. Nucleic acids such as chimeric polynucleotides and/or circular nucleic acids may be prepared by ligation of one or more regions or subregions. DNA fragments can be joined by a ligase catalyzed reaction to create recombinant DNA with different functions. Two oligodeoxynucleotides, one with a 5' phosphoryl group and another with a free 3' hydroxyl group, serve as substrates for a DNA ligase.

Purification

Purification of the nucleic acids described herein may include, but is not limited to, nucleic acid clean-up, quality assurance and quality control. Clean-up may be performed by methods known in the arts such as, but not limited to, AGENCOURT® beads (Beckman Coulter
25 Genomics, Danvers, MA), poly-T beads, LNATM oligo-T capture probes (EXIQON® Inc, Vedbaek, Denmark) or HPLC based purification methods such as, but not limited to, strong anion exchange HPLC, weak anion exchange HPLC, reverse phase HPLC (RP-HPLC), and hydrophobic interaction HPLC (HIC-HPLC). The term "purified" when used in relation to a nucleic acid such as a "purified nucleic acid" refers to one that is separated from at least one
30 contaminant. A "contaminant" is any substance that makes another unfit, impure or inferior. Thus, a purified nucleic acid (e.g., DNA and RNA) is present in a form or setting different from that in which it is found in nature, or a form or setting different from that which existed prior to subjecting it to a treatment or purification method.

A quality assurance and/or quality control check may be conducted using methods such as, but not limited to, gel electrophoresis, UV absorbance, or analytical HPLC.

In some embodiments, the nucleic acids may be sequenced by methods including, but not limited to reverse-transcriptase-PCR.

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Quantification

In some embodiments, the nucleic acids of the present invention may be quantified in exosomes or when derived from one or more bodily fluid. Bodily fluids include peripheral blood, serum, plasma, ascites, urine, cerebrospinal fluid (CSF), sputum, saliva, bone marrow, synovial fluid, aqueous humor, amniotic fluid, cerumen, breast milk, bronchoalveolar lavage fluid, semen, prostatic fluid, cowper's fluid or pre-ejaculatory fluid, sweat, fecal matter, hair, tears, cyst fluid, pleural and peritoneal fluid, pericardial fluid, lymph, chyme, chyle, bile, interstitial fluid, menses, pus, sebum, vomit, vaginal secretions, mucosal secretion, stool water, pancreatic juice, lavage fluids from sinus cavities, bronchopulmonary aspirates, blastocyl cavity fluid, and umbilical cord blood. Alternatively, exosomes may be retrieved from an organ selected from the group consisting of lung, heart, pancreas, stomach, intestine, bladder, kidney, ovary, testis, skin, colon, breast, prostate, brain, esophagus, liver, and placenta.

Assays may be performed using construct specific probes, cytometry, qRT-PCR, real-time PCR, PCR, flow cytometry, electrophoresis, mass spectrometry, or combinations thereof while the exosomes may be isolated using immunohistochemical methods such as enzyme linked immunosorbent assay (ELISA) methods. Exosomes may also be isolated by size exclusion chromatography, density gradient centrifugation, differential centrifugation, nanomembrane ultrafiltration, immunoabsorbent capture, affinity purification, microfluidic separation, or combinations thereof.

These methods afford the investigator the ability to monitor, in real time, the level of nucleic acids remaining or delivered. This is possible because the nucleic acids of the present disclosure, in some embodiments, differ from the endogenous forms due to the structural or chemical modifications.

In some embodiments, the nucleic acid may be quantified using methods such as, but not limited to, ultraviolet visible spectroscopy (UV/Vis). A non-limiting example of a UV/Vis spectrometer is a NANODROP® spectrometer (ThermoFisher, Waltham, MA). The quantified nucleic acid may be analyzed in order to determine if the nucleic acid may be of proper size, check that no degradation of the nucleic acid has occurred. Degradation of the nucleic acid may be checked by methods such as, but not limited to, agarose gel electrophoresis, HPLC based

purification methods such as, but not limited to, strong anion exchange HPLC, weak anion exchange HPLC, reverse phase HPLC (RP-HPLC), and hydrophobic interaction HPLC (HIC-HPLC), liquid chromatography-mass spectrometry (LCMS), capillary electrophoresis (CE) and capillary gel electrophoresis (CGE).

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Pharmaceutical Formulations

Provided herein are compositions (*e.g.*, pharmaceutical compositions), methods, kits and reagents for prevention or treatment of EBV in humans and other mammals, for example. EBV RNA (*e.g.*, mRNA) vaccines can be used as therapeutic or prophylactic agents. They may be used in medicine to prevent and/or treat infectious disease.

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In some embodiments, an EBV vaccine containing RNA polynucleotides as described herein can be administered to a subject (*e.g.*, a mammalian subject, such as a human subject), and the RNA polynucleotides are translated *in vivo* to produce an antigenic polypeptide (antigen).

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An "effective amount" of an EBV vaccine is based, at least in part, on the target tissue, target cell type, means of administration, physical characteristics of the RNA (*e.g.*, length, nucleotide composition, and/or extent of modified nucleosides), other components of the vaccine, and other determinants, such as age, body weight, height, sex and general health of the subject. Typically, an effective amount of an EBV vaccine provides an induced or boosted

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immune response as a function of antigen production in the cells of the subject. In some embodiments, an effective amount of the EBV RNA vaccine containing RNA polynucleotides having at least one chemical modifications are more efficient than a composition containing a corresponding unmodified polynucleotide encoding the same antigen or a peptide antigen.

Increased antigen production may be demonstrated by increased cell transfection (the percentage of cells transfected with the RNA vaccine), increased protein translation and/or expression from the polynucleotide, decreased nucleic acid degradation (as demonstrated, for example, by increased duration of protein translation from a modified polynucleotide), or altered antigen specific immune response of the host cell.

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The term "pharmaceutical composition" refers to the combination of an active agent with a carrier, inert or active, making the composition especially suitable for diagnostic or therapeutic use *in vivo* or *ex vivo*. A "pharmaceutically acceptable carrier," after administered to or upon a subject, does not cause undesirable physiological effects. The carrier in the pharmaceutical composition must be "acceptable" also in the sense that it is compatible with the active ingredient and can be capable of stabilizing it. One or more solubilizing agents can be utilized as

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pharmaceutical carriers for delivery of an active agent. Examples of a pharmaceutically acceptable carrier include, but are not limited to, biocompatible vehicles, adjuvants, additives, and diluents to achieve a composition usable as a dosage form. Examples of other carriers include colloidal silicon oxide, magnesium stearate, cellulose, and sodium lauryl sulfate.

- 5 Additional suitable pharmaceutical carriers and diluents, as well as pharmaceutical necessities for their use, are described in Remington's Pharmaceutical Sciences.

In some embodiments, RNA vaccines (including polynucleotides and their encoded polypeptides) in accordance with the present disclosure may be used for treatment or prevention of EBV. EBV RNA vaccines may be administered prophylactically or therapeutically as part of
10 an active immunization scheme to healthy individuals or early in infection during the incubation phase or during active infection after onset of symptoms. In some embodiments, the amount of RNA vaccines of the present disclosure provided to a cell, a tissue or a subject may be an amount effective for immune prophylaxis.

EBV RNA (*e.g.*, mRNA) vaccines may be administered with other prophylactic or
15 therapeutic compounds. As a non-limiting example, a prophylactic or therapeutic compound may be an adjuvant or a booster. As used herein, when referring to a prophylactic composition, such as a vaccine, the term "booster" refers to an extra administration of the prophylactic (vaccine) composition. A booster (or booster vaccine) may be given after an earlier
20 administration of the prophylactic composition. The time of administration between the initial administration of the prophylactic composition and the booster may be, but is not limited to, 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes, 6 minutes, 7 minutes, 8 minutes, 9 minutes, 10 minutes, 15 minutes, 20 minutes, 35 minutes, 40 minutes, 45 minutes, 50 minutes, 55 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21
25 hours, 22 hours, 23 hours, 1 day, 36 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 10 days, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 18 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, 11 years, 12 years, 13 years, 14 years, 15 years, 16 years, 17 years, 18 years, 19 years, 20 years, 25 years, 30 years, 35 years, 40 years, 45 years, 50
30 years, 55 years, 60 years, 65 years, 70 years, 75 years, 80 years, 85 years, 90 years, 95 years or more than 99 years. In exemplary embodiments, the time of administration between the initial administration of the prophylactic composition and the booster may be, but is not limited to, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 6 months or 1 year.

In some embodiments, EBV RNA vaccines may be administered intramuscularly, intranasally or intradermally, similarly to the administration of inactivated vaccines known in the art.

The EBV RNA vaccines may be utilized in various settings depending on the prevalence of the infection or the degree or level of unmet medical need. As a non-limiting example, the RNA vaccines may be utilized to treat and/or prevent a variety of infectious disease. RNA vaccines have superior properties in that they produce much larger antibody titers, better neutralizing immunity, produce more durable immune responses, and/or produce responses earlier than commercially available vaccines.

Provided herein are pharmaceutical compositions including EBV RNA vaccines and RNA vaccine compositions and/or complexes optionally in combination with one or more pharmaceutically acceptable excipients.

EBV RNA (*e.g.*, mRNA) vaccines may be formulated or administered alone or in conjunction with one or more other components. For instance, EBV RNA vaccines (vaccine compositions) may comprise other components including, but not limited to, adjuvants.

In some embodiments, EBV RNA vaccines do not include an adjuvant (they are adjuvant free).

EBV RNA (*e.g.*, mRNA) vaccines may be formulated or administered in combination with one or more pharmaceutically-acceptable excipients. In some embodiments, vaccine compositions comprise at least one additional active substances, such as, for example, a therapeutically-active substance, a prophylactically-active substance, or a combination of both. Vaccine compositions may be sterile, pyrogen-free or both sterile and pyrogen-free. General considerations in the formulation and/or manufacture of pharmaceutical agents, such as vaccine compositions, may be found, for example, in Remington: The Science and Practice of Pharmacy 21st ed., Lippincott Williams & Wilkins, 2005 (incorporated herein by reference in its entirety).

In some embodiments, EBV RNA vaccines are administered to humans, human patients or subjects. For the purposes of the present disclosure, the phrase “active ingredient” generally refers to the RNA vaccines or the polynucleotides contained therein, for example, RNA polynucleotides (*e.g.*, mRNA polynucleotides) encoding antigens.

Formulations of the vaccine compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient (*e.g.*, mRNA polynucleotide) into association with an excipient and/or one or more other accessory ingredients, and then, if

necessary and/or desirable, dividing, shaping and/or packaging the product into a desired single- or multi-dose unit.

Relative amounts of the active ingredient, the pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the disclosure will vary, depending upon the identity, size, and/or condition of the subject treated and further depending upon the route by which the composition is to be administered. By way of example, the composition may comprise between 0.1% and 100%, *e.g.*, between 0.5 and 50%, between 1-30%, between 5-80%, at least 80% (w/w) active ingredient.

In some embodiments, EBV RNA vaccines are formulated using one or more excipients to: (1) increase stability; (2) increase cell transfection; (3) permit the sustained or delayed release (*e.g.*, from a depot formulation); (4) alter the biodistribution (*e.g.*, target to specific tissues or cell types); (5) increase the translation of encoded protein *in vivo*; and/or (6) alter the release profile of encoded protein (antigen) *in vivo*. In addition to traditional excipients such as any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, excipients can include, without limitation, lipidoids, liposomes, lipid nanoparticles, polymers, lipoplexes, core-shell nanoparticles, peptides, proteins, cells transfected with EBV RNA vaccines (*e.g.*, for transplantation into a subject), hyaluronidase, nanoparticle mimics and combinations thereof.

Lipid Nanoparticles (LNPs)

In some embodiments, EBV RNA (*e.g.*, mRNA) vaccines of the disclosure are formulated in a lipid nanoparticle (LNP). Lipid nanoparticles typically comprise ionizable cationic lipid, non-cationic lipid, sterol and PEG lipid components along with the nucleic acid cargo of interest. The lipid nanoparticles of the disclosure can be generated using components, compositions, and methods as are generally known in the art, see for example PCT/US2016/052352; PCT/US2016/068300; PCT/US2017/037551; PCT/US2015/027400; PCT/US2016/047406; PCT/US2016000129; PCT/US2016/014280; PCT/US2016/014280; PCT/US2017/038426; PCT/US2014/027077; PCT/US2014/055394; PCT/US2016/52117; PCT/US2012/069610; PCT/US2017/027492; PCT/US2016/059575 and PCT/US2016/069491 all of which are incorporated by reference herein in their entirety.

Vaccines of the present disclosure are typically formulated in lipid nanoparticle. In some embodiments, the lipid nanoparticle comprises at least one ionizable cationic lipid, at least one

non-cationic lipid, at least one sterol, and/or at least one polyethylene glycol (PEG)-modified lipid.

In some embodiments, the lipid nanoparticle comprises a molar ratio of 20-60% ionizable cationic lipid. For example, the lipid nanoparticle may comprise a molar ratio of 20-50%, 20-40%, 20-30%, 30-60%, 30-50%, 30-40%, 40-60%, 40-50%, or 50-60% ionizable cationic lipid. In some embodiments, the lipid nanoparticle comprises a molar ratio of 20%, 30%, 40%, 50, or 60% ionizable cationic lipid.

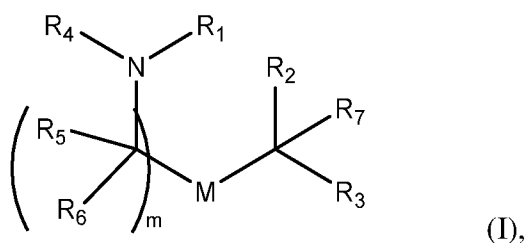
In some embodiments, the lipid nanoparticle comprises a molar ratio of 5-25% non-cationic lipid. For example, the lipid nanoparticle may comprise a molar ratio of 5-20%, 5-15%, 5-10%, 10-25%, 10-20%, 10-25%, 15-25%, 15-20%, or 20-25% non-cationic lipid. In some embodiments, the lipid nanoparticle comprises a molar ratio of 5%, 10%, 15%, 20%, or 25% non-cationic lipid.

In some embodiments, the lipid nanoparticle comprises a molar ratio of 25-55% sterol. For example, the lipid nanoparticle may comprise a molar ratio of 25-50%, 25-45%, 25-40%, 25-35%, 25-30%, 30-55%, 30-50%, 30-45%, 30-40%, 30-35%, 35-55%, 35-50%, 35-45%, 35-40%, 40-55%, 40-50%, 40-45%, 45-55%, 45-50%, or 50-55% sterol. In some embodiments, the lipid nanoparticle comprises a molar ratio of 25%, 30%, 35%, 40%, 45%, 50%, or 55% sterol.

In some embodiments, the lipid nanoparticle comprises a molar ratio of 0.5-15% PEG-modified lipid. For example, the lipid nanoparticle may comprise a molar ratio of 0.5-10%, 0.5-5%, 1-15%, 1-10%, 1-5%, 2-15%, 2-10%, 2-5%, 5-15%, 5-10%, or 10-15%. In some embodiments, the lipid nanoparticle comprises a molar ratio of 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, or 15% PEG-modified lipid.

In some embodiments, the lipid nanoparticle comprises a molar ratio of 20-60% ionizable cationic lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid.

In some embodiments, an ionizable cationic lipid of the disclosure comprises a compound of Formula (I):



or a salt or isomer thereof, wherein:

R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, -R*YR'', -YR'', and -R''M'R';

R₂ and R₃ are independently selected from the group consisting of H, C₁₋₁₄ alkyl, C₂₋₁₄ alkenyl, -R*YR'', -YR'', and -R*OR'', or R₂ and R₃, together with the atom to which they are attached, form a heterocycle or carbocycle;

R₄ is selected from the group consisting of a C₃₋₆ carbocycle, -(CH₂)_nQ, -(CH₂)_nCHQR, -CHQR, -CQ(R)₂, and unsubstituted C₁₋₆ alkyl, where Q is selected from a carbocycle, heterocycle, -OR, -O(CH₂)_nN(R)₂, -C(O)OR, -OC(O)R, -CX₃, -CX₂H, -CXH₂, -CN, -N(R)₂, -C(O)N(R)₂, -N(R)C(O)R, -N(R)S(O)₂R, -N(R)C(O)N(R)₂, -N(R)C(S)N(R)₂, -N(R)R₈, -O(CH₂)_nOR, -N(R)C(=NR₉)N(R)₂, -N(R)C(=CHR₉)N(R)₂, -OC(O)N(R)₂, -N(R)C(O)OR, -N(OR)C(O)R, -N(OR)S(O)₂R, -N(OR)C(O)OR, -N(OR)C(O)N(R)₂, -N(OR)C(S)N(R)₂, -N(OR)C(=NR₉)N(R)₂, -N(OR)C(=CHR₉)N(R)₂, -C(=NR₉)N(R)₂, -C(=NR₉)R, -C(O)N(R)OR, and -C(R)N(R)₂C(O)OR, and each n is independently selected from 1, 2, 3, 4, and 5;

each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-, -N(R')C(O)-, -C(O)-, -C(S)-, -C(S)S-, -SC(S)-, -CH(OH)-, -P(O)(OR')O-, -S(O)₂-, -S-S-, an aryl group, and a heteroaryl group;

R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

R₈ is selected from the group consisting of C₃₋₆ carbocycle and heterocycle;

R₉ is selected from the group consisting of H, CN, NO₂, C₁₋₆ alkyl, -OR, -S(O)₂R, -S(O)₂N(R)₂, C₂₋₆ alkenyl, C₃₋₆ carbocycle and heterocycle;

each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, -R*YR'', -YR'', and H;

each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₂₋₁₂ alkenyl;

each Y is independently a C₃₋₆ carbocycle;

each X is independently selected from the group consisting of F, Cl, Br, and I; and

m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13.

In some embodiments, a subset of compounds of Formula (I) includes those in which when R₄ is -(CH₂)_nQ, -(CH₂)_nCHQR, -CHQR, or -CQ(R)₂, then (i) Q is not -N(R)₂ when n is 1, 2, 3, 4 or 5, or (ii) Q is not 5, 6, or 7-membered heterocycloalkyl when n is 1 or 2.

5 In some embodiments, another subset of compounds of Formula (I) includes those in which

R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, -R*YR'', -YR'', and -R''M'R';

10 R₂ and R₃ are independently selected from the group consisting of H, C₁₋₁₄ alkyl, C₂₋₁₄ alkenyl, -R*YR'', -YR'', and -R*OR'', or R₂ and R₃, together with the atom to which they are attached, form a heterocycle or carbocycle;

R₄ is selected from the group consisting of a C₃₋₆ carbocycle, -(CH₂)_nQ, -(CH₂)_nCHQR, -CHQR, -CQ(R)₂, and unsubstituted C₁₋₆ alkyl, where Q is selected from a C₃₋₆ carbocycle, a 5- to 14-membered heteroaryl having one or more heteroatoms selected from N, O, and S, -OR, -O(CH₂)_nN(R)₂, -C(O)OR, -OC(O)R, -CX₃, -CX₂H, -CXH₂, -CN, -C(O)N(R)₂, -N(R)C(O)R, -N(R)S(O)₂R, -N(R)C(O)N(R)₂, -N(R)C(S)N(R)₂, -CRN(R)₂C(O)OR, -N(R)R₈, -O(CH₂)_nOR, -N(R)C(=NR₉)N(R)₂, -N(R)C(=CHR₉)N(R)₂, -OC(O)N(R)₂, -N(R)C(O)OR, -N(OR)C(O)R, -N(OR)S(O)₂R, -N(OR)C(O)OR, -N(OR)C(O)N(R)₂, -N(OR)C(S)N(R)₂, -N(OR)C(=NR₉)N(R)₂, -N(OR)C(=CHR₉)N(R)₂, -C(=NR₉)N(R)₂, -C(=NR₉)R, -C(O)N(R)OR, and a 5- to 14-membered heterocycloalkyl having one or more heteroatoms selected from N, O, and S which is substituted with one or more substituents selected from oxo (=O), OH, amino, mono- or di-alkylamino, and C₁₋₃ alkyl, and each n is independently selected from 1, 2, 3, 4, and 5;

each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

25 each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-, -N(R')C(O)-, -C(O)-, -C(S)-, -C(S)S-, -SC(S)-, -CH(OH)-, -P(O)(OR')O-, -S(O)₂-, -S-S-, an aryl group, and a heteroaryl group;

30 R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

R₈ is selected from the group consisting of C₃₋₆ carbocycle and heterocycle;

R₉ is selected from the group consisting of H, CN, NO₂, C₁₋₆ alkyl, -OR, -S(O)₂R, -S(O)₂N(R)₂, C₂₋₆ alkenyl, C₃₋₆ carbocycle and heterocycle;

each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, -R*YR'', -YR'', and H;

5 each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₂₋₁₂ alkenyl;

each Y is independently a C₃₋₆ carbocycle;

10 each X is independently selected from the group consisting of F, Cl, Br, and I; and m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13, or salts or isomers thereof.

In some embodiments, another subset of compounds of Formula (I) includes those in which

15 R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, -R*YR'', -YR'', and -R''M'R';

R₂ and R₃ are independently selected from the group consisting of H, C₁₋₁₄ alkyl, C₂₋₁₄ alkenyl, -R*YR'', -YR'', and -R*OR'', or R₂ and R₃, together with the atom to which they are attached, form a heterocycle or carbocycle;

20 R₄ is selected from the group consisting of a C₃₋₆ carbocycle, -(CH₂)_nQ, -(CH₂)_nCHQR, -CHQR, -CQ(R)₂, and unsubstituted C₁₋₆ alkyl, where Q is selected from a C₃₋₆ carbocycle, a 5- to 14-membered heterocycle having one or more heteroatoms selected from N, O, and S, -OR, -O(CH₂)_nN(R)₂, -C(O)OR, -OC(O)R, -CX₃, -CX₂H, -CXH₂, -CN, -C(O)N(R)₂, -N(R)C(O)R, -N(R)S(O)₂R, -N(R)C(O)N(R)₂, -N(R)C(S)N(R)₂, -CRN(R)₂C(O)OR, -N(R)R₈, -O(CH₂)_nOR, 25 -N(R)C(=NR₉)N(R)₂, -N(R)C(=CHR₉)N(R)₂, -OC(O)N(R)₂, -N(R)C(O)OR, -N(OR)C(O)R, -N(OR)S(O)₂R, -N(OR)C(O)OR, -N(OR)C(O)N(R)₂, -N(OR)C(S)N(R)₂, -N(OR)C(=NR₉)N(R)₂, -N(OR)C(=CHR₉)N(R)₂, -C(=NR₉)R, -C(O)N(R)OR, and -C(=NR₉)N(R)₂, and each n is independently selected from 1, 2, 3, 4, and 5; and when Q is a 5- to 14-membered heterocycle and (i) R₄ is -(CH₂)_nQ in which n is 1 or 2, or (ii) R₄ is 30 -(CH₂)_nCHQR in which n is 1, or (iii) R₄ is -CHQR, and -CQ(R)₂, then Q is either a 5- to 14-membered heteroaryl or 8- to 14-membered heterocycloalkyl;

each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-, -N(R')C(O)-, -C(O)-, -C(S)-, -C(S)S-, -SC(S)-, -CH(OH)-, -P(O)(OR')O-, -S(O)₂-, -S-S-, an aryl group, and a heteroaryl group;

R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

R₈ is selected from the group consisting of C₃₋₆ carbocycle and heterocycle;

R₉ is selected from the group consisting of H, CN, NO₂, C₁₋₆ alkyl, -OR, -S(O)₂R, -S(O)₂N(R)₂, C₂₋₆ alkenyl, C₃₋₆ carbocycle and heterocycle;

each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, -R*YR'', -YR'', and H;

each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₂₋₁₂ alkenyl;

each Y is independently a C₃₋₆ carbocycle;

each X is independently selected from the group consisting of F, Cl, Br, and I; and

m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13, or salts or isomers thereof.

In some embodiments, another subset of compounds of Formula (I) includes those in which

R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, -R*YR'', -YR'', and -R''M'R';

R₂ and R₃ are independently selected from the group consisting of H, C₁₋₁₄ alkyl, C₂₋₁₄ alkenyl, -R*YR'', -YR'', and -R*OR'', or R₂ and R₃, together with the atom to which they are attached, form a heterocycle or carbocycle;

R₄ is selected from the group consisting of a C₃₋₆ carbocycle, -(CH₂)_nQ, -(CH₂)_nCHQR, -CHQR, -CQ(R)₂, and unsubstituted C₁₋₆ alkyl, where Q is selected from a C₃₋₆ carbocycle, a 5- to 14-membered heteroaryl having one or more heteroatoms selected from N, O, and S, -OR, -O(CH₂)_nN(R)₂, -C(O)OR, -OC(O)R, -CX₃, -CX₂H, -CXH₂, -CN, -C(O)N(R)₂, -N(R)C(O)R, -N(R)S(O)₂R, -N(R)C(O)N(R)₂, -N(R)C(S)N(R)₂, -CRN(R)₂C(O)OR, -N(R)R₈, -O(CH₂)_nOR, -N(R)C(=NR₉)N(R)₂, -N(R)C(=CHR₉)N(R)₂, -OC(O)N(R)₂, -N(R)C(O)OR, -N(OR)C(O)R,

-N(OR)S(O)₂R, -N(OR)C(O)OR, -N(OR)C(O)N(R)₂, -N(OR)C(S)N(R)₂,
 -N(OR)C(=NR₉)N(R)₂, -N(OR)C(=CHR₉)N(R)₂, -C(=NR₉)R, -C(O)N(R)OR, and
 -C(=NR₉)N(R)₂, and each n is independently selected from 1, 2, 3, 4, and 5;

each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl,
 5 and H;

each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl,
 and H;

M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-,
 -N(R')C(O)-, -C(O)-, -C(S)-, -C(S)S-, -SC(S)-, -CH(OH)-, -P(O)(OR')O-, -S(O)₂-, -S-S-, an aryl
 10 group, and a heteroaryl group;

R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

R₈ is selected from the group consisting of C₃₋₆ carbocycle and heterocycle;

R₉ is selected from the group consisting of H, CN, NO₂, C₁₋₆ alkyl, -OR, -S(O)₂R,
 -S(O)₂N(R)₂, C₂₋₆ alkenyl, C₃₋₆ carbocycle and heterocycle;

each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl,
 15 and H;

each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl,
 -R*YR'', -YR'', and H;

each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄
 20 alkenyl;

each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₂₋₁₂
 alkenyl;

each Y is independently a C₃₋₆ carbocycle;

each X is independently selected from the group consisting of F, Cl, Br, and I; and

25 m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

or salts or isomers thereof.

In some embodiments, another subset of compounds of Formula (I) includes those in
 which

R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, -R*YR'', -YR'',
 30 and -R''M'R';

R₂ and R₃ are independently selected from the group consisting of H, C₂₋₁₄ alkyl, C₂₋₁₄
 alkenyl, -R*YR'', -YR'', and -R*OR'', or R₂ and R₃, together with the atom to which they are
 attached, form a heterocycle or carbocycle;

R₄ is -(CH₂)_nQ or -(CH₂)_nCHQR, where Q is -N(R)₂, and n is selected from 3, 4, and 5;

each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

5 M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-, -N(R')C(O)-, -C(O)-, -C(S)-, -C(S)S-, -SC(S)-, -CH(OH)-, -P(O)(OR')O-, -S(O)₂-, -S-S-, an aryl group, and a heteroaryl group;

R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

10 each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, -R*YR'', -YR'', and H;

each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

15 each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₁₋₁₂ alkenyl;

each Y is independently a C₃₋₆ carbocycle;

each X is independently selected from the group consisting of F, Cl, Br, and I; and

m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

20 or salts or isomers thereof.

In some embodiments, another subset of compounds of Formula (I) includes those in which

R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, -R*YR'', -YR'', and -R''M'R';

25 R₂ and R₃ are independently selected from the group consisting of C₁₋₁₄ alkyl, C₂₋₁₄ alkenyl, -R*YR'', -YR'', and -R*OR'', or R₂ and R₃, together with the atom to which they are attached, form a heterocycle or carbocycle;

R₄ is selected from the group consisting of -(CH₂)_nQ, -(CH₂)_nCHQR, -CHQR, and -CQ(R)₂, where Q is -N(R)₂, and n is selected from 1, 2, 3, 4, and 5;

30 each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-, -N(R')C(O)-, -C(O)-, -C(S)-, -C(S)S-, -SC(S)-, -CH(OH)-, -P(O)(OR')O-, -S(O)₂-, -S-S-, an aryl group, and a heteroaryl group;

R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

5 each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, -R*YR'', -YR'', and H;

10 each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₁₋₁₂ alkenyl;

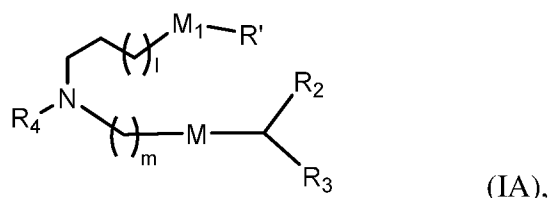
each Y is independently a C₃₋₆ carbocycle;

each X is independently selected from the group consisting of F, Cl, Br, and I; and

15 m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

or salts or isomers thereof.

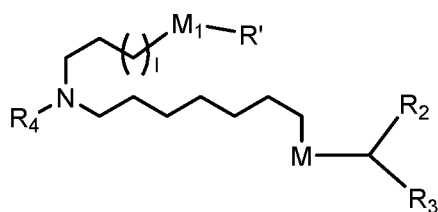
In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IA):



20 or a salt or isomer thereof, wherein l is selected from 1, 2, 3, 4, and 5; m is selected from 5, 6, 7, 8, and 9; M₁ is a bond or M'; R₄ is unsubstituted C₁₋₃ alkyl, or -(CH₂)_nQ, in which Q is OH, -NHC(S)N(R)₂, -NHC(O)N(R)₂, -N(R)C(O)R, -N(R)S(O)₂R, -N(R)R₈, -NHC(=NR₉)N(R)₂, -NHC(=CHR₉)N(R)₂, -OC(O)N(R)₂, -N(R)C(O)OR, heteroaryl or heterocycloalkyl; M and M' are independently selected from -C(O)O-, -OC(O)-, -C(O)N(R')-, -P(O)(OR')O-, -S-S-, an aryl group, and a heteroaryl group; and R₂ and R₃ are independently selected from the group

25 consisting of H, C₁₋₁₄ alkyl, and C₂₋₁₄ alkenyl.

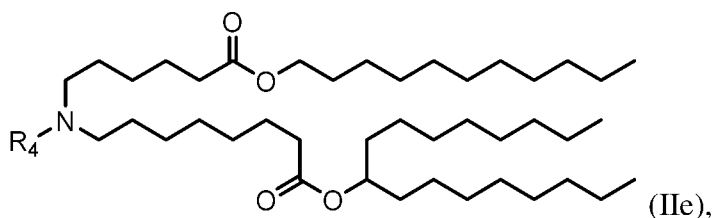
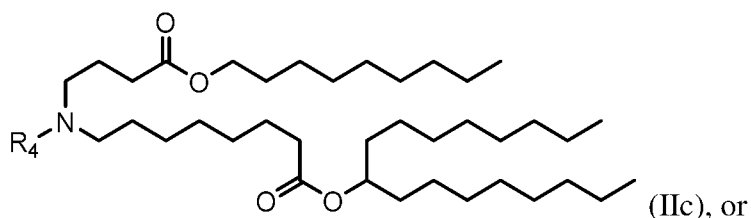
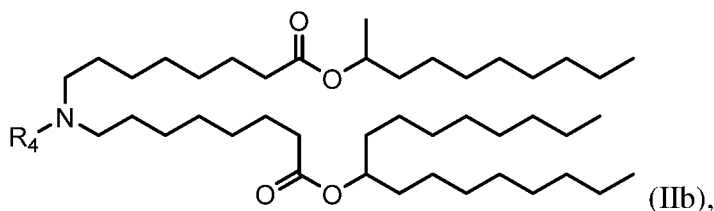
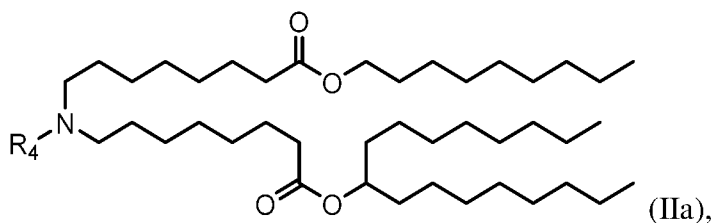
In some embodiments, a subset of compounds of Formula (I) includes those of Formula (II):



(II) or a salt or isomer thereof, wherein l is

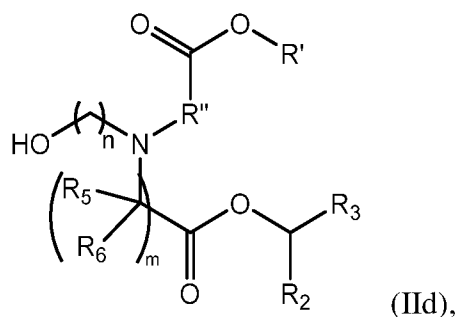
selected from 1, 2, 3, 4, and 5; M_1 is a bond or M' ; R_4 is unsubstituted C_{1-3} alkyl, or $-(CH_2)_nQ$, in which n is 2, 3, or 4, and Q is OH, $-NHC(S)N(R)_2$, $-NHC(O)N(R)_2$, $-N(R)C(O)R$, $-N(R)S(O)_2R$, $-N(R)R_8$, $-NHC(=NR_9)N(R)_2$, $-NHC(=CHR_9)N(R)_2$, $-OC(O)N(R)_2$, $-N(R)C(O)OR$, heteroaryl or heterocycloalkyl; M and M' are independently selected from $-C(O)O-$, $-OC(O)-$, $-C(O)N(R')$, $-P(O)(OR')O-$, $-S-S-$, an aryl group, and a heteroaryl group; and R_2 and R_3 are independently selected from the group consisting of H, C_{1-14} alkyl, and C_{2-14} alkenyl.

In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IIa), (IIb), (IIc), or (IIe):



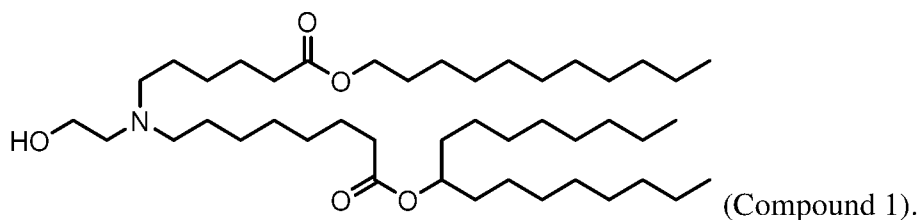
or a salt or isomer thereof, wherein R_4 is as described herein.

In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IIId):

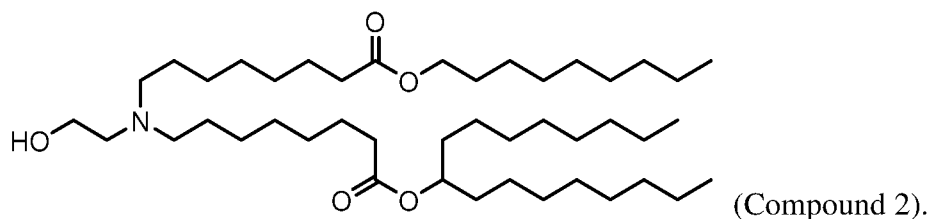


or a salt or isomer thereof, wherein n is 2, 3, or 4; and m , R' , R'' , and R_2 through R_6 are as described herein. For example, each of R_2 and R_3 may be independently selected from the group consisting of C_{5-14} alkyl and C_{5-14} alkenyl.

- 5 In some embodiments, an ionizable cationic lipid of the disclosure comprises a compound having structure:



In some embodiments, an ionizable cationic lipid of the disclosure comprises a compound having structure:



- 10 In some embodiments, a non-cationic lipid of the disclosure comprises 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC), 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE), 1,2-dilinoleoyl-sn-glycero-3-phosphocholine (DLPC), 1,2-dimyristoyl-sn-glycero-3-phosphocholine (DMPC), 1,2-dioleoyl-sn-glycero-3-phosphocholine (DOPC), 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC), 1,2-diundecanoyl-sn-glycero-phosphocholine (DUPC), 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC), 1,2-di-O-octadecenyl-sn-glycero-3-phosphocholine (18:0 Diether PC), 1-oleoyl-2-cholesterylhemisuccinoyl-sn-glycero-3-phosphocholine (OChemPC), 1-hexadecyl-sn-glycero-3-phosphocholine (C16 Lyso PC), 1,2-dilinolenoyl-sn-glycero-3-phosphocholine, 1,2-diarachidonoyl-sn-glycero-3-phosphocholine, 1,2-didocosahexaenoyl-sn-glycero-3-phosphocholine, 1,2-diphytanoyl-sn-glycero-3-phosphoethanolamine (ME 16.0 PE), 1,2-distearoyl-sn-glycero-3-phosphoethanolamine, 1,2-dilinoleoyl-sn-glycero-3-phosphoethanolamine, 1,2-dilinolenoyl-sn-glycero-3-phosphoethanolamine, 1,2-diarachidonoyl-sn-glycero-3-phosphoethanolamine, 1,2-

didocosahexaenoyl-sn-glycero-3-phosphoethanolamine, 1,2-dioleoyl-sn-glycero-3-phospho-rac-(1-glycerol) sodium salt (DOPG), sphingomyelin, and mixtures thereof.

In some embodiments, a PEG modified lipid of the disclosure comprises a PEG-modified phosphatidylethanolamine, a PEG-modified phosphatidic acid, a PEG-modified ceramide, a PEG-modified dialkylamine, a PEG-modified diacylglycerol, a PEG-modified dialkylglycerol, and mixtures thereof. In some embodiments, the PEG-modified lipid is PEG-DMG, PEG-c-DOMG (also referred to as PEG-DOMG), PEG-DSG and/or PEG-DPG.

In some embodiments, a sterol of the disclosure comprises cholesterol, fecosterol, sitosterol, ergosterol, campesterol, stigmasterol, brassicasterol, tomatidine, ursolic acid, alpha-tocopherol, and mixtures thereof.

In some embodiments, a LNP of the disclosure comprises an ionizable cationic lipid of Compound 1, wherein the non-cationic lipid is DSPC, the structural lipid that is cholesterol, and the PEG lipid is PEG-DMG.

In some embodiments, a LNP of the disclosure comprises an N:P ratio of from about 2:1 to about 30:1.

In some embodiments, a LNP of the disclosure comprises an N:P ratio of about 6:1.

In some embodiments, a LNP of the disclosure comprises an N:P ratio of about 3:1.

In some embodiments, a LNP of the disclosure comprises a wt/wt ratio of the ionizable cationic lipid component to the RNA of from about 10:1 to about 100:1.

In some embodiments, a LNP of the disclosure comprises a wt/wt ratio of the ionizable cationic lipid component to the RNA of about 20:1.

In some embodiments, a LNP of the disclosure comprises a wt/wt ratio of the ionizable cationic lipid component to the RNA of about 10:1.

In some embodiments, a LNP of the disclosure has a mean diameter from about 50 nm to about 150 nm.

In some embodiments, a LNP of the disclosure has a mean diameter from about 70 nm to about 120 nm.

Multivalent Vaccines

The EBV vaccines, as provided herein, may include an RNA (e.g. mRNA) or multiple RNAs encoding two or more antigens of the same or different EBV species. In some embodiments, an EBV vaccine includes an RNA or multiple RNAs encoding two or more antigens selected from gp350, gH, gL, gB, gp42, LMP1, LMP2, EBNA1 and EBNA3 antigens.

In some embodiments, the RNA (at least one RNA) of an EBV vaccine may encode 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or more antigens.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen and a gH antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen and a gL antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen and a gB antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gH antigen and a gL antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gH antigen and a gB antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gH antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gH antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gH antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gL antigen and a gB antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gL antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gL antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gL antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gB antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gB antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gB antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gp42 antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, gp42 antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp350 antigen, a LMP (e.g., LMP1 and/or LMP2) antigen, and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

5 In some embodiments, an EBV vaccine comprises at least one RNA encoding a gH antigen and a gL antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gH antigen and a gB antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gH antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gH antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a
10 gH antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gL antigen and a gB antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gL antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gL antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some
15 embodiments, an EBV vaccine comprises at least one RNA encoding a gL antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gB antigen and a gp42 antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gB antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an
20 EBV vaccine comprises at least one RNA encoding a gB antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp42 antigen and a LMP (e.g., LMP1 and/or LMP2) antigen. In some embodiments, an EBV vaccine comprises at least one RNA encoding a gp42 antigen and an EBNA (e.g., EBNA1 and/or
25 EBNA3) antigen.

In some embodiments, an EBV vaccine comprises at least one RNA encoding a LMP (e.g., LMP1 and/or LMP2) antigen and an EBNA (e.g., EBNA1 and/or EBNA3) antigen.

In some embodiments, two or more different RNA (e.g., mRNA) encoding antigens may be formulated in the same lipid nanoparticle. In other embodiments, two or more different RNA
30 encoding antigens may be formulated in separate lipid nanoparticles (each RNA formulated in a single lipid nanoparticle). The lipid nanoparticles may then be combined and administered as a single vaccine composition (e.g., comprising multiple RNA encoding multiple antigens) or may be administered separately.

Combination Vaccines

The EBV vaccines, as provided herein, may include an RNA or multiple RNAs encoding two or more antigens of the same or different EBV strains. Also provided herein are combination vaccines that include RNA encoding one or more EBV antigen(s) and one or more antigen(s) of a different organisms (e.g., bacterial and/or viral organism). Thus, the vaccines of the present disclosure may be combination vaccines that target one or more antigens of the same strain/species, or one or more antigens of different strains/species, e.g., antigens which induce immunity to organisms which are found in the same geographic areas where the risk of EBV infection is high or organisms to which an individual is likely to be exposed to when exposed to EBV.

Dosing/Administration

Provided herein are compositions (e.g., pharmaceutical compositions), methods, kits and reagents for prevention and/or treatment of EBV in humans and other mammals. EBV RNA vaccines can be used as therapeutic or prophylactic agents. In some aspects, the RNA vaccines of the disclosure are used to provide prophylactic protection from EBV. In some aspects, the RNA vaccines of the disclosure are used to treat an EBV infection. In some embodiments, the EBV vaccines of the present disclosure are used in the priming of immune effector cells, for example, to activate peripheral blood mononuclear cells (PBMCs) *ex vivo*, which are then infused (re-infused) into a subject.

A subject may be any mammal, including non-human primate and human subjects. Typically, a subject is a human subject.

In some embodiments, the EBV vaccines are administered to a subject (e.g., a mammalian subject, such as a human subject) in an effective amount to induce an antigen-specific immune response. The RNA encoding the EBV antigen is expressed and translated *in vivo* to produce the antigen, which then stimulates an immune response in the subject.

Prophylactic protection from EBV can be achieved following administration of an EBV RNA vaccine of the present disclosure. Vaccines can be administered once, twice, three times, four times or more but it is likely sufficient to administer the vaccine once (optionally followed by a single booster). It is possible, although less desirable, to administer the vaccine to an infected individual to achieve a therapeutic response. Dosing may need to be adjusted accordingly.

A method of eliciting an immune response in a subject against EBV is provided in aspects of the present disclosure. The method involves administering to the subject an EBV

RNA vaccine comprising at least one RNA (e.g., mRNA) having an open reading frame encoding at least one EBV antigen, thereby inducing in the subject an immune response specific to EBV antigen, wherein anti-antigen antibody titer in the subject is increased following vaccination relative to anti-antigen antibody titer in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against the EBV. An “anti-antigen antibody” is a serum antibody the binds specifically to the antigen.

A prophylactically effective dose is an effective dose that prevents infection with the virus at a clinically acceptable level. In some embodiments, the effective dose is a dose listed in a package insert for the vaccine. A traditional vaccine, as used herein, refers to a vaccine other than the mRNA vaccines of the present disclosure. For instance, a traditional vaccine includes, but is not limited, to live microorganism vaccines, killed microorganism vaccines, subunit vaccines, protein antigen vaccines, DNA vaccines, virus like particle (VLP) vaccines, *etc.* In exemplary embodiments, a traditional vaccine is a vaccine that has achieved regulatory approval and/or is registered by a national drug regulatory body, for example the Food and Drug Administration (FDA) in the United States or the European Medicines Agency (EMA).

In some embodiments, the anti-antigen antibody titer in the subject is increased 1 log to 10 log following vaccination relative to anti-antigen antibody titer in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against the EBV or an unvaccinated subject. In some embodiments, the anti-antigen antibody titer in the subject is increased 1 log, 2 log, 3 log, 4 log, 5 log, or 10 log following vaccination relative to anti-antigen antibody titer in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against the EBV or an unvaccinated subject.

A method of eliciting an immune response in a subject against an EBV is provided in other aspects of the disclosure. The method involves administering to the subject an EBV RNA vaccine comprising at least one RNA polynucleotide having an open reading frame encoding at least one EBV antigen, thereby inducing in the subject an immune response specific to EBV antigen, wherein the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine against the EBV at 2 times to 100 times the dosage level relative to the RNA vaccine.

In some embodiments, the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at twice the dosage level relative to the EBV RNA vaccine. In some embodiments, the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at three times the dosage level relative to the EBV RNA vaccine. In some embodiments, the immune response in

the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at 4 times, 5 times, 10 times, 50 times, or 100 times the dosage level relative to the EBV RNA vaccine. In some embodiments, the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at 10 times to 1000 times the dosage level relative to the EBV RNA vaccine. In some embodiments, the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at 100 times to 1000 times the dosage level relative to the EBV RNA vaccine.

In other embodiments, the immune response is assessed by determining [protein] antibody titer in the subject. In other embodiments, the ability of serum or antibody from an immunized subject is tested for its ability to neutralize viral uptake or reduce EBV transformation of human B lymphocytes. In other embodiments, the ability to promote a robust T cell response(s) is measured using art recognized techniques.

Other aspects the disclosure provide methods of eliciting an immune response in a subject against an EBV by administering to the subject an EBV RNA vaccine comprising at least one RNA polynucleotide having an open reading frame encoding at least one EBV antigen, thereby inducing in the subject an immune response specific to EBV antigen, wherein the immune response in the subject is induced 2 days to 10 weeks earlier relative to an immune response induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against the EBV. In some embodiments, the immune response in the subject is induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine at 2 times to 100 times the dosage level relative to the RNA vaccine.

In some embodiments, the immune response in the subject is induced 2 days, 3 days, 1 week, 2 weeks, 3 weeks, 5 weeks, or 10 weeks earlier relative to an immune response induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine.

Also provided herein are methods of eliciting an immune response in a subject against an EBV by administering to the subject an EBV RNA vaccine having an open reading frame encoding a first antigen, wherein the RNA polynucleotide does not include a stabilization element, and wherein an adjuvant is not co-formulated or co-administered with the vaccine.

EBV RNA (*e.g.*, mRNA) vaccines may be administered by any route which results in a therapeutically effective outcome. These include, but are not limited, to intradermal, intramuscular, intranasal, and/or subcutaneous administration. The present disclosure provides methods comprising administering RNA vaccines to a subject in need thereof. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease, the particular composition, its mode of administration,

its mode of activity, and the like. EBV RNA (*e.g.*, mRNA) vaccines compositions are typically formulated in dosage unit form for ease of administration and uniformity of dosage. It will be understood, however, that the total daily usage of EBV RNA (*e.g.*, mRNA) vaccines compositions may be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective, prophylactically effective, or appropriate imaging dose level for any particular patient will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific compound employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific compound employed; the duration of the treatment; drugs used in combination or coincidental with the specific compound employed; and like factors well known in the medical arts.

The effective amount of an EBV vaccine, as provided herein, may be as low as 20 µg, administered for example as a single dose or as two 10 µg doses. In some embodiments, the effective amount is a total dose of 20 µg-200 µg. For example, the effective amount may be a total dose of 20 µg, 25 µg, 30 µg, 35 µg, 40 µg, 45 µg, 50 µg, 55 µg, 60 µg, 65 µg, 70 µg, 75 µg, 80 µg, 85 µg, 90 µg, 95 µg, 100 µg, 110 µg, 120 µg, 130 µg, 140 µg, 150 µg, 160 µg, 170 µg, 180 µg, 190 µg or 200 µg. In some embodiments, the effective amount is a total dose of 25 µg-200 µg. In some embodiments, the effective amount is a total dose of 50 µg-200 µg.

In some embodiments, EBV RNA (*e.g.*, mRNA) vaccines compositions may be administered at dosage levels sufficient to deliver 0.0001 mg/kg to 100 mg/kg, 0.001 mg/kg to 0.05 mg/kg, 0.005 mg/kg to 0.05 mg/kg, 0.001 mg/kg to 0.005 mg/kg, 0.05 mg/kg to 0.5 mg/kg, 0.01 mg/kg to 50 mg/kg, 0.1 mg/kg to 40 mg/kg, 0.5 mg/kg to 30 mg/kg, 0.01 mg/kg to 10 mg/kg, 0.1 mg/kg to 10 mg/kg, or 1 mg/kg to 25 mg/kg, of subject body weight per day, one or more times a day, per week, per month, etc. to obtain the desired therapeutic, diagnostic, prophylactic, or imaging effect (*see e.g.*, the range of unit doses described in International Publication No. WO2013078199, herein incorporated by reference in its entirety). The desired dosage may be delivered three times a day, two times a day, once a day, every other day, every third day, every week, every two weeks, every three weeks, every four weeks, every 2 months, every three months, every 6 months, *etc.* In certain embodiments, the desired dosage may be delivered using multiple administrations (*e.g.*, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or more administrations). When multiple administrations are employed, split dosing regimens such as those described herein may be used. In exemplary embodiments, EBV RNA (*e.g.*, mRNA) vaccines compositions may be administered at dosage

levels sufficient to deliver 0.0005 mg/kg to 0.01 mg/kg, *e.g.*, about 0.0005 mg/kg to about 0.0075 mg/kg, *e.g.*, about 0.0005 mg/kg, about 0.001 mg/kg, about 0.002 mg/kg, about 0.003 mg/kg, about 0.004 mg/kg or about 0.005 mg/kg.

In some embodiments, EBV RNA (*e.g.*, mRNA) vaccine compositions may be administered once or twice (or more) at dosage levels sufficient to deliver 0.025 mg/kg to 0.250 mg/kg, 0.025 mg/kg to 0.500 mg/kg, 0.025 mg/kg to 0.750 mg/kg, or 0.025 mg/kg to 1.0 mg/kg.

In some embodiments, EBV RNA (*e.g.*, mRNA) vaccine compositions may be administered twice (*e.g.*, Day 0 and Day 7, Day 0 and Day 14, Day 0 and Day 21, Day 0 and Day 28, Day 0 and Day 60, Day 0 and Day 90, Day 0 and Day 120, Day 0 and Day 150, Day 0 and Day 180, Day 0 and 3 months later, Day 0 and 6 months later, Day 0 and 9 months later, Day 0 and 12 months later, Day 0 and 18 months later, Day 0 and 2 years later, Day 0 and 5 years later, or Day 0 and 10 years later) at a total dose of or at dosage levels sufficient to deliver a total dose of 0.0100 mg, 0.025 mg, 0.050 mg, 0.075 mg, 0.100 mg, 0.125 mg, 0.150 mg, 0.175 mg, 0.200 mg, 0.225 mg, 0.250 mg, 0.275 mg, 0.300 mg, 0.325 mg, 0.350 mg, 0.375 mg, 0.400 mg, 0.425 mg, 0.450 mg, 0.475 mg, 0.500 mg, 0.525 mg, 0.550 mg, 0.575 mg, 0.600 mg, 0.625 mg, 0.650 mg, 0.675 mg, 0.700 mg, 0.725 mg, 0.750 mg, 0.775 mg, 0.800 mg, 0.825 mg, 0.850 mg, 0.875 mg, 0.900 mg, 0.925 mg, 0.950 mg, 0.975 mg, or 1.0 mg. Higher and lower dosages and frequency of administration are encompassed by the present disclosure. For example, an EBV RNA (*e.g.*, mRNA) vaccine composition may be administered three or four times.

In some embodiments, EBV RNA (*e.g.*, mRNA) vaccine compositions may be administered twice (*e.g.*, Day 0 and Day 7, Day 0 and Day 14, Day 0 and Day 21, Day 0 and Day 28, Day 0 and Day 60, Day 0 and Day 90, Day 0 and Day 120, Day 0 and Day 150, Day 0 and Day 180, Day 0 and 3 months later, Day 0 and 6 months later, Day 0 and 9 months later, Day 0 and 12 months later, Day 0 and 18 months later, Day 0 and 2 years later, Day 0 and 5 years later, or Day 0 and 10 years later) at a total dose of or at dosage levels sufficient to deliver a total dose of 0.010 mg, 0.025 mg, 0.100 mg or 0.400 mg.

In some embodiments, the EBV RNA (*e.g.*, mRNA) vaccine for use in a method of vaccinating a subject is administered the subject a single dosage of between 10 µg/kg and 400 µg/kg of the nucleic acid vaccine in an effective amount to vaccinate the subject. In some embodiments, the RNA vaccine for use in a method of vaccinating a subject is administered the subject a single dosage of between 10 µg and 400 µg of the nucleic acid vaccine in an effective amount to vaccinate the subject. In some embodiments, an EBV RNA (*e.g.*, mRNA) vaccine for use in a method of vaccinating a subject is administered to the subject as a single dosage of 25-1000 µg (*e.g.*, a single dosage of mRNA encoding an EBV antigen). In some embodiments, an

EBV RNA vaccine is administered to the subject as a single dosage of 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950 or 1000 µg. For example, an EBV RNA vaccine may be administered to a subject as a single dose of 25-100, 25-500, 50-100, 50-500, 50-1000, 100-500, 100-1000, 250-500, 250-1000, or 500-1000 µg. In some
5 embodiments, an EBV RNA (*e.g.*, mRNA) vaccine for use in a method of vaccinating a subject is administered to the subject as two dosages, the combination of which equals 25-1000 µg of the EBV RNA (*e.g.*, mRNA) vaccine.

AN EBV RNA (*e.g.*, mRNA) vaccine pharmaceutical composition described herein can be formulated into a dosage form described herein, such as an intranasal, intratracheal, or
10 injectable (*e.g.*, intravenous, intraocular, intravitreal, intramuscular, intradermal, intracardiac, intraperitoneal, and subcutaneous).

Vaccine Efficacy

Some aspects of the present disclosure provide formulations of the EBV RNA (*e.g.*,
15 mRNA) vaccine, wherein the EBV RNA vaccine is formulated in an effective amount to produce an antigen specific immune response in a subject (*e.g.*, production of antibodies specific to an anti-EBV antigen). “An effective amount” is a dose of an EBV RNA (*e.g.*, mRNA) vaccine effective to produce an antigen-specific immune response. Also provided herein are methods of inducing an antigen-specific immune response in a subject.

As used herein, an immune response to a vaccine or LNP of the present invention is the development in a subject of a humoral and/or a cellular immune response to a (one or more) EBV protein(s) present in the vaccine. For purposes of the present invention, a “humoral” immune response refers to an immune response mediated by antibody molecules, including, *e.g.*, secretory (IgA) or IgG molecules, while a “cellular” immune response is one mediated by T-
25 lymphocytes (*e.g.*, CD4+ helper and/or CD8+ T cells (*e.g.*, CTLs) and/or other white blood cells. One important aspect of cellular immunity involves an antigen-specific response by cytolytic T-cells (CTLs). CTLs have specificity for peptide antigens that are presented in association with proteins encoded by the major histocompatibility complex (MHC) and expressed on the surfaces of cells. CTLs help induce and promote the destruction of intracellular
30 microbes or the lysis of cells infected with such microbes. Another aspect of cellular immunity involves an antigen-specific response by helper T-cells. Helper T-cells act to help stimulate the function, and focus the activity nonspecific effector cells against cells displaying peptide antigens in association with MHC molecules on their surface. A cellular immune response also leads to the production of cytokines, chemokines, and other such molecules produced by

activated T-cells and/or other white blood cells including those derived from CD4+ and CD8+ T-cells.

In some embodiments, the antigen-specific immune response is characterized by measuring an anti-EBV antigen antibody titer produced in a subject administered an EBV RNA (e.g., mRNA) vaccine as provided herein. An antibody titer is a measurement of the amount of antibodies within a subject, for example, antibodies that are specific to a particular antigen (e.g., an anti-EBV antigen) or epitope of an antigen. Antibody titer is typically expressed as the inverse of the greatest dilution that provides a positive result. Enzyme-linked immunosorbent assay (ELISA) is a common assay for determining antibody titers, for example.

In some embodiments, an antibody titer is used to assess whether a subject has had an infection or to determine whether immunizations are required. In some embodiments, an antibody titer is used to determine the strength of an autoimmune response, to determine whether a booster immunization is needed, to determine whether a previous vaccine was effective, and to identify any recent or prior infections. In accordance with the present disclosure, an antibody titer may be used to determine the strength of an immune response induced in a subject by the EBV RNA (e.g., mRNA) vaccine.

In some embodiments, an anti-EBV antigen antibody titer produced in a subject is increased by at least 1 log relative to a control. For example, anti-EBV antigen antibody titer produced in a subject may be increased by at least 1.5, at least 2, at least 2.5, or at least 3 log relative to a control. In some embodiments, the anti-EBV antigen antibody titer produced in the subject is increased by 1, 1.5, 2, 2.5 or 3 log relative to a control. In some embodiments, the anti-EBV antigen antibody titer produced in the subject is increased by 1-3 log relative to a control. For example, the anti-EBV antigen antibody titer produced in a subject may be increased by 1-1.5, 1-2, 1-2.5, 1-3, 1.5-2, 1.5-2.5, 1.5-3, 2-2.5, 2-3, or 2.5-3 log relative to a control.

In some embodiments, the anti-EBV antigen antibody titer produced in a subject is increased at least 2 times relative to a control. For example, the anti-EBV antigen antibody titer produced in a subject may be increased at least 3 times, at least 4 times, at least 5 times, at least 6 times, at least 7 times, at least 8 times, at least 9 times, or at least 10 times relative to a control. In some embodiments, the anti-EBV antigen antibody titer produced in the subject is increased 2, 3, 4, 5, 6, 7, 8, 9, or 10 times relative to a control. In some embodiments, the anti-EBV antigen antibody titer produced in a subject is increased 2-10 times relative to a control. For example, the anti-EBV antigen antibody titer produced in a subject may be increased 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, 2-3, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-10,

5-9, 5-8, 5-7, 5-6, 6-10, 6-9, 6-8, 6-7, 7-10, 7-9, 7-8, 8-10, 8-9, or 9-10 times relative to a control.

A control, in some embodiments, is the anti-EBV antigen antibody titer produced in a subject who has not been administered an EBV RNA (*e.g.*, mRNA) vaccine. In some
5 embodiments, a control is an anti-EBV antigen antibody titer produced in a subject administered a recombinant or purified EBV protein vaccine. Recombinant protein vaccines typically include protein antigens that either have been produced in a heterologous expression system (*e.g.*, bacteria or yeast) or purified from large amounts of the pathogenic organism.

10 In some embodiments, the ability of an EBV vaccine to be effective is measured in a murine model. For example, the EBV vaccines may be administered to a murine model and the murine model assayed for induction of neutralizing antibody titers. Viral challenge studies may also be used to assess the efficacy of a vaccine of the present disclosure. For example, the EBV vaccines may be administered to a murine model, the murine model challenged with EBV, and the murine model assayed for survival and/or immune response (*e.g.*, neutralizing antibody
15 response, T cell response (*e.g.*, cytokine response)).

In some embodiments, an effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a dose that is reduced compared to the standard of care dose of a recombinant EBV protein vaccine. A “standard of care,” as provided herein, refers to a medical or psychological treatment guideline and can be general or specific. “Standard of care” specifies appropriate treatment
20 based on scientific evidence and collaboration between medical professionals involved in the treatment of a given condition. It is the diagnostic and treatment process that a physician/clinician should follow for a certain type of patient, illness or clinical circumstance. A “standard of care dose,” as provided herein, refers to the dose of a recombinant or purified EBV protein vaccine, or a live attenuated or inactivated EBV vaccine, or an EBV VLP vaccine, that a
25 physician/clinician or other medical professional would administer to a subject to treat or prevent EBV, or an EBV-related condition, while following the standard of care guideline for treating or preventing EBV, or an EBV-related condition.

In some embodiments, the anti-EBV antigen antibody titer produced in a subject administered an effective amount of an EBV RNA vaccine is equivalent to an anti-EBV antigen
30 antibody titer produced in a control subject administered a standard of care dose of a recombinant or purified EBV protein vaccine, or a live attenuated or inactivated EBV vaccine, or an EBV VLP vaccine.

In some embodiments, an effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a dose equivalent to an at least 2-fold reduction in a standard of care dose of a recombinant or

purified EBV protein vaccine. For example, an effective amount of an EBV RNA vaccine may be a dose equivalent to an at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold reduction in a standard of care dose of a recombinant or purified EBV protein vaccine. In some embodiments, an effective amount of an EBV RNA vaccine is a dose equivalent to an at least 100-fold, at least 500-fold, or at least 1000-fold reduction in a standard of care dose of a recombinant or purified EBV protein vaccine. In some embodiments, an effective amount of an EBV RNA vaccine is a dose equivalent to a 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 20-, 50-, 100-, 250-, 500-, or 1000-fold reduction in a standard of care dose of a recombinant or purified EBV protein vaccine. In some embodiments, the anti-EBV antigen antibody titer produced in a subject administered an effective amount of an EBV RNA vaccine is equivalent to an anti-EBV antigen antibody titer produced in a control subject administered the standard of care dose of a recombinant or protein EBV protein vaccine, or a live attenuated or inactivated EBV vaccine, or an EBV VLP vaccine. In some embodiments, an effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a dose equivalent to a 2-fold to 1000-fold (*e.g.*, 2-fold to 100-fold, 10-fold to 1000-fold) reduction in the standard of care dose of a recombinant or purified EBV protein vaccine, wherein the anti-EBV antigen antibody titer produced in the subject is equivalent to an anti-EBV antigen antibody titer produced in a control subject administered the standard of care dose of a recombinant or purified EBV protein vaccine, or a live attenuated or inactivated EBV vaccine, or an EBV VLP vaccine.

In some embodiments, the effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a dose equivalent to a 2 to 1000-, 2 to 900-, 2 to 800-, 2 to 700-, 2 to 600-, 2 to 500-, 2 to 400-, 2 to 300-, 2 to 200-, 2 to 100-, 2 to 90-, 2 to 80-, 2 to 70-, 2 to 60-, 2 to 50-, 2 to 40-, 2 to 30-, 2 to 20-, 2 to 10-, 2 to 9-, 2 to 8-, 2 to 7-, 2 to 6-, 2 to 5-, 2 to 4-, 2 to 3-, 3 to 1000-, 3 to 900-, 3 to 800-, 3 to 700-, 3 to 600-, 3 to 500-, 3 to 400-, 3 to 300-, 3 to 200-, 3 to 100-, 3 to 90-, 3 to 80-, 3 to 70-, 3 to 60-, 3 to 50-, 3 to 40-, 3 to 30-, 3 to 20-, 3 to 10-, 3 to 9-, 3 to 8-, 3 to 7-, 3 to 6-, 3 to 5-, 3 to 4-, 4 to 1000-, 4 to 900-, 4 to 800-, 4 to 700-, 4 to 600-, 4 to 500-, 4 to 400-, 4 to 300-, 4 to 200-, 4 to 100-, 4 to 90-, 4 to 80-, 4 to 70-, 4 to 60-, 4 to 50-, 4 to 40-, 4 to 30-, 4 to 20-, 4 to 10-, 4 to 9-, 4 to 8-, 4 to 7-, 4 to 6-, 4 to 5-, 4 to 4-, 5 to 1000-, 5 to 900-, 5 to 800-, 5 to 700-, 5 to 600-, 5 to 500-, 5 to 400-, 5 to 300-, 5 to 200-, 5 to 100-, 5 to 90-, 5 to 80-, 5 to 70-, 5 to 60-, 5 to 50-, 5 to 40-, 5 to 30-, 5 to 20-, 5 to 10-, 5 to 9-, 5 to 8-, 5 to 7-, 5 to 6-, 6 to 1000-, 6 to 900-, 6 to 800-, 6 to 700-, 6 to 600-, 6 to 500-, 6 to 400-, 6 to 300-, 6 to 200-, 6 to 100-, 6 to 90-, 6 to 80-, 6 to 70-, 6 to 60-, 6 to 50-, 6 to 40-, 6 to 30-, 6 to 20-, 6 to 10-, 6 to 9-, 6 to 8-, 6 to 7-, 7 to 1000-, 7 to 900-, 7 to 800-, 7 to 700-, 7 to 600-, 7 to 500-, 7 to 400-, 7 to 300-, 7 to 200-,

7 to 100-, 7 to 90-, 7 to 80-, 7 to 70-, 7 to 60-, 7 to 50-, 7 to 40-, 7 to 30-, 7 to 20-, 7 to 10-, 7 to 9-, 7 to 8-, 8 to 1000-, 8 to 900-, 8 to 800-, 8 to 700-, 8 to 600-, 8 to 500-, 8 to 400-, 8 to 300-, 8 to 200-, 8 to 100-, 8 to 90-, 8 to 80-, 8 to 70-, 8 to 60-, 8 to 50-, 8 to 40-, 8 to 30-, 8 to 20-, 8 to 10-, 8 to 9-, 9 to 1000-, 9 to 900-, 9 to 800-, 9 to 700-, 9 to 600-, 9 to 500-, 9 to 400-, 9 to 300-, 9 to 200-, 9 to 100-, 9 to 90-, 9 to 80-, 9 to 70-, 9 to 60-, 9 to 50-, 9 to 40-, 9 to 30-, 9 to 20-, 9 to 10-, 10 to 1000-, 10 to 900-, 10 to 800-, 10 to 700-, 10 to 600-, 10 to 500-, 10 to 400-, 10 to 300-, 10 to 200-, 10 to 100-, 10 to 90-, 10 to 80-, 10 to 70-, 10 to 60-, 10 to 50-, 10 to 40-, 10 to 30-, 10 to 20-, 20 to 1000-, 20 to 900-, 20 to 800-, 20 to 700-, 20 to 600-, 20 to 500-, 20 to 400-, 20 to 300-, 20 to 200-, 20 to 100-, 20 to 90-, 20 to 80-, 20 to 70-, 20 to 60-, 20 to 50-, 20 to 40-, 20 to 30-, 30 to 1000-, 30 to 900-, 30 to 800-, 30 to 700-, 30 to 600-, 30 to 500-, 30 to 400-, 30 to 300-, 30 to 200-, 30 to 100-, 30 to 90-, 30 to 80-, 30 to 70-, 30 to 60-, 30 to 50-, 30 to 40-, 40 to 1000-, 40 to 900-, 40 to 800-, 40 to 700-, 40 to 600-, 40 to 500-, 40 to 400-, 40 to 300-, 40 to 200-, 40 to 100-, 40 to 90-, 40 to 80-, 40 to 70-, 40 to 60-, 40 to 50-, 50 to 1000-, 50 to 900-, 50 to 800-, 50 to 700-, 50 to 600-, 50 to 500-, 50 to 400-, 50 to 300-, 50 to 200-, 50 to 100-, 50 to 90-, 50 to 80-, 50 to 70-, 50 to 60-, 60 to 1000-, 60 to 900-, 60 to 800-, 60 to 700-, 60 to 600-, 60 to 500-, 60 to 400-, 60 to 300-, 60 to 200-, 60 to 100-, 60 to 90-, 60 to 80-, 60 to 70-, 70 to 1000-, 70 to 900-, 70 to 800-, 70 to 700-, 70 to 600-, 70 to 500-, 70 to 400-, 70 to 300-, 70 to 200-, 70 to 100-, 70 to 90-, 70 to 80-, 80 to 1000-, 80 to 900-, 80 to 800-, 80 to 700-, 80 to 600-, 80 to 500-, 80 to 400-, 80 to 300-, 80 to 200-, 80 to 100-, 80 to 90-, 90 to 1000-, 90 to 900-, 90 to 800-, 90 to 700-, 90 to 600-, 90 to 500-, 90 to 400-, 90 to 300-, 90 to 200-, 90 to 100-, 100 to 1000-, 100 to 900-, 100 to 800-, 100 to 700-, 100 to 600-, 100 to 500-, 100 to 400-, 100 to 300-, 100 to 200-, 200 to 1000-, 200 to 900-, 200 to 800-, 200 to 700-, 200 to 600-, 200 to 500-, 200 to 400-, 200 to 300-, 300 to 1000-, 300 to 900-, 300 to 800-, 300 to 700-, 300 to 600-, 300 to 500-, 300 to 400-, 400 to 1000-, 400 to 900-, 400 to 800-, 400 to 700-, 400 to 600-, 400 to 500-, 500 to 1000-, 500 to 900-, 500 to 800-, 500 to 700-, 500 to 600-, 600 to 1000-, 600 to 900-, 600 to 800-, 600 to 700-, 700 to 1000-, 700 to 900-, 700 to 800-, 800 to 1000-, 800 to 900-, or 900 to 1000-fold reduction in the standard of care dose of a recombinant EBV protein vaccine. In some embodiments, such as the foregoing, the anti-EBV antigen antibody titer produced in the subject is equivalent to an anti-EBV antigen antibody titer produced in a control subject administered the standard of care dose of a recombinant or purified EBV protein vaccine, or a live attenuated or inactivated EBV vaccine, or an EBV VLP vaccine. In some embodiments, the effective amount is a dose equivalent to (or equivalent to an at least) 2-, 3 -,4 -,5 -,6-, 7-, 8-, 9-, 10-, 20-, 30-, 40-, 50-, 60-, 70-, 80-, 90-, 100-, 110-, 120-, 130-, 140-, 150-, 160-, 170-, 1280-, 190-, 200-, 210-, 220-, 230-, 240-, 250-, 260-, 270-, 280-, 290-, 300-, 310-, 320-, 330-, 340-, 350-, 360-,

370-, 380-, 390-, 400-, 410-, 420-, 430-, 440-, 450-, 460-, 470-, 480-, 490-, 500-, 510-, 520-, 530-, 540-, 550-, 560-, 570-, 580-, 590-, 600-, 610-, 620-, 630-, 640-, 650-, 660-, 670-, 680-, 690-, 700-, 710-, 720-, 730-, 740-, 750-, 760-, 770-, 780-, 790-, 800-, 810-, 820-, 830-, 840-, 850-, 860-, 870-, 880-, 890-, 900-, 910-, 920-, 930-, 940-, 950-, 960-, 970-, 980-, 990-, or 1000-
 5 fold reduction in the standard of care dose of a recombinant EBV protein vaccine. In some embodiments, such as the foregoing, an anti-EBV antigen antibody titer produced in the subject is equivalent to an anti-EBV antigen antibody titer produced in a control subject administered the standard of care dose of a recombinant or purified EBV protein vaccine, or a live attenuated or inactivated EBV vaccine, or an EBV VLP vaccine.

10 In some embodiments, the effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a total dose of 50-1000 µg. In some embodiments, the effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a total dose of 50-1000, 50-900, 50-800, 50-700, 50-600, 50-500, 50-400, 50-300, 50-200, 50-100, 50-90, 50-80, 50-70, 50-60, 60-1000, 60-900, 60-800, 60-700, 60-600, 60-500, 60-400, 60-300, 60-200, 60-100, 60-90, 60-80, 60-70, 70-1000, 70- 900, 70-800, 70-700,
 15 70-600, 70-500, 70-400, 70-300, 70-200, 70-100, 70-90, 70-80, 80-1000, 80- 900, 80-800, 80-700, 80-600, 80-500, 80-400, 80-300, 80-200, 80-100, 80-90, 90-1000, 90- 900, 90-800, 90-700, 90-600, 90-500, 90-400, 90-300, 90-200, 90-100, 100-1000, 100-900, 100-800, 100-700, 100-600, 100-500, 100-400, 100-300, 100-200, 200-1000, 200-900, 200-800, 200-700, 200-600, 200-500, 200-400, 200-300, 300-1000, 300-900, 300-800, 300-700, 300-600, 300-500, 300-400, 400-
 20 1000, 400-900, 400-800, 400-700, 400-600, 400-500, 500-1000, 500-900, 500-800, 500-700, 500-600, 600-1000, 600-900, 600-900, 600-700, 700-1000, 700-900, 700-800, 800-1000, 800-900, or 900-1000 µg. In some embodiments, the effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a total dose of 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950 or 1000 µg. In some embodiments, the effective amount is a dose
 25 of 25-500 µg administered to the subject a total of two times. In some embodiments, the effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a dose of 25-500, 25-400, 25-300, 25-200, 25-100, 25-50, 50-500, 50-400, 50-300, 50-200, 50-100, 100-500, 100-400, 100-300, 100-200, 150-500, 150-400, 150-300, 150-200, 200-500, 200-400, 200-300, 250-500, 250-400, 250-300, 300-500, 300-400, 350-500, 350-400, 400-500 or 450-500 µg administered to the
 30 subject a total of two times. In some embodiments, the effective amount of an EBV RNA (*e.g.*, mRNA) vaccine is a total dose of 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 µg administered to the subject a total of two times.

Vaccine efficacy may be assessed using standard analyses (see, *e.g.*, Weinberg et al., J Infect Dis. 2010 Jun 1;201(11):1607-10). For example, vaccine efficacy may be measured by

double-blind, randomized, clinical controlled trials. Vaccine efficacy may be expressed as a proportionate reduction in disease attack rate (AR) between the unvaccinated (ARU) and vaccinated (ARV) study cohorts and can be calculated from the relative risk (RR) of disease among the vaccinated group with use of the following formulas:

- 5 Efficacy = $(ARU - ARV)/ARU \times 100$; and
 Efficacy = $(1 - RR) \times 100$.

Likewise, vaccine effectiveness may be assessed using standard analyses (see, e.g., Weinberg et al., J Infect Dis. 2010 Jun 1;201(11):1607-10). Vaccine effectiveness is an assessment of how a vaccine (which may have already proven to have high vaccine efficacy) reduces disease in a population. This measure can assess the net balance of benefits and adverse effects of a vaccination program, not just the vaccine itself, under natural field conditions rather than in a controlled clinical trial. Vaccine effectiveness is proportional to vaccine efficacy (potency) but is also affected by how well target groups in the population are immunized, as well as by other non-vaccine-related factors that influence the ‘real-world’ outcomes of hospitalizations, ambulatory visits, or costs. For example, a retrospective case control analysis may be used, in which the rates of vaccination among a set of infected cases and appropriate controls are compared. Vaccine effectiveness may be expressed as a rate difference, with use of the odds ratio (OR) for developing infection despite vaccination:

$$\text{Effectiveness} = (1 - OR) \times 100.$$

20 In some embodiments, efficacy of the EBV vaccine is at least 60% relative to unvaccinated control subjects. For example, efficacy of the EBV vaccine may be at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 95%, at least 98%, or 100% relative to unvaccinated control subjects.

Sterilizing Immunity. Sterilizing immunity refers to a unique immune status that prevents effective pathogen infection into the host. In some embodiments, the effective amount of an EBV vaccine of the present disclosure is sufficient to provide sterilizing immunity in the subject for at least 1 year. For example, the effective amount of an EBV vaccine of the present disclosure is sufficient to provide sterilizing immunity in the subject for at least 2 years, at least 3 years, at least 4 years, or at least 5 years. In some embodiments, the effective amount of an EBV vaccine of the present disclosure is sufficient to provide sterilizing immunity in the subject at an at least 5-fold lower dose relative to control. For example, the effective amount may be sufficient to provide sterilizing immunity in the subject at an at least 10-fold lower, 15-fold, or 20-fold lower dose relative to a control.

Detectable Antigen. In some embodiments, the effective amount of an EBV vaccine of the present disclosure is sufficient to produce detectable levels of EBV antigen as measured in serum of the subject at 1-72 hours post administration.

Titer. An antibody titer is a measurement of the amount of antibodies within a subject, for example, antibodies that are specific to a particular antigen (e.g., an anti-EBV antigen). Antibody titer is typically expressed as the inverse of the greatest dilution that provides a positive result. Enzyme-linked immunosorbent assay (ELISA) is a common assay for determining antibody titers, for example.

In some embodiments, the effective amount of an EBV vaccine of the present disclosure is sufficient to produce a 1,000-10,000 neutralizing antibody titer produced by neutralizing antibody against the EBV antigen as measured in serum of the subject at 1-72 hours post administration. In some embodiments, the effective amount is sufficient to produce a 1,000-5,000 neutralizing antibody titer produced by neutralizing antibody against the EBV antigen as measured in serum of the subject at 1-72 hours post administration. In some embodiments, the effective amount is sufficient to produce a 5,000-10,000 neutralizing antibody titer produced by neutralizing antibody against the EBV antigen as measured in serum of the subject at 1-72 hours post administration.

In some embodiments, the neutralizing antibody titer is at least 100 NT₅₀. For example, the neutralizing antibody titer may be at least 200, 300, 400, 500, 600, 700, 800, 900 or 1000 NT₅₀. In some embodiments, the neutralizing antibody titer is at least 10,000 NT₅₀.

In some embodiments, the neutralizing antibody titer is at least 100 neutralizing units per milliliter (NU/mL). For example, the neutralizing antibody titer may be at least 200, 300, 400, 500, 600, 700, 800, 900 or 1000 NU/mL. In some embodiments, the neutralizing antibody titer is at least 10,000 NU/mL.

In some embodiments, an anti-EBV antigen antibody titer produced in the subject is increased by at least 1 log relative to a control. For example, an anti-EBV antigen antibody titer produced in the subject may be increased by at least 2, 3, 4, 5, 6, 7, 8, 9 or 10 log relative to a control.

In some embodiments, an anti-EBV antigen antibody titer produced in the subject is increased at least 2 times relative to a control. For example, an anti-EBV antigen antibody titer produced in the subject is increased by at least 3, 4, 5, 6, 7, 8, 9 or 10 times relative to a control.

In some embodiments, a geometric mean, which is the n th root of the product of n numbers, is generally used to describe proportional growth. Geometric mean, in some embodiments, is used to characterize antibody titer produced in a subject.

A control may be, for example, an unvaccinated subject, or a subject administered a live attenuated EBV vaccine, an inactivated EBV vaccine, or a protein subunit EBV vaccine.

EXAMPLES

5

Example 1

EBV glycoprotein 350 (gp350) variants were produced and their expression tested in HeLa cells. HeLa cells were transiently transfected for 24 hours with mRNA encoding each of EBV glycoprotein 350 (gp350) variants (SEQ ID NOs: 185, 182, 207, and 208). Flow cytometry analyses (FIGS. 1A, 1 µg dose mRNA) and immunoassays (FIGS. 1B, 1 µg dose mRNA; FIG 10 1C, 0.5 µg dose mRNA) using an EBV neutralizing antibody that binds conformational epitopes in gp350 ("72A1") demonstrate that all EBV gp350 variants tested show equivalent expression at the surface of the transfected HeLa cells. Unless otherwise stated, all mRNA vaccines may be formulated in lipid nanoparticles comprising Compound 1 lipids, e.g., 20-60% ionizable cationic 15 lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid.

Example 2

EBV gp350 mRNA sequences with two different 5' UTR sequences (SEQ ID NOs: 81 and 204) were produced and their expression tested in HeLa cells. HeLa cells were transiently 20 transfected for 24 hours with a 0.5 µg dose of mRNA encoding the EBV gp350 antigens. Flow cytometry analyses (FIG. 2A) and immunoassays (FIG. 2B) using the anti-72A1 antibody demonstrate that both EBV gp350 mRNA constructs tested show equivalent expression at the surface of the transfected HeLa cells.

Example 3

Balb/c mice were vaccinated intramuscularly with EBV vaccines comprising mRNA encoding EBV gp350 variants (SEQ ID NOs: 185, 182, 207, and 208) formulated in a lipid nanoparticle. A 2 µg dose was administered on Day 1 and then again on Day 22. Mice were bled on Day 21 and Day 43. Results demonstrate that all the EBV gp350 vaccines tested induced 30 serum gp350-specific IgG antibody titers at day 21 (3 weeks post prime) and day 43 (3 weeks post boost) following vaccination (FIG. 3).

Example 4

Additional EBV antigens and antigen complexes were produced and their expression tested in HeLa cells. HeLa cells were transiently transfected for 24 hours with 0.25 µg of (1) mRNA encoding EBV gH (SEQ ID NO: 187), mRNA encoding EBV gL (SEQ ID NO: 188), and mRNA encoding EBV gp42 (SEQ ID NO:189) (EBV gH/gL/gp42 UTR A); (2) mRNA encoding EBV gH (SEQ ID NO: 201), mRNA encoding EBV gL (SEQ ID NO: 202), and mRNA encoding EBV gp42 (SEQ ID NO: 203) (EBV gH/gL/gp42 UTR B); (3) mRNA encoding EBV gH (SEQ ID NO: 187) and mRNA encoding gp42 (SEQ ID NO:189); or (4) mRNA encoding EBV gp42 (SEQ ID NO:189). Flow cytometry analyses (FIG. 4A) and immunoassays (FIG. 4B) using an anti-gH/gL/gp42 (2D4) antibody demonstrate that all EBV mRNA constructs tested show equivalent expression at the surface of the transfected HeLa cells.

Example 5

Balb/c mice were vaccinated intramuscularly with EBV vaccines comprising (1) mRNA encoding EBV gH (SEQ ID NO: 187), mRNA encoding EBV gL (SEQ ID NO: 188), and mRNA encoding EBV gp42 (SEQ ID NO: 189); (2) mRNA encoding EBV gp350 (SEQ ID NO: 185); or (3) mRNA encoding EBV gH (SEQ ID NO: 187), mRNA encoding EBV gL (SEQ ID NO: 188), mRNA encoding EBV gp42 (SEQ ID NO: 189), and mRNA encoding EBV gp350 (SEQ ID NO: 185). A 2 µg dose was administered on Day 1 and then again on Day 29. Mice were bled on Day 28 and Day 57. Results demonstrate that all the EBV vaccines tested induced neutralizing antibody titers at day 28 (4 weeks post prime) and day 57 (4 weeks post boost) following vaccination (FIG. 5).

Example 6

HeLa cells were transiently transfected for 24 hours with 0.5 µg of (1) mRNA encoding EBV gH (SEQ ID NO: 201) and mRNA encoding EBV gL (SEQ ID NO: 202); or (2) mRNA encoding EBV gH only (SEQ ID NO: 201). Flow cytometry analyses (FIG. 6A) using an anti-gH/gL (2A8) antibody or an anti-gH/gL/gp42 (2D4) antibody demonstrate that the 2A8 antibody binds specifically to EBV gL expressed on the surface of the HeLa cells (compare to data presented in Example 4). Immunoassays following 24 hour transfection with 0.25 µg of either (1) mRNA encoding EBV mRNA encoding EBV gH (SEQ ID NO: 187) and mRNA encoding EBV gL (SEQ ID NO: 188); or (2) mRNA encoding EBV mRNA encoding EBV gH (SEQ ID NO: 201) and mRNA encoding EBV gL (SEQ ID NO: 202) show comparable expression of both EBV antigen complexes at the surface of HeLa cells.

Example 7

Three additional immunogenicity studies were performed using various mRNA vaccines of the present disclosure (formulated in lipid nanoparticles) and various antigen-specific antibodies. Balb/c mice were vaccinated intramuscularly with (1) a 5 µg dose or a 1 µg dose of mRNA encoding EBV gH (SEQ ID NO: 187) and mRNA encoding EBV gL (SEQ ID NO: 188); (2) a 7.5 µg dose or a 1.5 µg dose of mRNA encoding EBV gH (SEQ ID NO: 187), mRNA encoding EBV gL (SEQ ID NO: 188), and mRNA encoding EBV gB (SEQ ID NO: 209); (3) a 7.5 µg dose or a 1.5 µg dose of mRNA encoding EBV gH (SEQ ID NO: 187), mRNA encoding EBV gL (SEQ ID NO: 188), and mRNA encoding EBV gp350 (SEQ ID NO: 185); or (4) a 10 µg dose or a 2 µg dose of mRNA encoding EBV gH (SEQ ID NO: 187), mRNA encoding EBV gL (SEQ ID NO: 188), mRNA encoding EBV gB (SEQ ID NO: 209), and mRNA encoding EBV gp350 (SEQ ID NO: 185). Mice were bled on Day 57. Results following detection with anti-gH/gL antibody (FIG. 7), anti-gB antibody (FIG. 8), or anti-gp350 antibody (FIG. 9) demonstrate induction of EBV antigen-specific neutralizing antibodies.

Example 8

Mice were vaccinated with a 2 µg dose of mRNA encoding one of four EBV latent genes (LMP1 (SEQ ID NO: 179), LMP2 (SEQ ID NO: 181), EBNA1^{Δ1-400} (SEQ ID NO: 178) or EBNA3A (SEQ ID NO: 177)) or a combination of all four mRNA vaccines (LMP1 (SEQ ID NO: 179), LMP2 (SEQ ID NO: 181), EBNA1^{Δ1-400} (SEQ ID NO: 178) and EBNA3A (SEQ ID NO: 177)). Cells were harvested from vaccinated mice and stimulated with LMP1, LMP2, EBNA1 or EBNA3A peptides. All peptide libraries comprise 15mer peptides overlapping by 11 amino acids. CD8 T cell responses are shown in FIGS. 10A-10D, and CD4 T cell responses are shown in FIGS. 11A-11D.

Example 9

mRNA encoding EBV glycoprotein H-glycoprotein L (gH-gL) linked constructs (SEQ ID NO: 218 or 221) were produced and their expression tested in HeLa cells. HeLa cells were transiently transfected for 24 hours with mRNA encoding two EBV gH-gL variants with different linkers (SEQ ID NO: 218 or SEQ ID NO: 221), or with mRNA encoding EBV gH (EBV gH mRNA; SEQ ID NO: 228) and mRNA encoding EBV gL (EBV gL mRNA; SEQ ID NO: 229). Flow cytometry analyses (FIG. 13A, 0.5 µg dose of EBV gH-gL linked mRNA or 0.25 µg dose of each of EBV gH mRNA and EBV gL mRNA) and immunoassays (FIG. 13B; 0.5 µg dose of gH-gL linked construct or 0.25 µg dose of each of gH and gL) using EBV

neutralizing antibodies 2A8 and CL40, which binds conformational epitopes in gH, demonstrate that both EBV gH-gL constructs (SEQ ID NO: 218 and 221) tested show expression at the surface of the transfected HeLa cells.

5 Example 10

In a further immunogenicity study to test the effect of different untranslated regions (UTRs), mice were vaccinated intramuscularly with lipid nanoparticles (comprising Compound 1 lipids, e.g., 20-60% ionizable cationic lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid) comprising (1) 10 µg mRNA encoding gp350 (SEQ ID NO: 185),
 10 mRNA encoding gH (SEQ ID NO: 187), mRNA encoding gL (SEQ ID NO: 188), mRNA encoding LMP2 antigen (SEQ ID NO: 181), and mRNA encoding EBNA1 antigen (SEQ ID NO: 178), each of the transcripts comprising UTRA; (2) 10 µg mRNA encoding gp350 (SEQ ID NO: 185), mRNA encoding gH (SEQ ID NO: 187), mRNA encoding gL (SEQ ID NO: 188), mRNA encoding LMP2 antigen (SEQ ID NO: 181), and mRNA encoding EBNA1 antigen (SEQ
 15 ID NO: 178), each of the transcripts comprising UTRB; (3) 2 µg mRNA encoding EBNA1 antigen (SEQ ID NO: 178) with UTRB; (4) 2 µg mRNA encoding LMP2 antigen with UTRB; or (5) empty lipid nanoparticles. The mice received one dose on Day 1 and a second dose on Day 29. Blood samples were taken just prior to dosing, and on Day 57. Spleens were collected from a subset of animals on Day 36. Cells were harvested from vaccinated mice and stimulated with
 20 peptides from an EBNA1 peptide library (FIG. 14) or an LMP2 library (FIG. 15). The peptide library comprised 15mer peptides overlapping by 11 amino acids. CD4 T cell cytokine responses for the EBV formulations (groups 1 and 2), the EBNA1 formulation (group 3), and the control (empty nanoparticles; group 5) are shown in the top row of FIG. 14; the bottom row of FIG. 14 shows CD8 T cell responses. FIG. 15 shows the CD4 T cell responses (top row) and CD8 T cell
 25 cytokine responses (bottom row) for EBV formulations (groups 1 and 2), the LMP2 formulation (group 4), and the control (empty nanoparticles; group 5). Similar T cell responses were found between groups regardless of the UTR used.

Example 11

30 The constructs were tested in a non-human primate (*Rhesus macaque*) model. The subjects were vaccinated intramuscularly with lipid nanoparticles comprising (1) 200 µg of mRNA encoding gp350 (SEQ ID NO: 185), mRNA encoding gH (SEQ ID NO: 187), mRNA encoding gL (SEQ ID NO: 188), mRNA encoding LMP2 antigen (SEQ ID NO: 181), and mRNA encoding EBNA1 antigen (SEQ ID NO: 178); (2) 50 µg of mRNA encoding gp350

(SEQ ID NO: 185), mRNA encoding gH (SEQ ID NO: 187), mRNA encoding gL (SEQ ID NO: 188), mRNA encoding LMP2 antigen (SEQ ID NO: 181), and mRNA encoding EBNA1 antigen (SEQ ID NO: 178); or (3) 200 µg of mRNA encoding a control. As shown in FIG. 16, the subjects received one dose on day 0 and a second dose on day 28. Blood samples were drawn on days 0, 27, 28, 60, 90, 120, 150, and 180. Results following detection with anti-gp350 titer and anti-gH/gL antibody demonstrate that vaccination with the selected formulations results in increased and durable anti-gp350 and anti-gH/gL antibody titers (FIG. 16). While neutralizing antibody titers were found to be durable at high doses, a significant drop in neutralizing antibody titers at low doses of the EBV vaccine was observed (FIG. 17).

Example 12

The effect of various downstream processes on EBV vaccine immunogenicity was examined. EBV vaccines comprising gp350 (SEQ ID NO: 185), gH (SEQ ID NO: 187), and gL (SEQ ID NO: 188) were synthesized using different downstream purification processes.

The resulting mRNA was used to form doses (10 µg, 3 µg, and 1 µg doses for each of the four groups; PBS was used as a control group; n=8/group) that were administered to mice on Days 1 and 22. Blood samples were collected on Days 1, 21, 22, 36, 82, and 142. Antibody titers from gp250 (FIG. 18) and for gH/gL (FIG. 19) were measured.

EQUIVALENTS

All references, patents and patent applications disclosed herein are incorporated by reference with respect to the subject matter for which each is cited, which in some cases may encompass the entirety of the document.

The indefinite articles “a” and “an,” as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean “at least one.” It should also be understood that, unless clearly indicated to the contrary, in any methods claimed herein that include more than one step or act, the order of the steps or acts of the method is not necessarily limited to the order in which the steps or acts of the method are recited.

In the claims, as well as in the specification above, all transitional phrases such as “comprising,” “including,” “carrying,” “having,” “containing,” “involving,” “holding,” “composed of,” and the like are to be understood to be open-ended, i.e., to mean including but not limited to. Only the transitional phrases “consisting of” and “consisting essentially of” shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03.

The terms “about” and “substantially” preceding a numerical value mean $\pm 10\%$ of the recited numerical value.

Where a range of values is provided, each value between the upper and lower ends of the range are specifically contemplated and described herein.

5 The entire contents of International Application Nos. PCT/US2015/02740, PCT/US2016/043348, PCT/US2016/043332, PCT/US2016/058327, PCT/US2016/058324, PCT/US2016/058314, PCT/US2016/058310, PCT/US2016/058321, PCT/US2016/058297, PCT/US2016/058319, and PCT/US2016/058314 are incorporated herein by reference.

SEQUENCE LISTING

It should be understood that any of the mRNA sequences described herein may include a 5' UTR and/or a 3' UTR. The UTR sequences may be selected from the following sequences, or other known UTR sequences may be used. It should also be understood that any of the mRNA constructs described herein may further comprise a polyA tail and/or cap (e.g., 7mG(5')ppp(5')NlmpNp). Further, while many of the mRNAs and encoded antigen sequences described herein include a signal peptide and/or a peptide tag (e.g., C-terminal His tag), it should be understood that the indicated signal peptide and/or peptide tag may be substituted for a different signal peptide and/or peptide tag, or the signal peptide and/or peptide tag may be omitted.

5' UTR: GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC (SEQ ID NO: 1)

5' UTR: GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGACCCC

GGCGCCGCCACC (SEQ ID NO: 104)

3' UTR: UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGG

CCUCCCCCAGCCCCUCCUCCCCUCCUGCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGU

GGGCGGC (SEQ ID NO: 3)

3' UTR: UGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCCCCUUGGG

CCUCCCCCAGCCCCUCCUCCCCUCCUGCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGU

GGGCGGC (SEQ ID NO: 106)

EBNA MO1		SEQ ID NO:
SEQ ID NO: 130 consists of from 5' end to 3' end, 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 2, and 3' UTR SEQ ID NO:3.		130
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGCGACGAGGGUCCGGGCACAGGACCCGGUAACGGG UUGGGCGAAAAGGGUGACACUAGCGGGCCCGAAGGUUCC GGCGGAUCUGGCCCGCAACGCAGAGGUGGUGAUAAACCAC GGUCGCGGUAGAGGCAGAGGCCGUGGCCGGGGUGGCGGA AGGCCCCGUGCCCCUGGAGGGGUCAGGGUCUGGCCCAAGG CACCGUGAUGGGGUGCGUCGCCCCCAGAAACGCCCCGUCCU GUAUCGGCUGCAAGGGCACGCAUGGCGGAACGGGAGGUG GCGCAGGAGCCGGAGGUGCAAGAGGUCGCGGGGGGUCAG GGGGGAGAGGUAGAGGGGGAUCAGGGGGGCGGAGAGGGC GGGGUCGAGAAAGAGCAAGAGGUGGCUCAGAGAGCGCG CUCGGGGUCGCGGGCGAGGCCGGGGUGAAAAACGGCCCC GGAGCCCAUCCUCGCAAUCAUAAGCUCGGGAUCGCCACC UCGGCGGCCGCCCCCGGCAGGCGUCCCUUUUCCACCCA GUGGGCGAAGCCGACUACUUCGAGUACCACCAGGAGGGA GGACCGGAUGGUGAGCCGGAUGUUCUCCCGGCGCCAU GAACAAGGUCCUGCCGAUGAUCCAGGCGAGGGGCCCUC ACAGGCCCCCGAGGGCAGGGGGACGGGGGACGUCGGAAG AAAGGAGGCUGGUUUGGCAAGCACCGAGGACAGGGGGGU	2

	AGCAACCCGAAAUUUGAGAACAUCCGAGGGGCUACAGG GCUCUCCUAGCCCGUAGCCACGUCGAAAGAACUACCGAU GAGGGCACCUGGGUUGCCGGCGUGUUCGUGUACGGGGGU AGCAAGACCUCUCUAUACAACCUUCGGAGGGGGACUGCA CUUGCUAUCCCCCAAUGCCGCCUCACACCACUGUCUCGCC UGCCAUUCGGCAUGGCCCCCGGCCGGGGCCACAGCCUGG GCCCCUACGGGAUUCUAUUGUUUGCUAUUUUAUGGUGUU CCUGCAGACCCAUUUCUUCGCAGAAGUCCUGAAAGACGC CAUCAAGACUUAGUUAUGACUAAACCCGCACCCACCUG CAACAUUCGCGUGACCGUAUGCAGCUUUGAUGAUGGCGU CGAUCUGCCCCCAUGGUUCCCCCUAUGGUCGAGGGGCGCC GCCGCCGAAGGGGACGACGGGGAUGACGGGGAUGAAGGC GGGGACGGCGAUGAGGGGCGAGGAGGGCCAGGAA	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MSDEGPGTGPNGNLGEKGDTSPEGSGGSGPQRRGGDNHGR GRGRGRGRGGGRPGAPGSGSGPRHRDGVRRPQKRPSICGCK GTHGGTGGGAGAGGARGRGGSGRGRGGSGRRGRGRERA RGGSRERARGRGRGRGEKRPRSPSSQSSSGSPRRPPPGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPST GPRGQGDGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALL ARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQC RLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVL KDAIKDLVMTKPAPTCNIRVTVCSDGVDLPPWFPPMVEGA AAEGDDGDDGDEGGDGEDEEGQE	4
PolyA tail	100 nt	
EBNA1_mod_002		
SEQ ID NO: 131 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 5, and 3' UTR SEQ ID NO:3		131
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAAGAGAGAAAAGAAGAGUAAGAAGAAAUUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGUGACGAGGGACCUGGGACUGGCCCCGGGAACGGU CUGGGUGAGAAAGGUGACACGUCUGGUCCUGAAGGAUCU GGCGGUUCAGGGCCGCAGCGCAGAGGAGGAGACAACCAC GGUAGAGGACGUGGACGCGGGAGAGGCCGAGGGGGCGGA AGACCUGGUGCACCGGGCGGUUCCGGCUCGGGGCCCCGCC ACAGGGAUGGGGUGCGGAGACCACAGAAGCGCCCCUCUU GCAUCGGCUGCAAGGGAACCAUGGGGGUACCGGAGGGG GAGCUGGUGCAGGUGGCGCCCGUGGUAGGGGUGGCAGCG GGGGGCGUGGAAGAGGUGGUUCAGGCGGACGGAGGGGAC GCGGACGUGAACGUGCCCCGGGGAGGAUCCCGGGAGAGGG CACGGGGCCGCGGCAGAGGCAGAGGGGAGAAGAGACCUA GAUCCCCUAGCUCUCAUCCAGCAGCAGUGGGUCCCCCCC GAGGCGACCGCCUCCAGGUAGGCGCCCUUUCUUCACCCC GUUGGCGAGGCAGAUUACUUCGAAUAUCAUAAGAGGGG GGGCCCCAUGGCGAGCCGGACGUACCAACCCGGUGCUAUC GAGCAAGGUCCGGCUGACGAUCCUGGUGAAGGGCCAAGU ACCGGACCUAGGGGGCAGGGCGACGGUGGUAGGCGUAAA AAAGGAGGGUGGUUCGGCAAACAUCGCGGCCAGGGAGGG AGCAACCCCAAGUUUGAAAAUAUCGCCGAAGGGCUACGA GCUUUGCUCGCGAGGUCCCAUGUGGAACGAACUACAGAC GAGGGCACCUGGGUGGCUGGUGUCUUCGUUUUAUGGCGGG AGCAAGACCUCUUGUAUAAUCUAAGGCGGGGCACAGCC CUGGCCAUACCGCAGUGUCGCCUGACACCCUGUCGCC UGCCUUUUGGCAUGGCGCCAGGGCCAGGACCACAACCU GGCCCCUGCGCGAAAGUAUUGUGUGUUACUUCAUGGUCU	5

	UCCUGCAGACACAUAUUUUCGCAGAAGUCCUAAAGGAUG CAAUAAAGGAUCUCGUAAUGACGAAGCCCCGCCAACGU GUAAUAUUAGGGUUAACGGUCUGUAGUUUCGAUGACGGGG UAGAUCUCCCCCCCUGGUUCCCACCUAUGGUCGAGGGGUGC CGCUGCGGAGGGGGACGAUGGCGACGACGGCGAUGAAGG CGGGGAUGGCGACGAGGGGGAGGAGGGACAGGAA	
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MSDEGPGTGPGNGLGEKGDTS GPEGSGGSGPQRRGGDNHGR GRGRGRGRGGGRPGAPGSGSGPRHRDGVRRPQKRPSICGCK GTHGGTGGGAGAGGARGRGGSGRGRGGSGRRGRGRERA RGGSRERARGRGRGRGEKRPRSPSSQSSSSGSPRRPPPGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPST GPRGQGDGGRRKKGWFGKHRGQGGSNPKFENIAEGLRALL ARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQC RLTPLSRLPFGMAPGPGPQGPLRESIVCYFMVFLQTHIFAEVL KDAIKDLVMTKPAPTCNIRVTVCSDDGVDLPPWFPPMVEGA AAEGDDGDDGDEGGDGDEGEEGQE	4
PolyA tail	100 nt	
EBNA1_mod_003		
SEQ ID NO: 132 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 6, and 3' UTR SEQ ID NO:3		132
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGUCAGACGAGGGGCCAGGCACGGGGCCUGGAAACGGA CUGGGAGAGAAGGGGGAUACCUCAGGGCCAGAGGGUAGU GGGGGUAGCGGGCCUCAGAGAAGGGGGGGCGACAAUCAC GGUCGGGGAAGAGGGAGAGGUAGGGGUAGAGGAGGAGGC CGUCCCGGGGCUCCUGGCGGUUCCGGGUCCGGCCUCGCC ACAGAGAUGGCGUGAGGAGACCUCAGAAGCGUCCGUCCU GUAUUGGGUGCAAGGGGACCCACGGUGGCACCGGUGGCG GAGCUGGGGCAGGAGGUGCUAGAGGAAGAGGCGGUUCAG GUGGAAGGGGUCGCGGUGGUUCAGGAGGACGGCGCGGCC GGGGGAGAGAGCGGGCAAGAGGCGGCAGCAGGGAGCGGG CAAGAGGACGAGGGAGGGGCCGAGGCGAGAAGCGACCUA GGUCGCCUAGUUCACAGAGCUCCAGUUCUGGGUCGCCCCC CCGGCGGCCGCCUCCUGGGCGAAGACCCUUUUUCCACCCC GUGGGGGAGGCUGACUACUUCGAGUACCACCAGGAGGGC GGCCAGACGAGAGCCCGAUGUUCGCGCUGGGGCCAUU GAACAAGGCCUGCAGAUAGCCAGGGGAAGGACCAUCA ACCGGCCCUAGGGGACAGGGCGAUGGGGGGAGACGGA AAGGGAGGGUGGUUCGGGAAGCACC GCGGCCAGGGGGGG UCUAAUCCGAAAUUCGAAAACAUUGCCGAGGGCCUCCGU GCUUUGUUGGCUAGAUCACACGUGGAAAGAACACGGAU GAAGGCACGUGGGUGGCGGGCGUCUUCGUGUAUGGUGGG AGUAAGACCUCUCCUGUAUAACCUCAGGCGUGGCACAGCC CUUGCCAUCCACAGUGCAGGCUCACACCCCUUAGCAGGC UCCCCUUUGGAUGGCUCCUGGUCCCGGCCCCAGCCCGG UCCACUGCGAGAAUCCAUGUAUGUUAUUAUGGUUUU CUUGCAGACACAUAUCUUCGCCGAGGUGCUGAAAGACGC CAUUAAGACCUGGUGAUGACAAAGCCUGCCCCACGUG CAUAUCCGUGUGACCGUCUGCUCCUUGAUGACGGAGU CGACCUGCCUCCUGGUUCCCCCAUGGUCGAGGGCGCU GCGGCGGAAGGGGACGACGGCGAUGAUGGUGACGAGGGC GGUGAUGGCGACGAAGGUGAAGAGGGUCAGGAG	6

3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MSDEGPGTGPNGNLGEKGDTSGPEGSGGSGPQRRGGDNHGR GRGRGRGRGGGRPGAPGGSGSGPRHRDGVRRPQKRPSICGCK GTHGGTGGGAGAGGARGRGGSGGRGRGGSGRRGRGRERA RGGSRERARGRGRGRGEKRPRSPSSQSSSSGSPRRPPPGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPST GPRGQGDGGRKKGGWFGKHRGQGGSNPKFENIAEGLRALL ARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQC RLTPLSRLPFMAPGPGPQGPLRESIVCYFMVFLQTHIFAEVL KDAIKDLVMTKPAPT CNIRVTVC SFDDGVDLPPWFPPMVEGA AAEGDDGDDGDEGGDGDEGEEGQE	4
PolyA tail	100 nt	
EBNA1_mod_004		
SEQ ID NO: 133 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 7, and 3' UTR SEQ ID NO:3		133
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAAGAGAGAAAAGAAGAGUAAGAAGAAAUUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGCGACGAGGGUCCAGGCACAGGCCCGGGGAACGGG UUGGGAGAAAAAGGGGACACUUCGGUCCAGAAGGCUCC GGGGGAGCGGACCUCAGAGAAGAGGUGUGAUAAUCAC GGGAGAGGGAGAGGGCGGGGCAGGGGACGUGGGGCGGU AGACCUGGGGCGCCGGGGGUUCCGGCUCCGGACACGG CAUAGGGAUGGUGUGCGAAGGCCCGCAGAAGCGGCCGUCU UGUAUAGGCUGCAAAGGCACUCACGGUGGUACCGGGGGG GGAGCAGGAGCAGGAGGCGCUCGAGGUCGGGGCGGGUCC GGCGGCAGAGGCCGCGUGGUUCUGGGGGAAGGAGGGGA AGAGGGAGAGAACGCGCCCGCGGAGGCUCUCGCGAACGG GCCAGAGGGCGGGGGAGGGGGCGCGGGGAGAAAAGGCC AGGUCGCCAAGUAGUCAGUCCUCCAGUAGCGGCAGCCCA CCCCGCAGACCUCCUCCAGGACGACGACCUUUCUUUAUC CCGUCGGCGAGGCCGAUUACUUUGAGUACCAUCAGGAAG GGGGGCCUGAUGGAGAACCAGGUAUGUCCUCCUGGUGCUA UCGAACAGGGCCCCGCGACGAUCCAGGCGAGGGCCCCAG UACGGGCCCUGAGAGGCCAGGGAGAUAGGAGGUAGAAGGAA GAAGGGGGGAUGGUUUGGCAAGCACAGAGGGCAGGGAGG UAGUAAUCCCAAUUUGAGAAUUAUGCCGAGGGUCUGCG GGCACUUCUGGCCCGGUCUCAUGUUGAGAGAACGACUGA UGAGGGAACAUGGGUGGCUGGCGUCUUUGUGUAUGGCGG UAGUAAAACCAGCCUCUACAAUUUACGGCGUGGGACAGC GCUAGCUAUUCCGCAAUGCCGGCUGACCCCUUUGUCUAG GCUGCCCUUUGGUUUGGCCCCCGCCCCGGCCACAGCCU GGGCCUUUGCGGGAAGCAUCGUCUGCUACUUUAUGGUG UCCUCCAGACCCACAUCUUUGCAGAGGUGCUUAAGGAC GCCAUAAAGGACCUGGUUAUGACCAAACCCGCCCCUACCU GCAAUUCCGCGUCACGGUGUGCUCCUUCGACGACGGGG UUGACUUGCCUCCAUUGGUUCCACCCAUUGGUAGAGGGCG CUGCUGCCGAGGGGAUGAUGGAGACGACGAGACGAGGAGG GCGGCGAUGGCGAUGAAGGCGAAGAAGGCCAGGAA	7
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3

Corresponding amino acid sequence	MSDEGPGTGPNGNLGEKGDTSGPEGSGSGSPQRRGGDNHGR GRGRGRGRGGGRPGAPGSGSGPRHRDGVRRPQKRPSICGCK GTHGGTGGGAGAGGARGRGSGGRGRGSGGRRGRGRERA RGGSRERARGRGRGRGEKRPRSPSSQSSSSGSPRRPPPGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPST GPRGQGDGGRKKGGWFGKHRGQGSNPKFENIAEGLRALL ARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIQC RLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVL KDAIKDLVMTKPAPT CNIRVTVC SFDDGVDLPPWFPPMVEGA AAEGDDGDDGDEGGDGDEGEEGQE	4
PolyA tail	100 nt	
EBNA1_mod_005		
SEQ ID NO: 134 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 8, and 3' UTR SEQ ID NO:3		134
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGUCUGACGAAGGCCCGGGCACAGGCCAGGCAACGGA UUGGGCGAAAAAGGUGAUACAAGCGGGCCAGAAGGGAGC GGGGGCUCUGGGCCCCAGAGACGGGGGGGUGACAAUCAC GGCCGAGGAAGGGGAAGGGGCAGGGGAAGAGGCGGAGGA CGGCCUGGCGCUCCUGGAGGCUCUGGCUCAGGUCCAAGA CAUAGGGAUGGGGUCAGAAGACCACAGAAGAGACCUAGC UGUAUUGGAUGCAAGGGUACACACGGUGGCACGGGCGGC GGUGCUGGCGCUGGGGGCGCGAGAGGACGUGGAGGUUCA GGCGGGAGAGGUCGAGGAGGCUCUGGAGGCCGCGAGGGGG AGAGGACGAGAGAGGGCCCCGGGGGGGUCCCCGGGAAAGA GCUAGAGGGAGGGGACGCGGGCGGGGGGAAAGACGGCCU CGCUCUCCUUCUUCUCAAUCUCCUCCUCUGGUUCCGC CCCCGACGCCCCCACCGGGCAGGAGGCCAUUUUUUACCC UGUCGGCGAGGCAGACUACUUCGAGUACCACCAAGAAGG AGGCCAGACGGCGAGCCUGAUGUGCCGCCAGGUGCCA CGAGCAGGGGCCAGCUGAUGACCCGGGGGAGGGACCUAG CACGGGGCCCCGCGGUCAGGGCGACGGAGGGAGGAGAAA AAAAGGUGGGUGGUUUGGCAAGCAUAGAGGGCAGGGUGG CUCAAACCCAAAGUUUGAAAACAUCGAGAAAGGUCUUCG GGCUCUGCUGGCCCGCUCUCAUGUAGAGCGCACUACUGA CGAAGGCACCUGGGUGGCCGGGGUGUUCGUGUACGGAGG AUCUAAGACCAGUCUGUACAACCUCCGAGGGGGACAGC UCUCGCUAUCCCCAGUGUAGGCUCACCCCUUUGAGUCGC CUUCCGUUCGGAUUGGCUCUGGCCCGGGCCCCAGCCCG GGCCACUAAGAGAGAGCAUCGUAUGCUACUUUAUGGUAU UUUUGCAAACCCACAUCUUCGCUGAAGUGCUUAAGGACG CCAUCAAGACCUGGUGAUGACAAAACCAGCUCCAACAU GCAAUAUAGGGUAACCGUAUGCUCCUUCGAUGAUGGCG UCGACCUUCCACCUUGGUUCCCCCAAUGGUGGAGGGAG CCGCAGCAGAAGGAGACGAUGGUGAUGAUGGAGACGAAG GCGGGGAUGGCGACGAAGGAGAGGAGGGACAGGAA	8
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MSDEGPGTGPNGNLGEKGDTSGPEGSGSGSPQRRGGDNHGR GRGRGRGRGGGRPGAPGSGSGPRHRDGVRRPQKRPSICGCK GTHGGTGGGAGAGGARGRGSGGRGRGSGGRRGRGRERA RGGSRERARGRGRGRGEKRPRSPSSQSSSSGSPRRPPPGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPST	4

	GPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALL ARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIPQC RLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVL KDAIKDLVMTKPAPTCNIRVTVCSDGVDLPPWFPPMVEGA AAEGDDGDDGDEGGDGDEGEEGQE	
PolyA tail	100 nt	
EBNA1_trunc_001		
SEQ ID NO: 135 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 9, and 3' UTR SEQ ID NO:3		135
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGCAGAAGACCCUUCUUUACCCCGUGGGAGAAGCC GACUAAUUCGAGUACCACCAGGAGGGCGGUCCUGACGGC GAGCCCGACGUGCCUCCAGGCGCCAUCGAACAGGGCCCCG CUGACGAUCCUGGCGAGGGGCCUCCACAGGCCCUCCGCG CCAGGGAGAUGGGGGAAGGCGGAAGAAGGGGGGCGUGGU UGGCAAGCAUAGGGGCCAGGGCGGCUCCAAUCCCAAGUU CGAGAAUAUCGCCGAGGGGCUCCGGGCUCUGCUGGCCCCG GUCGCACGUCGAACGUACCACUGACGAGGGGACGUGGGU GGCCGGCGUCUUUGUGUACGGAGGAUCCAAGACCUCCCU GUACAACCUGAGAAGGGGGACCGCCCUUGCCAUCCCUCA GUGCAGACUACCCCCCUGAGCAGGCUCUUUGGGAUG GCUCCUGGGCCAGGCCCCAGCCCGGGCCCCUCAGGGAAA GCAUCGUGUGUUACUUUAUGGUGUUUCUGCAGACACACA UUUUUGCAGAAGUUCUGAAAGAUGCAAUCAAGGAUCUGG UGAUGACCAAGCCUGCACCUCGUGCAAUAUCAGGGUGA CAGUAUGCUCCUUCGACGACGGUGUGGACCUCCCCCCCUG GUUCCCAACCAUGGUCGAGGGGGCCGCCCGGAGGGGAGA CGAUGGCGACGACGGUGAUGAGGGGGGAGACGGAGAUGA AGGCGAGGAGGGGGCAGGAG	9
3' UTR	UGAUAUUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRPPFFHPVGEADYFEYHQEGPDGEPDVPPGAIEQGPADD PGEPPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRG TALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQ THIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSDGVDLPPWF PPMVEGAAAEGDDGDDGDEGGDGDEGEEGQE	10
PolyA tail	100 nt	
EBNA1_trunc_002		
SEQ ID NO: 136 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 11, and 3' UTR SEQ ID NO:3		136
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGACGGAGACCAUUCUUCACCCCGUGGGAGAAGCC GACUACUUCGAGUACCACCAGGAGGGCGGUCCAGACGGC GAACCCGACGUCCUCCUGGAGCCAUCGAGCAGGGCCCCG CCGACGACCCUGGCGAGGGGCCUAGCACCGGACCUAGAGG ACAAGGCGACGGCGGGAGGAGAAAGAAGGGGGGCGUGGU CGGGAAGCACCGCGGGCAAGGCGGCAGCAACCCAAAGUU	11

	CGAGAACAU CGCCGAGGGGUUGCGGGCCUGCUCGCCCCG UUCCACGUGGAGCGGACAACCGACGAGGGAACCUGGGU UGCCGGGGU AUUUGUGUACGGCGGCAGUAAGACCAGCCU GUAUAACCUCAGAAGAGGAACAGCCCUGGCCAUCCCACA GUGCAGGCUGACACCCUCUCCCGGCUGCCAUUUGGAAU GGCACCCGGGCCUGGACCCAGCCUGGCCACUGCGCGAG UCUAUCGUGUGUACUUUAUGGUCUCCUGCAAACCCAC AUCUUCGCGGAGGUUUUAAAGGAUGCCAUCAAAGACCUC GUGAUGACAAAGCCCGCUCCACCUGCAAUAUCAGAGUG ACCGUAUGCAGCUUUGACGACGGCGUGGACCUGCCUCCC UGGUUCCCUCCUAUGGUGGAGGGCGCCGCCGAGAAGGG GACGACGUGACGAUGGCGAUGAGGGAGGGGAUGGAGAC GAAGGCGAGGAGGGGCCAGGAG	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADD PGE GPSTGPRGQGDGRRKKGGWFGKHRGQGGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRG TALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQ THIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSDDGVDLPPWF PPMVEGAAAEAGDDGDDGDEGGDGEDEEGQE	10
PolyA tail	100 nt	
EBNA1_trunc_003		
SEQ ID NO: 137 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 12, and 3' UTR SEQ ID NO:3		137
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGCCGCAGACCCUUCUUUACCCCGUGGGAGAGGCC GACUAUUUUGAGUACCACCAGGAGGGCGGGCCCGACGGC GAACCUGACGUGCCACCUGGCGCCAUGAACAAGGCCCA GCCGACGACCCUGGGGAGGGCCCUAGCACAGGGCCAGG GGCCAGGGAGACGGGGGUAGGCGUAAGAAGGGAGGCUGG UUCGGUAAGCACCGCGGCCAGGUGGCAGCAACCCUAAA UUCGAGAAUAUUGCCGAAGGUCUGCGAGCCCUUUGGCC AGAAGCCACGUGGAACGCACUACUGAUGAGGGCACCUGG GUCGCCGAGUGUUCGUGUACGGCGGAAGCAAAACCAGU CUGUACAACCUGCGCCGGGGAACCGCUCUUGCCAUCCCCC AGUGUCGCCUGACCCCAUUGUCCAGACUGCCAUUUGGCA UGGCCCCCGGCCCGGCCCCAGCCCGGCCCCUGAGGGA GAGCAUCGUGUGCUACUUAUGGUGUCCUGCAGACCCA CAUAUUCGCUGAGGUGCUGAAGGACGCCAUUAAGGACCU GGUGAUGACCAAGCCCGCCCUACCUGCAACAUCGCGUC ACCGUCUGUAGUUUCGAUGACGGCGUGGAUCUCCACCA UGGUUCCUCCAAUGGUGGAGGGCGCUGCUGCCGAGGGG GACGACGAGACGACGGAGACGAGGGCGGGGACGGGGAC GAAGGCGAAGAGGGGGCAAGAG	12
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADD PGE GPSTGPRGQGDGRRKKGGWFGKHRGQGGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRG TALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQ	10

	THIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLPPWF PPMVEGAAAEAGDDGDDGDEGGDGDEGEEGQE	
PolyA tail	100 nt	
EBNA1_trunc_004		
SEQ ID NO: 138 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 13, and 3' UTR SEQ ID NO:3		138
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGACGGAGACCUUUCUUUCACCCCGUAGGUGAAGCC GACUACUUUGAAUACCACCAGGAGGGCGGCCAGACGGC GAGCCCGACGUUCCCCCGGGCUAUCGAGCAGGGGCCUG CGGACGACCCAGGAGAGGGACCUAGCACUGGACCCCGAG GUCAGGGCGAUGGGGGGCGAAGAAAGAAGGGCGGCUGGU UCGGCAAACAUAGGGGCCAGGGCGGGUCUAACCCAAAGU UCGAGAACAUAAGCCGAGGGCCUGAGAGCCCUGCUGGCAA GAAGCCACGUGGAGCGAACCACAGAUGAAGGCACCUGGG UGGCCGCGUGUUCGUGUACGGGGGCAGCAAGACCUCCT UGUAUAACCUCAGAAGAGGGACCGCCUGGCCAUCCCCA GUGCCGACUGACCCCCCUGAGCAGGCUGCCCUUCGGAUG GCCCCUGGUCCCGUCCCCAACCGGGCCCGCUUCGGGAGU CCAUAGUGUGCUACUUAUGGUGUUCUGCAGACACACA UCUUCGCCGAGGUGCUGAAGGAUGCAAUCAAGGACCUGG UGAUGACCAAGCCAGCUCCACCUGCAACAUCGGGUGAC CGUGUGCAGCUUUGAUGACGGCGUGGACCUGCCACCCUG GUUCCCGCCUAUGGUGGAGGGCGCUGCAGCCGAGGGCGA CGACGGGGACGACGGCGACGAGGGCGGAGAUGGCGACGA GGGCGAGGAGGGGCCAGGAG	13
3' UTR	UGAUAUAAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADD PGE GPSTGPRGQGDGRRKKGWFGKHRGQGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFYGGSKTSLYNLRRG TALAIPQCRLTPLSRLPFGMAPGPGPQGPLRESIVCYFMVFLQ THIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLPPWF PPMVEGAAAEAGDDGDDGDEGGDGDEGEEGQE	10
PolyA tail	100 nt	
EBNA1_trunc_005		
SEQ ID NO: 139 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 14, and 3' UTR SEQ ID NO:3		139
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGCAGACGGCCCUUCUUCCACCCCGUGGGCGAAGCA GACUAUUUUGAGUAUCACCAGGAGGGGGGCCCCGACGGC GAGCCAGACGUCCACCUGGUGCAAUCGAGCAAGGUCCC GCCGACGACCCUGGGGAGGGCCCCAGCACCGGCCCCAGAG GCCAGGGGGACGGGGGCAGGAGAAAAAAGGGUGGCUGGU UCGGCAAGCACAGAGGGCAGGGGGGGAGCAACCCAAAGU UCGAGAACAUCGCCGAGGGCUUGAGAGCACUGCUGGCCA GAAGCCACGUGGAGAGAACCACCGAUGAGGGAACCUGGG UUGCUGGCGUGUUCGUCUACGGCGGCAGCAAGACCAGCC	14

	UGUACAACCUUAGAAGAGGCACCGCCUGGCCAUCCCCCA GUGCCGCCUGACACCGCUGAGCAGACUCCCCUUCGGCAUG GCUCCUGGCCCGGCCCCAGCCCGGGCCCCUGAGAGAGA GCAUCGUGUGCUACUUAUGGUGUUUCUUCAGACGCACA UCUUCGCUGAGGUCCUGAAAAGACGCCAUUAAGGACCUGG UGAUGACAAAACCAGCUCCGACCUGCAACAUCAGGGUCA CUGUCUGUAGCUUCGACGAUGGCGUGGAUCUCCUCCCU GGUCCCCCCAAUGGUGGAGGGCGCUGCCGCUGAGGGGG ACGACGGCGACGACGGGAUGAAGGCGGCGACGGCGACG AGGGGAAGAGGGCCAGGAG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADD PGE GPSTGPRGQGDGGRRKKGGWFGKHRGQGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRG TALAIPQCRLTPLSRLPFGMAPGPGPQGPLRESIVCYFMVFLQ THFAEVLKDAIKDLVMTKPAPTCNIRVTVC SFDDGDVLPWF PPMVEGAAAE GDDGDDGDEGGDGDGE EEGQE	10
PolyA tail	100 nt	
LMP1_001		
SEQ ID NO: 140 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 15, and 3' UTR SEQ ID NO:3		140
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGCACGACCUGGAGAGGGGGCCACCAGGCCCCAGG CGACCCCCAAGAGGACCACACUGAGCUCCAGCCUGGGAC UGGCCCCUCCUGCUGUUGCUCUCCUCGCUUUACUGUUUUGGC UGUAUAUAGUCAUGUCUGACUGGACAGGCGGGGCAUUAU UGGUGCUCUACAGCUUUGCACUGAUGCUCAUUAUCAUUA UUCUGAUUAUCUUUAUUUUUAGACGGGACUUGCUCUGUC CAUUAGGCGCGCUGUGUAUUUUGCUGCUGAUGAUCACAC UGCUGCUGAUUGCUGCUGUGGAACCUCCACGGUCAGGCCC UUUUUCUCGGCAUCGUGCUGUUUAUCUUUGGGUGCCUCU UGGUGCUUGGGAAUUUGGAUCUACCUUCUCGAAAGUUUAU GGCGGCUCGGCGCUACAAUCUGGCAGCUCCUGGCCUUCU UCUUAGCAUUUUUUCUGGAUCUGAUCCUGCUGAUAAUAG CCCUGUACCUACAACAGAACUGGUGGACUCUGCUGGUUG ACCUGUUAUGGCUGCUCUCCUGUUCUCCUGCCAUCUCAUUU GGAUGUACUACCACGGGCAGCGUCAUUCAGACGAACACC ACCACGAUGAUAGCCUGCCGCACCCUCAACAAGCUACGGA UGACUCCGGACACGAGUCCGAUAGUAACUCCAACGAGGG ACGCCAUCACUUGCUGGUCUCUGGGGCGUGGCGACGGGCC UCCACUGUGUAGCCAAAUCUGGGAGCCCCCGGCGGGGG CCCUGAUAAUGGGCCUCAGGAUCCUGAUAAACACGAUGA UAACGGCCCACAGGAUCCAGAUAAUACCGACGAUAAUGG ACCUCAUGAUCCUCUCCACAGGAUCCCGACAUAACAGA UGACAAUGGGCCGCAGGAUCCAGACAAUACUGACGAUAA UGGCCCACAUGAUCCCCUGCCACACAGCCCCUCAGACUCA GCGGGAAAUGAUGGCGGGCCCCCACAGUUAACCGAGGAA GUGGAAAACAAAGGGGGAGAUACGGGUCCUCCCUCAUG ACAGAUGGCGGGGGCGGCCACAGUCAUGAUAGUGGGCAC GGGGGUGGCGAUCCACAUCUCCCAACACUGCUGCUAGGC AGCUCCGGUAGCGGGGGAGAUAGACGAUCCCAACGGC CCUGUGCAGUUGAGCUAUUACGAC	15

3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEHDLERGPPGPRRPPRGPLSSSLGLALLLLLALLFWLYIV MSDWTGGALLVLYSFALMLIIIIILIFRRLDLCPLGALCILLM ITLLLIALLWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRL GATIWQLLAFFLAFFLDLILLIALLYLQQNWWTLLVDLLWLLL FLAILIWMYYHQRHSDEHHHDDSLPHPQQATDDSGHESDSN SNEGRHLLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTD DNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTDDNG PHDPLPHSPSDSAGNDGGPPQLTEEVENKGGDQGPPLMTDGG GGHSHDSHGSGGDPHLPITLLLGSSSGGDDDDPHGPVQLSYY D	16
PolyA tail	100 nt	
LMP1_002		
SEQ ID NO: 141 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 17, and 3' UTR SEQ ID NO:3		141
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGCACGACCUGGAGCGCGGGCCUCCAGGACCCCGAC GGCCGCCCAGGGGGCCACCGCUGUCAUCCAGUCUGGGCCU UGCUCUGUUGCUGUUAACUCCUUGCCUGCUAUUCUGGUU GUACAUCGUCAUGAGCGAUUGGACAGGGGGUGCUCUCGU GGUGUUGUACAGCUUUGCGCUGAUGUUGAUUAUUAUCAU CCUGAUUAUCUUUAUAUUAUUCGAAGGGACCUCUUUGUCC CCUGGGAGCGCUGUGCAUACUGCUCUUAUGAUCACGUU GCUCCUCAUUGCUUUAUGGAAUCUGCACGGACAGGCUCU AUUCCUCGGCAUCGUUUUAUUCAUUUUCGGGUGCCUCCU UGUGCUGGGAAUCUGGAUCUAUCUGCUAGAGAUGCUGUG GCGGCUCGGCGCCACCAUUGGCAGCUUCUGGCAUUUUU CCUAGCGUUUUUUCUGGAUCUCAUCCUACUUAUUAUCGC CUUGUAUUUGCAGCAGAACUGGUGGACUCUCCUGGUGGA UCUCCUGUGGCUCUCCUGUUCUCCUGCCAUAUUGAUUUG GAUGUACUACCACGGACAGCGCCACAGCGACGAGCACCAC CACGAUGAUAGUCUGCCUCACCCUCAACAGGCUACAGAU GACUCAGGCCACGAAAGCGAUUCCAACUCAAUAUGAAGGC CGGCACCACUUGUUGGUGUCCGGAGCCGGCGACGGGCCA CCACUCUGCAGCCAGAAUCUGGGCGCUCGCGGCGGAGGUC CAGACAAUGGGCCACAGGACCCUGAUAAACACGGAUGAU ACGGACCGCAGGAUCCUGACAAUACAGAUACAACGGCC CGAUGAUCCACUGCCUCAGGAUCCUGAUAAUACUGACG AUAACGGACCCAGGAUCCUGAUAAACACCGACGACAACG GGCCUCACGAUCCCCUACCCCAUCCCCAUCUGACUCUGC UGGCAACGAUGGCGGGCCACCGCAGCUGACCGAAGAGGU AGAAAACAAGGGCGGGGAUCAGGGCCCUCCACUGAUGAC AGACGGCGGGCGGGGACACUCCCAUGAUUCGGGCCAUGG GGGAGGGGAUCCUACCUUCCACACUCUUGCUGGGAAG UAGCGGGUCCGGCGGGGACGAUGAUGAUCCCAUGGUCC AGUCCAGUUGUCAUAUUACGAU	17
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3

Corresponding amino acid sequence	MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLLLLALLFWLYIV MSDWTGGALLVLYSFALMLIIIIIFIFRRDLLCPLGALCILLML ITLLIIALWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRL GATIWQLLAFFLAFFLDLILLIIALYLQQNWWTLLVDLLWLLL FLAILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSN SNEGRHLLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTD DNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTDDNG PHDPLPHSPSDSAGNDGGPPQLTEEVENKGGDQGPPLMTDGG GGHSHDSGHGGDPHLPTLLLGSSSGGDDDDPHGPVQLSYY D	16
PolyA tail	100 nt	
LMP1_003		
SEQ ID NO: 142 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 18, and 3' UTR SEQ ID NO:3		142
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGCACGACCUUGAGCGGGGUCCACCAGGCCACGG CGCCCUCCGCGCGGGCCUCCUUUGUCAUCCUCCUGGGAC UGGCACUGCUGCUGUUGCUUCUGGCCUGCUGUUCUGGC UGUACAUCGUUAUGUCUGAUUGGACAGGAGGAGCUCUGC UGGUUCUUUACUCUUUCGCGCUGAUGCUGAUCAUCAUCA UCUUGAUCAUUUUCAUUUUCAGACGAGACCUCCUUUGUC CUCUCGGAGCCUGUGUAUCCUCCUGCUGAUGAUAACCC UUCUGCUGAUUGCUUUGUGGAUUCUGCAUGGGCAAGCUC UGUUUCUUGGAUUGUCUUAUUUAUUUUUGGGUGUCUGC UGGUGUUGGGAAUCUGGAUCUAUCUUCUUGAAAUGCUGU GGCGGCUGGGCGCCACAAUCUGGCAGCUACUCGCCUUUU UCCUAGCUUUCUUUUUGGAUCUGAUUCUGCUGAUUAUUG CUCUCUACCUGCAGCAGAAUUGGUGGACCCUCUAGUCG AUCUGCUGUGGCUGUUGCUCUUUCUGCCAUCUGAUUU GGAUGUACUAUCAUGGGCAGCGCAUAGUGAUGAACAU AUCACGAUGAUUCCUGCCACAUCUCCAGCAGGCCACAGA UGAUUCAGGCCACGAUACAGACAGCAAUAGCAAUGAGGG CCGCCACCACUUGCUUUCAGGUUUCAGGGGCCGUGACGGCCU CCAUGUGCAGUCAGAACCUGGGAGCCCCGGGGGUGGA CCUGAUAAACGGGCCGAGGAUCCUGACAAUACUGAUGAC AACGGACCCAGGAUCCAGAUAAACACUGACGACAAUGGC CCCCAUGACCCCUACCCAGGAUCCGACAAUACAGACG ACAACGGACCGCAGGACCCCGACAACACUGAUGAUAAUG GGCCACACGAUCCUCUGCCUCACUCUCCAUCAGACUCUGC CGGAAAUGACGGUGGACCGCCACAGUUAACUGAAGAAGU CGAAAACAAGGGCGGCGAUCAGGGGCCGCGCUCUAUGAC AGAUGGCGGGGGAGGUCACAGCCACGAUAGCGGACACGG AGGAGGUGACCCUCAUCUGCCUACACUUCUGUUGGGUAG CUCUGGGAGUGGGGGGGAUGACGACGACCCUCACGGACC UGUUCAGCUCUCAUACUACGAC	18
3' UTR	UGAUAUAAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLLLLALLFWLYIV MSDWTGGALLVLYSFALMLIIIIIFIFRRDLLCPLGALCILLML ITLLIIALWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRL GATIWQLLAFFLAFFLDLILLIIALYLQQNWWTLLVDLLWLLL FLAILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSN SNEGRHLLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTD DNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTDDNG	16

	PHDPLPHSPSDSAGNDGGPPQLTEEEVENKGGDQGPPLMTDGG GGHSHDSGHGGGDPHLP TLLL GSSGSGGDDDDPHGPVQLSYY D	
PolyA tail	100 nt	
LMP1_004		
SEQ ID NO: 143 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 19, and 3' UTR SEQ ID NO:3		143
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAACACGAUCUUGAACGGGGGCCCGGGACCGAGG AGGCCGCCACGGGGGGCCCCCUGAGCAGUAGCUUGGGG UUGCGCUGCUUCUCCUGCUGUUGGCCCUCCUGUUUUGG UGUAUAUUGUGAUGUCCGACUGGACCGGCGGCGCCUGC UCGUCCUGUAUAGCUUUGCUUUGAUGCUGAUAAUUAUA UAUUGAUCAUUUUAUUUCCGGCGUGAUUUGCUCUGUC CUCUUGGUGCCCUUUGUAUCCUGCUGUAAUGAUCACUC UGCUCUCAUUGCCCUAUGGAACCUCCACGGACAAGCCCU GUUUCUUGGCAUCGUUCUCUUUAU AUUCGGAUGCCUCU AGUGCUUGGGAUCUGGAUAUACCUGUUGGAAUUGCUGUG GAGGCUUGGAGCCACGAUAUGGCAAUAUUGGCAUUCU UCUGGCCUUCUUCUGGAUCUGAUCCUGUUGAUAAUUGC UCUGUACCUGCAGCAGAACUGGUGGACACUACUUGUUGA CCUGCUCUGGCUACUCCUGUCCUUGCGAUCCUGAUUUG GAUGUACUAUCACGGACAGAGACACUCCGACGAGCAUCA UCACGACGAUUCUUUACCACACCCUCAGCAGGCGACAGAU GAUUCUGGCCAUGAGAGCGAUUCCAACAGCAACGAGGGC CGGCACCAUUUGCUGGUGUCGGGGGCGUGGAGACGGGCCU CCGUUAUGUAGCCAAAACUUGGGCGCGCCCGGCGGCGGG CCCGAUACGGCCCGCAGGACCCGGACAAUACCGACGAUA AUGGGCCUCAAGAUCCTCGACAAUACUGAUGACAAUGGAC CACACGAUCCUCUGCCACAGGAUCCCGACAACACAGAUGA CAAUGGGCCGCAAGACCCCGACAAUACAGACGAUAAUGG CCCCACGACCCACUACCACAUUCUCCUCUGACAGUGCG GGGAAUGAUGGUGGUCCCCACAACUGACCGAGGAGUG GAGAAUAAGGGGGGGACCAAGGUCCACCCUCAUGACU GAUGGAGGAGGAGGACACUCGCACGAUUCAGGUCACGGC GGGGGGGACCCUCACUUGCCACUCUGCUGCUGGGCAGC AGCGGUUCUGGGGGGCGACGAUGAUGAUCCCCACGGCCCG GUGCAGCUAAGUUAUUACGAC	19
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLLALLFWLYIV MSDWTGGALLVLYSFALMLIIILIIIFIFRRDLLCPLGALCILLM ITLLLIALLWNLHGQALFLGIVLFIFGCLLVGIWIYLLLEMLWRL GATIWQLLAFFLAFFLDLILLIALLYLQQNWWTLLVDLLWLLL FLAILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSN SNEGRHLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTD DNGPQDPDNTDDNGPHDPLQDPDNTDDNGPQDPDNTDDNG PHDPLPHSPSDSAGNDGGPPQLTEEEVENKGGDQGPPLMTDGG GGHSHDSGHGGGDPHLP TLLL GSSGSGGDDDDPHGPVQLSYY D	16
PolyA tail	100 nt	
LMP1_005		

SEQ ID NO: 144 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 20, and 3' UTR SEQ ID NO:3		144
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGCACGAUUUAGAGAGGGGCCCACCUGGCCCCAGGCGCCCACCAGAGGGCCACCCUUGUCGUCGUCAUUAGGGCUGGCAUUGCUCUCCUGCUCUCCUGGCCUUGCUGUUCUGGCUUUACAUCGUGAUGAGCGACUGGACUGGCGGGGCCCUGCUGGUCCUCUAUAGCUUUGCACUGAUGCUGAUUAUAAUCAUAUUGAUCAUUCUUCUCCGACGGGAUUUACUUUGCCCCCUGGGGGCAUUAUGUAUUCUAUUGCUGAUGAUAAACACUUCUGCUUAUUGCUIUAUGGAAUCUACACGGUCAGGCUCUUUUUCUGGGAAUCGUGCUCUUUAUCUUUGGAUGCCUUCUGGUACUAGGAUUUGGAUUAUACCUCUUAAGAAAUGCUGUGGCGGCUCGGCGCAACCAUCUGGCAACUCCUUGCGUUUUUUCUCGCGUUUUUCCUCGACCUGAUUCUGCUAAUAAUCGCCUUAUACCUUCAGCAGAAUUGGUGGACACUCCUGGUGGACCUGCUGUGGCUCCUGCUAUUCCUUGCAAUCCUCAUUUGGAUGUAUUACCAUGGCCAGAGGCACUCUGAUGAGCACCACCACGAUGAUAGUCUACCUCAUCCACAGCAGGCUACGGACGAUUCAGGGCAUGAGUCAGAUUCUAAUCCAACGAAGGAAGACACCAUCUGUUGGUGUCAGGGGCCGGAGACGGCCCCCUCUGUGUAGCCAGAACCUCGGGGCACCAGGGGGAGGUCCUGACAAUGGGCCGCAAGACCCUGACAAUACUGAUGAUAUUGGCCCCCAAGAUCUAGACAAUACCGAUGACAACGGCCGCACGACCCCCUGCCGCAGGAUCCGGAUAACACCGGACGACAAUGGACCCAGGACCCCGAUAAACACGGACGAUAAACGCCCCUCACGAUCCCUUACCCCAUUCUCCGUCCGACUCGAGGGAACGACGGGGGCCUCCUCAGUUAACCGAAGAGGUCGAAAAUAAGGGGGGAGACCAGGGCCCCCAUUAUAGACAGACGGGGGCGGCGGUCACAGUCACGACUCAGGUCACGGCGGCGGGGACCCCCAUUUGCCUACACUGCUGUUAAGGUUCUUCUGGCUCAGGCGGGGACGAUGAUGAUCCACACGGUCCGGUGCAGCUGUCAUUAUUGAU	20
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACCUGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGGC	3
Corresponding amino acid sequence	MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLLALLFWLYIVMSDWTGGALLVLYSFALMLIIIIIFIFRRDLLCPLGALCILLMITLLLIALLWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRLGATIWQLLAFFLAFFLDLILLIALLYLQQNWWTLLVDLLWLLFLAILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSNNEGRHHLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTDNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTDDNGPHDPLPHSPSDSAGNDGGPPQLTEEVENKGGDQGPPLMTDGGGHSHDSHGSGGDPHLPPTLLLGSSGSGGDDDDPHGPVQLSYYD	16
PolyA tail	100 nt	
LMP2_001		
SEQ ID NO: 145 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 21, and 3' UTR SEQ ID NO:3		145
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1

ORF of mRNA Construct (excluding the stop codon)	AUGGGUAGUCUUGAGAUGGUACCAAUGGGCGCAGGUCCA CCGAGCCCUGGAGGCGAUCCUGACGGGUACGACGGGGGA AAUAAUCUCGCAAUAUCCCUAGCCUCAGGCUCAUCGGGU AAUACUCCGACCCCUCAAACGACGAGGAAAGGGAAUCC AAUGAGGAACCGCCUCCACCAUAUGAGGAUCCGUACUGG GGGAACGGUGAUAGGCACAGUGACUACCAGCCACUUGGG ACACAAGACCAAAGCCUGUACCUCGGACUUCAGCACGAU GGUAAACGACGGUUUGCCGCCUCCCCCUUAUAGCCCUAGA GAUGAUAGCUCCAGCAUAUAUACGAGGAGGCUGGUAGG GGCUCCAUGAAUCCAGUAUGCUUGCCCGUUAUCGUAGCC CCCUACCUCUUCUGGCUUGCGGCGAUCGCAGCUAGCUGU UUUACAGCUUCCGUGAGCACAGUCGUAACCGCGACAGGA CUGGCACUGUCUCUACUCCUCUUGGCAGCGGUUGCCAGC AGCUACGCCGCCGCUCAGCGGAAACUGCUCACCCCUGUUA CAGUCUUAACUGCAGUUGUGACCUUCUUCGCCAUUUGUU UGACAUGGAGGAUCGAAGAUCUCCAUUUAAUAGUCUCC UGUUUGCACUGCUGGCCGCUGCGGGCGGGCUACAAGGGA UAUAUGUGCUAGUAAUAGCUCGUCCUACUUAUUCUGGCCU AUAGGCGGAGGUGGCGGCGCCUGACAGUGUGCGGAGGGA UAAUGUUCUAGCCUGUGUGCUCGUGCUCAUUGUGGACG CUGUUCUACAGUUGUCUCCUCUGCUGGGUGCAGUGACGG UGGUCUCAUGACCCUGCUGUUAUUGCCUUCGUGCUUU GGUUGUCAUCUCCAGGGGGACUGGGCACACUGGGCGCCG CCUGUUAACCCUGGCGGCCGCUCUGGCACUCCUGGCCUC ACUGAUUCUGGGAACUCUGAAUCACACCACUAUGUUUCU UCUGAUGUUAUUGUGGACUUUGGUGUGUUGCUGAUUUG CAGCUCCUGCAGUUCUUGCCCCCUAUCCAAAAUAUUAU GGCGCGGCUGUUCUUUAUGCCCUCGCCUACUGCUGCUC GCUAGCGCCUUAUUGCUGGGGGCUCCAUUCUUCAGACC AACUUUAAAUCCUGUCCAGCACUGAAUUCAUCCCCAACCC UUUUUUGCAUGCUGCUCCUAAUCGUGGCUGGGAUUCUGU UUAUUCUGGCCAUUUUGACCGAGUGGGGCGAGUGGCAACA GGACCUACGGCCCUGUGUUCUUGUGUCUGGGGGGGCUCU UAACGAUGGUCGUGGCGCUGUCUGGCUCACGGUGAUGA GUAACACUUUGCUCAGCGCGUGGAUCCUGACAGCCGGCU UUCUCAUUUUUCUGAUUGGGUUCGCUUUGUUUGGAGUCA UUCGGUGUUGCCGCUAUUGCUGUUACUUAUUGUUUGACAU UGGAGUCCGAGGAGAGGCCACCCACCCCUACCGAAAUAAC GGUA	21
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWNGDRHSDYQPLGTQDQSL YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTA VVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRLTVCGGIMFLACVL VLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTNL TTMFLLMLLWTLVLLICS SCSSCPLSKILLARLFLYALALLLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLLIVAGILFILAILTEWGSNGRNTYGPVFMCLGG LLTMVAGAVWLTVM SNTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	22
PolyA tail	100 nt	
LMP2_002		
SEQ ID NO: 146 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 23, and 3' UTR SEQ ID NO:3		146
Chemistry	1-methylpseudouridine	

Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGAUCCUUGGAAAUGGUGCCCAUGGGAGCCGGACCC CCCUCACCAGGGGGAGACCCAGACGGAUACGACGGGGGA AACAAUUCUCAGUAUCCGAGCGCGUCCGGCAGCUCAGGA AACACACCCACCCCCCAACGACGAGGAGAGAGAAUCCA ACGAGGAGCCUCCUCCCCCAUACGAAGACCCUACUGGGG GAAUGGAGACCGUCAUUCUGACUAUCAACCUCUAGGCAC UCAGGACCAGUCUCUUUACCUAGGGUACAACACGAUGG UAAUGAUGGGUUGCCCCCGCCGCCCUAUAGUCCCCGGGAC GACAGUAGUCAGCAUAUAUAGAGGAAGCCGGCAGAGGU UCUAUGAAUCCCGUUUGUCUACCGGUCAUUGUCGCCCC UAUUUAUUCUGGCUUGCAGCCAUCGCCGCUUCGUGCUUC ACCGCCUCCGUGUCCACGGUGGUGACAGCUACAGGGCUG GCACUCUCUCUGCUACUCCUGGCUGCUGUGGCCAGCUCCU ACGCAGCGGCUCAGCGGAAGCUUCUCACUCCUGUAACUG UCCUCACCGCGGUAGUGACCUUUUUUGCCAU AUGCCUGA CAUGGAGGAUUGAGGACCCACCCUUAAUUCUCUGCUGU UUGCGCUUUUGGCCGUGCCGGAGGACUGCAAGGAUUU AUGUGCUGGUA AUGUUGGUUCUACUUAUUCUCGCAUACC GGCGACGGUGGCGGAGGCUGACUGUAUGCGGGGGGAUUA UGUUCCUGGCGUGUGUUCUGGUUUUGAUCGUCGAUGCCG UGCUGCAGUUGUCACCGCUGCUCGGGGCGGUCACCGUUG UGAGUAUGACACUGCUUCUGCUGGCUUUCGUGCUCUGGC UAUCUCCCCCGGGGGGCGUGGGGACCUUGGGCGCUGCGC UUCUGACUCUGGCAGCUGCUCUGGCCUGCUGGCCUCUCU UAUUCUUGGCACACUGAAUUUGACUACCAUGUCCUCUU GAUGUUGCUGUGGACCUUAGUUGUGCUGCUGAUCUGUUC UUCUGUAGCAGCUGUCCACUGUCCAAGAUUCUCCUGGC CAGGUUGUUUCUGUAUGCCCUAGCGCUGCUGCUGUAGC UUCUGCUCUGAUAGCCGGCGGCAGUAUCCUGCAAACCAA CUUCAAGAGCCUCUCCAGCACAGAAUUAUCCCUAAUCUC UUUUGCAUGCUACUGCUCAUCGUGGCAGGCAUACUGUUC AUUCUUGCUAUCCUGACUGAAUGGGGCUCUGGCAAUAGA ACAUACGGGCCAGUGUUAUGUGCUUGGGCGGCCUGUUG ACAAUGGUUGCUGGAGCCGUGUGGCUGACGGUAAUGUCC AACACUCUGCUGAGCGCAUGGAUCUUAACAGCCGGAUUC CUGAUCUUUUUAAUCGGAUUCGCACUCUUCGGAGUGAUC CGGUGCUGUAGGUAUUGUUGUUAUACUGCCUGACACUC GAGUCGGAAGAGAGGCCCCCUACACCUUACCGGAUACA GUU	23
3' UTR	UGAUA AUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWGNGDRHSDYQPLGTQDQSL YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMNPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAQQRKLLTPVTVLTA VVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRRRLTVCGGIMFLACVL VLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTNLNLT MFLMLLWTLVLLICS SCSSCPLSKILLARFLYALALLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLIVAGILFILAILTEWGSGRNRTYGPVFMCLGG LLTMVAGAVWLTVM SN TLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	22
PolyA tail	100 nt	
LMP2_003		

SEQ ID NO: 147 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 24, and 3' UTR SEQ ID NO:3		147
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAGAGAGAAAAGAAGAGUAAGAAGAAAUUAUAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGGUCGUUGGAGAUGGUCCCCAUGGGCGCUGGUCCUCCAAGCCCCGGCGGGGACCCGGACGGAUACGACGGGGGC AAUAAUAGUCAGUAUCCGAGUGCAAGCGGAAGCAGUGGG AAUACGCCUACACCACCAACGACGAGGAGCGGGAGUCU AACGAGGAGCCUCCACCCCUUACGAGGAUCCUUACUGG GGGAACGGAGAUUCGACAUUCUGACUACCAGCCUUUAGGG ACACAGGAUCAGUCUCUCUAUCUCGGACUGCAGCAUGAU GGCAACGACGGACUGCCCCACCACCUUAUUCUCCACGCG ACGACAGCUCACAGCACAUUAACGAAGAGGCCGGGCGCG GGUCUAUGAACCCGGUUUGCCUGCCAGUCAUCGUCGCAC CCUACCUCUUUUGGCUGGCGGCCAUUGCCGCGUCCUGUU UCACAGCCUCAGUGUCGACUGUGGUAACCGCAACAGGGC UCGCACUCAGCCUACUGCUGCUCGCGUGCCGUCGCGUCCUC UUAUGCUGCUGCCCAGCGCAAACUGCUCACCCCAGUUACG GUGCUCACUGCUGUUGUUACCUUUUUCGCUAUUUGUCUC ACCUGGAGAAUCGAAGACCCGCGGUCAACAGUCUGUUA UUUGCCCUUUGGCUGCAGCAGGCGGCCUUCAGGGCAUC UAUGUCCUGGUGAUGCUGGUCCUGCUAUCCUGGCUUAC AGGAGAAGAUGGCGUCGGCUGACCGUGUGUGGUGGCAUC AUGUUUCUCGCGUGUGUUCUGGUGCUAUCGUCGAUGCC GUGCUACAGCUGAGCCACUGCUUGGAGCCGUGACAGUC GUUAGCAUGACACUCCUGCUAUUGGCUUUCGUGCUCUGG CUGAGUAGCCCAGGUGGGCUCGGCACACUUGGUGCCGCG CUUUUAACACUGGCCGCGGCCUCGCACUGCGUCCUCUC UAAUUCUCGGAACAUUGAACCUAGACAACCAUGUUCUCC UGAUGCUCCUCUGGACACUGGUGGUACUGUUAUUCUGUA GCUCUUGCUCAUCAUGCCCACUGAGCAAGAUACUCCUGG CGAGACUUUUCUUAUACGCCUUGGCCUGCUGCUGUUGG CAUCGGCUCUGAUCGCUUGGGGAAGCAUCCUUCAAACA AUUUCAGAGCCUUAAGCAGUACUGAGUUUAUACCUAAC UGUUCUGUAUGCUUCUGCUGAUAGUCGCGUGGGAUACUU UUAUUCUGGCAUCCUACAGAGUGGGGGUCAGGUAACA GGACCUAUGGGCCUGUUUUUAUGUGCCUCGGAGGCCUCC UCACCAUGGUUGCCGGCGCAGUUUGGUUGACAGUGAUGU CCAACACCCUACUGAGUGCUUGGAUACUGACGGCCGGGU UCCUGAUUUUCCUAAUAGGAUUUGCCUGUUUGGGGUUA UCCGGUGCUGCCGUUACUGCUGCUACUUAUGUUUGACCC UUGAGUCUGAAGAAAGGCCGCCACCCCCUACAGAAACA CUGUA	24
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWNGDRHSDYQPLGTQDQSL YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTAVVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRRRLTVCGGIMFLACVL VLIVDAVLQLSPLLGAVTVVSMTLLLLAFLVLWSSPGGLGTL GAALLTLAALALLASLILGTLNLTMTFLLMLLWTLNVLLICS SCSSCPLSKILLARFLYALALLLASALIAGGSILQTNFKLSSTEFIPNLCMLLLIVAGILFILAILTEWGSNGRNTYGPVFMCLGG	22

	LLTMVAGAVWLTVMSTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	
PolyA tail	100 nt	
LMP2_004		
SEQ ID NO: 148 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 25, and 3' UTR SEQ ID NO:3		148
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGGUCAUUGGAGAUGGUGCCUAUGGGGGCCGGCCCA CCCAGCCCAGGGGGCGAUCCUGACGGAUACGACGGGGGC AAUAAUUCACAAUAUCCUAGCGCCAGCGGAUCUUCUGGG AAUACCCCCACACCACCUAACGACGAGGAACGGGAGUCA AACGAGGAACCCCCACCGCCGUACGAGGACCCAUACUGGG GGAACGGGGAUCGACACUCAGACUACCAGCCUCUCGGAA CGCAGGAUCAAAAGCCUGUACCUGGGACUGCAGCACGAUG GUAACGAUGGACUGCCACCACCUCCUACAGUCCAAGGG AUGACUCCAGCCAGCACAUUUAUGAAGAAGCCGGCCGAG GUAGUAUGAAUCCAGUGUGUCUGCCCGUGAUUGUCGCCC CUUAUCUCUUUUGGCUGGCCGCCAUUGCCGCCAGCUGUU UCACCGCGUCGGUUUCAACCGUAGUGACCGCCACAGGCCU GGCUCUCAGCUUGUUACUGUUGGCCGCGUGUGGCGAGCUC CUACGCCGCCGCCAGCGCAAGCUACUUAACCCUGUGACA GUGCUGACGGCGGUGGUACAUCUUCGCCAUUUGCCUG ACCUGGCGAAUUGAGGAUCCACCAUUAUUAUCCUUAUUG UUUGCCCUCCUCGCCGCGUCUGGAGGGCUCCAGGGUAUC UACGUGCUGGUGAUGCUCGUUUUGCUGAUAAUUGGCUUAC CGGCGGGCGCUGGCGCCGCCUUAACCGUCUGCGGAGGAAUC AUGUUUUUGGCAUGCGUGCUCGUUCUCAUUGUGGAUGCU GUUUUGCAGCUGUCACCCUGUUGGGUGCCGUGACAGUU GUAAGUAUGACCCUGCUCUCCUGCUGCAUUCGUGCUCUGG CUGAGCUCUCCCGGGGGGCGUGGGCACUCUCGGAGCAGCU CUGCUGACACUAGCCGCGAGCACUAGCCCUUCUGGCCAGUC UUAUCCUCGGAACGCUGAACCUGACGACCAUGUUCUCC UGAUGUUGCUCUGGACCCUCGUAGUGCUGUUAUUAUGCU CUAGCUGUAGCUCCUGCCCUCUGAGCAAGAUUCUCCUUG CUAGGCUGUUCUUAUACGCCUCGCUCUCCUUAUUGCUGGC GAGCGCUCUCAUCGCCGGUGGGAGCAUCCUGCAGACUAA CUUCAAGUCCCUGAGUUAACAGAAUUAUUAUCCCAACCU CUUUUGUAUGCUGCUGCUUAUCGUGGGCCGGCAUCCUCUU UAUCCUCGCCAUUCUUGACUGAGUGGGGGUCCGAAAUUCG CACAU AUGGCCAGUUUUAUGUGUCUGGGGGGCCUGCU CACGAUGGUGGCCGGCGCAGUGUGGCUGACGGUAAUGUC AAACACUUUGCUCUCUGCGUGGAUCUUGACCGCAGGCUU CCUGAUCUUUUUGAUCGGCUUCGCCCUGUUCGGUGUCAU CCGGUGCUGCAGAUACUGCUGCUACUUAUUGCCUCACACU CGAAUCCGAAGAGAGGCCUCCACACCUUACCGAAAUAC AGUG	25
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPNDEERESNEEPPPPYEDPYWGNDRHSDYQPLGTQDQSL YGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLP VIVAPYLFWLAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTA VVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRRRLTVCGGIMFLACVL	22

	VLIVDAVLQLSPLLGAVTVVSM TLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTLNLTMMFLMLLWTLVVLLICS SCSSCPLSKILLARFLYALALLLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLLIVAGILFILAILTEWGSNRTYGPVFMCLGG LLTMVAGAVWLTVMSNTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	
PolyA tail	100 nt	
LMP2_005		
SEQ ID NO: 149 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 26, and 3' UTR SEQ ID NO:3		149
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGGUCUUUAGAAAUGGUCCCCAUGGGUGCCGGCCCA CCCUCGCCAGGAGGCGAUCCAGACGGCUACGACGGGGGA AACACAGCCAGUACCCCAGCGCCAGCGGUAGCAGCGGCA ACACCCGACCCACCAACGACGAAGAGCGGGAGAGCAA UGAGGAGCCCCACCCCUAUGAGGACCCUACUGGGGA AAUGGCGAUCGACACAGCGAUUACCAGCCCCUGGGCACA CAGGAUCAGAGCCUGUACCUGGGCUUGCAGCAUGAUGGU AACGACGGGCUUCCGCCCCACCAUACUCACCCAGAGACG AUUCAAGUCAGCACAUUCACGAGGAGGCUGGUAGGGGUA GUAUGAAUCCUGUGUGUCUCCUGUGAUCGUCGCCCCCU ACCUAUUUUGGUUAGCUGCGAUCGCGGCCUCCUGCUUCA CCGCUAGCGUGUCAACAGUGGUUACGGCAACCGGGCUGG CGUUAAGUCUGCUUCUGCUUGCGGCAGUGGCAUCUUCU AUGCAGCGGCCAGCGGAAGCUUUUGACCCUGUGACAG UACUGACCGCAGUGGUUACGUUUUUUGCGAUUUGCUUGA CGUGGAGAAUAGAGGAUCCCCCUUUUAACUCACUGCUCU UUGCACUGCUCGCGGCUGCUGGGGGCCUGCAGGGGAUUU ACGUCCUCGUUAUGCUGGUGCUCCUGAUCUUAAGCCUACA GAAGGAGAUGGCGCCGACUGACAGUAUGCGGGGGGAUUA UGUUUUUGGCAUGUGUACUCGUAUUGAUCGUGGAUGCCG UCUUGCAGCUUCCCCCUGCUGGGGCGCAGUCACCGUCGU GAGUAUGACUCUGCUGUACUGGCCUUCGUACUGUGGC UAGCAGCCCUGGAGGACUAGGCACGCUGGGCGCCGCUU AUUGACCCUGGCAGCCGCCUGGCUCUGCUGGCCUCCUG AUACUGGGGACAUUAAAUUUAAACAACUAUGUUUCUGCUG AUGCUGCUGUGGACUCUAGUUGUGCUCUUGAUUAUGUUC UCCUGUUCAGCUGCCUCUGAGCAAGAUCUGUUGGCU CGGCUAUUCCUGUACGCGCUGGCUCUCCUCCUGCUAGCUU CAGCGCUAAUUGCAGGCGGGUCUAUUCUCCAGACGAAU UUAAGAGCCUCAGUAGCACUGAGUUUAUCCCGAAUCUGU UCUGCAUGUUGCUAUUGAUCGUCGAGGCAUUCUCUUA UUCUGGCCAUACUUAACAGAGUGGGGUAGCGGCAACCGGA CUUAUGGCCUGUGUUAUGUGCUUGGGGGGCUUCUCA CAAUGGUGGCAGGGGCGGU AUGGCUGACCGUGAUGUCUA ACACCUUGUUAUCAGCCUGGAUCCUUAACCGCCGGCUUCCU AAUUUUUCUGAUCGGCUUCGCCCUCUUCGAGUAAUACG AUGCUGUCGGUACUGCUGCUACUUAUUGCCUUAUUUGGA GAGCGAAGAGCGGCCUCCACUCCCUAUAAGAAACACCGU U	26
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWGNGDRHSDYQPLGTQDQSL	22

	YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMNPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTAVVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRRRLTVCGGIMFLACVL VLIVDAVLQLSPLLGAFTVVSMTLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTNLNTTMFLLMLLWTLVLLICS SCSSCPLSKILLARFLYALALLLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLLIVAGILFILAILTEWGSNGRTYGPVFMCLGG LLTMVAGAVWLTVMSNTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	
PolyA tail	100 nt	
gp350_mod_001		
SEQ ID NO: 150 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 27, and 3' UTR SEQ ID NO:3		150
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UUUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCUAGUGGGUAUAAUUGCAAUUCACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUAUCUCUACCUACUUCUGCCCAAGACUCCAAUUUU UCUGUCAAGACCGAGAUAGCUCGGGAAUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUAUUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACCCCAUUCUCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAUAAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUAUACCUACGUGGGCGA CAAUGCCACGUUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUGUUAUCUGUAACAGCUUUUUGGGC CUGGCCAAUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUUA CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAAACAUUAAUUAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUACCAACCCCCGCAGGUACAACCUCAGGCG CCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUGG AACGGAGUCCAAGGCUCUGAUUAGACUUCUCCUACAG CCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAACC CCAGCUGUGACGACCCCAACCCGAACGCGACAUCUCCCA	27

	CACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCCC UACCCUAGGUAAGACCAGUCCGACUAGCGCCGUUACAAC CCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGACU UCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGGG ACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAACG CUACCUCGCGUGUCACUACCGGACAGCACAACAUCACCAG CUAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAAA UCCCCGAGACCCUACACCAUCCACAUCAGACAACAGUACU UCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGCG GCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCCA CCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAGG GACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUAC AAGCACAAAACCAGGCGAAGUUAACGUGACAAAAGGAAC GCCCCCCCAGAACGCAACAGUCCUCAGGCCCCCAGCGGG CAGAAAACUGCGGUGCCAACUGUGACCAGCACCGGUGGC AAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGGG CACGGCGCCCGGACCUCCACUGAACCCACGACCGAUUACG GAGGUGACAGCACAACACCGCGGCCACGAUAUAUGCCA CCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGCC ACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCAA GCGACGGUGCCAGUGCCCCCUACAAGCCAGCCACGCUUCU CCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUUG CUGUUCUGACCCUCCUCCUGCUCGUGAUGGCCGAUU GCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUACA CCACGCCCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCGUGGAGCCUCGUGGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDTITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLTTS AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLV MADCAFRRLSTSHTYTTPPYDDAETVY	28
PolyA tail	100 nt	
gp350_mod_002		
SEQ ID NO: 151 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 29, and 3' UTR SEQ ID NO:3		151
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct	AUGGAGGCUGCUCUAUUGGUGUGCCAAUACACCAUUCAG UCGCUGAUCCACUUGACUGGGGAGGAUCCCGGAUUUUUC	29

(excluding the stop codon)	AACGUGGAGAUUCCGGAAUUCCCUUUUUACCCACCUGC AACGUGUGCACUGCCGACGUAACGUGACCAUAAACUUU GACGUCGGUGGGAAGAAGCACCAGCUGGACCUGGACUUC GGGCAGUUAACACCCACACAAAGGCAGUUUACCAGCCC AGAGGAGCCUUCGGCGGAUCGGAGAAUGCAACAAAUUU UCCUGCUAGAACUGCUCGGCGCCGGCGAGUUGGCCUG ACAAUGAGAAGCAAGAAACUCCUUAUCAACGUAACCACA GGGAGGAGCAGCAGGUCAGCCUCGAAAGUGUUGACGUC UAUUUCCAGGAUGUCUUUGGGACUUGUGGUGCCAUCAC GCCGAAUAGCAGAAUCCCGUGUACCUCAUCCCCGAGACA GUACCCUUAUCAAGUGGGACAACUGCAACUCUACUAAU AUUACAGCCGUGGUGCGCGCUCAGGGACUUGAUGUAACA UUGCCUUUGUCUUUGCCCACAAGCGCUCAGGAUUCUAAU UUCUCUGUAAAGACGGAGAUGCUGGGGAAUGAAAUCGAC AUAGAAUGUAUUAUGGAAGACGGUGAAAUCAGUCAGGUG CUACCGGGAGACAACAAAUUCAUAUUACAUGUUCUGGC UAUGAGAGCCACGUGCCGAGCGGGGGCAUCCUGACUUCG ACUUCUCCCGUCGCCACACCCAUACCAGGCACAGGCUACG CUUAUAGUCUGAGGCUGACUCCAGGCCAGUAUCCCGAU UUCUGGGUAAUAAUCCAUCUUUAUGUGUUUUACUCCG GUAACGGCCCCAAAGCUUCGGGGGGCGACUAUUGUAUCC AGUCUAAUUAUGUGUUCUCCGAUGAGAUUCCCGCGAGUC AGGAUAUGCCCACCAACACCACCGACAUCACGUAUGUUG GGGAUAACGCUACCUAUAGUGUGCCGAUGGUGAACCCG AGGACGCAAACUCUCCUAACGUAACCGUGACCGCCUUUU GGGCAUGGCCAAAUAAUACCGAAACCGAUUUUAAAUGCA AGUGGACCCUGACAUCCGGGACUCCCUCCGGAUGCGAAA AUUUUUCUGGAGCUUUUGCCAGCAAUCGGACCUUUGAUA UCACUGUGAGUGGUUUAGGCACCGCCCCAAAAACACUGA UCAUAACCAGGACAGCCACAAUUGCGACCACAACUACAC ACAAAGUUAUAUUUAGUAAAGCACCUGAGUCCACCACAA CUUCUCCGACCCUCAACACUACCGGCUUCGCUGAUCCGAA UACCACCACAGGUCUCCAUCUUCACCCACGUCCAACU AAUCUACGGCGCCUGCUAGCACCGGUCCAACCGUGUCCA CCGCCGAUGUGACUAGCCCCACGCCGGCUGGAACAACAUC AGGGGCCAGCCUGUAACCCCAAGCCCUACCCUGGGAC AAUGGUACCGAGAGUAAGGGCGCCGACAUGACCUCAUCA ACUUCUCCUGUUAACAACUCCAACACCAAUGCCACUAGUC CUACCCCCGAGUCACUACCCCAACGCCUAAUGCAACGUC ACCAACUCCUGCAGUGACCACACCAACACCCAAUGCUACU UCGCCGACCCUGGGCAAGACCAGCCCAACCAGUGCCGUGA CGACACCGACUCCAAUUGCGACCGGACCUACUGUCGGUG AGACAAGCCCCAGGCAAACGCGACCAACCACACCCUCGG CGGGACUUCUCCAACACCCGUCGUAACGUCCCAACCAAAA AAUGCUACAUCGGCCGUGACUACCGGACAGCAUAAUUAUC ACCUCAAGCUCCACGUCGUCUAAUGAGCCUGCGGCCGUCAA GUAAUCCAGAGACUCUGUCGCCAUCUACCUCAGAUAAU CAACUAGCCACAUGCCUCUACUCACUAGUGCCCACCCAC CGGCGGGGAGAACAUCACGCAGGUAACACCAGCGUCUAU CAGUACUCACCAUGUGAGUACCAGCUCCCCCGCUCCUGCA CCGGGAACACAGAGCCAGGCCAGCGGACCGGGUAAUAGU AGCACUUCUACUAAACCGGGAGAGGUCAAUGUGACUAAG GGGACUCCCCCCCCAAAACGCUACCAGCCACAGGCUCCCU CAGGGCAGAAGACCGCUGUCCAACAGUUAACUACUG GGGGCAAGGCAAAUAGCACAACCGGUGGCAAGCAUACUA CUGGGCACGGUGCCCGCACAAGCACCGAGCCUACAACGGA CUAUGGGGGGGGAUUCUACCACACCACGUCCCCGGUAUAA CGCCACCACGUACUUCGCGCUAGCACAUAAGCAAACUC AGACCUCGCUGGACAUUUAUACUACCCCCAGUUACCACUG CUCAGGCAACCGUCCCGGUGCCUCCUACUUCACAACCACG UUUCAGCAACUUGAGCAUGCUGGUCCUGCAGUGGGCUUC CCUCGCCGUGCUGACAUUACUGUUAUUGCUGGUGAUGGC	

	CGAUUGCGCGUUCGCGAGGAACCUGUCUACCAGCCACAC AUACACAACGCCCCCGUAUGACGACGCAGAGACUUAUGU G	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLITRTATNATTTTHKVFISKAPESTTTS PTLNTTGFADPNTTTGLPSSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETYV	28
PolyA tail	100 nt	
gp350_mod_003		
SEQ ID NO: 152 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 30, and 3' UTR SEQ ID NO:3		152
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAAGCCGCUCUUCUGGUCUGCCAGUAUACAAUCCAG UCGCUGAUUCAUCACCGGCGAGGAUCCAGGUUUCUUU AACGUGGAGAUUCCAGAAUCCCUUUCUAUCCAACUUGU AACGUGUGUACUGCCGACGUUAACGUUACUAUUAACUUU GACGUGGGCGGAAAGAAGCACCAGCUGGAUCUUGAUUUC GGCCAGCUAACACCUCUAUACCAAGGCCGUCUACCAACCAC GCGGGGCAUUUGGCGGUUCUGAGAAUGCUACAAACCUGU UCCUUUUGGAACUCCUCGGAGCAGGGGAACUGGCACUUA CAAUGAGGAGUAAGAAGCUGCCCAUCAACGUCACCACGG GGGAAGAACAGCAGGUGUCCUGGAGUCCGUUGAUGUGU AUUUCAGGACGUUUUCGGGACAAUGUGGUGUCAUCAUG CCGAAAUGCAGAAUCCGGUGUAUCUCAUUCUGAGACCG UGCCCUAUUAUAAAUGGGAUAACUGUAAUUCGACAAACA UAACUGCCGUAGUGCGUGCCCAGGGUCUGGAUGUAACUU UGCCUCUCUCCCUUCCACUUCUGCCCAGGACUCCAAUUU UUCAGUGAAGACCGAAUUGCUUGGGAACGAGAUCCGACAU CGAGUGUAUCAUGGAGGAUGGGGAGAUCAUCAGGUGUU GCCUGGUGACAAUAAGUUUAAUAUACAUGUUCGGGCUA UGAAUCACAUGUCCAAGCGGAGGUAUUCUCACAAGUAC AUCUCCCGUAGCCACGCCGAUUCGGGAACCGGAUACGCC UAUUCACUUCGGCUGACUCCUCGGCCAGUGUCACGAUUC CUGGGCAAUAACUCAAUUCUGUACGUCUUUACAGCGGC AACGGCCCCAAAGGCCAGUGGAGGCGAUUACUGUAUCCAG UCUAAACAUCGUAUUUUCAGAUAGAUUCCAGCAAGCCAA	30

	GACAUGCCAACUAAUACUACAGACAUUACAUAACGUCGGU GAUAACGCCACUUAUUCAGUCCCUAUGGUCACAUCCGAG GACGCGAACUCACCCAAUGUUACCGUUACCGCAUUCUGG GCAUGGCCCAAUAAUACGGAAACAGACUUCAAAUGUAAG UGGACCCUGACCAGUGGCACCCCUUCUGGCUGCGAAAAU AUAAGCGGGGCAUUUGCUAGCAACAGAACAUUCGAUAAU ACUGUGUCUGGGCUGGGGACCGCCCCCAAACACUCAUU AUAACGCGAACAGCUACGAACGCUACCACAACCACACAU AAAGUGAUUUUCAGCAAGGCUCCAGAAUCAACUACAACC AGUCCGACCCUUAUUAACCACAGGCUUCGCAGACCCGAACA CAACGACGGGACUGCCCUCCUCAACGCAUGUGCCGACUAA UCUGACUGCUCCCGCAAGUACCGGCCAACAGUCUCCACA GCAGACGUCACCUCUCCGACUCCCGCCGGCACUACAUCUG GAGCCUCACCGGUGACUCCUAGUCCUUCUUUUUGGACAA UGGGACCGAGUCUAAAGCCCCGGACAUGACGAGUUCUAC CUCACCAGUUACAACCCCAACACCUAAUGCCACAAGCCCU ACGCCAGCCGUGACCACCCCUACCCCAUUGCCACCAGCC CAACACCCGCUGUUACAACGCCAACCCCAACGCUACUUC UCCAACGCUAGGAAAAACAUCACCCACCUCAGCUGUAACC ACCCCAACACCAAACGCUACCGGGCCAACCGUUGGCGAAA CCUUUUUUAGGCCAAUGCGACAAACCACACCCUUGGGGG GACUUCUCCACUCCUGUGGUGACUUCACAACCGAAGAA CGCGACGUCGGCCGUUACGACCGGGCAGCACAAUAUACCC UCGUCCUCCACGUCGUCCAUGUCCUUGCGGCCUUCAGUA ACCCAGAGACACUGUCUCCUAGUACCAGUGACAACAGCA CCUCUCACAUGCCAUUACUGACUUCGCCCCACCAACCGG CGGAGAGAAACAUCACUCAGGUGACCCCGCAUCUAAUUC UACCCACCACGUGAGCACUAGCAGCCCGGCACCAAGACCA GGGACCACCUCUCCAGGCUAGCGGCCCGGGCAACUCCUCCA CUAGCACGAAACCAGGAGAGGUGAACGUGACCAAGGGCA CACCGCCACAGAAUGCAACUUCUCCACAGGCCCCCUCCGG CCAGAAAACUGCUGUACCUACGGUCACUAGCACUGGCGG AAAAGCGAAUUAACCACCGGUGGUAAGCAUACCACCGG ACACGGCGCUCGGACUAGCACAGAGCCAACCACUGAUUA CGGGGGUGACUCAACGACCCCGAGGCCAGGUACAACGC AACCACCUAUCUCCACCAUCCACAUCUCCAAGCUCAGG CCUCGUUGGACUUAUACCUCCCGCCUGUGACUACAGCGC AGGCCACAGUGCCAGUGCCUCCAACGUCACAGCCGCGGUU UAGCAAUCUCUCCAUGCUGGUCCUGCAGUGGGCAUCUCU GGCAGUCCUGACACUGCUUCUUUUGCUCGUGAUGGCCGA UUGUGCGUUUAGACGCAACCUUUAACAUCCACACAUA UACAACUCCACCCUAUGAUGACGCAGAGACUUAUGUG	
3' UTR	UGAUAUAGGCUUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTGLPSSTHVPTNLTAPOSTGPTVSTADVTS PTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGSPTPVVTSQPKNATS AVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT	28

	AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLVLMADCAFRRLNSTSHTYTTPPYDDAETYV	
PolyA tail	100 nt	
gp350_mod_004		
SEQ ID NO: 153 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 31, and 3' UTR SEQ ID NO:3		153
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAAGCCGCCCUAUUAGUCUGCCAGUACACCAUUCAA AGCCUCAUCCACUUGACUGGGGAGGAUCCUGGGUUCUUU AACGUGGAAAUCCCGGAAUUCCCUUUCUACCCAACUUGC AACGUGUGCACGGCUGACGUCAACGUGACUAUCAACUUC GAUGUGGGGGGAAGAAACAUAACUUGAUCUGGACUUU GGCCAGCUUACUCCCCACACCAAGGCCGUGUACCAGCCCC GCGGCGCAUUCGGUGGGAGCGAGAACGCGACAAAUCUAU UCUUGCUGGAACUGCUGGGCGCAGGAGAGCUCGCCCUGA CGAUGCGAUCUAAAAAGCUUCCCAUCAACGUUACCACUG GCGAGGAGCAGCAGGUGUCCCUCGAAAGCGUCGACGUCU AUUCCAAGACGUCUUCGGAACAAUGUGGUGCCACCACG CUGAGAUGCAGAACCCCGUAUAUCUUAUUCCCGAAACCG UGCCAUACAUAAGUGGGACAACUGCAACUCAACUAACA UCACUGCAGUAGUGCGCGCCCAGGGACUGGACGUCACUU UGCCACUGUCACUGCCCAUAUCAGCCCAAGACAGCAACUU CAGCGUCAAGACAGAAAUGCUGGGCAACGAAAUCGACAU CGAAUGCAUAAUGGAGGAUGGGGAAAUUUCCAGGUCCU CCCCGGUGAUAAACAAGUUUAAUUAUACUUGUUCUGGAUA UGAAUCCCAUGUGCCGUCUGGUGGUUAUACUGACGAGUAC AUCGCCAGUGGCUACCCCAUCCCGGGACAGGCUAUGCC UACAGCCUGAGACUGACGCCAAGACCAGUUUCCAGGUUU CUGGGGAAUAACUCUAUCCUGUAUGUGUUUUUUAUCUGGU AACGGACCCAAAGGCAUCCGGCGGUGAUUAUUGUAUCCAG AGCAAUAUAGUGUUCUCUGAUGAGAUUCCGGCCUCCAG GAUAUGCCAACCAACACGACAGAUUAUACCUAUGUCGGG GACAACGCCACAUAUAGCGUGCCAAUGGUGACCAGCGAA GAUGCCAAUUCUCCCAACGUCACAGUGACAGCCUUUUGG GCGUGGCCUAAUAACACAGAAACUGACUUUAAAUGCAAA UGGACUCUAACCUCAGGCACCCCAUCUGGCUGCGAGAAC AUAAGCGGCGCGUUUGCAUCGAACAGAACUUUUGAUUU ACAGUAUCUGGGUUGGGCACUGCCCCCAAACUCUAAUA AUUACACGGACGGCCACUAACGCCACCACGACGACUCACA AGGUGAUCUUCAGCAAAGCUCCCGAAUCUACUACUACCU CGCCGACACUGAAUACGACAGGAUUCGCCGACCCAAUA CUACGACCGGCCUUCCAGCUCGACACAUGUGCCUACAAA CUUAACGGCCCCCGCCAGUACCGGCCCCACCGUGAGCACC GCUGACGUCACCUCUCCUACCCUGCCGGGACUACAAGUG GUGCUUCCCCAGUUACUCCAGCCCUAGCCCUUGGGACAA CGGCACUGAGAGCAAAGCUCCGGACAUGACCAGCAGUAC CAGUCCAGUGACAACUCCGACACCCAAUGCGACGUCCCCA ACUCCCGCCGUGACCACGCCAACACCAAUGCCACGUCAC CUACUCCAGCGGUCACCACCCCAACGCCAAACGCUACUAG UCCACUCUAGGCAAGACAUCUCCACCUCGUGUCACC ACCCUACACCCAAUGCUACCGGUCCACGGUGGGUGAGA CUAGCCCACAGGCCAACGCAACUAAUCAUACAUUGGGGG GCACAAGCCCAACCCCGUCGUCACUAGCCAGCCUAAAA	31

	CGCCACAAGCGCUGUAACUACCGGCCAGCACAAUAUAAC AAGUUCCAGUACUAGCAGUAUGUCUCUGAGACCCAGCUC AAAUCCUGAAACCCUCUCCCCCUCUACGUCGGAUAACUCC ACGUCCCACAUGCCUCUACUCACAAGCGCGCACCCUACCG GGGGAGAAAAUAUCACUCAGGUUACCCCAGCUUCUAUCU CGACUCACCAUGUCUCUACUUCUCCCCAGCGCCACGGCC CGGCACUACCAGCCAGGCUAGCGGGCCAGGUAUUUCCUCC ACUAGCACUAAACCUGGCGAAGUCAACGUUACCAAGGGA ACACCCCCCAGAAUGCAACCUCCCCCCAAGCUCCUCUG GACAGAAAACAGCCGUCCCUACCGUCACAAGCACCCGGUG GGAAGGCGAAUUCUACGACAGGCGGGAAGCACACUACCG GACACGGAGCAAGGACAUCCACUGAGCCCACGACCGACU ACGGUGGCGACUCCACCACCCCCAGACCCAGGUACAAUGC GACUACCUACCUGCCCCCUUCCACUUCAGCAAACUGAGG CCUCGUUGGACUUUCACUUCUCCCCCAGUACCAACCGCUC AGGCUACCGUGCCUGUCCCGCCGACCUCUCAGCCCCGGUU UUCAAAUUUGAGUAUGCUCGUGCUGCAGUGGGCCAGCCU GGCAGUGCUUACCCUCCUGCUCUUGCUGGUUAUGGCUGA CUGCGCCUUCGACGUAACUUAUCCACCAGUCAUACUAC ACUACACCCCCUUAUGACGACGCGGAGACCUACGUG	
3' UTR	UGAUAUUAGGCUAGGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGAFADPNTTTGLPSSTHVPTNLTAPOSTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWFTSPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLNSTSHTYTTTPPYDDAETYV	28
PolyA tail	100 nt	
gp350_mod_005		
SEQ ID NO: 154 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 32, and 3' UTR SEQ ID NO:3		154
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAAGCCGCCUUACUGGUCUGCCAGUACACUAUUCAG UCCCUCAUCCAUCUCACAGGCGAGGACCCGGGGUUCUUA ACGUCGAAAUCCCCGAAUUCCTTAUUCUUAUCCACCUGUAA CGUCUGCACAGCCGACGUUAACGUUACAAUCAAUUUCGA CGUGGGCGGGAAAAAACACCAGCUGGACCUCGACUUUGG GCAGCUGACGCCCCACACUAAAGCCGUUUUACCAGCCCAGG GGUGCAUUCGGUGGAUCUGAAAAUGCUACAAACCUCUUU	32

	CUGCUUGAGCUGCUUGGUGCUGGAGAGCUGGCCUGACA AUGCGCAGCAAAAAGUUGCCAAUCA AUGUGACCACAGGU GAAGAACAGCAGGUGUCCCUAGAAUCCGUGGAUGUGUAC UCCAGGACGUUUUCGGCACAAUGUGGUGCCAUCACGCA GAGAUGCAAAAUCCGGUGUACCUUAUCCCCGAAACAGUG CCGUACAUAUAAUUGGGAUAAUUGUAACUCCACAAACAU ACGGCAGUGGUGCGCGCUCAGGGGCUGGACGUGACACUC CCCCUUCCUUACCAACAAGUGCUCAAGAUUCCAACUUU UCUGUGAAAACCGAGAUGCUGGGCAACGAGAUUGAUUU GAAUGCAUCAUGGAGGAUGGCGAGAUUAGCCAGGUGUUG CCCGGCGACAAUAAUUAUUAUUAUUAUUAUUAUUAUUAU GAGUCACACGUGCCAAGUGGAGGCAUUCUCACGAGCACC UCUCCCGUUGCAACACCCAUUCCUGGGACAGGGUACGCA UAUAGUCUCAGGCUGACACCGAGACCGGUAUCGCGCUUC UUAGGUAACAAUCCAUCUUGUAUGUGUUUACAGCGGA AACGGGCCAAAGGCCUCAGGAGGAGACUACUGCAUCCAG AGCAAUUAAGUUUUAGCGACGAGAUCCUGCCUCACAA GACAUGCCCACCAACACCACCGACAUCACGUACGUCGGUG AUAUUGCCACUACAGCGUGCCU AUGGUGACCUCUGAAG ACGCAAAUUCACCCAAUGUCACGGUUAACGCAUUCUGGG CUUGGCCAAUAACACUGAAACCGACUUAAGUGUAAA GGACCCUAACAGCGGCACCCCAUCAGGGUGCGAGAAUA UCAGCGGGGCCUUCGCCAGCAACCGGACAUCGACAUCAC CGUGUCAGGACUAGGGACUGCUCCAAAAACAUAUAAUUA UACACGGACAGCAACUAACGCUACGACUACGACUCACAA AGUGAUUUUAGCAAAGCCCCGAAUCGACUACUACGAG CCCGACCCUAAACACCACCGGUUUCGCCGAUCCCAACACA ACUACUGGUCUCCCAUCUUCGACCCAUUGUCCAACGAUUC UGACAGCUCCAGCAAGUACGGGGCCACUGUGAGUACAG CCGACGUUACUAGCCCAACUCCCGCGGGUACGACUAGUG GCGCGUCUCCAGUGACCCCUUCGCCUUCUCCGUGGGAAUA UGGAACCGAGUCAAGGCUCCUGAU AUGACCAGCUCCAC CAGUCCCGUUAACAACGCCAACCCCAAUGCAACGAGUCCA ACUCCGGCGGUUACACUCCGACACCAAACGCCACCUCCC CCACGCCUGCAGUUAUACGCCACCCCUAAUGCUACGUC ACCCACUCUGGGAAAGACCUCACCAACCUCUGCCGUGACU ACUCCUACACCUAAUGCCACAGGACCCACAGUUGGGGAA ACCAGCCCACAGGCUAACGCAACUAAUCAUACGCUUGGG GGGACCUCUCCACGCCCGUGGUCACUUCACAGCCUAAGA AUGCCACAAGCGCUGUGACUACAGGCCAGCAUAUAUAA CCAGCAGUUAACAGUAGCAUGUCCUGCGUCCUUAUC CAAUCCUGAGACUCUGAGCCCCAGCACUAGUGACAACUC AACUUCUCACAUGCCGUUGCUGACCUCGCGCAUCCACG GGCGGUGAGAAUAUCACACAGGUGACACCCGCGUCUAU AGCACACAUCACGUGAGUACGUCCUCCCCCGCACCCCGCC CAGGCACAACCUCACAAGCAUCAGGUCCGGGGAACAGCA GCACAAGUACCAAGCCUGGCGAAGUGAAUGUAACCAAGG GCACGCCCCCGCAGAACGCCACAUCCCUCAAGCCCCAUC CGGCCAGAAGACCGCUGUACCCACCGUGACAUAACUGG GGGAAAGCGAACUCAACUACCGGGGGGAAGCAUACAAC AGGGCACGGUGCCAGAACUUCUACAGAGCCAACCACGGA CUACGGAGGGGACAGCACAACGCCCAGACCGCGGUACAA UGCGACCACAUACCUGCCUCCCUCAACUUCGAGUAAGCUG CGACCCAGAUGGACCUUUAUUCUCCCCUGUACCAACCG CUAAGCCACCGUCCCGGUUCCACCUACUUCACAGCCUAG AUUCUCCAUCUGAGCAUGCUUGUCCUACAGUGGGCAUC ACUCGCGGUACUAACCUUGCUGCUACUGUUGGUGAUGGC GGACUGCGCGUUUCGCCGAACUUAUCCACCUCCCACACG UACACAACACCUCCCUAUGAUGACGCUAGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC	3

	CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNN SILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDTITYVGD NATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTGLPSSSTHVPTNLTA PASTGPTVSTADVTS PTPAGTTS GASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPL LTS AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQA TVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLV MADCAFRRLSTSHTYTTTPYDDAETYV	28
PolyA tail	100 nt	
EBV gp42 (B95-8) DX		
SEQ ID NO: 155 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 33, and 3' UTR SEQ ID NO:3		155
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGUGAGCUUCAAGCAGGUGAGAGUGCCCCUGUUCACC GCCAUCGCCCUGGUGAUCGUGCUGCUGGCCUACUUC UGCCCCCAGAGUGAGAGGCGGCGGCAGAGUGGCCGCGC CCGCCAUCACCUGGGUGCCCAAGCCCAACGUGGAGGUGU GGCCCGUGGACCCCCACCCCCGUGAACUUAACAAGAC CGCCGAGCAGGAGUACGGCGACAAGGAGGUGAAGCUGCC CCACUGGACCCCCACCCUGCACACCUUCCAGGUGCCCCAG AAUACACCAAGGCCAACUGCACCACUGCAACACCCAGAG AGUACACCUUCAGCUACAAGGGCUGCUGCUUCUACUUA CCAAGAAGAAGCACACCUGGAACGGCUGCUUCCAGGCCU GCGCCGAGCUGUACCCUGCACCACUUCUACGGCCCCAC CCCCGACAUCUGCCCGUGGUGACCAGAAACCUGAACGCC AUCGAGAGCCUGUGGGUGGGCGUGUACAGAGUGGGCGAG GGCAACUGGACCAGCCUGGACGGCGGCACCUUCAAGGUG UACCAGAUUCUGGCAGCCACUGCACCACGUGAGCAAG UUCAGCACCGUGCCCGUGAGCCACCACGAGUGCAGCUUCC UGAAGCCCUGCCUGUGCGUGAGCCAGAGAAGCAACAGC	33
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVRRGGGRVAAA ITWVPKPNVEVWPVDPPPPVNFNKTAEQEYGDKEVKLPHW TPTLHTFQVPQNYTKANCTYCNTRYTFYSYKGCCFYFTKKK HTWNGCFQACAELYPTIFYGPTPDILPVVTRNLNAIESLWV GVYRVGEGNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPVSH HECSFLKPCLCVSQRSNS	34
PolyA tail	100 nt	

EBV gL (B95-8)		
SEQ ID NO: 156 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 35, and 3' UTR SEQ ID NO:3		156
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUUCUGGCCAUCUGCCUGGUGACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAUCAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUCUACAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCGGCCACCUGAGA GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUAC GCCUGGCACAGAGGCGGC	35
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MRAVGVFLLAICLVITIFVLPWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFVSDLFGANLNR YAWHRGG	36
PolyA tail	100 nt	
EBV gH (BXL2)_RX		
SEQ ID NO: 157 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 37, and 3' UTR SEQ ID NO:3		157
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGCAGUUGUUGUGCGUGUUCUGCCUCGUGUACUCUGG GAGGUGGGCGCCGCCAGCCUUAAGCGAGGUGAAGCUCCAC UUGGACAUCGAGGGCCACGCCAGCCACUACACCAUCCCCU GGACCGAGCUCAUGGCCAAGGUGCCCGGCCUUAAGCCCCGA GGCCUGUGGGCGGGAGGCCAACGUGACCGAGGACCUGGC CAGCAUGCUGAACCGGUACAAGCUGAUCUACAAGACCAG CGGCACCCUGGGCAUCGCCCUGGCCGAGCCCGUGGACAUC CCCGCCGUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGC AAGGUGCACCCCGGCGUGAUCAGCGGCCUGAACAGCCCCG CCUGUAUGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCU ACUACAUCGGCACCAUGCUGCCCAACACCCGGCCCCACAG CUACGUGUUCUACCAGCUGCGGUGCCACCUGAGCUACGU UGCCUGAGCAUCAACGGCGACAAGUCCAGUACACCGG CGCCAUGACCAGCAAGUCCUGAUGGGCACCUCACAAGCG GGUCACCGAGAAGGGCGACGAGCACGUGCUGUCACUGGU GUUCGGCAAGACCAAGGACCUGCCCCGACCUGCGGGGCCCC UUCAGCUACCCUAGUUUGACCAGCGCCCAGAGCGGCGAC UACAGCUUGGUGAUCGUGACCACCUUCGUGCACUACGCC AACUCCACAACUACUUCGUGCCCAACCUGAAGGACAUG UUCAGCCGGGGCCGUGACCAUGACUGCCGCUUCUACGCC GGUACGUGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGG GCGGCUGCCGGGAGCCCGAGCUGGACACCGAAACACUGA CCACCAUGUUCGAGGUGAGCGUGGCCUUCUUCACAGGUGG	37

	GUACACGCGGUGGGCGAAACCGGCAACGGCUGCGUGGACU UACGCUGGCUGGCCAAGAGCUUCUUCGAGCUGACCGUGC UGAAGGAUAUCAUCGGCAUCUGCUACGGCGCCACCGUGA AGGGCAUGCAGAGCUACGGCCUGGAGCGGCUGGCCGCCA UGCUUAUGGCAACAGUGAAGAUGGAGGAGCUGGGACACC UGACAACAGAGAAGCAGGAGUACGCCUGAGACUGGCCA CAGUGGGCUACCCAAAGGCCGGCGUGUACAGUGGACUGA UCGGCGGCGCAACCAGCGUGCUGCUAUCCGCUUACAACCG GCACCCGCGUUCAGCCCCUGCACACCGUGAUGCGGGAA ACCCUGUUAUCGGAAGCCACGUCGUGCUGCGGGAGCUG AGGCUGAACGUAACCACCCAGGGCCCUAAUCUGGCCCU UAUCAGCUCCUCAGUACCGCCUGUGCAGCGCCCUUGAGA UCGGCGAGGUGCUCAGAGGCCUGGCCCUCCGUACCGAGA GCGGCCUCUUCAGCCCAUGCUACUUAAGCCUGCGGUUCG ACCUGACCCGGGACAAGUUGCUGAGCAUGGCCCCGCAGG AGGCCACACUGGACCAGGCAGCUGUAUCCAACGCCGUGG ACGGCUUCCUGGGCAGACUGUCCUGGAACGGGAGGACC GGGACGCCUGGCACCUGCCUGCCUACAAGUGUGUGGAUC GGCUGGACAAGGUGCUGAUGAUAUCCUCUGAUUAAUG UCACCUUCAUCAUCAGCAGCGACCGGGAGGUGCGGGGAU CCGCCUCUACGAGGCCAGCACACCUAUCUGAGCAGCAG CCUGUUCUGUCUCCUGUGAUGAUGAACAAGUGCAGCCA GGGCGCCGUGGCCGGCGAGCCCCGGCAGAUCCCCAAGAUC CAGAACUUCACCCGGACCCAGAAGUCUUGCAUCUUCUGC GGCUUCGCCCUIUUGUCCUACGACGAGAAGGAGGGGUG GAGACUACAACCUACAUCACCAGCCAGGAGGUGCAGAAC AGCAUCCUGUCAUCUAAUUAUUCGACUUCGACAACCUG CACGUUCAUUAACCGUCCUCACCACCAACGGUACCGUCA UGGAAAUCGCCGGACUGUACGAGGAGCGGGCCCAUGUUG UGCUGGCCAUCAUCCUGUACUUAUCGCUUUCGCACUUG GCAUCUUCUGGUGCACAAGAUCGUGAUGUUCUUCUG	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MQLLCVFCLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTE LMAKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGLGI ALAEPVDIPAVSEGSMQVDASKVHPGVISGLNSPACMLSAPLE KQLFYIYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFQYT GAMTSKFLMGTYKRVTEKGDEHVLVLVFGKTKDLPDLRGPF YPSLTSAQSGDYSLVIVTTFVHYANFHNYPVNLKDMFSRAV TMTAASYARYVLQKLVLLEMKGCCREPELDTETLTMTFEVS VAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIGICYG ATVKGMQSYGLERLAAMLATVKMEELGHLTTEKQEYALR LATVGYPKAGVYSGLIGGATSVLLSAYNRHPLFQPLHTVMRE TLFIGSHVVLRELRLNVTQGPNLALYQLLSTALCSALEIGEV RGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAA VSNVVDGFLGRSLEREDRDWHLPAYKCVDRDLKVLMIPL INVTFISSDREVRGSALYEASTTYLSSSLFLSPVIMNKCSQGAV AGEPRQIPKIQNFTRTQKSCIFCGFALLSYDEKEGLETTTYITSQ EVQNSILSSNYFDFDNLHVHYLLLTNGTVMEIAGLYEERAH VVLAILYFIAFALGIFLVHKIVMFFL	38
PolyA tail	100 nt	
EBV LMP1_DX (modified)		
SEQ ID NO: 158 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 39, and 3' UTR SEQ ID NO:3		158
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	

5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAACACGACCUUGAGAGGGGCCCACCGGGCCCGCGACGGCCACCUCGAGGACCUCUUUCCUUCUAGGCCUUGCUCUCCUUCUCCUCCUUGGCGCUACUGUUUUGGCUGUACAUCGUUAUGAGUGACUGGACUGGAGGAGCCCUCCUUGUCCUCUAUUCUUUUGCUCUCAUGCUUAUAAUUAUAAUUUUGAUCAUUUUAUCUUCAGAAGAGACCUUCUCUGUCACUUGGAGCCCUUUGUAUACUCCUACUGAUGAUCACCCUCCUGCUCAUUCGUCUCUGGAAUUUGCACGGACAGGCAUUGUCCUUGGAAUUGUGCUGUUCUUCUUCGGGUGCUUACUUGUCUUAGGUAUCUGGAUCUACUUAUUGGAGAUGCUCUGGCGACUUGGUGCCACCAUCUGGCAGCUUUUGGCCUUCUCCUAGCCUUCUCCUAGACCUCUCCUGCUCAUUAUUGCUCUCUAUCUACAACAGAACUGGUGGACUCUAUUGGUUGAUCUCCUUUGGCUCCUCCUGUUUCUGGCGAUUUUAAUCUGGAUGUAUUACCAUGGACAACGACACAGUGAUGAACACCAACACGAUGACUCCUCCCGCACCCUCAACAAGCUACCGAUGAUUCUGGCCAUGAAUCUGACUCUAAUCUCCAACGAGGGCAGACACCACUGCUCGUGAGUGGAGCCGGCGACGGACCAACACUCUGCUCUCAGAACCUAGGCGCACCUUGGAGGUGGUCCUGACAAUGGCCCACAGGACCCUGACAACACGGAUGAUAAUGGCCCACAGGACCCUGAUAAACACUGAUGACAAUGGCCACAUGACCCGCGUGCCUCAAGACCCAGACAAUACUGAUGACAAUGGCCCACAGGACCCUGACAACACUGAUGACAAUGGCCGCGACGACCCGUUACCUCUAGCCCUAGCGACUGCUGGAAAUGAUGGAGGCCCUCCACAAUUGACGGAAGAGGUGAGAACAAAGGAGGUGACCAGGGCCCGCCUUUGAUGACAGACGGAGGCGGCGGUCUAGUCAUGAUUCCGGCCAUGGCGGCGGUGAUCCACACCUUCCUACGCUGCUGUUGGGUUCUUCUGGUUCCGGUGGAGAUGAUGACGACCCGCACGGCCCAGUUCAGCUAAGCUACUAGAC	39
3' UTR	UGAUAUUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCCCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLLLLALLFWLYIVMSDWTGGALLVLYSFALMLIIIIILIFIFRRDLLCPLGALCILLMITLLLIALLWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRLGATIWQLLAFFLAFFLDLILLIALLYLQQNWWTLLVDLLWLLFLAILIWMYYHGRHSDEHHHDDSLPHPQQATDDSGHESDSNSNEGRHLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTDNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTDDNGPHDPLPHSPSDSAGNDGGPPQLTEEVENKGGDQGPPLMTDGGGGHSHDSHGSGGDPHPLPTLLGSSGSGGDDDDPHGPVQLSYYD	16
PolyA tail	100 nt	
EBV LMP2		
SEQ ID NO: 159 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 40, and 3' UTR SEQ ID NO:3		159
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGGUCCCUAGAAAUGGUGCCAAUGGGCGCGGGUCCUCCUAGCCCCGGCGGGGAUCCGGAUGGGUACGAUGGCGGAACAACUCCCAAUAUCCAUCUGCUUCUGGCUCUUCUGGGAACACGCCACCCACCGAACGAUGAGGAACGUGAAUCUAAUGAAGAGCCACCACCGCCUUAUGAGGACCCAUAUUGG	40

	GGCAAUGGCGACCGUCACUCGGACUAUCAACCACUAGGA ACCCAAGAUCAAAGUCUGUACUUGGGAUUGCAACACGAC GGGAAUGACGGGCUCCCUCCACCUCUCCUACUCUCCACGGG AUGACUCAUCUCAACACAUAUACGAAGAAGCGGGCAGAG GAAGUAUGAAUCCAGUAUGCCUGCCUGUAAUUGUUGCGC CCUACCUCUUUUGGCUGGCGGCUAUUGCCGCCUCGUGUU UCACGGCCUCAGUUAGUACCGUUGUGACCGCCACCGGCU UGGCCCUCUCACUUCUACUCUUGGCAGCAGUGGCCAGCUC AUAUGCCGCUGCACAAGGAAACUGCUGACACCGGUGAC AGUGCUUACUGCGGUUGUCACUUCUUGCAAUUUGCCU ACAUGGAGGAUUGAGGACCCACCUUUUAAUUCUCUUCU GUUUGCAUUGCUGGCCGCAGCUGGCGGACUACAAGGCAU UUACGUUCUGGUGAUGCUUGUGCUCCUGAUACUAGCGUA CAGAAGGAGAUGGCGCCGUUUGACUGUUUGUGGCGGCAU CAUGUUCUUGGCAUGUGUACUUGUCCUCAUCGUCGACGC UGUUUUGCAGCUGAGUCCCCUCCUUGGAGCUGUAAACUGU GGUUUCCAUGACGCUGCUGCUACUGGCUUUCGUCCUCUG GCUCUCUUCGCCAGGUGGCCUAGGUACUCUUGGUGCAGC CCUUUUAACAUUGGCAGCAGCUCUGGCACUGCUAGCGUC ACUGAUUUUGGACACACUUAACUUGACUACAAUGUCCU UCUCAUGCUCUUAUGGACACUUGUGGUUCUCCUGAUUUG CUCUUCGUGCUCUUAUGUCCACUGAGCAAGAUCUUCU GGCAGCAGUGUCCUUAUGCUCUCGCACUCUUGUUGCU AGCCUCCGCGCUAAUCGCUGGUGGCAGUAAUUUGCAAAC AAACUUCAAGAGUUUAAGCAGCACUGAAUUUAUACCCAA UUUGUUCUGCAUGUUAAUACUGAUUGUCGCGGCAUACU CUUCAUUCUUGCUAUCCUGACCGAAUGGGGCAGUGGAAA UAGAACAUACGGUCCAGUCUUUAUGUGCCUCGGUGGCCU GCUCACCAUGGUAGCCGGCGCUGUGUGGCUGACGGUGAU GUCUAAACACGCUUUUGUCUGCCUGGAUUCUACAGCAGG AUUCCUGAUUUUCCUCAUUGGCUUUGCCUCUUUGGGGU CAUUAGAUGCUGCCGCUACUGCUGCUACUACUGCCUAC ACUGGAAAGUGAGGAGCGCCACCGACCCCAUAUCGCAA CACUGUA	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWNGDRHSDYQPLGTQDQSL YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTA VVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRLTVCGGIMFLACVL VLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTLNL TTMFLLMLLWTLVLLICS SCSSCPLSKILLARFLYALALLLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLLIVAGILFILAILTEWGSNGRNTYGPVFMCLGG LLTMVAGAVWLTVMSNTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	22
PolyA tail	100 nt	
EBNA1_trunc_001 (modified)		
SEQ ID NO: 160 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 41, and 3' UTR SEQ ID NO:3		160
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1

ORF of mRNA Construct (excluding the stop codon)	AUGGGCAGAAGACCCUUCUUUCACCCCGUGGGAGAAGCC GACUAUUUCGAGUACCACCAGGAGGGCGGUCCUGACGGC GAGCCCGACGUGCCUCCAGGCGCCAUCGAACAGGGCCCCG CUGACGAUCCUGGCGAGGGGGCCUCCACAGGCCCUCGCGG CCAGGGAGAUGGCGGAAGGCGGAAGAAGGGCGGCUGGUU UGGCAAGCAUAGGGGGCCAGGGCGGCUCCAAUCCCAAGUU CGAGAAUAUCGCCGAGGGGCUCCGGGCUCUGCUGGCCCCG GUCGCACGUCGAACGUACCACUGACGAGGGGACGUGGGU GGCCGGCGUCUUUGUGUACGGAGGAUCCAAGACCUCCCU GUACAACCUGAGAAGGGGGCACCGCCCUUGCCAUCCUCAG UGCAGACUCACGCCCCUGAGCAGGCUCCCCUUUGGGAUG GCUCCUGGGCCAGGCCCCGAGCCCCGGGCCCCUCAGGGAAA GCAUCGUGUGUUACUUUAUGGUGUUUCUGCAGACACACA UCUUUGCAGAAGUUCUGAAAGAUGCAAUCAAGGAUCUGG UGAUGACCAAGCCUGCACCUCGUGCAAUAUCAGGGUGA CAGUAUGCUCCUUCGACGACGGUGUGGACCUCCCGCCCUG GUUCCCAACCAUGGUCGAGGGUGCCGCCGCCGAGGGAGA CGAUGGCGACGACGGUGAUGAGGGUGGAGACGGAGAUGA AGGCGAGGAGGGGGCAGGAG	41
3' UTR	UGAUAUUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADD PEGGPSTGPRGQGDGRRKKGGWFGKHRGQGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRG TALAI PQRLTPLSR L PFGMAPGPGPQPGPLRESIVCYFMVFLQ THIFAEVLKDAIKDLVMTKPAPTCNIRVTVC SFDDGVDLPPWF PPMVEGAAAE GDDGDGDEGGDGDEGE EGQE	10
PolyA tail	100 nt	
EBV EBNA3 (B95-8)_RX		
SEQ ID NO: 161 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 42, and 3' UTR SEQ ID NO:3		161
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACAAGGACAGGCCCCGGCCCUCCCGCCUUGGACGACA ACAUGGAGGAGGAGGUGCCCGACACGAGCGUGGUGCAGG AGCAGGUGAGCGCCGGCGACUGGGAGAACGUGUUAUUCG AGUUGAGCGACAGCAGCAGCGAGAAGGAGGCCGAGGACG CCCACCUGGAGCCCGCCAGAAAGGGCACCAAGAGGAAGA GGGUGGACCACGACGUGGCGGAUCUGCCCCUGCCAGGCC CAUGCUGCCACCCAGCCCGACCUGCCCGGCAGGGAGGCC AUCCUGAGGAGGUUCCACUGGACCUGAGGACCCUGCUG CAGGCCAUCGGCGCCGCCGCCACCAGGAUCGACACCAGGG CCAUCGACCAGUUCUUCGGCAGCCAGAUCAAGCAACACCGA GAUGUACAUAUGUACGCCAUGGCCAUCAGACAAGCAAU UAGGGAUCGACGCAGAAAUCCUGCCAGCAGGAGGGACCA GGCCAAGUGGAGGCUGCAGACCCUGGCCGCCGGCUGGCCC AUGGGCUACCAGGCCUACAGCAGCUGGAUGUACAGCUAC ACCGACCACCAGACCACUCCGACCUUCGUGCACCUCAGG CUACCCUGGGCUGCACUGGCGGUCGAGGUGCCACGUGA CCUUCUCAGCGGGCACCUUCAAGCUGCCAGGUGCACACC UGGCGACAGGCAGUGGCUGUACGUGCAGAGCAGCGUGGG CAACAUUGUUCAGAGUUGCAACCCAGGUACAGCAUCUU CUUCGACUACAUGGCGAUUCACAGGAGCCUGACCAAGAU CUGGGAGGAAGUCCUGACCCUGACCAGAGGGUGAGCUU CAUGGAGUUCUGGGCUUCCUGCAGAGGACCGACCUGAG	42

	CUACAUCAAGAGCUUCGUGAGCGACGCCUGGGCACCACC AGCAUCCAGACUCCUUGGAUCGACGAUAACCCUAGCACC GAAACCGCCCAGGCCUGGAACGCCGGUUUCCUGAGGGGC AGGGCCUACGGCAUCGACCUGCUCCGGACCGAGGGCGAG CACGUGGAGGGCGCCACCGGCGAGACUAGGGAGGAGAGC GAGGACACUGAGAGCGACGGCGACGACGAGGAUCUGCCG UGCAUCGUGAGCAGGGGCGGCCCCAAGGUGAAGAGGCCU CCCAUCUUAUCCGGAGGCUUCACAGGCUGCUGCUGAUG AGGGCCGGCAAGCGUACUGAACAGGGCAAGGAGGUACUG GAGAAGGCCAGGGGCAGCACAU AUGGCACCCCUAGACCG CCUGUGCCCAAGCCGCGUCCUGAAGUCCCGCAGAGUGAU GAGACAGCGACUAGCCAUGGCAGUGCUCAGGUGCCCGAG CCACCCACCAUCCAUCUCGCCGCACAGGGCAUGGCCUACC CACUGCACGAGCAGCACGGCAUGGCGCCUGCCCCGUGGC CCAGGCUCCUCCAACCCCGCUUCCUCCAGUAUCCCCUGGU GACCAGUUGCCAGGCGUGUUCAGCGACGGUAGGGUGGCC UGCGCGCCAGUUCCUGCACCAGCAGGCCCAUUGUGAGG CCCUGGGAGCCCUCCCUAACCCAGGCGGCAGGUCAGGCCU UCGCUCCAGUUAGACCACAGCACAU GCCCGUGGAACCGG UGCCAGUGCCUACGGUGGCGCUGGAGAGGCCCGUGUACC CAAAGCCUGUGCGACCUGCGCCUCCU AAGAUCGCCAUGCA AGGCCCCGGGCGAGACUAGCGGU AUCAGGCGGGCCAGGGA GAGGUGGCGCCCGGCACCGUGGACUCCCAACCCACCAAGG UCACCUAGUCAGAUGAGCGUGCGUGAUAGGCUGGACCG CUUCGGGCAGAGGCUACAGGUA AAGCAGGCCAGUGUGGAG GUGCAGCCACCACAGCUGACUCAGGUGUCCCGCAGCAGC CCAUGGAGGGCCACUGGUGCCGGAACAGCAGAUGUUC CCGGCGCCCCGUUCAGCCAGGUGGCCGACGUGGUUAGGG CUCCUGGCGUGCCUGCUAUGCAGCCUCAGUACUUCGACCU ACCGCUGAUCCAGCCCAUCAGUCAAGGUGCCCCAGUGGCC CCACUGAGGGCUAGCAUGGGCCCCGUCCCUCCUGUUCAG CCACCCAGCCUCAAUAUUUCGACAUUCCUCUGACCGAGCC UAUAAACCAGGGCGCGUCUGCGGCCACUUCUGCCUCA CAGCCAAUGGAAGGCCCGCUGGUCCCAAGACAGUGGAUG UUCCUGGAGCUGCCCUGAGCCAAUCAGUGAGGCCGGGA GUUGCCCAGAGCCAGUAUUUCGAUCUCCCUUUGACACAG CCUAUCAAUACCGGAGCACCUGCCGCUCACUCCUUCACC AGCCUCCGAUGGAAGGUCCUUGGGUUC CAGAGCAAUGGA UGUCCAAGGUGCGCCACCAUCUCAGGGCACAGACGUGG UCCAGCAUCAGCUGGACGCGCUUGGCUACACUCUACACG GCCUGAACCACCCGGGCGUCCAGUGAGUCCAGCCGUGA ACCAGUACCAUCUCUCUCAGGCUGCCUUCGGCCUGCCCAU UGACGAGGACGAGAGCGGCGAGGGCAGCGAUACCAGCGA GCCUGCGAAGCCUGGAUCUUUCCAUCCACGGCCGACCU UGCCCACAGGCUCCAGAGUGGCCCGUACAGGAAGAAGGC GGCCAGGACGCCACCGAGGUCCUGGACUUGUCCAUA CAU GGCAGACCGCGCCCUAGGACCCCGGAGUGGCCAGUUCAG GGUGAAGGUGGUCAGAACGUGACCGGCCCGGAAACCCGA AGGGUGGUCGUGUCCGCUUGUCCACAUGUGUCAGGAU GACGAAUCCCCAGAUUCUGCAAGAUCCACCCGACGAGGCC	
3' UTR	UGAUAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDKDRPGPPALDDNMEEV PSTSVVQE QVSAGDWENVLIELS DSSSEKEAEDAHLEPAQKGT KRKRVDHDAGGSAPARPMLPPQ PDLPGREAILRRFPLDLRTL LQAIGAAATRIDTRAIDQFFGSQIS NTEMYIMYAMAIRQAIRDRRRNPASRRDQAKWRLQTLAAGW PMGYQAYSSWMYSYTDHQT TPTFVHLQATLGCTGGRRCHVT FSAGTFKLPRCTPGDRQWLYVQSSVGNIVQSCNPRYSIFFDYM AIHRS�TKIWEEVLTPDQRV SFMEFLGFLQRTDLSYIKSFVSDA	43

	LGTTSIQTPWIDDPSTETAQAWNAGFLRGRAYGIDLLRTEGE HVEGATGETREESEDTESDGDEDLPCIVSRGGPKVKRPPIFIR RLHRLLLMRAGKRTEQKKEVLEKARGSTYGTTPRPVVKPRPE VPQSDDETATSHGSAQVPEPPTIHLAAQGMAYPLHEQHGMAPC PVAQAPPTPLPPVSPGDQLPGVFS DGRVACAPVPAPAGPIVRP WEPSLTQAAGQAFAPVRPQHMPVEPVVPVPTVALERPVPKPV RPAPPKIAMQGPGETSGIRRARERWRPAPWTPNPPRSPSQMSV RDRLARLRAEAQVKQASVEVQPPQLTQVSPQQPMEGPLVPEQ QMFPGAPFSQVADVVRAPGV PAMQPQYFDLPLIQIPISQGAPV APLRASMGPVPPVPATQPQYFDIPLTEPINQGASAAHFLPQQP MEGPLVPEQWMFPGAALSQSVRPGVAQSQYFDLPLTQPINHG APAAHFLHQPPMEGPWVPEQWMFQGAPPSQGTDVVQHQLD ALGYTLHGLNHPGV PVPSPAVNQYHLSQA AFGLPIDEDES GEG SDTSEPCEALDLSIHGRPCPQAPEWPVQEEGGQDATEVLDLSI HGRPRPRTPEWPVQEGGQNV TGPETRRVVVSAVVHMCQDD EFPDLQDPPDEA	
PolyA tail	100 nt	
EBV gp350 A44Y V10 Stab		
SEQ ID NO: 162 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 44, and 3' UTR SEQ ID NO:3		162
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUUCGACGUGAACGUGACAAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAUAAUUGCAAUUAACAAUUAU UACGGCUGUGGUGAGGGCCAGGGCUUGGACGUGACUCU GCCCUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUGCUCGGGAAUGAGAUCGAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUAUAUACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAAUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAUAACACUGAGACUGACUCAA AUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU	44

	GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUCACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUCACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUAAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTY DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNLSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGAFADPNTTTGLPSSTHVPTNLTAPOSTGPTVSTADVTS PTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTDYGGDSTPRPRYNATTYLP STSSKLRPRWTFSTPPVTTAQAATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLVLMADCAFRRNLSTSHTYTTPPYDDAETV	45
PolyA tail	100 nt	
EBV gp350 I150F V11 Stab		
SEQ ID NO: 163 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 46, and 3' UTR SEQ ID NO:3		163
Chemistry	1-methylpseudouridine	

Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAUAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUAUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCCTCAUACGUAUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUAAGUGGGAAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCCUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC UCUGUCAAGACCGAGAUAGCUCGGGAAUGAGAUCAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUAUAUACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAAUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAUUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCCT CGACUCUUAACACUACGGGCUUCGUGAUCCTAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCUUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCTCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAGC GCUACCUCGCGUGACUACCGGACAGCACAACAUCACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUAUCACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAAACAUCACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC	46

	GGAGGUGACAGCACAAACACCGCGGCCACGAUAAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAUAGGUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTFNFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNISILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLITRTATNATTTTHKVFISKAPESTTTS PTLNTTGAFADPNTTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSATV TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLTTS AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTIDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLVMA DCAFRRNLSTSHTYTTPPYDDAETYV	47
PolyA tail	100 nt	
EBV gp350 M202I V12 Stab		
SEQ ID NO: 164 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 48, and 3' UTR SEQ ID NO:3		164
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAUUCUGU UCUUAUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUACUCGGGAAUGAGAU CGAU AUC GAGUGCAUCAUGGAGGACGGUGAGAU AAGCCAGGUUCUG CCCGGCGACAACAAGUCAAUAUCACUUGUUCUGGCUAC GAGUCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU	48

	UCUCCCGUAGCCACGCCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAGCGUCCGGAGGGGACUUAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGUUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAUAAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUUAG GUGAUCUUUCCAAGGCACCUAGAGUCCACCACUACCUC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUUAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGGCCGACCGUGGGCGAGAC UCCCCGCAAGCCAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAACAUCACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCAGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAACACCGCGGCCACGAUAAUAGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACGACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUACGUC	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTS AQDSNFSVKTEILGNEIDIECIME DGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGTG YAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQSN VFSDEIPASQDMPTNTTDITYVGD NATYSVPMVTSEDANSPNV TVTAFWAWPNN TETDFKCKWTLTSGTPSGCENISGAFASNRT FDITVSGLTAPKTLITRTATNATTTTHKVI FSKAPESTTTTSPT	49

	LNTTGAFADPNTTTGLPSSTHVPTNLTAFASTGPTVSTADVTSTPT PAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNA TSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVTTP TPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATSAV TTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLTSAH PTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTST KPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKANST TGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPSTST SKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQWAS LAVLTLLLLLVLMADCAFRRLSTSHTYTTPPYDDAETVYV	
PolyA tail	100 nt	
EBV gp350 H417W V13 Stab		
SEQ ID NO: 165 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 50, and 3' UTR SEQ ID NO:3		165
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCUAGUGGGUAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGCCCCAGGGCUUGGACGUGACUCU GCCCCUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUAGCUCGGGAAUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUAUUAUACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAUAAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUAUACCUACGUGGGCGA CAAUGCCACGUUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUGUUAUCUGUAACAGCUUUCUGGGC CUGGCCAAUUAACACUGAGACUGACUCAAUUAUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUUAU AACACGGACCGCCACCAACGCCACGACUACAACCGUGAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCGAACGCGACAUCUCC	50

	ACACCGUCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAG GCUACCUCCGUGUCACUACCGGACAGCACAACAUCACCA GCUCAAGCAGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUACACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAACACCGCGGCCACGAUAAUAAUGCC ACCACUUACUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCUACGAUGACGCCGAGACUACGUC	
3' UTR	UGAUAUAGGCGUGGAGCCUCGGUGGCCAUGCUUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNLSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTWKVIFSKAPESTTTS PTLNTTGFADPNTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLS AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKA NSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLVMDCAFRRLSTSHTYTTPPYDDAETYV	51
PolyA tail	100 nt	
EBV gp350 V14 Stab4 mut		
SEQ ID NO: 166 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 52, and 3' UTR SEQ ID NO: 3		166
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU	52

(excluding the stop codon)	AACGUGGAAAUCCCAGAGUUCCCUUUCUAUCCAACCUGU AACGUUUGCACUUAACGACGUGAACGUGACAUUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUUC UCUGUCAAGACCGAGAUACUCGGGAAUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUUAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGUUUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUUGUUAACUGUAACAGCUUUUCUGGC CUGGCCAAUUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUUA CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUUAU AACACGGACCGCCACCAACGCCACGACUACAACCUGGAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGACGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCUUGAUUAGACUUCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCCCACCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAAGAAC GCUACCUCGCGUGACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUUCUUGAGCUUUGCGGCCGAGCUAA AUCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUUAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUACAAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU	

	UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTY DVNVTFNFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEILGNEIDIECIME DGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGTG YAYSLRLTPRPVSRFLGNNILYVFYSGNGPKASGGDYCIQSN VFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSPNV TVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRT FDITVSGLGTAPKTLITRTATNATTTTWKVIFSKAPESTTTSTPT LNTTGFADPNTTGLPSSTHVPTNLTAPOSTGPTVSTADVTSTPT PAGTTSGASPVTSPSPWDNGTESKAPDMSTSTSPVTTPTPNA TSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVTTP TPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATSAV TTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLTSAH PTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTST KPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKANST TGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPSTST SKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQWAS LAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETYV	53
PolyA tail	100 nt	
EBV gp350 V15 Stab4_NGM6		
SEQ ID NO: 167 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 54, and 3' UTR SEQ ID NO:3		167
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUU AACGUGGAAAUCCAGAGUCCCUUUCUAUCCAACCGU AACGUUUGCACUACGACGUGAACGUGACAUUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUGCGAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGGAUAAUUGCAAUUCAGCGAAUAU UACGGCUGUGGUGAGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC GCGGUCAAGACCGAGAUACUCGGGAUUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUCAAUAUCGCGUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUACCUACGUGGGCGA	54

	CAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAAUGUUGCGGUAACAGCUUUCUGGGC CUGGCCAAAUAAACACUGAGACUGACUCAAUUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCGCGACUACAACCCAUAAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCUGG GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGACUACCGGACAGCACAACAUCACCA GCUAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUACACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAAUACACCCAGGUGACUCCGGCGUCUAAUUC ACCACACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUAAUAGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTY DVNVTNFNFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENAANLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSAN ITAVVRAQGLDVTPLSLPTSAQDSNFAVKTEILGNEIDIECIM EDGEISQVLPDGNKFNIACSGYESHVPSSGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGVDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVAVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLITRTATNAATTHKVIKFAPESTTTS PTLNTTGFADPNTTTGLPSSTHVPTNLTAPOSTGPTVSTWDVT SPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTP NATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS SAVTTTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNAT SAVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT SAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNS	55

	STSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGK ANSTTGKKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYL PPSTSSKLRPRWFTSPVTTAQTVPVPPTSQPRFSNLSMLVL QWASLAVLTLTLLLLVMADCAFRRLNSTSHTYTTTPPYDDAETY V	
PolyA tail	100 nt	
V1_NGM 36 mut_EBV_gp350_001		
SEQ ID NO: 168 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 56, and 3' UTR SEQ ID NO:3		168
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGGCGAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUGCGAAUCUGU UCUUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUGCGACCG GGGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGU ACUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACG CUGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUG UACCCUACAUAAGUGGGAUAAUUGCAAUUCAGCGAAUA UUGCGGCUGUGGUGAGGGCCCAGGGCUUGGACGUGACUC UGCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAAUUU CGCGGUCAAGACCGAGAUUGCUCGGGAAUGAGAUCAUAU CGAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCU GCCCGGCGACAACAAGUCAAUAUCGCGUGUUCUGGCUA CGAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUAC UUCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCC UACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCC UGGGUAAACAUGCGAUCUUAUACGUGUUUUAUAGCGGAA ACGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGA GUAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGG ACAUGCCGACAAACACAGCGGAUAUUAACCUACGUGGGCG ACAAUGCCGCGUAUUCAGUGCCCAUGGUCACGAGCGAGG ACGCCAAUUCACCAAUUGUUGCGGUAACAGCUUUCUGGG CCUGGCCAAUAACGCGGAGACUGACUCAAUUGUAAGU GGACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUA UCGCGGGGGCCUUGCUUCCAACAGGGCGUUCGACAUA CUGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUA UAACACGGACCGCCACCAACGCCGCGACUACAACCCAUAA GGUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUC CCGACUCUUAACACUGCGGGCUUCGCUGAUCCCAACACCG CGACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACC UGGCGGGCCUGCAUCGACCGGGCCACAGUUUCGACCGC CGAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAGCGGAGUCCAAGGCUCCUGAUUAUGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAGCGAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGGCGUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCGCGAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAGCGGGCCCGACCGUGGGCGAGAC UCCCCGCAAGCCAAUGCGGCGAAUCACGCGUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC	56

	GCUGCGUCCGUGUCACUACCGGACAGCACAACAUCGCGA GCUCAAGCACGAGUUCUUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUAGACAACAGUGC GUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAAACUAGCGCAGGUGACUCCGGCGUCUUAUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCGCGA CAAGCACAAAGCCAGGCGAAGUUAACGUGGCGAAGGGAA CGCCUCCCCAGAACGCAGCGAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAGCGACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCCGCGGCCACGAUAUAAUGCC GCGACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUGCGAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCGCGACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAUUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVAINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENAANLFLLELLGAGELALTMRSKKLPINVATGEEQQVSLESV DVYFQDVFGTMVCHHAEMQNPVYLIPETVPYIKWDNCNSAN IAAVVRAQGLDVTLP LSLPTSAQDSNFAVKTEMLGNEIDIECI MEDGEISQVLPDGNKFNIACSGYESHVPSGGILTSTSPVATPIP GTGYAYSLRLTPRPVSRFLGNNAILYVFYSGNGPKASGGDYCI QSNIVFSDEIPASQDMPTNTADITYVGDNAAYSVPMTSEDAN SPNVAVTAFWAWPNNAETDFKCKWTLTSGTPSGCENIAGAF ASNRAFDITVSGLTAPKTLIITRTATNAATTTTHKVFISKAPEST TTSPTLNTAGFADPNTATGLPSSTHVPTNLAAPASTGPTVSTA DVTSPTPAGTTSGASPVTPSPSPWDNGAESKAPDMTSSTSPVT TPTPNAASPTPAVTTPTPNAASPTPAVTTPTPNAASPTLGKTSP TSAVTTPTPNAAGPTVGETSPQANAANHALGGTSPTPVVTSQP KNAASAVTTGQHNIASSSTSSMSLRPSSNPETLSPSTSDNSASH MPLLTAHPTGGENIAQVTPASISTHHVSTSSPAPRPGTTSQAS GPGNSATSTKPGEVNVAKGTPPQNAASPQAPSGQKTAVPTVT STGGKANSATGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYN AATYLPSTSSKLRPRWTFSTPPVTTAQTVPVPPTSQPRFSNL AMLVLQWASLAVLTLLLLVMADCAFRRLATSHTYTTPPY DDAETYV	57
PolyA tail	100 nt	
V2_NGM 18 mut_EBV_gp350_001		
SEQ ID NO: 169 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 58, and 3' UTR SEQ ID NO:3		169
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGGCGAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA	58

	GGGGUGCAUUUGGAGGGAGCGAGAAUGCUGCGAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCCAUCAACGUUGCGACCG GGGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGU ACUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACG CUGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUG UACCCUACAUCAAGUGGGAAUAAUUGCAAUUCAGCGAAUA UUGCGGCUGUGGUGAGGGCCCAGGGCUUGGACGUGACUC UGCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAAUUU CGCGGUCAAGACCGAGAUUGCUCGGGAAUGAGAUCGAU CGAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCU GCCCCGGCGACAACAAGUCAAUAUCGCGUGUUCUGGCCUA CGAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUAC UUCUCCCGUAGCCACGCCCAUUCCCGGAACCGGAUACGCC UACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCC UGGGUAAACAAUGCGAUCUUAUACGUGUUUAUAGCGGAA ACGGCCCUAAAGCGUCCGGAGGGGACUUAUGUAUUCAGA GUAUAUACGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGG ACAUGCCGACAAACACAGCGGAUUAUACCUACGUGGGCG ACAAUGCCGCGUAUUCAGUGCCCAUGGUCACGAGCGAGG ACGCCAAUUCACCAAUGUUGCGGUAACAGCUUUCUGGG CCUGGCCAAAUAACGCGGAGACUGACUCAAUUGUAAGU GGACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUA UCGCGGGGGCCUUUGCUUCCAACAGGGCGUUCGACAUA CUGUCUCAGGGCUGGGGACAGCACCGAAGACAUAAUA UAACACGACCGCCACCAACGCCGCGACUACAACCCAUAA GGUGAUCUUUUCCAAGGCACCUGAGUCCACCACUACCUC CCGACUCUUAACACUGCGGGCUUCGCUGAUCCCAACACCG CGACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACC UGGCGGGCCCCUGCAUCGACCGGGCCCACAGUUUCGACCGC CGAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCGUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCCGCUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUACAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUACGGCGCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCCGCGGCCACGAUUAUAAUGCC ACCACUUUUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACGACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC	3

	CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVAINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENAANLFLLELLGAGELALTMRSKKLPINVATGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSAN IAAVVRAQGLDVTPLSLPTSAQDSNFAVKTEMLGNEIDIECI MEDGEISQVLPGDNKFNIACSGYESHVPSGGILTSTSPVATPIP GTGYAYSLRLTPRPVSRFLGNNAILYVFYSGNGPKASGGDYCI QSNIVFSDEIPASQDMPTNTADITYVGDNAAYSVPMVTSEDAN SPNVAVTAFWAWPNNAETDFKCKWTLTSGTPSGCENIAGAF ASNRAFDITVSGLTAPKTLITRTATNAATTTTHKVIFSKAPEST TTSPTLNTAGFADPNTATGLPSSTHVPTNLAAPASTGPTVSTA DVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVT TTPNATSPTPAVTTTPNATSPTPAVTTTPNATSPTLGKTSPT SAVTTTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPK NATSAVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHM PLL TSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGP GNSSTSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTG GKANSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATT YLPPSTSSKLRPRWTFSTPPVTTAQA TVPVPPTSQPRFSNL SML VLQWASLAVLTL LLLL VMADCAFRRLSTSHTYTTPPYDDAE TYV	59
PolyA tail	100 nt	
V4_NGM N87_EBV_gp350_001		
SEQ ID NO: 170 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 60, and 3' UTR SEQ ID NO:3		170
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUC GGCCAACUGACGCCACACACCAAGCGGUGUACCAACCAA GGGUGCAUUGGAGGAGCGAGAAUGCUGCGAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUGCUCGGGAAUGAGAUCAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUACCUACGUGGGCGA CAAUGCCACGUAAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAAUGUUAUCUGUAACAGCUUUCUGGGC CUGGCCAAUAACACUGAGACUGACUCAAUUGUAAGUG	60

	GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAUGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGGCCGACCGUGGGCGAGAC UCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUAAUUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENAANLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNLSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANS NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSLGTAPKTLITRTATNATTTTHKVFISKAPESTTTS PTLNTTGAFADPNNTTGLPSSTHVPTNLTAPOSTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP	61

	STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLVMDCAFRRLSTSHYTTTPPYDDAETYV	
PolyA tail	100 nt	
V5_NGM N166_EBV_gp350_001		
SEQ ID NO: 171 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 62, and 3' UTR SEQ ID NO:3		171
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAAUCUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAAUAAUUGCAAUUCAGCGAAUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUUC UCUGUCAAGACCGAGAUGCUCGGGAAUGAGAUCCGAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAUAGCCACGUUAUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCGCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGACUACCGGACAGCACAACAUCACCA GCUCAAGCACGAGUCCAUGAGCUUUGCGGCCGAGCUCAA AUCCCGAGACCCUAUCACCAUCCACAUCAGACAACAGUAC	62

	UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAAACAUCACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCCGCGGCCACGAUUAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGUGGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSAN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDTITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTTLPSSTHVPTNLTAPOSTGPTVSTADVTS PTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWFTSPPVTTAQA TVPVPTSPQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETYV	63
PolyA tail	100 nt	
V6_NGM N195_EBV_gp350_001		
SEQ ID NO: 172 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 64, and 3' UTR SEQ ID NO:3		172
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAAUCUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA	64

	CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAAUAAUUGCAAUUAACUAAU UACGGCUGUGGUGAGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC GCGGUCAAGACCGAGAUGCUCGGGAAUGAGAUCGAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAGCGUCCGGAGGGGACUUAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUACCUACGUGGGCGA CAAUGCCACGUAAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAAUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAUAAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCCC CGACUCUUAACACUACGGGCUUCGUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUCACCAUCCACAUACAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUCACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAAGACUGCGGUGCCAAUCUGUGACCAGACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACACCGCGGCCACGAUAAUAGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3

Corresponding amino acid sequence	MEALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTLP LSLPTS AQDSNFAVKTEMLGNEIDIECI MEDGEISQVLP GDNKFNITCSGYESHVPSGGILTSTSPVATPIPG TGYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQ SNIVFSDEIPASQDMPTNTTDTITYVGDNATYSVPMVTSEDANS PNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFAS NRTFDITVSGLTAPKTLIITRTATNATTTTHKVIFSKAPESTTT SPTLNTTG FADPNTTGLPSSTHVPTNLTA PASTGPTVSTADVT SPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTP NATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AV TTPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNAT SAVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT SAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNS STSTKPGEVNVTKGTTPPNATSPQAPSGQKTAVPTVTSTGGK ANSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYL PPSTSSKL RPRWTF TSPPVTTA QATVPVPPTSQPRFSNLSMLVL QWASLAVLTLLLLLV MADCAFRRLSTSHTYTTPPYDDAETY V	65
PolyA tail	100 nt	
V7_NGM N229_EBV_gp350_001		
SEQ ID NO: 173 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 66, and 3' UTR SEQ ID NO:3		173
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAUACUUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUGCUCGGGAUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUCAAUAUCGCGUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCC UAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUACCUACGUGGGCGA CAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUGUUAUCUGUAACAGCUUUCUGGGC CUGGCCAAUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUGCUUCCAACAGGACUUCGACAUCAC	66

	UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAU AAG GUGAUCUUUUCCAAGGCACCUAGUCCACCACUACCUC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGU AAGACCAGUCCGACUAGCGCCGUUACAA CCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACAUACCA GCUCAAGCACGAGUUCUUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCU AUCACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GCGGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCACACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGA CGCCUCCCCAGAACGCAACAGUCCUAGGCGCCGAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUAAUUGCC ACCACUU AUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACGACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTS AQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNIACSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGD NATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLIITRTATNATTTTHKVIFSKAPESTTS PTLNTTG FADPNTTTGLPSSTHVPTNLTA PASTGPTVSTADVTS PTPAGTTS GASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSP TLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPL LTS AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTG HGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFNSMLVLQ WASLAVLTLLLLLV MADCAFRRNLSTSHTYTTPPYDDAETYV	67
PolyA tail	100 nt	

V8_NGM N345_EBV_gp350_001		
SEQ ID NO: 174 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 68, and 3' UTR SEQ ID NO:3		174
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAGUCGCUCAUUCAUCUGACAGGCGAGGACCCCGGCUUCUUUAACGUGGAAAUCCCAGAGUUCUUUCUAUCCAACCUGUAACGUAUUGCACUGGCUGACGUGAACGUGACAAUCAAUUCGACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUCGGCCAACUGACGCCACACACCAAAAGCGGUGUACCAACCAAGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGUUCUUAUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGGGGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUACUUUCAGGAUGUUUCGGCACCAUGUGGUGUCACCACGUGAGAUAGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGUACCCUACAUAAGUGGGAUAAUUGCAAUUAACUAAUUAACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCUGCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUCUCUGUCAAGACCGAGAUAGCUCGGGAAUGAGAUCAUUCGAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUGCCCAGGACAAAGUUAUUAUCACUUGUUCUGGCUACGAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACUUCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCUACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCUGGGUAAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAACGGCCUAAAGCGUCCGGAGGGGACUAAUUGUAUUCAGAGUAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGACAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGCAUAUGCCACGUUUCAGUGCCCAUGGUCACGAGCGAGGACGCCAAUUCACCAAAUGUUGCGGUAACAGCUUUCUGGGCUGGGCCAAUUAACACUGAGACUGACUCAAUUGUAAGUGGACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAUCAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCACUGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAUAACACGGACCGCCACCAACGCCACGACUACAACCCAUAAAGUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCGCCACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCACUACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCUGACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCCGAUGUGACAUACCAACGCCCGCAGGUACAACCCUAGGCGCCAGCCCAGUACCCCUUCCCCAAGCCCCUGGGAUAAUGAACGGAGUCCAAGGCUCCUGAUUAGACUUCUUAACAGCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAACCCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCCACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCCCUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAAACCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGACUUCUCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGGGACCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAGGCUACCUCGUGUCACUACCGGACAGCACAAACUACCAACGCUAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAAUCCCGAGACCCUUAUCACCAUCCACAUCAGACAACAGUACUUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGCGGAGAAACUACCCAGGUGACUCCGGCGUCUAAUUCACCCACCAGUCAGCACGUCGUCUCCCGCACCGAGACCAGGGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA	68

	CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACACCGCGGCCACGAUAAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNLSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVAVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGAFADPNTTGLPSSTHVPTNLTAPOSTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLVMA DCAFRRNLSTSHTYTTPPYDDAETVY	114
PolyA tail	100 nt	
V9_NGM N411_EBV_gp350_001		
SEQ ID NO: 175 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 69, and 3' UTR SEQ ID NO:3		175
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUUCUUUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGCCCAGGGCUUGGACGUGACUCU	69

	GCCCCUUAUCUCUACCUACUUCUGCCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUGCUCGGGAAUGAGAU CGAU AUC GAGUGCAUCAUGGAGGACGGUGAGAU AAGCCAGGUUCUG CCCGGCGACAACAAGUUC AAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCCAUUC CCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCC UAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAU AUUACCUACGUGGGCGA CAAUGCCACGU AUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAA AUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAAU AACACUGAGACUGACUCAA AUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAU AU CAGCGGGGCCUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCGCGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUC C CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAU AUGACUCCCUAACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGU AAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUC CGCUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUAUCACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACGACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINF DVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIM	70

	EDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLIITRTATNAATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSGASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTL LLLL VMADCAFRRLSTSHTYTTPPYDDAETYV	
PolyA tail	100 nt	
EBV gp42 (B95-8)_DX		
SEQ ID NO: 176 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 70, and 3' UTR SEQ ID NO:3		176
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGUGAGCUUCAAGCAGGUGAGAGUGCCCCUGUUCACC GCCAUCGCCCUGGUGAUCGUGCUGCUGGCCUACUUC UGCCCCCAGAGUGAGAGGCGGCGGCAGAGUGGCCGCCG CCGCCAUCACCUGGGUGCCCCAAGCCCAACGUGGAGGUGU GGCCCGUGGACCCCCACCCCCCGUGAACUUAACAAGAC CGCCGAGCAGGAGUACGGCGACAAGGAGGUGAAGCUGCC CCACUGGACCCCCACCCUGCACACCUUCCAGGUGCCCCAG AACUACACCAAGGCCAACUGCACCUACUGCAACACCAGAG AGUACACCUUCAGCUACAAGGGCUGCUGCUUCUACUUA CCAAGAAGAAGCACACCUGGAACGGCUGCUUCCAGGCCU GCGCCGAGCUGUACCCUGCACCUACUUCUACGGCCCCAC CCCCGACAUCCUGCCCGUGGUGACCAGAAACCUGAACGCC AUCGAGAGCCUGGGUGGGCGUGUACAGAGUGGGCGAG GGCAACUGGACCAGCCUGGACGGCGGCACCUUCAAGGUG UACCAGAUUUUGGCAGCCACUGCACCUACGUGAGCAAG UUCAGCACCGUGCCCGUGAGCCACCACGAGUGCAGCUUCC UGAAGCCCUGCCUGUGCGUGAGCCAGAGAAGCAACAGC	71
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVRGGRVAAA ITWVPKPNVEVWPVDP PPPVNFNKTAEQEYGDKEVKLPHW TPTLHTFQVPQNYTKANCTYCNTREYTFSYKGCCFYFTKKK HTWNGCFQACAELYPCTYFYGPTPDILPVVTRNLNAIESLW VG VYRVGEGNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPV SHHECSFLKPCLCVSQRSNS	34
PolyA tail	100 nt	
EBV EBNA3 (B95-8)_RX		
SEQ ID NO: 177 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 72, and 3' UTR SEQ ID NO:3		177
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	

5' UTR	GGGAAAUAGAGAGAAAAGAAGAGUAAGAAGAAAUUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACAAGGACAGGCCCGGCCUCCCGCCUUGGACGACA ACAUGGAGGAGGAGGUGCCAGCACCAGCGUGGUGCAGG AGCAGGUGAGCGCCGCGACUUGGAGAACGUGUUAUUCG AGUUGAGCGACAGCAGCAGCGAGAAGGAGGCCGAGGACG CCCACCUGGAGCCCGCCAGAAGGGCACCAAGAGGAAGA GGGUGGACCACGACGCUGGCGGAUCUGCCCCUGCCAGGCC CAUGCUGCCACCCAGCCCGACCUGCCCGGCAGGGAGGCC AUCCUGAGGAGGUUCCACUGGACCUGAGGACCCUGCUG CAGGCCAUCGGCGCCGCCGCCACCAGGAUCGACACCAGGG CCAUCGACCAGUUCUUCGGCAGCCAGAUCAGCAACACCGA GAUGUACAUAUGUACGCCAUGGCCAUCAGACAAGCAAU UAGGGAUCGACGCAGAAAUCCUGCCAGCAGGAGGGACCA GGCCAAGUGGAGGCUGCAGACCCUGGCCGCCGGCUGGCC AUGGGCUACCAGGCCUACAGCAGCUGGAUGUACAGCUAC ACCGACCACCAGACCACUCCGACCUUCGUGCACCUCAGG CUACCCUGGGCUGCACUGGCGGUCGACGGUGCCACGUGA CCUUCUCAGCGGGCACCUUCAAGCUGCCAGGUGCACACC UGGCGACAGGCAGUGGCUGUACGUGCAGAGCAGCGUGGG CAACAUUGUUCAGAGUUGCAACCCAGGUACAGCAUCUU CUUCGACUACAUGGCGAUUCACAGGAGCCUGACCAAGAU CUGGGAGGAAGUCCUGACCCUGACCAGAGGGUGAGCUU CAUGGAGUUCUGGGCUUCCUGCAGAGGACCGACCUGAG CUACAUAAGAGCUUCGUGAGCGACGCCUGGGCACCACC AGCAUCCAGACUCCUUGGAUCGACGAUAACCCUAGCACC GAAACCGCCAGGCCUGGAACGCCGUUUCUGAGGGGGC AGGGCCUACGGCAUCGACCUGCUCCGGACCGAGGGCGAG CACGUGGAGGGCGCCACCGGCGAGACUAGGGAGGAGAGC GAGGACACUGAGAGCGACGGCGACGACGAGGAUCUGCCG UGCAUCGUGAGCAGGGGCGGCCCAAGGUGAAGAGGCCU CCCAUCUUAUCCGGAGGCUUCACAGGCUGCUGCUGAUG AGGGCCGGCAAGCGUACUGAACAGGGCAAGGAGGUACUG GAGAAGGCCAGGGGCAGCACAUAGGGACCCCUAGACCG CCUGUGCCCAAGCCGCGUCCUGAAGUCCCGCAGAGUGAU GAGACAGCGACUAGCCAUGGCAGUGCUCAGGUGCCCGAG CCACCCACCAUCCAUCUCGCCGCACAGGGCAUGGCCUACC CACUGCACGAGCAGCACGGCAUGGCGCCUGCCCCGUGGC CCAGGCUCCUCCAACCCCGCUUCCUCCAGUAUCCCCUGGU GACCAGUUGCCAGGCGUGUUCAGCGACGGUAGGGUGGCC UGCGCGCCAGUUCCUGCACCAGCAGGCCCAAUUGUGAGG CCCUGGGAGCCCUCCCUAACCCAGGCGGCAGGUCAGGCCU UCGCUCCAGUUAGACCACAGCACAUGCCCGUGGAACCGG UGCCAGUGCCUACGGUGGCGCUGGAGAGGCCCGUGUACC CAAAGCCUGUGCGACCUGCGCCUCCUAAGAUCGCCAUGCA AGGCCCGGGCGAGACUAGCGGUUACAGGCGGGCCAGGGA GAGGUGGCGCCCGGCACCGUGGACUCCCAACCCACCAAGG UCACCUAGUCAGAUGAGCGUGCGUGAUAGGCUGGCACGG CUUCGGGCAGAGGCUCAGGUAAAGCAGGCCAGUGUGGAG GUGCAGCCACCACAGCUGACUCAGGUGUCCCCGCAGAGC CCAUGGAGGGCCACUGGUGCCGGAACAGCAGAUUGUCC CCGGCGCCCCGUUCAGCCAGGUGGCCGACGUGGUUAGGG CUCCUGGCGUGCCUGCUAUGCAGCCUCAGUACUUCGACCU ACCGCUGAUCCAGCCCAUCAGUCAAGGUGCCCCAGUGGCC CCACUGAGGGCUAGCAUGGGCCCGGUCCUCCUGUUCAG CCACCCAGCCUCAAUAUUUCGACAUUCCUCUGACCGAGCC UAUAAACCAGGGCGCGUCUGCGGCCACUUCUGCCUCAA CAGCCAAUGGAAGGCCCGCUGGUCCCAAGACAGUGGAUG UUCCUGGAGCUGCCUGAGCCAAUCAGUGAGGCCGGGA GUUGCCCAGAGCCAGUAUUUCGAUCUCCCUUUGACACAG CCUAUCAUAUCACGGAGCACCUGCCGCUCACUCCUUCACC AGCCUCCGAUGGAAGGUCCUUGGGUCCAGAGCAAUGGA	72

	UGUCCAAGGUGCGCCACCAUCUCAGGGCACAGACGUGG UCCAGCAUCAGCUGGACGCGCUUGGCUACACUCUACACG GCCUGAACCACCCGGGCGUCCAGUGAGUCCAGCCGUGA ACCAGUACCAUCUCUCUCAGGCUGCCUUCGGCCUGCCCAU UGACGAGGACGAGAGCGGCGAGGGCAGCGAUACCAGCGA GCCCUGCGAAGCCCUGGAUCUUUCCAUCCACGGCCGACCU UGCCACAGGCUCAGAGUGGCCCAGACAGGAAGAAGGC GGCCAGGACGCCACCGAGGUCCUGGACUUGUCCAUAACAU GGCAGACCGCGCCCUAGGACCCCGAGUGGCCAGUUCAG GGUGAAGGUGGUCAGAACGUGACCGGCCCGGAAACCCGA AGGGUGGUCGUGUCCGCGUUGUCCACAUGUGUCAGGAU GACGAAUUCCCAGAUCUGCAAGAUCACCCGACGAGGCC	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDKDRPGPPALDDNMEEEVPSTSVVQEQVSAGDWENVLIELS DSSEKEAEDAHLEPAQKGTKRKRVDHDAGGSAPARPMPLPPQ PDLPGREAILRRFPLDLRLTLQAIGAAATRIDTRAIDQFFGSQIS NTEMYIMYAMAIRQAIRDRRRNPASRRDQAKWRLQTLAAGW PMGYQAYSSWMYSYTDHQTTPTFVHLQATLGCTGGRCHVT FSAGTFKLPRCTPGDRQWLYVQSSVGNIVQSCNPRYSIFFDYM AIHRS�TKIWEEVLTPDQRVSFMEFLGFLQRTDLSYIKSFVSDA LGTTSIQTPWIDNPNSTETAQAWNAGFLRGRAYGIDLLRTEGE HVEGATGETREESEDTESDGDDDELPCIVSRGGPKVKRPPIFIR RLHRLLLMRAGKRTEQGKEVLEKARGSTYGTPRPPVPKPRPE VPQSDATATSHGSAQVPEPPTIHLAAQGMAYPLHEQHGMAPC PVAQAPPTPLPPVSPGDQLPGVFS DGRVACAPVPAPAGPIVRP WEPSLTQAAGQAFAPVRPQHMPVEPVVPVPTVALERPVPYKPV RPAPPKIAMQGPGETSGIRRARERWRPAPWTPNPPRSPSQMSV RDRLARLRAEAQVKQASVEVQPPQLTQVSPQQPMEGPLVPEQ QMFPGAPFSQVADVVRAPGV PAMQPQYFDLPLIQIPISQGAPV APLRASMGPVPPVPATQPQYFDIPLTEPINQGASAAHFLPQQP MEGPLVPEQWMFPGAALSQSVRPGVAQSQYFDLPLTQPINHG APAAHFLHQPPMEGPWVPEQWMFQGAPPSQGTDVVQHQLD ALGYTLHGLNHPGV PVPSPAVNQYHLSQAAFGLPIDEDESSEG SDTSEPCEALDLSIHGRPCPQAPWVPVQEEGGQDATEVLDLSI HGRPRPRTPEWPVQEGGQNVGTGPETRRVVVSAVVHMCQDD EFPDLQDPPDEA	43
PolyA tail	100 nt	
EBNA1_trunc_001 (modified)		
SEQ ID NO: 178 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 73, and 3' UTR SEQ ID NO:3		178
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGCAGAAGACCCUUCUUUCACCCCGUGGGAGAAGCC GACUAAUUCGAGUACCACCAGGAGGGCGGUCCUGACGGC GAGCCCGACGUGCCUCCAGGCGCCAUCGAACAGGGCCCCG CUGACGAUCCUGGCGAGGGGCCUUCACAGGCCCCUCGCGG CCAGGGAGAUGGCGGAAGGCGGAAGAAGGGCGGCUGGUU UGGCAAGCAUAGGGGCCAGGGCGGCUCCAAUCCCAAGUU CGAGAAUAUCGCCGAGGGGCUCGCGGCUCUGCUGGCCCCG GUCGCACGUCGAACGUACCACUGACGAGGGGACGUGGGU GGCCGGCGUCUUUGUGUACGGAGGAUCCAAGACCUCCCU GUACAACCUGAGAAGGGGACCCGCCCUUGCCAUCCCUACAG UGCAGACUCACGCCCCUGAGCAGGCUCUCCCUUUGGGAUG GCUCCUGGGCCAGGCCCGCAGCCCGGGCCCCUCAGGGAAA	73

	GCAUCGUGUGUUACUUUAUGGUGUUUCUGCAGACACACA UCUUUGCAGAAGUUCUGAAAGAUGCAAUCAAGGAUCUGG UGAUGACCAAGCCUGCACCUACGUGCAAUAUCAGGGUGA CAGUAUGCUCCUUCGACGACGGUGUGGACCUCGCCGCCUG GUUCCACCCAUUGGUCGAGGGUGCCGCCGCCGAGGGAGA CGAUGGCGACGACGGUGAUGAGGGUGGAGACGGAGAUGA AGGCGAGGAGGGGGCAGGAG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADD PGE GPSTGPRGQGDGRRKKGWFGKHRGQGSNPKFENIA EGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRG TALAIPQCRLTPLSRLPFGMAPGPGPQGPLRESIVCYFMVFLQ THIFAEVLKDAIKDLVMTKPAPTCNIRVTVC SFDDGVDLPPWF PPMVEGAAAEGDDGDDGDEGGDGDEGEEGQE	10
PolyA tail	100 nt	
EBV LMP1_DX_(modified)_DX		
SEQ ID NO: 179 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 74, and 3' UTR SEQ ID NO:3		179
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAACACGACCUUGAGAGGGGCCACCGGGCCCGCGA CGGCCACCUCGAGGACCUCUCCUUCUCCCUAGGCC UUGCUCUCCUUCUCCUCCUUCUUGGCGCUACUGUUUUGGC UGUACAUCGUUAUGAGUGACUGGACUGGAGGAGCCCUCC UUGUCCUCUAUUCUUUGCUCUCAUGCUUAUAAUUAUAA UUUUGAUCAUUCUUUAUCUUCAGAAGAGACCUUCUCUGUC CACUUGGAGCCCUUUGUAUACUCCUACUGAUGAUCACCC UCCUGCUCAUUCGUCUCUGGAAUUGCAGGACAGGCAU UGUCCUUGGAAUUGUGCUGUUCAUUCUGGGUGCUUAC UUGUCUUAGGUAUCUGGAUCUACUUAUUGGAGAUGCUCU GGCGACUUGGUGCCACCAUCUGGCAGCUUUUGGCCUUCU UCCUAGCCUUCUCCUAGACCUCAUCCUGCUCAUUAUUGC UCUCUAUCUACAACAGAACUGGUGGACUCUAUUGGUUGA UCUCCUUGGCUCCUCCUGUUUCUGGCGAUUUUAUCUG GAUGUAUUACCAUGGACAACGACACAGUGAUGAACACCA CCACGAUGACUCCUCCCGCACCCUCAACAAGCUACCGAU GAUUCUGGCCAUGAAUCUGACUCUAACUCCAACGAGGGC AGACACCACCUGCUCGUGAGUGGAGCCGGCGACGGACCA CCACUCUGCUCUCAGAACCUAGGCGCACCUGGAGGUGGU CCUGACAAUGGCCACAGGACCCUGACAACACGGAUGAU AAUGGCCACAGGACCCUGAUAAACACUGAUGACAAUGGC CCACAUGACCCGUGCCUCAAGACCCAGACAAUACUGAUG ACAAUGGCCACAGGACCCUGACAACACUGAUGACAAUG GCCCCGACGACCCGUUACCUCUAGCCCUAGCGACUCUGC UGGAAAUGAUGGAGGCCCUCCACAAUUGACGGAAGAGGU UGAGAACAAAGGAGGUGACCAGGGGCCCGCCUUGAUGAC AGACGGAGGCGGCGGUCAUAGUCAUGAUUCCGGCCAUGG CGGCGGUGAUCCACACCUUCCUACGCUGCUGUUGGGUUC UUCUGGUUCCGGUGGAGAUGAUGACGACCCGCACGGCCC AGUUCAGCUAAGCUACUAUGAC	74
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3

Corresponding amino acid sequence	MEHDLERGPGRPRRPPRGPPPLSSSLGLALLLLLLLALLFWLYIV MSDWTGGALLVLYSFALMLIIILIIIFIRRDLLCPLGALCILLML ITLLLIALLWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRL GATIWQLLAFFLAFFLDLILLIIALYLQQNWWTLLVDLLWLLL FLAILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSN SNEGRHLLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTD DNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTDDNG PHDPLPHSPSDSAGNDGGPPQLTEEVENKGGDQGPPLMTDGG GGSHDSGHGGGDPHLP TLLLGSSSGGDDDDPHGPVQLSYY D	16
PolyA tail	100 nt	
EBV LMP2		
SEQ ID NO: 180 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 75, and 3' UTR SEQ ID NO:3		180
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGGUGCCCUAGAAAUGGUGCCAAUGGGCGCGGGUCCU CCUAGCCCCGGCGGGGAUCCGGAUGGGUACGAUGGCGGA AACAAUCUCCAAUAUCCAUCUGCUUCUGGCUCUUCUGGG AACACGCCACCCACCGAACGAUGAGGAACGUGAAUCU AAUGAAGAGCCACCACCGCCUUAUGAGGACCCAUAUUGG GGCAAUGGCGACCGUCACUCGGACUAUCAACCACUAGGA ACCCAAGAUCAAAGUCUGUACUUGGGAUUGCAACACGAC GGGAAUGACGGGCUCCCUCCACCUCUCCUACUCUCCACGGG AUGACUCAUCUCAACACAUAUACGAAGAAGCGGGCAGAG GAAGUAUGAAUCCAGUAUGCCUGCCUGUAAUUGUUGCGC CCUACCUCUUUUGGCGUGGCGGCUAUUGCCGCCUCGUGUU UCACGGCCUCAGUUAGUACCGUUGUGACCGCCACCGGCU UGGCCUCUCACUUCUACUCUUGGCAGCAGUGGCCAGCUC AUUGCCGCUGCACAAAGGAAACUGCUGACACCGGUGAC AGUGCUUACUGCGGUUGUCACUUUCUUUGCAAUUUGCCU ACAUGGAGGAUUGAGGACCCACCUUUUAAUUCUCUUCU GUUUGCAUUGCUGGCCGCAGCUGGCCGACUACAAGGCAU UUACGUUCUGGUGAUGCUUGUGCUCCUGAUACUAGCGUA CAGAAGGAGAUGGCGCCGUUUGACUGUUUGUGGCGCAU CAUGUUCUUGGCAUGUGUACUUGUCCUCAUCGUCGACGC UGUUUUGCAGCUGAGUCCCCUCCUUGGAGCUGUAAACUGU GGUUUCCAUGACGCUGCUGCUACUGGCUUUCGUCCUCUG GCUCUCUUCGCCAGGUGGCCUAGGUACUCUUGGUGCAGC CCUUUUAACAUUGGCAGCAGCUCUGGCACUGCUAGCGUC ACUGAUUUUGGCACACUUAACUUGACUACAAUGUCCU UCUCAUGCUCCUAGGACACUUGUGGUUCUCCUGAUUUG CUCUUCGUGCUCUUCUUGUCCACUGAGCAAGAUCUUCU GGCACGACUGUCCUUAUUGCUCUCGCACUCUUGUUGCU AGCCUCCGCGCUAAUCGCUUGGUGGCAGUAUUUUGCAAAC AAACUUCAAGAGUUUAAGCAGCACUGAAUUUAUACCCAA UUUGUUCUGCAUGUUUAUACUGAUUGUCGCGUGGCAUACU CUUCAUUCUUGCUAUCCUGACCGAAUGGGGCAGUGGAAA UAGAACAUACGGUCCAGUCUUUAUGUGCCUCGGUGGCCU GCUCACCAUGGUAGCCGGCGCUGUGUGGCUGACGGUGAU GUCUAAACACGCUUUUGUCUGCCUGGAUUCUUAACAGCAGG AUUCCUGAUUUUCCUCAUUGGCUUUGCCUCUUUGGGGU CAUUAAGAUGCUGCCGCUACUGCUGCUACUACUGCCUAC ACUGGAAAGUGAGGAGCGCCACCGACCCCAUAUCGCAA CACUGUA	75
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC	3

	CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWGNDRHSDYQPLGTQDQSL YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTAVVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRLTVCGGIMFLACVL VLIVDAVLQLSPLLGAFTVVSMTLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTNLNLTMTFLLMLLWTLVLLICS SCSSCPLSKILLARLFLYALALLLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLLIVAGILFILAILTEWGSGRNTYGPVFMCLGG LLTMVAGAVWLTVMSNTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	22
PolyA tail	100 nt	
EBV LMP2		
SEQ ID NO: 181 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 76, and 3' UTR SEQ ID NO:3		181
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGGGUCCCUAGAAAUGGUGCCAAUGGGCGCGGGUCCU CCUAGCCCCGGCGGGGAUCCGGAUGGGUACGAUGGCGGA AACACUCCCAUAUCCAUCUGCUUCUGGCUCUUCUGGG AACACGCCACCCACCGAACGAUGAGGAACGUGAAUCU AAUGAAGAGCCACCACCGCCUUAUGAGGACCCAUAUUGG GGCAAUGGCGACCGUCACUCGGACUAUCAACCACUAGGA ACCCAAGAUCAAAGUCUGUACUUGGGAUUGCAACACGAC GGGAAUGACGGGCUCCCUCCACCUCUCCUACUCUCCACGGG AUGACUCAUCUCAACACAUAUACGAAGAAGCGGGCAGAG GAAGUAUGAAUCCAGUAUGCCUGCCUGUAAUUGUUGCGC CCUACCUCUUUUGGCUGGCGGCUAUUGCCGCCUCGUGUU UCACGGCCUCAGUUAGUACCGUUGUGACCGCCACCGGCU UGGCCCUCUCACUUCUACUCUUGGCAGCAGUGGCCAGCUC AUAUGCCGCUGCACAAAGGAAACUGCUGACACCGGUGAC AGUGCUUACUGCGGUUGUCACUUCUUGCAAUUGCCU ACAUGGAGGAUUGAGGACCCACCUUUUAAUUCUCUUCU GUUUGCAUUGCUGGCCGCGAGCUGGCGGACUACAAGGCAU UUACGUUCUGGUGAUGCUUGUGCUCCUGAUACUAGCGUA CAGAAGGAGAUGGCGCCGUUUGACUGUUUGUGGCGGCAU CAUGUUCUUGGCAUGUGUACUUGUCCUCAUCGUCGACGC UGUUUUGCAGCUGAGUCCCCUCCUUGGAGCUGUAAACUGU GGUUUCCAUGACGCUGCUGCUACUGGCUUUCGUCCUCUG GCUCUCUUCGCCAGGUGGCCUAGGUACUCUUGGUGCAGC CCUUUUAACAUUGGCAGCAGCUCUGGCACUGCUAGCGUC ACUGAUUUUGGACACACUUAACUUGACUACAAUGUUCU UCUCAUGCUCCUAGGACACUUGUGGUUCUCCUGAUUUG CUCUUCGUGCUCUUCUUGUCCACUGAGCAAGAUCUUCU GGCACGACUGUCCUUAUUGCUCUCGCACUCUUGUUGCU AGCCUCCGCGCUAAUCGUGGUGGCAGUAUUUUGCAAAC AAACUUCAAGAGUUUAAGCAGCACUGAAUUUAUACCCAA UUUGUUCUGCAUGUUAUACUGAUUGUCGCGUGGCAUACU CUUCAUUCUUGCUAUCCUGACCGAAUGGGGCAGUGGAAA UAGAACAUACGGUCCAGUCUUUAUGUGCCUCGGUGGCCU GCUCACCAUGGUAGCCGGCGCUGUGUGGCUGACGGUGAU GUCUAAACGCUUUUGUCUGCCUGGAUUCUUAACAGCAGG AUUCCUGAUUUUCCUACUUGGCUUUGCCCUUUUGGGGU CAUAGAUGCUGCCGCUACUGCUGCUACUACUGCCUAC	76

	ACUGGAAAGUGAGGAGCGCCACCGACCCCAUAUCGCAA CACUGUA	
3' UTR	UGAUAUAAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNT PTPPNDEERESNEEPPPPYEDPYWGNGDRHSDYQPLGTQDQSL YLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGSMPVCLP VIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVAS SYAAAQRKLLTPVTVLTAVVTFFAICLTWRIEDPPFNSLLFALL AAAGGLQGIYVLVMLVLLILAYRRRWRRRLTVCGGIMFLACVL VLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTL GAALLTLAAALALLASLILGTNLNLTMMFLMLLWTLVLLICS SCSSCPLSKILLARFLYALALLLLASALIAGGSILQTNFKSLSS TEFIPNLFCMLLIVAGILFILAILTEWGSGNRITYGPVFMCLGG LLTMVAGAVWLTVMSTLLSAWILTAGFLIFLIGFALFGVIRC CRYCCYYCLTLESEERPPTPYRNTV	22
PolyA tail	100 nt	
EBV gp350 _003 (modified)		
SEQ ID NO: 182 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 77, and 3' UTR SEQ ID NO:3		182
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAAGCCGCUCUUCUGGUCUGCCAGUAUACAAUCCAG UCGCUGAUUCAUCUCACCGGCGAGGAUCCAGGUUUCUUU AACGUGGAGAUUCCAGAAUUCCCUUUCUAUCCAACUUGU AACGUGUGUACUGCCGACGUUAACGUUACUAUUAACUUU GACGUGGGCGGAAAGAAGCACCAGCUGGAUCUUGAUUUC GGCCAGCUAACACCUCUAUACCAAGGCCGUCUACCAACCAC GCGGGGCAUUGGCGGUUCUGAGAAUGCUACAAACCUGU UCCUUUUGGAACUCCUCGGAGCAGGGGAACUGGCACUUA CAAUGAGGAGUAAGAAGCUGCCCAUCAACGUCACCACGG GUGAAGAACAGCAGGUGUCCUGGAGUCCGUUGAUGUGU AUUCCAGGACGUUUUCGGGACAAUGUGGUGUCAUACUG CCGAAUGCAGAAUCCGGUGUAUCUAUCCUGAGACCAGG UGCCCUAUAAUAAAUGGGAUAACUGUAAUUCGACAAACA UACUGCCGUAGUGCGUGCCCAGGGUCUGGAUGUAACUU UGCCUCUCUCCCUUCCACUUCUGCCCAGGACUCCAUUU CUCAGUGAAGACCGAAAUGCUUGGGAACGAGAUUCGACAU CGAGUGUAUCAUGGAGGAUGGGGAGAUCAUGCAGGUGUU GCCUGGUGACAAUAGUUUAAUUAACAUGUUCGGGCUA UGAAUCACAUGUCCAAGCGGAGGUAUUCUCACAAGUAC AUCUCCCGUAGCCACGCCGAUUCGGGAACCGGAUACGCC UAUUCACUUCGGCUGACUCCUCGGCCAGUGUCACGAUUC CUGGGCAUAACUCAAUUCUGUACGUCUUUUACAGCGGC AACGGCCCAAAGGCCAGUGGAGGCGAUUACUGUAUCCAG UCUAACAUCGAUUUUUCAGAUAGAUUCCAGCAAGCCAA GACAUGCCAACUAAUACUACAGACAUUACAUACGUCGGU GAUAAACGCCACUUAUUCAGUCCCUAUGGUCACAUCGAG GACGCGAACUCACCCAAUGUUACCGUUAACCGCAUUCUGG GCAUGGCCCAAUAUACGGAACAGACUUCAAAUGUAAG UGGACCCUGACCAGUGGCACCCCUUCUGGCUGCGAGAAU AUAAGCGGGGCAUUUGCUAGCAACAGAACAUUCGAUAAU ACUGUGUCUGGCCUGGGGACCGCGCCCAAGACACUCAU AUAACGCGAACAGCUACGAACGCUACCAACAACACACAU AAAGUGAUUUUCAGCAAGGCUCCAGAAUCAACUACAACC	77

	AGUCCGACCCUUAUACCACAGGCUUCGCAGACCCGAACA CAACGACGGGACUGCCCUCCUCAACGCAUGUGCCGACUAA UCUGACUGCUCCCGCAAGUACCGGCCCAACAGUCUCCACA GCAGACGUCACCUCUCCGACUCCCGCCGGCACUACAUCUG GAGCCUCACCGGUGACUCCUAGUCCUUCGCCCUGGGACAA UGGGACCGAGUCUAAAGCCCCGGACAUGACGAGUUCUAC CUCACCAGUUACAACCCCAACACCUAAUGCCACAAGCCCU ACGCCAGCCGUGACCACCCCUACGCCCAUGCCACCAGCC CAACACCCGCUGUUAACAACGCCAACGCCAACGCUACUUC UCCAACGCUAGGAAAGACAUCACCCACCUCAGCUGUAACC ACGCCACACCAAACGCUACCGGGCCAACCGUUGGCGAAA CCUCGCCCCAGGCCAAUGCGACAAACCACACCCUUGGCGG GACUUCUCCACUCCUGUGGUGACUUCACAACCGAAGAA CGCGACGUCGGCCGUUACGACCGGGCAGCACAAUAUACC UCGUCCUCCACGUCGUCCAUGUCCUUGCGGCCUUCAGUA ACCCAGAGACACUGUCUCCUAGUACCAGUGACAACAGCA CCUCUCACAUGCCAUUACUGACUUCGCCCCACCCAACCGG CGGAGAGAACAUCACUCAGGUGACGCCCCGCAUCUAAUUC UACCCACCACGUGAGCACUAGCAGCCCCGGCACCAAGACCA GGGACCACCUCUCCAGGCUAGCGGCCCGGGCAACUCCUCCA CUAGCACGAAACCAGGAGAGGUGAACGUGACCAAGGGCA CACCGCCACAGAAUGCAACUCCCCACAGGCGCCCUCCGG CCAGAAGACUGCUGUACCUACGGUCACUAGCACUGGCGG AAAGGCGAAUUAACACCGGUGGUAAGCAUACCACCGG ACACGGCGCUCGGACUAGCACAGAGCCAACCACUGAUUA CGGAGGUGACUAAACGACCCCGAGGCCAGGUACAACGC AACCACCUAUCUCCACCAUCCACAUCUCCAAGCUCAGG CCUCGUUGGACUUAUACCUCUCCCGCCUGUGACUACAGCGC AGGCCACAGUGCCAGUGCCUCCAACGUCACAGCCGCGGUU UAGCAAUCUCUCCAUGCUGGUCUGCAGUGGGCAUCUCU GGCAGUCCUGACACUGCUUCUUAUUGCUCGUGAUGGCCGA UUGUGCGUUUAGACGCAACCUUUAACAUCCACACAUA UACAACUCCACCCUUGAUGACGCAGAGACUUAUGUG	
3' UTR	UGAUAUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPNTTDDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNTTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFA DPNTTGLPSSTHVPTNLTA PASTGPTVSTADVTS PTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKA NSTTGGKHHTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETYV	78
PolyA tail	100 nt	
EBV gH (BXL F2)_RX		

SEQ ID NO: 183 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 79, and 3' UTR SEQ ID NO:3		183
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGCAGUUGUUGUGCGUGUUCUGCCUCGUGUACUCUGG GAGGUGGGCGCCGCCAGCCUUAAGCGAGGUGAAGCUCCAC UUGGACAUCGAGGGGCCACGCCAGCCACUACACCAUCCCCU GGACCGAGCUCAUGGCCAAGGUGCCCGGCCUAGCCCCGA GGCCUGUGGCGGGAGGCCAACGUGACCGAGGACCUGGC CAGCAUGCUGAACCAGGUACAAGCUGAUCUACAAGACCAG CGGCACCCUGGGCAUCGCCCUGGCCGAGCCCGUGGACAUC CCCGCCGUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGC AAGGUGCACCCCGGCGUGAUCAGCGGCCUGAACAGCCCCG CCUGUAUGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCU ACUACAUCGGCACCAUGCUGCCCAACACCCGGCCCCACAG CUACGUGUUCUACCAGCUGCGGUGCCACCUGAGCUACGU UGCCCUGAGCAUCAACGGCGACAAGUUCAGUACACCGG CGCCAUGACCAGCAAGUUCUGAUGGGCACCUCACAAGCG GGUCACCGAGAAGGGCGACGAGCACGUGCUGUCACUGGU GUUCGGCAAGACCAAGGACCUGCCCCGACCUGCGGGGCCCC UUCAGCUACCCUAGUUUGACCAGCGCCAGAGCGGGCGAC UACAGCUUGGUGAUCGUGACCACCUUCGUGCACUACGCC AACUCCACAACUACUUCGUGCCCAACCUGAAGGACAUG UUCAGCCGGGCGGUGACCAUGACUGCCGCUUCUACGCCC GGUACGUGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGG GCGGCUGCCGGGAGCCCGAGCUGGACACCGAAACACUGA CCACCAUGUUCGAGGUGAGCGUGGCCUUCUUAAGGUGG GUCACGCGGUGGGCGAAACCGGCAACGGCUGCGUGGACU UACGCUGGCUGGCCAAGAGCUUCUUCGAGCUGACCGUGC UGAAGGAUAUCAUCGGCAUCUGCUACGGCGCCACCGUGA AGGGCAUGCAGAGCUACGGCCUGGAGCGGCUGGCCGCCA UGCUUAUGGCAACAGUGAAGAUGGAGGAGCUGGGACACC UGACAACAGAGAAGCAGGAGUACGCCUGAGACUGGCCA CAGUGGGCUACCCAAAGGCCGGCGUGUACAGUGGACUGA UCGGCGGCGCAACCAGCGUGCUGCUAUCCGCUUACAACCG GCACCCGCGUUCAGCCCCUGCACACCGUGAUGCGGGAA ACCUGUUCUACUGGAAGCCACGUCGUGCUGCGGGAGCUG AGGCUGAACGUAACCACCCAGGGCCCUAAUCUGGCCCUG UAUCAGCUCCUCAGUACCGCCCUGUGCAGCGCCCUUGAGA UCGGCGAGGUGCUCAGAGGCCUGGCCCUCCGUACCGAGA GCGGCCUCUUCAGCCCAUGCUACUUAAGCCUGCGGUUCG ACCUGACCCGGGACAAGUUGCUGAGCAUGGCCCCGCAGG AGGCCACACUGGACCAGGCAGCUGUAUCCAACGCCGUGG ACGGCUUCCUGGGCAGACUGUCCUGGAACGGGAGGACC GGGACGCCUGGCACCUGCCUGCCUACAAGUGUGUGGAUC GGCUGGACAAGGUGCUGAUGAUAUCCCUUGAUUAAUG UCACCUUCAUCAUCAGCAGCGACCGGGAGGUGCGGGGAU CCGCCCUCUACGAGGCCAGCACCACCUAUCUGAGCAGCAG CCUGUUCUGUCUCCUGUGAUGAUGAACAAGUGCAGCCA GGGCGCCGUGGCCGGCGAGCCCCGGCAGAUCCCCAAGAUC CAGAACUUCACCCGGACCCAGAAGUCUUGCAUCUUCUGC GGCUUCGCCCUCUUGUCCUACGACGAGAAGGAGGGGCUUG GAGACUACAACCUACAUCACCAGCCAGGAGGUGCAGAAC AGCAUCCUGUCAUCUAAUUAUCUUCGACUUCGACAACCUG CACGUUCAUUAACCGUCCUACACCAACGGUACCGUCA UGGAAAUCGCCGGACUGUACGAGGAGCGGGCCCAUGUUG UGCUGGCCAUCAUCCUGUACUUAUCGCUUUCGCACUUG GCAUCUUCUGGUGCACAAGAUCGUGAUGUUCUUCUG	79

3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MQLLCVFLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTE LMAKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGLGI ALAEPVDIPAVSEGSMQVDASKVHPGVISGLNSPACMLSAPLE KQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFQYT GAMTSKFLMGTYKRVTEKGDEHVLVSLVFGKTKDLPLDRGPF YPSLTSAQSGDYSLVIVTTFVHYANFNHYFVPNLKDMFSRAV TMTAASYARYVLQKLVLEMKGGCREPELDTETLTMTFEVS VAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIGICYG ATVKGMQSYGLERLAAMLATVKMEELGHLTTEKQEYALR LATVGYPKAGVYSGLIGGATSVLLSAYNRHPLFQPLHTVMRE TLFIGSHVVLRELRLNVTQGPNLALYQLLSTALCSALEIGEVL RGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAA VSNVVDGFLGRLSLEREDRDWHLPAYKCVDRDLKVLMIPL INVTFISSDREVRGSALYEASTTYLSSSLFLSPVIMNKCSQGAV AGEPRQIPKIQNFTRTQKSCIFCGFALLSYDEKEGLETTTYITSQ EVQNSILSSNYFDFDNLHVHYLLLTNGTVMEIAGLYEERAH VVLAILYFIAFALGIFLVHKIVMFFL	38
PolyA tail	100 nt	
EBV gL (B95-8)		
SEQ ID NO: 184 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 80, and 3' UTR SEQ ID NO:3		184
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUUCUGGCCAUCUGCCUGGUG ACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAACAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUAUCAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCGGCCACCUGAGA GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUAC GCCUGGCACAGAGGCGGC	80
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MRAVGVFLAICLVITFVLPTWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFVSVDLFGANLNR YAWHRGG	36
PolyA tail	100 nt	
EBV gp350 _001 (modified)		
SEQ ID NO: 185 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 81, and 3' UTR SEQ ID NO:3		185
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1

ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUUCCCUUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGUAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGCCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC UCUGUCAAGACCGAGAUGCUCGGGAAUGAGAUCCGAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAAUAAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAA GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCUGAUUAGACUUCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGACUACCGGACAGCACAAACUACCA AUCCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAAACAACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCAGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUUAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCACCCGUGACGACUGCCCA AGCGACGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC	81

	UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUUGCUGUUCUGACCCUCCUCCUGCUGCUGAUGGCCGAUUGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUACACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRFTDITVSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTSTPTLNTTGAFADPNTTGLPSSSTHVPTNLTAPASTGPTVSTADVSTPTPAGTTSGASPVTPSPSPWDNGTESKAPDMSTSTSPVTTPTPNATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLTSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKANSTTGKKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPSTSSKLRPRWFTTSPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHYTTTPPYDDAETYV	28
PolyA tail	100 nt	
LMP1 del 1-44_RX		
SEQ ID NO: 186 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 82, and 3' UTR SEQ ID NO:3		186
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGUGACUGGACAGGAGGAGCCCUCCUUGUCCUCUAU UCCUUUGCUCUCAUGCUUAUAAUUAUCAUCCUGAUAAUC UUAUUCUUCAGACGGGACCUUCUCUGUCCACUUGGAGCC CUUUGUAUACUCCUAUUGAUGAUCACCCUCCUCCUCAUC GCUCUCUGGAAUUGCACGGACAGGCAUUGUCCUUGGA AUUGUGCUGUUAUCUUCGGGUGCUUACUUGUCUUAAGGU AUCUGGAUCUACUUAUUGGAGAUGCUCUGGCGACUUGGU GCCACCAUCUGGCAGCUUUUGGCCUUCUCCUAGCGUUC UCCUCGACCUCAUUCUACUCAUUAUUGCUCUCUAUCUA CAACAGAACUGGUGGACUCUAUUGGUUGAUCUCCUUGG CUCCUCCUGUUUCUGGCGAUUUUAAUCUGGAUGUAUUAC CAUGGACAACGACACAGUGAUGAACACCACCACGAUGAC UCCCUCGCGACCCUCAACAAGCUACCGAUGAUUCUGGCC AUGAAUCUGACUCUAACUCCAACGAGGGCAGACACCACC UGCUCGUGAGUGGAGCCGGCGACGGACCACCACUCUGCU CUCAGAACCUAGGCGCACCUGGAGGUGGUCCUGACAAUG GCCACAGGACCCUGACAACACGGAUGAUAAACGGUCCAC AAGACCCAGAUAAACACUGACGACAAUGGACCGCAUGACC CGCUGCCUCAGGAUCCUGAUAAACACAGACGACAACGGCCC ACAAGAUCCGGACAAUACCGACGAUAAACGGACCGCACGA CCCGUUACCUCAUAGCCCUAGCGACUCUGCUGGAAUUGA UGGAGGCCCUCCACAAUUGACGGAAGAGGUUGAGAACAA AGGAGGUGACCAGGGCCCGCCUUUGAUGACAGACGGAGG	82

	CGGCGGUCAUAGUCAUGAUUCCGGCCAUGGCGGAGGAGA UCCACACCUUCCUACGCUGCUGUUGGGUUCUUCUGGUUC CGGUGGAGAUGAUGACGACCCGCACGGCCCAGUUCAGCU AAGCUACUAUGAC	
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MSDWTGGALLVLYSFALMLIIIIILIFRRDLLCPLGALCILLM ITLLLIALLWNLHGQALFLGIVLFIFGCLLVLGIWIYLLLEMLWRL GATIWQLLAFFLAFFLDLILLIALLYLQQNWWTLLVDLLWLLL FLAILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSN SNEGRHLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTD DNGPQDPDNTDDNGPHDPLQDPDNTDDNGPQDPDNTDDNG PHDPLPHSPDSAGNDGGPPQLTEEVENKGGDQGPPLMTDGG GGSHDSGHGGGDPHLPTLLLGSSGSGGDDDDPHGPVQLSYY D	83
PolyA tail	100 nt	
EBV gH (BXL2)_RX		
SEQ ID NO: 187 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 84, and 3' UTR SEQ ID NO:3		187
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGCAGUUGUUGUGCGUGUUCUGCCUCGUGUACUCUGG GAGGUGGGCGCCGCCAGCCUUAGCGAGGUGAAGCUCCAC UUGGACAUCGAGGGGCCACGCCAGCCACUACACCAUCCCCU GGACCGAGCUC AUGGCCAAGGUGCCCGGCCUUAGCCCCGA GGCCCUUGUGCGGGAGGCCAACGUGACCGAGGACCUGGC CAGCAUGCUGAACCUGUACAAGCUGAUCUACAAGACCAG CGGCACCCUGGGCAUCGCCCUGGCCGAGCCCGUGGACAUC CCCGCCGUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGC AAGGUGCACCCCGCGUGAUCAGCGGCCUGAACAGCCCCG CCUGUAUGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCU ACUACAUCGGCACCAUGCUGCCCAACACCCGGCCCCACAG CUACGUGUUCUACCAGCUGCGGUGCCACCUGAGCUACGU UGCCCUAGCAUCAACGGCGACAAGUUCAGUACACCCGG CGCAUGACCAGCAAGUUCUGAUGGGCACCUACAAGCG GGUACCGAGAAGGGCGACGAGCACGUGCUGUCACUGGU GUUCGGCAAGACCAAGGACCUGCCCGACCUGCGGGGCCCC UUCAGCUACCCUAGUUUGACCAGCGCCAGAGCGGCGAC UACAGCUUGGUGAUCGUGACCACCUUCGUGCACUACGCC AACUCCACAACUACUUCGUGCCCAACCUGAAGGACAUG UUCAGCCGGGCGGUGACCAUGACUGCCGCUUCUACGCC GGUACGUGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGG GCGGCUGCCGGGAGCCCGAGCUGGACACCGAAACACUGA CCACCAUGUUCGAGGUGAGCGUGGCCUUCUUAAGGUGG GUCACGCGGUGGGCGAAACCGGCAACGGCUGCGUGGACU UACGCUGGCUGGCCAAGAGCUUCUUCGAGCUGACCGUGC UGAAGGAUAUCAUCGGCAUCUGCUACGGCGCCACCGUGA AGGGCAUGCAGAGCUACGGCCUGGAGCGGCUGGCCGCCA UGCUUAUGGCAACAGUGAAGAUGGAGGAGCUGGGACACC UGACAACAGAGAAGCAGGAGUACGCCUGAGACUGGCCA CAGUGGGCUACCCAAAGGCCGGCGUGUACAGUGGACUGA UCGGCGGCGCAACCAGCGUGCUGCUAUCCGCUUACAACCG GCACCCGCUUUCAGCCCCUGCACACCGUGAUGCGGGAA ACCCUGUUCAGGAAAGCCACGUCGUGCUGCGGGAGCUG AGGCUAAGCUAACCAACCCAGGGCCCUAAUCUGGCCCU	84

	UAUCAGCUCCUCAGUACCGCCUGUGCAGCGCCCUUGAGA UCGGCGAGGUGCUCAGAGGCCUGGCCUCGGUACCGAGA GCGGCCUCUUCAGCCCAUGCUACUUAAGCCUGCGGUUCG ACCUGACCCGGGACAAGUUGCUGAGCAUGGCCCCGCAGG AGGCCACACUGGACCAGGCAGCUGUAUCCAACGCCGUGG ACGGCUUCCUGGGCAGACUGUCCUGGAACGGGAGGACC GGGACGCCUGGCACCUGCCUGCCUACAAGUGUGUGGAUC GGCUGGACAAGGUGCUGAUGAUCAUCCUCUGAUUAAUG UCACCUUCAUCAUCAGCAGCGACCGGGAGGUGCGGGGAU CCGCCCUCUACGAGGCCAGCACCACCUAUCUGAGCAGCAG CCUGUCCUGUCUCCUGUGAUGAUGAACAAGUGCAGCCA GGGCGCCGUGGCCGGCGAGCCCCGGCAGAUCCCCAAGAUC CAGAACUUCACCCGGACCCAGAAGUCUUGCAUCUUCUGC GGCUUCGCCCUIUUGUCCUACGACGAGAAGGAGGGCUUG GAGACUACAACCUACAUCACCAGCCAGGAGGUGCAGAAC AGCAUCCUGUCAUCUAAUUAUUCGACUUCGACAACCGUG CACGUUCAUUAACCGUCUCCUACACCACCAACGGUACCGUCA UGGAAAUCGCCGGACUGUACGAGGAGCGGGCCCAUGUUG UGCUGGCCAUCAUCCUGUACUUAUCGCUUUCGCACUUG GCAUCUCCUGGUGCACAAGAUCGUGAUGUUCUCCUG	
3' UTR	UGAUAUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MQLLCVFCLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTE LMAKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGLGI ALAEVPDIPAVSEGSMQVDASKVHPGVISGLNSPACMLSAPLE KQLFYIYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFYT GAMTSKFLMGTYKRVTEKGDEHVLVLVFGKTKDLPDLRGPFS YPSLTSAQSGDYSLVIVTTFVHYANFHNYPVNLKDMFSRAV TMTAASYARYVLQKLVLLEMKGCCREPELDTETLTMTFEVS VAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIIGICYG ATVKGMQSYGLERLAAMLATVKMEELGHLTTEKQEYALR LATVGYPKAGVYSGLIGGATSVLLSAYNRHPLFQPLHTVMRE TLFIGSHVVLRELRLNVTQGPNLALYQLLSTALCSALEIGEVL RGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAA VSNVDGFLGRSLEREDRDAWHLPAYKCVDRDLKVLMIPL INVTFISSDREVRGSALYEASTTYLSSSLFLSPVIMNKCSQGAV AGEPRQIPKIQNFTRTQKSCIFCGFALLSYDEKEGLETTTYITSQ EVQNSILSSNYFDFDNLHVHYLLLTNGTVMEIAGLYEERAH VVLAILLYFIAFALGIFLVHKIVMFFL	38
PolyA tail	100 nt	
EBV gL (B95-8)		
SEQ ID NO: 188 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 85, and 3' UTR SEQ ID NO:3		188
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUCCUGGCCAUCUGCCUGGUG ACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAUCAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUAUCAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCGGCCACCUGAGA GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC	85

	AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUACGCCUGGCACAGAGGCGGC	
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MRAVGVFLAICLVITIFVLPTWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFSVEDLFGANLNR YAWHRGG	36
PolyA tail	100 nt	
EBV gp42 (B95-8)_DX		
SEQ ID NO: 189 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 86, and 3' UTR SEQ ID NO:3		189
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGUGAGCUUCAAGCAGGUGAGAGUGCCCCUGUUCACC GCCAUCGCCCUGGUGAUCGUGCUGCUGGCCUACUUC UGCCCCCAGAGUGAGAGGCGGCGGCAGAGUGGCCGCCG CCGCCAUCACCUGGGUGCCCAAGCCCAACGUGGAGGUGU GGCCCGUGGACCCCCACCCCCCGUGAACUUAACAAGAC CGCCGAGCAGGAGUACGGCGACAAGGAGGUGAAGCUGCC CCACUGGACCCCCACCCUGCACACCUUCCAGGUGCCCCAG AACUACACCAAGGCCAACUGCACCUCUGCAACACCAGAG AGUACACCUUCAGCUACAAGGGCUGCUGCUUCUACUUA CCAAGAAGAAGCACACCUUGAACGGCUGCUUCCAGGCCU GCGCCGAGCUGUACCCUGCACCUCUUCUACGGCCCCAC CCCCACAUCCUGCCCUGGUGACCAGAAACCUGAACGCC AUCGAGAGCCUGUGGGUGGGCGUGUACAGAGUGGGCGAG GGCAACUGGACCAGCCUGGACGGCGGCACCUUCAAGGUG UACCAGAUUCUUCGGCAGCCACUGCACCUCUGAGCAAG UUCAGCACCGUGCCCGUGAGCCACCACGAGUGCAGCUUCC UGAAGCCCUGCCUGUGCGUGAGCCAGAGAAGCAACAGC	86
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVRRGGGRVAAAIT WVPKPNVEVWPVDPPPPVNFNKTAEQEYGDKEVKLPHWTPT LHTFQVPQNYTKANCTYCNTREYTFSYKGCCFYFTKKKHTW NGCFQACAELYPTCYFYGPTPDILPVVTRNLNAIESLWVG VYR VGEGNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPVSHHECSFL KPCLCVSQRSNS	34
PolyA tail	100 nt	
gp350 D123_LS_RX		
SEQ ID NO: 190 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 87, and 3' UTR SEQ ID NO:3		190
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct	AUGGACAGCAAGGGCAGCAGCCAGAAGGGAAGCAGGUUG UUAUUGCUUUUAGUGGUGAGCAACUACUCUUAACCCAG GGCGUGGUGGAGGCAGCACUCCUCGUCUGCCAGUAUACA	87

(excluding the stop codon)	A U C C A G U C G C U C A U U C A U U U G A C A G G C G A G G A C C C C G G C U U C U U U A A C G U G G A A A U C C C A G A G U U C C C U U U C U A U C C A A C C U G U A A C G U U U G C A C A G C C G A C G U G A A C G U G A C A A U C A A U U U C G A C G U G G G A G G A A A G A A G C A U C A G C U U G A U C U G G A U U U C G G C C A A C U G A C G C C A C A C A C C A A A G C G G U G U A C C A A C C A A G G G G U G C A U U U G G A G G G A G C G A G A A U G C U A C A A A U C U G U U C U U A C U G G A A C U G C U U G G U G C A G G A G A G C U G G C A C U A A C C A U G C G A A G C A A G A A G C U C C C C A U C A A C G U U A C C A C C G G G G A A G A A C A G C A A G U C A G C C U U G A A U C C G U G G A U G U G U A C U U U C A G G A U G U U U C G G C A C C A U G U G G U G U C A C C A C G C U G A G A U G C A G A A U C C C G U G U A U C U C A U A C C C G A G A C U G U A C C C U A C A U C A A G U G G G A U A A U U G C A A U U C A A C U A A U A U U A C G G C U G U G G U G A G G G C C C A G G G C U U G G A C G U G A C U C U G C C C U U A U C U C U A C C U A C U U C U G C C C A A G A C U C C A A U U U C U C U G U C A A G A C C G A G A U G C U C G G G A A U G A G A U C G A U A U C G A G U G C A U C A U G G A G G A C G G U G A G A U A A G C C A G G U U C U G C C C G G C G C A C A A C A A G U U C A A U A U C A C U U G U U C U G G C U A C G A G U C C C A U G U G C C U A G U G G U G G C A U A C U C A C A A G U A C U U C U C C C G U A G C C A C G C C C A U U C C C G G A A C C G G A U A C G C C U A C A G U C U G C G U C U G A C C C C A C G G C C U G U G U C C A G A U U C C U G G G U A A C A A U A G U A U C U U A U A C G U G U U U U A U A G C G G A A A C G G C C C U A A A G C G U C C G G A G G G G A C U A U U G U A U U C A G A G U A A U A U C G U U U U C U C U G A U G A G A U C C C U G C C A G U C A G G A C A U G C C G A C A A C A C A C U G A U A U U A C C U A C G G U G G G C G A C A A U G C C A C G U A U U C A G U G C C C A U G G U C A C G A G C G A G G A C G C C A A U U C A C C A A A U G U U A C U G U A A C A G C U U U C U G G G C C U G G C C A A A U A A C A C U G A G A C U G A C U U C A A A U G U A A G U G G A C U U U G A C C U C U G G A A C U C C G U C G G G U U G C G A G A A U A U C A G C G G G G C C U U U G C U U C C A A C A G G A C U U U C G A C A U C A C U G U C U C A G G G C U G G G G A C A G C A C C G A A G A C A U U A A U C A U A A C A C G G A C C G C C A C C A A C G C C A C G A C U A C A A C C C A U A A G G U G A U C U U U U C C A A G G C A C C U G G C A G C G G C A G C G C A G G C U C U G C A A G C G G C G G C G C C U C C A G C G G C U C C G G A G G U G C C A G C A U G C A G A U C U A C G A G G G C A A G C U G A C C G C C G A G G G C C U G A G G U U C G G C A U C G U G G C C A G C A G G U U C A A C C A C G C C C U G G U G G A C A G G C U G G U G G A A G G C G C C A U C G A C G C C A U C G U G A G G C A C G G C G G C A G G G A G G A G G A C A U C A C C C U G G U G C G G G U G C C C G G C A G C U G G G A G A U C C C C G U G G C C G C C G G C G A G C U G G C C A G G A A G G A A G A U A U U G A U G C A G U G A U C G C C A U C G G C G U G C U G A U C A G G G G C G C C A C C C C A C A C U U C G A C U A C A U C G C C A G C G A A G U G A G C A A G G G A C U G G C G G A C C U G A G C C U G G A G C U G A G G A A G C C C A U C A C C U U C G G C G U G A U C A C C G C C G A C A C C C U G G A G C A G G C C A U C G A G A G G G C C G G C A C C A A G C A C G G C A A C A A G G G A U G G G A G G C C G C C C U G A G C G C U A U C G A A A U G G C C A A C C U C U U C A A G A G C C U G A G G	
3' UTR	U G A U A A U A G G C U G G A G C C U C G G U G G C C A U G C U U C U U G C C C C U U G G G C C U C C C C C A G C C C C U C C U C C C U U C C U G C A C C C G U A C C C C C G U G G U C U U U G A A U A A A G U C U G A G U G G G C G G C	3
Corresponding amino acid sequence	M D S K G S S Q K G S R L L L L L V V S N L L L P Q G V V E A A L L V C Q Y T I Q S L I H L T G E D P G F F N V E I P E F P F Y P T C N V C T A D V N V T I N F D V G G K K H Q L D L D F G Q L T P H T K A V Y Q P R G A F G G S E N A T N L F L L E L L G A G E L A L T M R S K K L P I N V T T G E E Q Q V S L E S V D V Y F Q D V F G T M W C H H A E M Q N P V Y L I P E T V P Y I K W D N C N S T N I T A V V R A Q G L D V T L P L S L P T S A Q D S N F S V K T E M L G N E I D I E C I M E D G E I S Q V L P G D N K F N I T C S G Y E S H V P S G G I L T S T S P V A T P I P G T G Y A Y S L R L T P R P V S R F L G N N S I L Y V F Y S G N G P K A S G G D Y C I Q S N I V F S D E I P A S Q D M P T N T T D I T Y V G D N A T Y S V P M V T S E D A N S P N V T V T A F W A W P N N T E T D F K C K W T L T S G T P S G C E N I S G A F A S N R T F D I T V S G L G T A P K T L I I T R T A T N A T T T T H K V I F S K A P G S G S A G S A S G G A S S G S G G A S M	88

	QIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAIDAIVRHGGR EEDITLVRVPGSWEIPVAAGELARKEDIDAVIAIGVLIRGATPH FDYIASEVSKGLADLSLELRKPITFGVITADTLEQAIERAGTKH GNKGWEAALSAIEMANLFKSLR	
PolyA tail	100 nt	
gp350_D123_HBsAg_RX		
SEQ ID NO: 191 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 89, and 3' UTR SEQ ID NO:3		191
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACAGCAAGGGCAGCAGCCAGAAGGGCAGUAGGCUC CUUUUGCUACUUGUGGUGAGCAACCUCUUGUUACCCAG GGCGUGGUGGAGGCAGCACUCCUCGUCUGCCAGUAUACA AUCCAGUCGCUCAUUAUUUGACAGGCGAGGACCCCGGC UUCUUUAACGUGGAAAUCCAGAGUUCUUUUAUCCA ACCUGUAACGUUUGCACGGCAGACGUGAACGUGACAAUC AAUUUCGACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUG GAUUUCGGCCAACUGACGCCACACACCAAAGCGGUGUAC CAACCAAGGGGUGCAUUUGGAGGGAGCGAGAAUGCUACA AAUCUGUUCUACUGGAACUGCUUGGUGCAGGAGAGCUG GCACUAACCAUGCGAAGCAAGAAGCUCCCCAUCAACGUU ACCACCGGGGAAGAACAGCAAGUCAGCCUUGAAUCCGUG GAUGUGUACUUUCAGGAUGUUUUCGGCACCAUGUGGUGU CACCACGCUGAGAUGCAGAAUCCCGUGUAUCUCAUACCC GAGACUGUACCCUACAUCAAGUGGGGAUAAUUGCAAUUA ACUAAUAUUACGGCUGUAGUGAGGGCCCAGGGCUUGGAC GUGACUCUGCCCUUAUCUCUACCUACUUCUGCCCAAGACU CCAAUUUCUCUGUCAAGACCGAGAUUGCUCGGGAUAGAGA UCGAUAUCGAGUGCAUCAUGGAGGACGGUGAGAUAAAGCC AGGUUCUGCCCGGCGACAACAAGUUCAAUAUCACUUGUU CUGGCUACGAGUCCCAUGUGCCUAGUGGUGGCAUACUCA CAAGUACUUCUCCCGUAGCCACGCCCAUUCCCGGAACCGG AUACGCCUACAGUCUGCGUCUGACCCACGGCCUGUGUCC AGAUUCCUGGGUAACAUAAGUAUCUUAUACGUGUUUAU AGCGGAAACGGCCCUAAAGCGUCCGGAGGGGACUAUUGU AUUCAGAGUAAUAUCGUUUUCUCUGAUGAGAUUCCAGCC AGUCAGGACAUGCCGACAAACACAACUGAUAAUACCUAC GUGGGCGACAAUGCCACGUAAUUCAGUGCCCAUGGUCACG AGCGAGGACGCCAAUUCACCAAAUGUUACUGUAACAGCU UUCUGGGCCUGGCCAAAUAACACUGAGACUGACUUCAAA UGUAAGUGGACUUUGACCUCUGGAACUCCGUCGGGUUGC GAGAAUAUCAGCGGGGCCUUUGCUUCCAACAGGACUUUC GACAUCACUGUCUCAGGGCUGGGGACAGCACCGAAGACA UUAUAUCAUAACACGGACCGCCACCAACGCCACGACUACAA CCCAUAAGGUGAUCUUUCCAAGGCACCUGGCAGCGGCA GCGCUGGCUCCGCUAGCGGCGGCCCUUAGCGGAUCAG GAGGCGCAUCCAUGGAGAACAUUGCAUCUGGCCUGCUGG GACCUCUACUGGUGCUGCAGGCCGGAUUCUUCUGCUGA CCAAGAUCUGACCAUCCCUACAGAGCCUGGACAGCUGGU GGACCAGCCUGAACUUCUGGGCGGCACCCAGUGUGCCU GGGCCAGAACAGCCAGAGCCAGAUCCUCCACAGCCCC ACCUGCUGUCCGCCCAUCUGCCCCGGCUACCGUUGGAUGU GCCUGAGGAGGUUCAUCAUCUUCUGUGCAUACUCCUGU UGUGUCUAAUUUCCUGCUCGUUCUGCUCGACUACCAGG GCAUGCUGCCGGUGUGUCCUCUGAUCCCCGGCUCCUCCAC CACCAGCACCGGCCCUUGCAGGACCUGCACACACCAGCA CAAGGUACCAGCAUGUCCCCAGCUGUUGCUGUACCAAG	89

	CCCACCGACGGCAACUGCACCUGCAUCCCCAUCCCCAGCA GCUGGGCCUUCGCCAAGUACCUGUGGGAGUGGGCCAGCG UGAGGUUCAGCUGGCUGUCACUUCUUGCGCCAUCUGUGC AGUGGUUCGUGGGCCUGAGCCCUACUGUGUGGCUGUCGG UAAUCUGGAUGAUGUGGUUCUGGGGCCCCAGCCUGUACA ACAUCUGUCACCGUUC AUGCCUCUCCUACCGCUGUUCU CUGCCUGUGGGUGUACAUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLLLVSNLLLPQGVVEAALLVCQYTIQS LIHLTGEDPGFFNVEIPEFPFYPTCNVCTADVNVTFNFDVGGKK HQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLELLGAG ELALTMRSKKLPINVTTGEEQVVSLESVDVYFQDVFGTMWCH HAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNKF NITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSRLTPRPVSR FLGNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPT NTTDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNT ETDFKCKWTLTSGTPSGCENISGAFASNRTFDITVSGLTAPKT LIITRTATNATTTTHKVIFSKAPGSGSAGSASGGASSGSGGASM ENIASGLLGPLLVLQAGFFLLTKILTIPQSLDSWWTSLNFLGGT PVCLGQNSQSQISSHSPTCCPPICPGYRWMCLRRFIIFLCILLC LIFLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMF PSCCCTKPTDGNCTCIPISSWAFAYLWEWASVRFSWLSLLA PFVQWFVGLSPTVWLSVIWMMWFWGPSLYNILSPFMPLPLF FCLWVYI	90
PolyA tail	100 nt	
gp350 D123_HBcAg_heterotandem_RX		
SEQ ID NO: 192 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 91, and 3' UTR SEQ ID NO:3		192
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACAGCAAGGGCAGCAGCCAGAAGGGAUCCAGGCUA UUGUUACUAUUAGUGGUGAGCAACCUCCUCUUGCCCCAG GGCGUGGUGGACAUCGACCCCUACAAGGAGUUCGGCGCC ACCGUGGAGUUGUUAAGCUUCCUCCCCAGCGACUUCUUC CCCAGCGUGAGGGACCUGCUGGACACCGCCGCCGCCUGU ACAGGGAGGCCUUGGAGAGCCCCGAGCACUGCUCGCCUCA CCACACCGCCCUGAGGCAGGCCAUCCUGUGCUGGGGCGAG CUGAUGACCCUGGCCACCUGGGUGGGCAACAACCUGGAG GACCCCGCCAGCCGCGACCUCGUUGUGAACUACGUGAACA CCAACAUGGGCCUGAAGAUCAGGCAGCUGCUGUGGUUCC ACAUCAGCUGCCUGACCUUCGGCAGGGAGACAGUGCUGG AGUACCUGGUGAGCUUCGGCGUGUGGAUCAGGACUCCAC CCGCCUACAGGCCUCCCAACGCGCCAAUCCUGAGCACCCU GCCCCGAGACAACAGUGGUGGGCAGCGGCAGCGCAGGUUC CGCCAGCGGCGGCGCAUCCAGUGGCUCUGGAGGAGCUUC UGACAUUGACCCAUAUAAGGAUUCGGUGCUACAGUAGA GCUACUGUCUUUCUUGCCUAGUGAUUUCUCCCCGAGUGU AAGGGAUCUCCUAGAUACAGCCGCUGCUCUAUAUAGAGA GGCACUGGAAUUCUCCAGAGCACUGUUCUCCACACCAUACC GCUCUCCGGCAGGCAAUCCUGUGUUGGGGUGAACUUAUG ACACUGGCAACCUGGGUCGGUAACAACGGAUCAGGUGAG GCGGCUCUGCUGGUCUGCCAGUAUACAAUCCAGUCGCUC AUUCAUCUGACAGGCGAAGAUCAGGUUUCUUUAACGUG	91

	GAAAUCCAGAGUUCCCUUUCUAUCCAACCUGUAACGUU UGUACAGCUGACGUGAACGUGACAAUCAAUUCGACGUG GGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUCGGCCAA CUGACGCCACACACCAAAGCGGUGUACCAACCAAGGGGU GCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGUUCUUA CUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAACCAUG CGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGGGGAA GAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUACUUU CAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGCUGAG AUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGUACCC UACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAUACG GCUGUGGUGAGGGCCCAGGGCUUGGACGUGACUCUGCCC UUAUCUCUACCUACUUCUGCCCAAGACUCCAAUUCUCU GUCAAGACCGAGAUGCUCGGGAUGAGAUCGAUAUCGAG UGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUGCCC GGCGACAACAAGUUCAAUAUCACUUGUUCUGGCUACGAG UCCCAUGUGCCUUCUGGUGGCAUACUCACAAGUACUUCU CCCGUAGCCACGCCCAUUCUCCGGAACCGGAUAUGCGUAUA GUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCUGG GUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAACG GCCCUAAAGCGUCCGGAGGGGACUAAUGUAUUCAGAGUA AUUCGUUUUCUCUGAUGAAAUUCCUGCCAGUCAGGACA UGCCGACAAACACAACUGAUAAUACCUACGUGGGCGACA AUGCCACGUAAUCAGUGCCCAUGGUCACGAGCGAGGACG CCAAUUCACCAAAUGUUAACUGUAACAGCUUUCUGGGCCU GGCCAAUAACACUGAGACUGACUUCAAUUGAAGUGGA CUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAUCA GCGGGGCCUUGCUUCCAACAGGACUUCGACAUCACUG UCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAUAA CACGGACCGCCACCAACGCCACGACUACAACCCAUAAGGU GAUCUUUCCAAGGCACCUGGAUCCGGACUGGUGGUCAA CUAUGUGAAUACAAUAUGGGCCUCAAGAUUAGGCAGCU CCUAUGGUUCCAUAUUUCCUGCUUACUUCGGUAGGGA AACUGUCCUGGAUAUUCUGUAGCUUCGGAGUGUGGAU UCGGACUCCUCCUGCCUACAGACCACCUAACGCUCCAAU CUGUCAACUCUCCAGAGACGACUGUGGUCAGAAGGAGG GGCAGGAGCCCCAGACGGCGGACACCAAGCCCUCGCCGAA GAAGAAGCCAAAGCCCCGCGCGCCGGAGAUCUCAGUCCA GAGAGAGCCAGUGC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLLVVSNNLLPQGVVDIDPYKEFGATVE LLSFLPSDFFPSVRDLLDTAAALYREALSPEHCSPHHTALRQ AILCWGELMTLATWVGNNLEDPASRDLVVNYVNTNMGLKIR QLLWFHISCLTFGRETVLEYLVSGVWIRTPPAYRPPNAPILST LPETTVVSGSGSAGSASGGASSGSGGASDIDPYKEFGATVELLS FLPSDFFPSVRDLLDTAAALYREALSPEHCSPHHTALRQAILC WGELMTLATWVGNNNGSGEAALLVCQYTIQSLIHLTGEDPGFF NVEIPEFPFYPTCNVCTADVNTINFVVGKKHQLDLDFGQLT PHTKAVYQPRGAFGGSENATNLFLELLGAGELALTMRSKKL PINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPNVYLI PETVPYIKWDNCNSTNITAVVRAQGLDVTLP LSLPTS AQDSNF SVKTEMLGNEIDIECIMEDGEISQVLPDGNKFNITCSGYESHVP SGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNSILYVFY SGNGPKASGGDYCIQSNIVFSDEIPASQDMPTNTTDITYVGDN ATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLT SGTPSGCENISGAFASNRTFDITVSGLGTA PKTLIITRTATNATT TTHKVIFSKAPGSGLVVNYVNTNMGLKIRQLLWFHISCLTFGR	92

	ETVLEYLVSFVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSP RRRTSPRRRRSQSPRRRRSQSRESQC	
PolyA tail	100 nt	
EBV gp350 Ecto_RX		
SEQ ID NO: 193 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 93, and 3' UTR SEQ ID NO:3		193
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACAGCAAGGGCAGCAGCCAGAAGGGUAGCAGGCUA CUCUUGCUCCUAGUGGUGAGCAACUUGCUUCUUCUCCAG GGCGUGGUGGAGGCAGCAUUGCUUGUCUGCCAGUAUACA AUCCAGUCGCUCAUUAUCUAAACAGGCGAGGACCCCGGC UUCUUUAACGUGGAAAUCCAGAGUUCUUUUAUCCA ACCUGUAACGUUUGCAGUGCCGACGUGAACGUGACAAUC AAUUUCGACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUG GAUUUCGGCCAACUGACGCCACACACCAAAGCGGUGUAC CAACCAAGGGGUGCAUUUGGAGGGAGCGAGAAUGCUACA AAUCUGUUCUACUGGAACUGCUUGGUGCAGGAGAGCUG GCACUAACCAUGCGAAGCAAGAAGCUCCCCAUCAACGUU ACCACCGGGGAAGAACAGCAAGUCAGCCUUGAAUCCGUG GAUGUGUACUUUCAGGAUGUUUUCGGCACCAUGUGGUGU CACCACGCUGAGAUGCAGAAUCCCGUGUAUCUCAUACCC GAGACUGUACCCUACAUCAAGUGGGGAUAAUUGCAAUUA ACUAAUUAUACGGCUGUGGUGAGGGCCCAGGGCUUGGAC GUGACUCUGCCCUUAUCUCUACCUACUUCUGCCCAAGACU CCAAUUUCUCUGUCAAGACCGAGAUGCUCGGGAUUGAGA UCGAUAUCGAGUGCAUCAUGGAGGACGGUGAGAUAAAGCC AGGUUCUGCCCCGGCGACAACAAGUUCAAUAUCACUUGUU CUGGCUACGAGUCCCAUGUGCCUUCGGCGGGCAUACUCAC AAGUACUUCUCCCGUAGCCACGCCCAUUCGGGAACCGGA UACGCCUACAGUCUGCGUCUGACCCACGGCCUGUGUCCA GAUUCUGGGUAACAAUAGUAUCUUAUACGUGUUUUAUA GCGGAAACGGCCCUAAAGCGUCCGGAGGGGACUAUUGUA UUCAGAGUAAUAUCGUUUUCUGAUGAGAUUCCAGCCA GUCAGGACAUGCCGACAAACACAACUGAUAAUACCUACG UGGGCGACAAUGCCACGUAUUCAGUGCCCAUGGUCACGA GCGAGGACGCCAAUUCACCAAUGUUAUCUGUAACAGCUU UCUGGGCCUGGCCAAAUAAACACUGAGACUGACUUCAAA GUAAGUGGACUUUGACCUCUGGAACUCCGUCGGGUUGCG AGAAUAUCAGCGGGGCCUUUGCUUCCAACAGGACUUUCG ACAUCACUGUCUCAGGGCUGGGGACAGCACCGAAGACA UAAUCAUAACACGGACCGCCACCAACGCCACGACUACAAC CCAUAAGGUGAUCUUUCCAAGGCACCUAGUCCACCAC UACCUCCCCGACUCUUAACACUACGGGCUUCGCUGAUCCC AAUACUACUACUGGGUUGCCUAGCUCGACACAUGUGCCG ACGAACCUGACUGCCCCUGCAUCGACCGGGCCCACAGUUU CGACCGCCGAUGUGACAAGCCUACGCCCCGAGGUACAAC CUCAGGCGCCAGCCAGUGACCCCUUCCCCAAGCCCCUGG GACAACGGAACGGAGUCCAAGGCUCUGAUUAUGACUUC UCUACCGCCCCGUGACUACACCCACUCCCAACGCAACUA GCCCAACCCAGCUGUGACGACGCCACCCGAACGCGAC AUCUCCACACCGUCUGUGACAACCCCUACCCCUAACGCC ACUAGCCCUACCCUAGGUAAGACCAGUCCGACUAGCGCCG UUACUACACCGACCCCUAAUGCAACCGGCCCGACUGUCGG CGAGACUCCCCGCAAGCCAAUGCGACAAAUCACACAUU GGGCGGGACCUCUCCUACACCAGUCGUUACAUCUCAGCCU AAGAACGCUACCUCCGCUGUCACUACCGGCCAGCACAACA	93

	UCACAAGCUCUAAGCACGAGUUCUCAUGAGCUUGCGGCCGA GCUCAAUCCCCGAGACACUAUCACCAUCCACAUCAGACAA CAGUACUUCACACAUGCCACUCUUGACGAGCGCUCACCCC ACCGGCGGCGGAGAACAUAUACCCAGGUGACUCCGGCGUCU AUUUCCACCCACCACGUCAGCACGUCGUCUCCCGCACCAC GGCCAGGGACGACUUCUCAGGCCAGCGGCCAGGAAACU CCUCUACAAGCACAAAGCCAGGCGAAGUUAACGUCACCA AGGGAACGCCUCCCCAGAACGCAACCUCCCCACAGGCUC CAGCGGGCAGAAGACUGCGGUGCCAACUGUGACCAGCAC CGGUGGCAAGGCCAACUCAACAACUGGAGGCAAGCAUAC GACGGGGCACGGCGCCCGGACCUCACUGAACCCACGACC GAUUACGGAGGUGAUAGUACCACCCCGCGGCCACGAUUA AAUGCCACCACUUAUCUGCCACCUAGCACUUCUCCAAGC UCCGGCCACGGUGGACCUUCACAAGCCCACCCGUGACGAC AGCCCAGGCGACGGUGCCAGUCCACCUACAAGCCAGCCA CGCUUCUCCAACCUUAGU	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLLVVSNLLLPQGVVEAALLVCQYTIQS LIHLTGEDPGFFNVEIPEFPFYPTCNVCTADVNTINFVGGKK HQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLELLGAG ELALTMRSKKLPINVTTGEEQVSLESVDVYFQDVFGTMWCH HAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNKF NITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSR FLGNNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPT NTDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNT ETDFKCKWTLTSGTPSGCENISGAFASNRTFDITVSGLTAPKT LIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGFAADPNTTTG LPSSTHVPTNLTAPASTGPTVSTADVSTPTPAGTTSGASPVTPS PSPWDNGTESKAPDMTSSTSPVTTPTPNATSPTPAVTTPTPNAT SPTPAVTTPTPNATSPTLGKTSPTS AVTTPTPNATGPTVGETSP QANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSS MSLRPSSNPETLSPSTSDNSTSHMPLLTSAHPTGGENTQVTPA SISTHHVSTSSPAPRPGTTSQASGPGNSSTSTKPGEVNVTKGTP PQNATSPQAPSGQKTAVPTVTSTGGKANSTTGGKHHTTGHGAR TSTEPTTDYGGDSTTPRPRYNATTYLPPSTSSKLRPRWFTTSP VTTAQATVPVPPTSQPRFSNLS	94
PolyA tail	100 nt	
EBV gL-gH_LS_RX		
SEQ ID NO: 194 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 95, and 3' UTR SEQ ID NO:3		194
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACUCGAAGGGAUCUAGUCAGAAAGGCUCUAGGCUC CUACUCCUCUUGGUGGUGAGCAACUACUCCUCCCCAG GGCGUGGUGAGAGCAGUGGGCGUUUUCUAGCAAUCUGC CUCGUGACAAUCUUUGUGUUGCCGACCUGGGGCAACUGG GCCUACCCUGCUGCCACGUGACCCAGCUGAGAGCUCAAC ACCUGCUUGCCUGGAGAACAUACAGCGACAUCUACCUUG UAAGCAACCAGACAUGCGACGGCUUCAGUCUGGCCAGCC UGAACAGCCCCAAGAACGGCUCAAACCAGCUAGUGAUCA GCCGGUGCGCUAACGGUCUGAACGUUGUGAGCUUCUUA UCAGCAUCUUGAAGAGAAGUAGUAGCGCGCUGACCGGCC ACCUGAGAGAGCUGCUGACCACUCUCGAGACACUCUAUG	95

	GCAGCUUCAGCGUGGAGGACCUGUUCGGCGCAAACCUGA ACCGCUACGCCUGGCACAGAGGCGGCGGAAGCGGUAGCG CUGGCAGCGCCAGCGGAGGCGCUUCAUCCGGAUCCGGCG GCGCAAGCAGCCUUUCUGAGGUGAAGCUCCACUUGGACA UCGAAGGCCACGCCAGCCAUUACACCAUACCAUGGACCGA GCUGAUGGCAAAGGUGCCCCGGCCUUAGCCCAGAAGCCCU GUGGCGAGAGGCCAACGUUACCGAAGACUUGGCUAGUAU GUUAAACAGGUACAAACUUUCUACAAGACUAGCGGCAC CCUGGGCAUCGCAUAGCCGAGCCCGUGGACAUCCCCGCC GUUAGCGAGGGCAGCAUGCAGGUGGACGCCAGCAAGGUU CACCCUGGUGUAAUUAGUGGCCUCAACAGCCAGCCUGU AUGUUGAGCGCCCCACUGGAGAAGCAGCUGUUUUACUAU AUCGGGACCAUGUUGCCCAAUACCCGGCCACACAGUAC GUGUUCUACCAGCUGCGGUGUCACCUGAGCUACGUGGCC CUGUCUAUCAACGGCGACAAGUUCAGUACACCGGCGCC AUGACCAGCAAGUUCUGAUGGGCACCUACAAGCGGGUC ACCGAGAAGGGCGACGAGCACGUGCUGUCACUUGUGUUC GGUAAGACCAAGGACCUGCCCCGACCUUCGGGGCCCCUUU UCAUACCCUAGUUUGACCAGCGCCCAAAGUGGCGACUAC AGCCUUGUGAUAGUGACCACCUUCGUGCAUACGCCAAC UCCACAACUACUUCGUGCCCAACCUGAAGGACAUGUUC AGCCGGGCGGUAACCAUGACGGCCGCUUCUUAUGCCCGG UAUGUGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGGGC GGGUGCCGGGAGCCCGAGUUGGACACCGAAACCCUGACC ACCAUGUUCGAGGUUAGCGUGGCCUUCUUAAGGUGGGU CACGCGGUGGGCGAAACCGGCAAUGGAUGCGUGGACUUA CGCUGGCUGGCCAAGAGUUUCUUGAGCUUACCGUGCUG AAGGAUAUCAUCGGCAUCUGCUACGGCGCCACCGUAAAG GGAAUGCAGAGCUAUGGGCUGGAGAGACUUGCCGCCAUG CUCAUGGCUACCGUGAAGAUGGAGGAGCUGGGACACCUG ACAACAGAGAAGCAGGAGUACGCCUGAGACUGGCCACC GUGGGCUACCCUAAGGCCGGCGUGUACAGUGGACUCAUA GGCGGAGCUACCAGCGUGCUCCUAUCCGCUUAUAACAGA CACCCCUUAUUUCAGCCCCUGCACACAGUGAUGCGGGAG ACUUUAUUCAUUCGGAUCUCACGUCGUACUGCGGGAGUUG CGGCUGAACGUAACCACCCAGGGCCCUAAUUUAGCACUU UAUCAGCUGCUCAGUACUGCCCUGUGCAGCGCACUUGAG AUCGGCGAGGUACUCAGAGGCCUGGCCUCGGUACGGAG AGUGGCCUGUUUCUCCAUGCUACCUUAGCCUGCGGUUU GAUCUGACCAGAGACAAGUUGCUGAGCAUGGCUCCUCA GAGGCGACCCUUGACCAGGCAGCCGUGUCAACGCCGUG GACGGAUUCUGGGCAGACUGUCUCUGGAACGGGAAGAC CGGGAUGCUUGGCACCUUCCUGCCUAUAAGUGUGUGGAU CGGCUGGAUAAGGUCCUGAUGAUAAUCCUCUGAUUAAC GUUACUUUCAUCUUCUAGCGAUCGGGAGGUCCGAGGG UCCGCCCUACGAGGCCAGCACCAUUCUGAGCAGCA GCCUCUUCUUGUCUCCUGUGAUUAUGAACAAGUGCAGCC AGGGUGCAGUAGCCGGCGAGCCCCGGCAGAUCCCGAAGA UCCAGAACUUCACUCGGACCCAGAAGUCUUGUAUCUUCU GCGGCUUCGCCCUCUGAGUUACGACGAGAAGGAGGGCC UGGAGACUACAACUUAUCAACAAGCCAGGAGGUGCAGA ACAGCAUCCUGUCAUCUAAUUACUUUGACUUCGACAACC UGCACGUUCAUUAUCUACUGCUAACAACUAACGGUACCG UCAUGGAAAUCGCAGGACUGUAUGAGGAGCGGGCCGGCA GCGGGAGCGCGGGCUCUGCCAGCGGUGGUGCCAGCAGCG GCAGUGGAGGUGCCUCCAUGCAGAUUUACGAAGGAAAGC UGACCGCCGAAGGCCUGAGGUUCGGCAUCGUGGCUUCCA GAUUCAACCACGCACUGGUGGACAGGCUGGUGGAGGGCG CCAUCGACGCAAUCGUGCGCCACGGCGGCAGGGAGGAGG ACAUCACCCUCGUAAGAGUCCUGGUAGCUGGGAAAUUC CCGUGGCCGCGGGCGAGCUGGCUAGGAAGGAGGAUAUCG ACGCCGUCAUCGCCAUCGGCGUUCUCAUCCGGGGUGCCAC	

	ACCACAUUUCGACUACAUCGCAAGCGAGGUUUCAAAGGG ACUCGCCGACUUAAGUCUGGAGCUGAGGAAGCCCAUCAC CUUUGGCGUGAUCACCGCCGACACCCUGGAGCAGGCCAUC GAGCGCGCCGGCACCAAGCACGGGAACAAGGGCUGGGAG GCAGCCUUAUCAGCCAUCGAAAUGGCGAAUCUGUUAAG AGCCUGCGG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLLLVVSNLLLPQGVVRAVGVFLAICLVTI FVLPTWGNWAYPCCHVTQLRAQHLLALENISDIYLVSNQTC GFSLASLNSPKNGSNQLVISRCANGLNVVSFFISILKRSSSALTG HLRELLTTLETLYGSFVEDLFGANLNRYAWHRGGSGSAGS ASGGASSSGGASSLSEVKLHLDIEGHASHYTIPWTELMKVP GLSPEALWREANVTEDLASMLNRYKLIYKTSGLGIALAEPV DIPAVSEGSMQVDASKVHPGVISGLNSPACMLSAPLEKQLFYY IGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFQYTGAMTS KFLMGTYKRVTEKGDEHVLSLVFGKTKDLPDLRGPFYSPLT SAQSGDYSLVIVTTFVHYANFHNYPVNLKDMFSRAVMTAA SYARYVLQKLVLEMKGCCREPELDTETLTMTFEVSVAFFKV GHAVGETGNGCVDLRWLAKSFFELTVLKDIIGICYGATVKGM QSYGLERLAAMLMA TVKMEELGHLTTEKQEYALRLATVGY KAGVYSGLIGGATSVLLSAYNRHPLFQPLHTVMRETFIGSHV VLRELRLNVTTQGP NLALYQLLSTALCSALEIGEVLRLALGT ESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAAVSNVADG FLGRLSLEREDRDAWHLPA YKCVDRDLKVLMIPLINVTFISS DREVRGSALYEASTTYLSSSLFLSPVIMNKCSQGAVAGEPRQI PKIQNFTRTQKSCIFCGFALLSYDEKEGLETTTYITSQEVQNSIL SSNYFDNHLHVHYLLLTNGTVMEIAGLYEERAGSGSAGSA SGGASSSGGASMQIYEGKLTAEGLRFGIVASRFNHALVDRL VEGAIDAIVRHGGREEDITLVRVPGSWEIPVAAGELARKEDID AVIAIGVLIRGATPHFDYIASEVSKGLADLSLELRKPITFGVITA DTLEQAIERAGTKHGNKGWEAALSAIEMANLFKSLR	96
PolyA tail	100 nt	
EBV gBEcto_LS_RX		
SEQ ID NO: 195 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 97, and 3' UTR SEQ ID NO:3		195
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGACUCUAAGGGCAGCAGCCAGAAGGGCAGUAGGCUC CUACUUCUCCUCGUGGUGAGCAACUUAUUGCUUCCCCAG GGAGUGGUGCAGACUCCGGAACAGCCCGCUCCGCCCGCUA CCACCGUCCAGCCUACCGCCACGCGCCAGCAGACUCCU CCCGUUCGCGUCUGCGAGCUCUCCUCUCACGGCGAUCUC UCCGCUUCUCCUCCGAUAUUCAGUGCCCCUCCUUCGGCA CCCGCGAGAACCAUACCGAGGGCCUCCUCAUGGUCUUUA AGGACAACAUAUCCCUUACUCCUUAAGGUACGCUCU ACACAAAGAUAGUCACCAACAUCUUAUCUAUAUAAUGGAU GGUACGCUGACUCUGUUAACCAUCCGACGAGGAGAAGU UCUCCGUUGAUUCCUACGAGACUGACCAGAUGGAUACCA UCUACCAGUGCUACAAUGCCGUCAAGAUGACCAAGGACG GCCUGACCCGCGUCUAUGUCGACCGCGACGGCGUUAACA UACUGUCAACCUCAAGCCUACAGGCGGCCUGGCCAAUG GCGUCAGACGCUACGCCUCCAGACCGAGCUCUACGACGC UCCUGGCUGGCUGAUCUGGACCUACCGGACCCGCACCACU GUCAAUUGCCUCAUUAACCGACAUGAUGGCCAAGUCCAAU	97

	AGCCCAUUCGAUUUCUUCGUAACCACCACCGGCCAGACCG UCGAGAUGUCGCCAUUCUAUGACGGCAAGAAUAAGGAAA CUUUCACGAGAGAGCCGAUAGCUUCCACGUCCGCACGA ACUACAAGAUUGUCGACUACGACAAUCGCGGCACCAAUC CACAGGGCGAGCGCCGCGCCUUCUGGACAAGGGCACCUA CACCCUCUCCUGGAAACUCGAGAACAGAACCGCCUACUGU CCCCUCCAGCACUGGCAGACUUUUGAUUCCACCAUCGCCA CUGAGACUGGCAAGAGUAUCCAUUUCGUCACCGACGAAG GAACAUCUUCAUUCGUCACAAUACCACUGUGGGCAUUG AGCUCCCCGACGCCUUCAGUGCAUCGAGGAACAGGUCA ACAAGACAAUGCACGAGAAGUACGAGGCCGUGCAGGACC GGUAUACCAAGGGCCAGGAGGCCAUUACAUACUUCAUCA CCAGCGGUGGAUUGCUUCUCGCCUGGCUUCCACUCACACC UCGCAGUCUGGCCACAGUUAAGAACCUCACUGAGUUGAC CACUCCAACAUCGUCACCACCUUCUUCACCUAGCCCUCCU GCUCCUUCGCGCCGCGCGGCUCCACUCCUGCCGCUUGUCU UAAGGGGUCUGGGCAGCGCCGGCAGCGCAUCGGGAGGGG CGAGUUCAGGGUCAGGCGGUGCCUCCGCAGGCAAUGCUA CCACACCAGUGCCACCAACCGCCCCUGGCAAGUCCUAGG UACCCUGAACAUAUCCAGCGACAGUUCAGAUCCAGUUCGC UUACGAUUCACUCAGGCGCCAGAUCAACCGCAUGCUUGG UGACCUUGCCCGGGCCUGGUGCCUCGAACAGAAGCGCCA GAACAUGGUACUUAGGGAAACUUACCAAGAUUAAUCCUAC UACAGUCAUGUCCUCUAUCUACGGCAAGGCCGUUGCUGC CAAGCGCCUGGGCGACGUCAUCAGCGUGUCGCAGUGCGU CCCAGUCAACCAGGCUACCGUUAACCCUCAGGAAGUCCAUG AGAGUGCCAGGCUCCGAAACAAUGUGCUAUUCCCGCCCU CUGGUUUCAUUUCCUUCAUCAACGACACAAAGACCUAC GAGGGCCAGUUAGGAACUGACAAUGAGAUUUCUUGACU AAGAAGAUGACUGAGGUUAGCCAGGCAACUUCUCAAUAC UACUCCAGUCUGGAAAUGAAAUCCACGUAAUUAACGAC UAUCAUCACUUUAAGACUAUCGAACUCGACGGAAUUGCU ACACUCCAAACAUAUCUCACUGAAUACCUCCCUUAUCG AGAACAUCGACUUCGCAUCCCUCGAGCUGUAUAGCAGAG ACGAGCAGAGAGCCAGCAACGUGUUCGACCUGGAGGGUA UCUUUCGCGAGUACAACUCCAGGCACAGAAUUAAGCCG GCCUCCGUAAGGACCUGGAUAACGCCGUGUCCA AUGGCC GCAACCAGUUCGUCGACGGUCUUGGCGAACUCAUGGACU CUCUGGGAUCCGUGGGGCAAUCCAUCACAAACUUAUGUCU CUACUGUCGGUGGACUAUUCAGCAGCCUGGUUAGCGGAU UUAUCUCUUUCUUUAAGAACCCAGGCAGUGGUUCUGCCG GCUCAGCCAGCGGCGGCGCUAGUAGCGGCAGCGGAGGCG CCUCA AUGCAGAUUAUGAGGGUAAGUUGACAGCCGAAG GCUUGAGGUUUGGCAUCGUAGCCAGCCGGUUAACCACG CCCUGGUGGACAGGCUGGUUGAGGGUGCCAUGACGCCA UUGUGAGGCACGGCGGCAGGGAGGAGGACAUUACCCUGG UCAGAGUCCCCGGAUCAUGGGAGAUCCCCGUGGCCGCCG GGGAGCUGGCCAGGAAGGAAGACAUCGACGCUGUGAUCG CCAUCGGCGUGCUGAUCCGAGGAGCCACACCCCAUUAUCGA CUACAUCGCCAGUGAGGUUAGCAAAGGCCUAGCGGACCU GAGCCUGGAGCUGCGCAAGCCAUACCUUCGGCGUCAU UACUGCCGACACCUUGGAACAGGCCAUCGAAAGGGCCGG UACAAAGCACGGCAACAAGGGCUGGGAGGCAGCCCUUAG CGCCAUCGAGAUUGGCAAACCUGUUUAAGUCCUUGAGG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLVSNNLLPQGVVQTPEQPAPPATTV QPTATRQQTSPFRVCELSSHGDLFRFSSDIQCPSFGTRENHTE GLLMVFKDNIIPYSFKVRSYTKIVTNILYNGWYADSVNTRHE	98

	EKFSVDSYETDQMDTIYQCYNAVKMTKDGLTRVYVDRDGV NITVNLKPTGGLANGVRRYASQTELYDAPGWLIIWYRTRTTV NCLITDMMAKSNSPFDFVTTTGQTVEMSPFYDGKNKETFHE RADSFHVRTNYKIVDYDNRGTNPQGERRAFLDKGTYTLSWK LENRTAYCPLQHWQTFDSTIATETGKSIHFVTDEGTSSFVTNT TVGIELPDAFKCIEEQVNKTMHEKYEAVQDRYTKGQEAITYFI TSGGLLLAWLPLTPRSLATVKNLTELTTPTSSPPSSPPAPSAA RGSTPAAVLRGSGSAGSASGGASSGGSGGASAGNATTPVPPTAP GKSLGTLNNPATVQIQFAYDSLRRQINRMLGDLARAWCLEQK RQNMVLRELTKINPTTVMSSYIGKAVAAKRLGDVISVSQCVP VNQATVTLRKSMRVPGSETMCYSRPLVSFSFINDTKTYEGQL GTDNEIFLTKKMTEVCQATSQYYFQSGNEIHVYNDYHHFKTIE LDGIATLQTFISLNTSLIENIDFASLELYSRDEQRASNVDLEGI FREYNFQAQNIAGLRKDLDNAVSNGRNQFVDGLGELMDSL SVGQSITNLVSTVGGLFSSLVSGFISFFKNPGSGSAGSASGGAS SGSGGASMQUIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAID AIVRHGGREEDITLVRVPGSWEIPVAAGELARKEDIDAVIAIGV LIRGATPHFDYIASEVSKGLADLSLELRKPITFGVITADTLEQAI ERAGTKHGNKGWEAALSAIEMANLFKSLR	
PolyA tail	100 nt	
EBV gp350 A44Y V10 Stab		
SEQ ID NO: 196 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 99, and 3' UTR SEQ ID NO:3		196
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUUAUCCAACCUGU AACGUUUGCACUACGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAGUGUGA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCUAAUGGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC UCUGUCAAGACCGAGAUGCUCGGGAUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCCAUUCUCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUUAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUUAACUACGUGGGCGA CAAUGCCACGUAAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUUGUUAUCUGUAACAGCUUUCUGGGC CUGGCCAAUUAACACUGAGACUGACUCAAUUAUGUAAGUG GACUUUGACCUCUGGAACUCCGUGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAAG	99

	GUGAUCUUUUCCAAGGCACCUAGAGUCCACCACUACCUCCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGCCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UCCCCGCAAGCCAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACAUACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCAGCUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCCGCGGCCACGAUAAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUACAAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTY DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPNTNTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNTTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFA DPNTTTGLPSSTHVPTNLTA PASTGPTVSTADVTS PTPAGTTS GASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKA NSTTGKKHTTG HGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETYV	45
PolyA tail	100 nt	
EBV gp350 V15 Stab4_NGM6		

SEQ ID NO: 197 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 100, and 3' UTR SEQ ID NO:3		197
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAGAGAGAAAAGAAGAGUAAGAAGAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAGUCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUUAACGUGGAAAUCCCAGAGUCCCCUUUCUAUCCAACCUGUAACGUUUGCACUUAACGACGUGAACGUGACAUAUUAUUCGACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUCGGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAAAGGGUGCAUUUGGAGGGAGCGAGAAUGCUGCGAAUCUGUUCUUAUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAAACCAUGCGAAGCAAGAAGCUCCCCAUCAACGUUACCACCGGGGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUACUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGCUAGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGUACCCUACAUAAGUGGGUAUUAUUGCAAUUCAGCGAAUAUUAACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCUGCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUCGCGUCAAGACCGAGAUACUCGGGAAUGAGAUCAUUCGAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUGCCCGGCGACAACAAGUUCAAUAUCGCGUGUUCUGGCUACGAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACUUCUCCCCGUAGCCACGCCAUUCCCCGGAACCGGAUACGCCUACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCUGGGUAACAUAAGUAUCUUAUACGUGUUUUAUAGCGGAAACGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAGUAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGAUAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGACAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGACGCCAAUUCACCAAAUGUUGCGGUAACAGCUUUCUGGGCUGGGCCAAUAACACUGAGACUGACUUCAAAUGUAAGUGGACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAUCAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCACUGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAAACACGGACCGCCACCAACGCCGCGACUACAACCCAUAAAGUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCGCCACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCACUACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCUGACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCUGGGAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGGGCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUGGAACGGAGUCCAAGGCUCCUGAUUAGACUUCUUCUACCAAGCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCCAACCCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCCACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCCCUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAAACCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGACUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGGGACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAGCUACCUCGCGUGACUACCGGACAGCACAACAUCACCAACGCUAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUAAAUCCCGAGACCCUACACCAUCCACAUAGACAAACAGUACUUCACACAUUGCCACUCUUGACGAGCGCUCACCCACCGGCGGAGAAACAUCACCCAGGUGACUCCGGCGUCUAUUUCCACCCACCAGUCAGCACGUCGUCUCCCGCACCGAGACCAGGGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUACAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA	100

	CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACACCGCGGCCACGAUAAUAAUGCC ACCACUUUCUGGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTY DVNVTFNFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENAANLFLLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSAN ITAVVRAQGLDVTPLSLPTS AQDSNFAVKTEILGNEIDIECIM EDGEISQVLPDGNKFNIACSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNLSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGD NATYSVPMVTSEDANSP NVAVTAFWAWPNNTETDFKCKWLTLSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNAATTHKVIKFAPESTTTS PTLNTTG FADPNTTGLPSSTHVPTNLTA PASTGPTVSTWDVT SPTPAGTTS GASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTP NATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AV TTPTPNATGPTVGETSPQANATNHTLGTSPTPVVTSQPKNAT SAVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT SAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNS STSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGK ANSTTGKKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYL PPSTSSKLRPRWTFSTPPVTTAQA TVPVPPTSQPRFSNLSMLVL QWASLAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETY V	55
PolyA tail	100 nt	
V6_NGM N195_EBV_gp350_001		
SEQ ID NO: 198 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 101, and 3' UTR SEQ ID NO:3		198
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCUACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGCCCAGGGCUUGGACGUGACUCU	101

	GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC GCGGUCAAGACCGAGAUGCUCGGGAAUGAGAU CGAU AUC GAGUGCAUCAUGGAGGACGGUGAGAU AAGCCAGGUUCUG CCCGGCGACAACAAGUUC AAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCCAUUC CCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUAUAGCGGAAA CGGCCC UAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAU AUUACCUACGUGGGCGA CAAUGCCACGU AUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAA AUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAAU AACACUGAGACUGACUCAA AUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAU AU CAGCGGGGCCUUGCUUCCAACAGGACUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUC C CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCUCUGAU AUGACUCCCUAACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGU AAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUAUCACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUACCCAGGUGACUCCGGCGUCUAUUUCC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCCGCGGCCACGAUAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUACAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINF DVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTLP LSLPTSAQDSNFAVKTEMLGNEIDIECI	65

	MEDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPG TGYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQ SNIVFSDEIPASQDMPTNTTDDITYVGDNATYSVPMVTSEDANS PNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFAS NRTFDITVSGLGTA PKTLIITRTATNATTTTHKVIKFAPESTTT SPTLNNTGTFADPNTTTGLPSSTHVPTNLTA PASTGPTVSTADVT SPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTP NATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAV TTPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNAT SAVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT SAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNS STSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGK ANSTTGKKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYL PPSTSSKLRPRWFTSPPVTTA QATVPVPPTSQPRFSNLSMLVL QWASLAVL TLLLLVMADCAFRRLSTSHYTTTPPYDDAETY V	
PolyA tail	100 nt	
V8_NGM N345_EBV_gp350_001		
SEQ ID NO: 199 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 102, and 3' UTR SEQ ID NO:3		199
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUAUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCCUAUCUCUACCUACUUCUGCCCAAGACUCCA AUUUC UCUGUCAAGACCGAGAUGCUCGGGAAUGAGAUCGAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUAUAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAUUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUACCUACGUGGGCGA CAAUGCCACGAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAA AUGUUGCGGUAACAGCUUUCUGGGC CUGGCCAAUAACACUGAGACUGACUCAA AUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCACGACUACAACCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU	102

	GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC GCUACCUCGCGUGUCACUACCGGACAGCACAAACUACCA GCUCAAGCACGAGUCCAUGAGCUUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUCACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAACAUCACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCGCGGCCACGAUAAUUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAUUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGG ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVAVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFA DPNTTTGLPSSTHVPTNLTA PASTGPTVSTADVTS PTPAGTTS GASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTDYGGDSTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQA TVPVPTSPQPRFSNLSMLVLQ WASLAVLTLLLLLV MADCAFRRNLSTSHTYTTPPYDDAETVY	114
PolyA tail	100 nt	
V9_NGM N411_EBV_gp350_001		
SEQ ID NO: 200 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 103, and 3' UTR SEQ ID NO:3		200
Chemistry	1-methylpseudouridine	

Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCCTCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAAUAAUUGCAAUUCACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCCUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC UCUGUCAAGACCGAGAUUGCUCGGGAAUGAGAUCAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUUGUUACUGUAACAGCUUUCUGGGC CUGGCCAAUUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCCGGACUACAACCCAUAAG GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCCT CGACUCUUAACACUACGGGCUUCGUGAUCCTAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUUCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCCGAACGCGACAUUCCTC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCTCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAGAAGC GCUACCUCGCGUGUCACUACCGGACAGCACAACAUCACCA GCUCAAGCACGAGUUCUUAUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GGCGAGAAACAUCACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGCACCGAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC	103

	GGAGGUGACAGCACAAACACCGCGGCCACGAUAAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUCGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAUAGGUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPNTTDTITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLITRTATNAATTTHKVIKFAPESTTTS PTLNTTGAFADPNTTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSATV TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMLRPSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTIDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHTYTTPPYDDAETVYV	70
PolyA tail	100 nt	
EBV gH (BXL2)		
SEQ ID NO: 201 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 106, and 3' UTR SEQ ID NO:106		201
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGCAGUUGUUGUGCGUGUUCUGCCUCGUGUACUCUGG GAGGUGGGCGCCGCCAGCCUUAGCGAGGUGAAGCUCCAC UUGGACAUCGAGGGCCACGCCAGCCACUACACCAUCCCCU GGACCGAGCUCAUGGCCAAGGUGCCCGGCCUUAGCCCCGA GGCCUGUGGGCGGGAGGCCAACGUGACCGAGGACCUGGC CAGCAUGCUGAACCAGGUAACAAGCUGAUCUACAAGACCAG CGGCACCCUGGGCAUCGCCCUGGCCGAGCCGUGGACAUC CCCGCCGUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGC AAGGUGCACCCCGGCGUGAUCAGCGGCCUGAACAGCCCCG CCUGUAUGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCU ACUACAUCGGCACCAUGCUGCCCAACACCCGCCCCACAG CUACGUGUUCUACCAGCUGCGGUGCCACCUGAGCUACGU UGCCUGAGCAUCAACGGCGACAAGUCCAGUACACCGG CGCAUGACCAGCAAGUCCUGAUGGGCACCUCACAAGCG GGUCACCGAGAAGGGCGACGAGCACGUGCUGUCACUGGU GUUCGGCAAGACCAAGGACCUGCCCCGACCUGCGGGGCCCC UUCAGCUACCCUAGUUUGACCAGCGCCCAGAGCGGCGAC UACAGCUUGGUGAUCGUGACCACCUUCGUGCACUACGCC AACUCCACAACUACUUCGUGCCCAACCUGAAGGACAUG	105

	UUCAGCCGGGCCGUGACCAUGACUGCCGCUUCUACGCCC GGUACGUGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGG GCGGCUGCCGGAGCCCGAGCUGGACACCGAAACACUGA CCACCAUGUUCGAGGUGAGCGUGGCCUUCUUAAGGUGG GUCACGCGGUGGGCGAAACCGGCAACGGCUGCGUGGACU UACGCUGGCUGGCCAAGAGCUUCUUCGAGCUGACCGUGC UGAAGGAUAUCAUCGGCAUCUGCUACGGCGCCACCGUGA AGGGCAUGCAGAGCUACGGCCUGGAGCGGCUGGCCGCCA UGCUUAUGGCAACAGUGAAGAUGGAGGAGCUGGGACACC UGACAACAGAGAAGCAGGAGUACGCCCUGAGACUGGCCA CAGUGGGCUACCCAAAGGCCGGCGUGUACAGUGGACUGA UCGGCGGCGCAACCAGCGUGCUGCUAUCCGCUUACAACCG GCACCCGCGUUCAGCCCCUGCACACCGUGAUGCGGGAA ACCCUGUUAUCGGAAGCCACGUCGUGCUGCGGGAGCUG AGGCUGAACGUAACCACCCAGGGCCCUAAUCUGGCCCU UAUCAGCUCCUCAGUACCGCCCUGUGCAGCGCCCUUGAGA UCGGCGAGGUGCUCAGAGGCCUGGCCCUUGGUACCGAGA GCGGCCUCUUCAGCCCAUGCUACUUAAGCCUGCGGUUCG ACCUGACCCGGGACAAGUUGCUGAGCAUGGCCCCGCAGG AGGCCACACUGGACCAGGCAGCUGUAUCCAACGCCGUGG ACGGCUUCCUGGGCAGACUGUCCUGGAACGGGAGGACC GGGACGCCUGGCACCUGCCUGCCUACAAGUGUGUGGAUC GGCUGGACAAGGUGCUGAUGAUAUCCUCUGAUUAAUG UCACCUUCAUCAUCAGCAGCGACCGGGAGGUGCGGGGAU CCGCCCUCUACGAGGCCAGCACCCUAUCUGAGCAGCAG CCUGUUCUGUCCUGUGAUGAUGAACAAGUGCAGCCA GGGCGCCGUGGCCGGCGAGCCCCGGCAGAUCCCCAAGAUC CAGAACUUCACCCGGACCCAGAAGUCUUGCAUCUUCUGC GGCUUCGCCCUIUUGUCCUACGACGAGAAGGAGGGCUUG GAGACUACAACCUACAUCACCAGCCAGGAGGUGCAGAAC AGCAUCCUGUCAUCUAAUUAUCUUCGACUUCGACAACCG CACGUUCAUUAACCGUCCUCACCACCAACGGUACCGUCA UGGAAAUCGCCGGACUGUACGAGGAGCGGGCCCAUGUUG UGCUGGCCAUCAUCCUGUACUUAUCGCUUUCGCACUUG GCAUCUUCUGGUGCACAAGAUCGUGAUGUUCUUCUG	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MQLLCVFLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTE LMAKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGLGI ALAEPVDIPAVSEGSMQVDASKVHPGVISGLNSPACMLSAPLE KQLFYIYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFQYT GAMTSKFLMGTYKRVTEKGDEHVLVSLVFGKTKDLPLDRGPF YPSLTSAQSGDYSLVIVTTFVHYANFHNYPVNLKDMFSRAV TMTAASYARYVLQKLVLLEMKGCCREPELDTETLTMTFEVS VAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIIGICYG ATVKGMQSYGLERLAAMLATVKMEELGHLTTEKQEYALR LATVGYPKAGVYSGLIGGATSVLLSAYNRHPLFQPLHTVMRE TLFIGSHVVLRELRLNVTQGPNLALYQLLSTALCSALEIGEV RGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAA VSNVDGFLGRLSLEREDRDWHLPAYKCVDRDLKVLMIPL INVTFIISDREVRGSALYEASTTYLSSSLFLSPVIMNKCSQGA VAGEPRQIPKIQNFTRTQKSCIFCGFALLSYDEKEGLETTTYITSQ EVQNSILSSNYFDFDNLHVHYLLLTNGTVMEIAGLYEERAH VVLAILYFIAFALGIFLVHKIVMFFL	38
PolyA tail	100 nt	
EBV gL (B95-8)		
SEQ ID NO: 202 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 107, and 3' UTR SEQ ID NO:106		202

Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUUCUGGCCAUCUGCCUGGUG ACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAACAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUCAUCAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCGGCCACCUGAGA GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUAC GCCUGGCACAGAGGCGGC	107
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MRAVGVFLAICLVITIFVLPTWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFVEDLFGANLNR YAWHRGG	36
PolyA tail	100 nt	
EBV gp42 (B95-8)		
SEQ ID NO: 203 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 108, and 3' UTR SEQ ID NO:1-6		203
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGGUGAGCUUCAAGCAGGUGAGAGUGCCCCUGUUCACC GCCAUCGCCCUGGUGAUCGUGCUGCUGGCCUACUUC UGCCACCCAGAGUGAGAGGCGGCGGCAGAGUGGCCGCGG CCGCCAUCACCUGGGUGCCCAAGCCCAACGUGGAGGUGU GGCCCGUGGACCCGCCACCUCGUGAACUACAACAGAC CGCCGAGCAGGAGUACGGCGACAAGGAGGUGAAGCUGCC CCACUGGACGCCGACCCUGCACACCUUCCAGGUGCCCCAG AACUACACCAAGGCCAACUGCACCUACUGCAACACCAGAG AGUACACCUUCAGCUACAAGGGCUGCUGCUUCUACUUA CCAAGAAGAAGCACACCUGGAACGGCUGCUUCCAGGCCU GCGCCGAGCUGUACCCUGCACCUACUUCUACGGCCCCAC CCCAGACAUCCGCCGUGGUGACCAGAAACCUGAACGCC AUCGAGAGCCUGUGGGUGGGCGUGUACAGAGUGGGCGAG GGCAACUGGACCAGCCUGGACGGCGGCACCUUCAAGGUG UACCAGAUUCUGGCAGCCACUGCACCUACGUGAGCAAG UUCAGCACCGUGCCCGUGAGCCACCACGAGUGCAGCUUCC UGAAGCCCUGCCUGUGCGUGAGCCAGAGAAGCAACAGC	108
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MVSFKQVRVPLFTAIALVIVLLLAYFLPPVRGGGRVAAAAT WVPKPNVEVWVPDPPPPVNFNKTAQEYGDKEVKLPHWTPT LHTFQVPQNYTKANCTYCNTREYTFSYKGCCFYFTKKKHTW NGCFQACAELYPCTYFYGPTDILPVVTRNLNAIESLWVG VYR VGEGNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPVSHHECSFL KPCLCVSQRSNS	34

PolyA tail	100 nt	
EBV gp350 _001 (modified)		
SEQ ID NO: 204 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 109, and 3' UTR SEQ ID NO:106		204
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCGCCAGUAUACAAUCCAG UCGCUCAUUCUAUCUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCAGAGUUCCCUUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUACAAAUUCUGU UCUUACUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGAAUAAUUGCAAUUAACUAAUUAU UACGGCUGUGGUGAGGGGCCAGGGCUUGGACGUGACUCU GCCCUUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC UCUGUCAAGACCGAGAUGCUCGGGAUGAGAUCAUUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUCAAUAUCACUUGUUCUGGCUAC GAGUCCCAUGUGCCUAGUGGUGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCAUUCCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUAAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUCAGGA CAUGCCGACAAACACAACUGAUAAUACCUACGUGGGCGA CAAUGCCACGUAAUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUGUUACUGUAACAGCUUUUCUGGGC CUGGCCAAUAACACUGAGACUGACUCAAUAAUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUUA CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUUAU AACACGGACCGCCACCAACGCCACGACUACAACCCAUAA GUGAUCUUUCCAAGGCACCUGAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGCUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCCGAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGAUAAUG GAACGGAGUCCAAGGCUCUGAUUAGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UUCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAAGAAC GCUACCUCGCGUGACUACCGGACAGCACAAACAUACCA GCUCAAGCACGAGUUCUUGAGCUUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUCAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCCGGC GGCGAGAACAUCACCCAGGUGACUCCGGCGUCUAUUUCC	109

	ACCCACCACGUCAGCAGCUCGUCUCCCGCACCAGACACG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCCAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACACCGCGGCCACGAUAUAAUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGUGGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAUGCUCGUUCUCCAGUGGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPDGNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDTITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISEGAFASN RTFDITVSGLGTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSASPVTTPSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWFTFTSPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLVMADCAFRRLNSTSHTYTTTPYDDAETVY	28
PolyA tail	100 nt	
EBV D123_Ferritin_RX		
SEQ ID NO: 205 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 110, and 3' UTR SEQ ID NO:106		205
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGGACAGCAAGGGCAGCAGCCAGAAGGGAUCGAGGCUA UUAUUGUUACUUGUGGUGAGCAACUUGCUCUCCUGCCUCAG GCGUGGUGGGCGAGGCCGCCUUGUUGGUGUGCCAGUAC ACCAUCCAGAGCCUCAUCCACCUCACCGGCGAGGACCCCG GCUUCUUAACGUGGAGAUCCCCGAGUCCCCUUCUACCC CACCUGCAACGUGUGCACCGCCGACGUGAACGUGACCAUC AACUUCGACGUGGGCGGCAAGAAGCACCAGCUGGACCUG GACUUCGGCCAGCUGACCCCGCACACCAAGGCCGUGUACC AGCCCAGGGGCGCCUUCGGCGGCAGCGAGAACGCCACCAA CCUGUUCUGCUGGAGCUGCUGGGCGCCGGCGAGCUGGC CCUGACCAUGAGGUCCAAGAAGCUGCCCAUCAUUGUGAC CACAGGAGAGGAGCAGCAGGUGAGCCUGGAGAGCGUGGA	110

	CGUGUACUCCAGGACGUGUUCGGCACCAUGUGGUGCCA CCACGCCGAGAUGCAGAACCCAGUUUACUUGAUUCCUGA GACAGUGCCCUACAUCAAGUGGGACAACUGCAACAGCAC CAACAUCACCGCCGUGGUGAGGGCCCAGGGCCUGGACGU GACCCUGCCCCUGAGCCUGCCCACCAGCGCCCAGGAUAGC AACUUCAGCGUGAAGACCGAAAUGCUGGGCAACGAGAUC GACAUCGAGUGCAUCAUGGAGGACGGCGAGAUCAGCCAG GUGCUGCCCGGCGACAACAAGUUCAACAUUACCUGCAGC GGCUACGAGAGCCACGUGCCCAGCGGCGGCAUCCUGACCU CAACUUCACCCGUGGCCACUCCGAUCCCCGGCACCCGGCUA CGCCUACAGCCUGCGUCUGACACCUAGGCCCCGUGAGCAGG UUCCUGGGCAAUAACAGCAUCCUGUACGUGUUCUACAGC GGCAACGGCCCCAAGGCUUCCGGCGGCGACUACUGUAUU CAAUCAAACAUCGUGUUCAGCGACGAGAUACCAGCCAGC CAGGACAUGCCUACUAAACACCACCGACAUCACCUAUGUG GGAGACAAUGCUACUACAGCGUGCCCAUGGUGACCAGC GAGGACGCCAACAGCCCAAUGUCACCGUGACCGCCUUCU GGGCCUGGCCCAACAACACUGAGACAGACUUAAGUGCA AGUGGACCCUCACAUCCGGCACCCCUAGCGGAUGCGAGA ACAUCAGCGGAGCGUUCGCCAGCAACAGGACCUUCGAUA UACAGUGAGCGGCCUGGGCACCCGUCCUAGACCCUGA UCAUCACCAGGACGGCCACAAAUGCAACUACUACAC ACAAGGUGAUCUUCAGCAAGGCUCCGGAAUCACAAGUGA GGCAGCAGUUCUCAAGGAUAUCGAGAAGCUUCUUAACG AGCAAGUUAACAAGGAAAUGCAGAGCAGUAUUCUCUACA UGAGCAUGAGCAGCUGGUGCUACACCCACUCCUGGACG GAGCAGGCCUCUCCUGUUCGACCACGCAGCCGAGGAGU ACGAGCACGCUAAGAAGUUGAUCAUUUUCUUGAACGAGA ACAACGUGCCCGUGCAGCUAACGUCAAUCAGCGCACCUG AGCACAAGUUCGAGGGCCUGACCCAGAUCUUCAGAAAGG CCUACGAACACGAACAGCACAUCUCCGAGAGCAUCAACA AUUUGUGGAUCACGCUAUCAGUCCAAGGACCACGCUA CCUUCACUCCUGCAGUGGUACGUGGCCGAGCAACAUG AGGAGGAGGUGCUGUUAAGGACAUCUGGACAAGAUCG AGCUGAUCGGUAAUGAGAAUCACGGCCUGUACCUGGCCG ACCAGUACGUGAAGGGCAUCGCCAAGAGCCGGAAGUCA	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLTVSNLLLPQGVVGEAALLVCQYTIQ SLIHLTGEDPGFFNVEIPEFFPYPTCNVCTADVNTINFVGGK KHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLELLGA GELALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFMTWC HHAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVT PLSLPTS AQDSNFSVKTEMLGNEIDIECIMEDGEISQVLP GDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSL RLTPRPVSRFLGNSILYVFYSGNGPKASGGDYCIQSNIVFS DEIPASQDMP TTTDITYVGD NATYSVPMVTSEDANSPNVT VTAFAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRT FDITVSGLTAPK TLITRTATNATTTTHKVIFSKAPESQVR QQFSKDIEKLLNEQV NKEMQSSNLYMSMSSWCYTHSLD GAGLFLFDHAAEEYEHAK KLIIFLNENNPVQLT SISAPEHKFEGLTQIFQKAYEHEQHISESI NNIVD HAIKSKDHATFNFLQWYVAEQHEEEVLFKDILDKIELI GNENHGLYLADQYVKGIKSRKS	111
PolyA tail	100 nt	
EBV D123_LS		
SEQ ID NO: 206 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 112, and 3' UTR SEQ ID NO:106		206
Chemistry	1-methylpseudouridine	

Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGGACAGCAAGGGCAGCAGCCAGAAGGGCUCCCGGUUG UUGCUCUUGCUCGUGGUGAGCAACUUGUUGUUGCCUCAG GGCGUGGUGGGCGAGGCCGCCUUGUUGGUGUGCCAGUAC ACCAUCCAGAGCCUCAUCCACCUCACCGGCGAGGACCCUG GCUUCUUAACGUGGAGAUCCCUAGAUUCCCUUUCUACC CUACCUGCAACGUGUGCACCGCCGACGUGAACGUGACCA UCAACUUCGACGUGGGCGGCAAGAAGCACCAGCUGGACC UGGACUUCGGCCAGCUGACCCCUACACCAAGGCCGUGUA CCAGCCUAGAGGCGCCUUCGGCGGCAGCGAGAACGCCACC AACCUGUUCUGCUGGAGCUGCUGGGCGCCGGCGAGCUG GCCCUGACCAUGAGAAGUAAGAAGCUGCCUAUCAACGUC ACUACUGGCGAGGAGCAGCAGGUGAGCCUGGAGAGCGUG GACGUGUACUUCAGGACGUGUUCGGCACCAUGUGGUGC CACCACGCCGAGAUGCAGAACCCUGUGUACCUGAUCCCAG AAACCGUGCCUUAUCAUAAGUGGGACAACUGCAACAGCA CCAACAUCACCGCUGUGGUGAGAGCCAGGGCCUGGACG UGACCCUGCCUCUGAGCCUGCCUACCAGCGCCCAAGACAG UAACUUCAGCGUGAAGACGGAGAUGCUGGGCAACGAGAU CGACAUCGAGUGCAUCAUGGAGGACGGCGAGAUACGCCA GGUGCUGCCUGGCGACAACAAGUUAACAUAACAUGCAG CGGCUACGAGAGCCACGUGCCUAGCGGCGGCAUCCUGACC UCCACCAGCCCUGUGGCCACCCCUAUCCCUGGCACCGGCU ACGCCUACAGCCUGAGACUCACGCCAAGACCUGUGAGCA GAUUCUUAAGGAAACAACAGCAUCCUGUACGUGUUCUACA GCGGCAACGGCCCUAAGGCCUCCGGCGGUGACUACUGUA UCCAGUCUAACAUCGUGUUCAGCGACGAAAUCCCAGCCA GCCAGGACAUGCCUACAAACACCACCGACAUCACUUAUG UCGGCGACAAUGCGACAUAACAGCGUGCCUAUGGUGACCA GCGAGGACGCCAACAGCCCUAACGUAACCGUGACCGCCUU CUGGGCCUGGCCUAACAACACCGAAACCGACUUAAGUG CAAGUGGACUUUAACUAGUGGCACCCCUUCUGGCUGCGA GAACAUCAGCGGCGCAUUCGCCAGCAACAGAACCUUCGA UAUCACCGUGAGCGGCCUGGGCACCGCCCUAAGACCCUG AUCAUCACCAGAACCGCAACUAAUGCAACUACAACAACCC ACAAGGUGAUCUUCAGCAAGGCCCUUGGCUCCGGCUCUG CCGGCAGUGGCGAGCGCAGGCAGUGGAUCCGCCGUGUACG GUUCCGCCAUGCAGAUUCUACGAGGGCAAGCUGACCGCCG AGGGCCUGAGAUUCGGCAUCGUGGCCAGCAGGUUCAACC ACGCCUUGGUGGACAGACUGGUGGAGGGCGCCAUCGACG CCAUCGUGAGACACGGAGGAAGAGAGGAGGAUAUAACAC UGGUCAGAGUGCCUGGAUCAUGGGAAAUCCCUGUCGCCG CUGGUGAGCUGGCAAGAAAGGAGGACAUCGAUGCGGUGA UCGCCAUCGGCGUGCUGAUCCGCGGUGCAACUCCACACUU CGACUACAUCGCCUCUGAAGUGUCAAGGGCCUUGCGGA CCUGUCCCUCGAACUCAGAAAGCCUAUCACAUUCGGAGU GAUUACUGCAGAUACCCUGGAGCAGGCCAUCGAGAGAGC CGGCACCAAGCACGGCAACAAGGGCUGGGAAGCCGCGCU GUCUGCCAUAAGAAAUGGCAAACCUUUUCAAGUCCCUUAG A	112
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCGGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MDSKGSSQKGSRLLLLVLVSNLLLPQGVVGEAALLVCQYTIQ SLIHLTGEDPGFFNVEIPEFPFYPTCNVCTADVNTINFVGGK KHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLELLGA GELALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFMTWC HHAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVTL	113

	PLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNK FNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVS RFLGNNILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMP TNTTDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNN TETDFKCKWTLTSGTPSGCENISGAFASNRTFDITVSGLTAPK TLIITRTATNATTTTHKVFISKAPGSGSAGSGSAGSGSAGSGSA MQIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAIDAIVRHGG REEDITLVRVPGSWEIPVAAGELARKEDIDAVIAIGVLIRGATP HFDYIASEVSKGLADLSLELRKPITFGVITADTLEQAIERAGTK HGNKGWEAALSAIEMANLFKSLR	
PolyA tail	100 nt	
EBV gp350 _004 (modified)		
SEQ ID NO: 207 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 124, and 3' UTR SEQ ID NO:3		207
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAAGCCGCCCUAUUAGUCUGCCAGUACACCAUUCAA AGCCUCAUCCACUUGACUGGGGAGGAUCCUGGGUUCUUU AACGUGGAAAUCCCGGAAUUCCCUUUCUACCCAACUUGC AACGUGUGCACGGCUGACGUCAACGUGACUAUCAACUUC GAUGUGGGAGGGAAGAAACAUCAACUUGAUCUGGACUUU GGCCAGCUUACUCCCCACACCAAGGCCGUGUACCAGCCCC GCGGCGCAUUCGGUGGGAGCGAGAACGCGACAAAUCUAU UCUUGCUGGAACUGCUGGGCGCAGGAGAGCUCGCCCUGA CGAUGCGAUCUAAGAAGCUUCCCAUCAACGUUACCACUG GCGAGGAGCAGCAGGUGUCCCUCGAAAGCGUCGACGUCU AUUCCAAGACGUCUUCGGAACAAUGUGGUGCCACCACG CUGAGAUGCAGAACCCCGUAUAUCUUAUUCCCGAAACCG UGCCAUACAUCAAGUGGGACAACUGCAACUCAACUAACA UCACUGCAGUAGUGCGCGCCCAGGGACUGGACGUCACUU UGCCACUGUCACUGCCCACAUCAGCCCCAAGACAGCAACUU CAGCGUCAAGACAGAAAUGCUGGGCAACGAAAUCGACAU CGAAUGCAUAAUGGAGGAUGGGGAAAUUCCAGGUCCU CCCCGGUGAUAAACAAGUUUAAUUAUACUUGUUCUGGAUA UGAAUCCCAUGUGCCGUCUGGUGGUUAUACUGACGAGUAC AUCGCCAGUGGCUACCCCAAUCCCCGGGACAGGCUAUGCC UACAGCCUGAGACUGACGCCAAGACCAGUUUCCAGGUUU CUGGGGAAUAACUCUAUCCUGUAUGUGUUUUUUCUGGU AACGGACCCAAGGCAUCCGGCGGUGAUUAUUGUAUCCAG AGCAAUAUAGUGUUCUCUGAUGAGAUUCCGGCCUCCCAG GAUAUGCCAACCAACACGACAGAUUACACCUAUGUCGGG GACAACGCCACAUAUAGCGUGCCAAUGGUGACCAGCGAA GAUGCCAAUUCUCCCAACGUCACAGUGACAGCCUUUUGG GCGUGGCCUAAUAACACAGAAACUGACUUUAAAUGCAAA UGGACUCUAACCUCAGGCACCCCAUCUGGCUGCGAGAAC AUAAGCGGCGCGUUUGCAUCGAACAGAACUUUUGAUUU ACAGUAUCUGGGUUGGGCACUGCGCCCAAGACUCUAAUA AUUACACGGACGGCCACUAACGCCACCACGACGACUCACA AGGUGAUCUUCAGCAAAGCUCCCGAAUCUACUACUACCU CGCCGACACUGAAUACGACAGGAUUCGCCGACCCAAAUA CUACGACCGGCCUUCCCAGCUCGACACAUGUGCCUACAAA CUUAAACGGCGCCCGCCAGUACCGGCCCCACCGUGAGCACC GCUGACGUCACCUUCUCCUACCCUUGCCGGGACUACAAGUG GUGCUUCCCCAGUUACUCCAGCCCUAGCCCUUGGGACAA CGGCACUGAGAGCAAAGCUCCGGACAUGACCAGCAGUAC CAGUCCAGUGACAACUCCGACACCCAAUGCGACGUCCCCA ACUCCCGCCGUGACCACGCCAACACCAAUGCCACGUCAC	124

	CUACUCCAGCGGUCACCACCCCAACGCCAAACGCUACUAG UCCCACUCUAGGCAAGACAUUCCCACCUCCGCUGUACC ACCCCUACACCCAAUGCUACCGGUCCCACGGUGGGUGAGA CUAGCCCACAGGCCAACGCAACUAAUCAUACAUUGGGUG GCACAAGCCCAACGCCCUGCGUCACUAGCCAGCCUAAGAA CGCCACAAGCGCUGUAAACUACCGGCCAGCACAAUUAAC AAGUUCAGUACUAGCAGUAUGUCUCUGAGACCCAGCUC AAAUCCUGAAACCCUCUCGCCCUCUACGUCGGAUAACUCC ACGUCCCACAUGCCUCUACUCACAAGCGCGCACCCUACCG GAGGAGAGAAUUAUCACUCAGGUUACCCAGCUUCUAUCU CGACUCACCAUGUCUCUACUUCUCCCCAGCGCCACGGCC CGGCACUACCAGCCAGGCUAGCGGGCCAGGUAAUUCCUCC ACUAGCACUAAACCUGGCGAAGUCAACGUUACCAAGGGA ACACCUCCCCAGAAUGCAACCUCGCCCCAAGCUCCUCUG GACAGAAGACAGCCGUCCUACCGUCACAAGCACCCGGUG GGAAGGCGAAUUCUACGACAGGCGGGAAGCACACUACCG GACACGGAGCAAGGACAUCCACUGAGCCCACGACCGACU ACGGUGGCGACUCCACCACGCCCAGACCCAGGUACAAUGC GACUACCUACCUGCCGCCUCCACUUCAGCAAACUGAGG CCUCGUUGGACUUCACUUCUCCACCAGUACACCCGCUC AGGCUACCGUGCCUGUCCCGCCGACCUCUCAGCCCCGGUU UUCAAAUUUGAGUAUGCUCGUGCUGCAGUGGGCCAGCCU GGCAGUGCUUACCCUCCUGCUCUUGCUGGUUAUGGCUGA CUGCGCCUUCCGACGUAACUUAUCCACCAGUCAUACUAC ACUACACCUCCUUAUGACGACGCGGAGACCUACGUG	
3' UTR	UGAUAUAGGCUAGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNISILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGFADPNTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLTTS AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFSNLSMLVLQ WASLAVLTLLLLLV MADCAFRRLSTSHTYTTPPYDDAETVY	125
PolyA tail	100 nt	
EBV gp350_005 (modified)		
SEQ ID NO: 208 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 126, and 3' UTR SEQ ID NO:3		208
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct	AUGGAAGCCGCCUACUGGUCUGCCAGUACACUAUUCAG UCCCUCAUCCAUCUCACAGGCGAGGACCCGGGGUUCUUA	126

(excluding the stop codon)	ACGUCGAAAUCCCCGAAUUCCCAUUCUAUCCCAACUGUAA CGUCUGCACAGCCGACGUUAACGUUACAAUCAAUUCGA CGUGGGCGGGAAGAAACACCAGCUGGACCUCGACUUUGG GCAGCUGACGCCCCACACUAAAGCCGUUUACCAGCCCAGG GGUGCAUUCGGUGGAUCUGAGAAUGCUACAAACCUCUUU CUGCUUGAGCUGCUUGGUGCUGGAGAGCUGGCCUCGACA AUGCGCAGCAAGAAGUUGCCAAUCAAUGUGACCACAGGU GAAGAACAGCAGGUGUCCCUAGAAUCCGUGGAUGUGUAC UCCAGGACGUUUUCGGCACAAUGUGGUGCCAUCACGCA GAGAUGCAGAAUCCGGUGUACCUUAUCCCCGAAACAGUG CCGUACAUAUAAUUGGGAUAAUUGUAACUCCACAAACAUC ACGGCAGUGGUGCGCGCUCAGGGGCUGGACGUGACACUC CCGCUUCCUUAACCAACAAGUGCUCUAGAUUCCAACUUU UCUGUGAAGACCGAGAUGCUGGGCAACGAGAUUGAUUU GAAUGCAUCAUGGAGGAUGGGCAGAUUAGCCAGGUGUUG CCCGGCGACAAUAAUUAUUAUUAUUAUUAUUAUUAUUAU GAGUCACACGUGCCAAGUGGAGGCAUUCUCACGAGCACC UCUCCCGUUGCAACACCCAUUCUCCUGGGACAGGGUACGCA UAUAGUCUCAGGCUGACACCGAGACCGGUUACGCGCUUC UUAGGUAAACAAUCCAUCUUGUAUGUGUUUUACAGCGGA AACGGGCCAAAGGCCUCAGGAGGAGACUACUGCAUCCAG AGCAAUAUAGUCUUUAGCGACGAGAUCUCCUGCCUCACAA GACAUGCCCACCAACACCACCGACAUCACGUACGUCGGUG AUAUAGCCACUACAGCGUGCCUUAUGGUGACCUCUGAAG ACGCAAAUUCACCCAAUGUCACGGUUAACGCAUUCUGGG CUUGGCCAAUAACACUGAAACCGACUUAAGUGUAAAU GGACCCUAAACAGCGGCACCCCAUCAGGGUGCGAGAAUA UCAGCGGGGCCUUCGCCAGCAACCGGACAUUCGACAUCAC CGUGUCAGGACUAGGGACUGCUCCAAAGACAUUAAUUAU UACACGGACAGCAACUAAACGCUACGACUACGACUCACAA AGUGAUUUUAGCAAAGCGCCCGAAUCGACUACUACGAG CCCGACCCUAAACACCACCGGUUUCGCCGAUCCCAACACA ACUACUGGUCUCCCAUCUUCGACCCAUUGUCCAACGAAUC UGACAGCUCCAGCAAGUACGGGGCCACUGUGAGUACAG CCGACGUUACUAGCCCAACUCCCGCGGGUACGACUAGUG GCGCGUCUCCAGUGACCCCUUCGCCUUCUCCGUGGGAAUA UGGAACCGAGUCAAAAGGCUCCUGAUUAGACCAGCUCCAC CAGUCCCGUUAACAACGCCAACGCCAAUGCAACGAGUCCA ACUCCGGCGGUUACCACUCCGACACCAACGCCACCUCGC CCACGCCUGCAGUUAUACGCCCACCCUAAUAGCUACGUC ACCCACUCUGGGAAAGACCUCACCAACCUCUGCCGUGACU ACUCCUACACCUAAUGCCACAGGACCCACAGUUGGGGAA ACCAGCCCACAGGCUAACGCAACUAAUCAUACGCUUGGC GGGACCUCUCCACGCCCCGUGGUCACUUCACAGCCUAAGA AUGCCACAAGCGCUGUGACUACAGGCCAGCAUAAUUAUA CCAGCAGUUAACAGUAGCAUGUCCUGCGUCCUUAUC CAAUCCUGAGACUCUGAGCCCCAGCACUAGUGACAACUC AAUUCUCACAUGCCGUUGCUGACCUCGCGCAUCCACAG GGCGGUGAGAAUAUCACACAGGUGACACCCGCGUCUAU AGCACACAUCAGUGAGUACGUCCUCGCCCCGACCCCGCC CAGGCACAACCUCACAAGCAUCAGGUCCGGGGAUAAGCA GCACAAGUACCAAGCCUGGCGAAGUGAAUGUAACCAAGG GCACGCCACCGCAGAACGCCACAUCCCUCAAGCCCCAUC CGGCCAGAAGACCGCUGUACCCACCGUGACAUCAACUGG GGGGAAAGCGAACUCAACUACCGGUGGGAAGCAUACAAC AGGGCACGGUGCCAGAACUUCUACAGAGCCAACCACGGA CUACGGAGGGGACAGCACAAACGCCAGACCGCGGUACAA UGCGACCACAUACCUGCCUCCCUCAACUUCGAGUAAGCUG CGACCCAGAUGGACCUUUAUUCUCCUCCUGUACCAACCG CUAAGCCACCGUCCCGGUUCCACCUACUUCACAGCCUAG AUUCUCCAAUCUGAGCAUGCUUGUCCUACAGUGGGCAUC ACUCGCGGUACUAAACUUGCUGCUACUGUUGGUGAUGGC	

	GGACUGCGCGUUCGCCGCAACUUAUCCACCUCACACG UACACAACACCUCUUAUGAUGACGCUGAGACUACGUC	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENATNLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTN ITAVVRAQGLDVTPLSLPTSAQDSNFSVKTEMLGNEIDIECIM EDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGT GYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQS NIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSP NVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASN RTFDITVSGLGTAPKTLITRTATNATTTTHKVIFSKAPESTTTS PTLNTTGAFADPNTTTGLPSSTHVPTNLTAPASTGPTVSTADVTS PTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPTPN ATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS AVT TPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNATS AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLLT AHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSS TSTKPGEVNVTKGTPPQNATSPQAPSGQKTA VPTVTSTGGKA NSTTGKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYLPP STSSKLRPRWTFSTPPVTTAQATVPVPPTSQPRFNSMLVLQ WASLAVLTLLLLVMADCAFRRLSTSHYTTTPYDDAETYV	127
PolyA tail	100 nt	
SE_EBV gB_019		
SEQ ID NO: 209 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 128, and 3' UTR SEQ ID NO:3		209
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGACCCGGCGGGGUGUUAAGCGUGGUGGUGCUCUUA GCCGCCUUAAGCCUGCCGGCUUGGCGCCAGACUCCGGAGC AGCCCGCUCCUCCCGCCACCACCGUCCAGCCACCGCCAC CCGCCAGCAGACCUCCUUCUCCUUCGCGUCUGCGAGCUC UCCUCCACGGCGACCUCUUCGCGUUCUCCUCCGACAUC AGUGCCCCUCCUUCGGCACCCGCGAGAACCACACCGAGGG CCUCCUCAUGGUCUUAAGGACAACAUAUCCCCUACUCC UUAAGGUCCGCUCCUACACCAAGAUCGUCACCAACAUC UCAUCUACAACGGCUGGUACGCCGACUCUGUGACUAAUC GCCACGAGGAGAAGUUCUCCGUCGACUCCUACGAGACUG ACCAGAUGGACACCAUCUACCAGUGCUACAACGCCGUCA AGAUGACCAAGGACGGCCUCACCCGCGUCUACGUCGACCG CGACGGCGUCAACAUCACCGUCAACCUCAAGCCUACAGGC GGCCUCGCCAACGGCGUCCGCCGCUACGCCUCCAGACCG AGCUCUACGACGCCCCUGGCUGGCUCUACUGGACCUACCG CACCAGGACCACUGUCAAUUGCCUCAUACCGACAUGAU GGCCAAGUCCAACUCCCCUUCGACUUCUUCGUGACCACC ACAGGCCAGACCGUCGAGAUGUCGCCAUUCUAUGACGGC AAGAACAAGGAGACUUUCCACGAGAGAGCGGACUCUUUC CAUGUCCGCACCAACUACAAGAUUGUCGACUACGACAAC CGCGGCACCAAUCCACAGGGCGAGCGCCGCGCCUUCUUCG ACAAGGGCACCUACACCCUCUCCUGGAAGCUCGAGAACCG CACCGCCUACUGUCCUCUCCAGCACUGGCAGACCUUCGAU UCCACCAUCGCCACCGAGACUGGCAAGUCCAUCAUUCG UCACCGACGAAGGAACAUCUUAUUCGUCACAAUACAA	128

	CCGUGGGCAUCGAGCUCCCCGACGCCUUCAAGUGCAUCGA GGAGCAGGUCAACAAGACCAUGCACGAGAAGUACGAGGC CGUCCAGGACCGGUUAUACAAAGGGCCAGGAGGCCAUAC CUACUUAUCACCAGCGGAGGUCUGCUUCUCGCCUGGCU UCCACUCACACCUCGCUCCCUGGCCACAGUGAAGAACCUC ACUGAGUUGACCACCCCAACAAGUCCCCACCUAGUAGUC CUAGCCCUCCUGCUCCUUCGCGCGCCGCGGCCUCCACGCC UGCCGCGGUCCUGCGGAGACGGAGAAGGGACGCCGGCAA CGCUACCACUCCUGUGCCGCCGACAGCCCCUGGAAAGUCC CUAGGUACCCUCAACAACCCAGCGACAGUUCAGAUCCAG UUCGCCUACGACUCUCUCAGGCGCCAGAUCAACCGCAUGC UUGGUGACCUUGCCCGCGCCUGGUGCCUCGAGCAGAAGC GCCAGAACAUUGGUGCUUCGUGAACUAACAAAGAUUAUC CUACUACAGUGAUGUCCUCCAUCUACGGCAAGGCCGUCG CCGCCAAGCGCCUCGGCGACGUCAUCUCCGUCUCCAGUG CGUCCCAGUGAACCAGGCUACCGUGACCCUCAGGAAGUCC AUGAGAGUGCCAGGCUCCGAGACAAUGUGCUACUCCCGC CCACUCGUCUCCUUCUCCUUAUCAACGACACAAAGACCU ACGAGGGCCAGUUAAGGCACUGACAACGAGAUCUUCUUGA CUAAGAAGAUGACUGAGGUUAUGCCAGGCAACUUCUCAAU ACUACUCCAGUCUGGAAAUGAGAUCCACGUUAUAACG ACUACCACCACUUAAGACUAUUGAACUCGACGGAAUUG CCACCCUCCAAACAUAUCUACUGAAUACCUCCCUCAU CGAGAACAUUGACUUCGCCUCCUCCUGAGCUGUAUAGCAG AGACGAGCAGCGCGCCUCCAACGUCUUCGACCUAGGGGC AUCUUCGCGAGUACAACUUCAGGCACAGAACAUAGCC GGCCUCCGUAAGGAUCUGGACAAUGCCGUGUCCAACGGC CGCAACCAGUUCGUCGACGGUUUGGGUGAACUCAUGGAC UCUCUGGGCUCGUGCGGCCAGUCCAUAACUAAUAGUC UCUACGGUGGGAGGCCUAUUCAGCAGCCUGGUGAGCGGC UUAUCUCUUAUCUUAAGAACCCUUCGGCGGCAUGCUC AUCCUCGUCCUCGUCGCCGGCGUCGUCAUACUGGUGAUC UCACUCACAAGGAGGACGCGCCAAAUGUCCCAGCAGCCA GUGCAGAUUCUCUACCCAGGCAUAGACGAGCUCGCUCAG CAGCACGCGUCGGGUGAGGGACCAGGCAUCAAUCCUAUC UCCAAGACUGAGCUGCAAGCCAUAUAGCUCGCCCCUCCACG AGCAGAACCAGGAACAGAAAGCGGGCCGCCAGCGAGCUG CCGGCCCCUCCGUCGCCAGUAGGGCACUACAAGCCGCCG GGACCGCUUCCAGGCCUGAGAAGGAGGAGAUACCACGA CCCAGAGACAGCCGUGCCCUCCUUGGCGAAGCAGAAACC GAGUUC	
3' UTR	UGAUAUUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MTRRRVLSVVLLAALACRLGAQTPEQPAPPATTVQPTATRQ QTSFPRVCELSSHGDLFRFSSDIQCPSTRENHTEGLLMVFK DNIIPYSFKVRSYTKIVTNILIYNGWYADSVNTRHEEKFSVDSY ETDQMDTIYQCYNAVKMTKDGLTRVYVDRDGVNITVNLKPT GGLANGVRRYASQTELYDAPGWLIWYRTRTTVNCLITDMM AKSNSPFDFVTTTGQTVEMSPFYDGKNKETFERADSFHVR TNYKIVDYDNRGTNPQGERRAFLDKGTYTLSWKLENRTAYC PLQHWQTFDSTIATETGKSIHFVTDEGTSSFVTNTTVGIPLDA FKCIEEQVNKTMHEKYEAVQDRYTKGQEAITYFITSGGLLLA WLPLTPRSLATVKNLTELTTPTSSPPSSPSPPAPSAARGSTPAA VLRRRRRRDAGNATTPVPPTAPGKSLGTLNPNPATVQIQFAYDSL RRQINRMLGDLARAWCLEQKRQNMVLRELTKINPTTVMSSIIY GKAVAAKRLGDVISVSQCVPVNQATVTLRKSMRVPGETMC YSRPLVSFSFINDTKTYEQLGTDNEIFLTKKMTVEVCQATSQY YFQSGNEIHVYNDYHHFKTIELDGIATLQTFISLNTSLIENIDFA SLELYSRDEQRASNVDLEGIFREYNFQAQNIAGLRKDLDNAV	129

	SNGRNQFVDGLGELMDSLGSVGSITNLVSTVGGFLFSSLVSGF ISFFKNPFGGMLILVLVAGVVILVISLTRRTRQMSQQPVQMLY PGIDELAQQHASGEGPGINPISKTELQAIMLALHEQNQEKKRA AQRAAGPSVASRALQAARDRFPGLRRRRYHDPETAAALLGE AETEF	
PolyA tail	100 nt	
V3_NGM 6mut CR2_EBV_gp350_001		
SEQ ID NO: 210 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 1, mRNA ORF SEQ ID NO: 211, and 3' UTR SEQ ID NO:3.		210
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGAGCCACC	1
ORF of mRNA Construct (excluding the stop codon)	AUGGAGGCAGCACUGCUGGUCUGCCAGUAUACAAUCCAG UCGCUCAUUCUACUGACAGGCGAGGACCCCGGCUUCUUU AACGUGGAAAUCCCAGAGUCCCCUUCUAUCCAACCUGU AACGUUUGCACUGCUGACGUGAACGUGACAAUCAAUUUC GACGUGGGAGGAAAGAAGCAUCAGCUUGAUCUGGAUUUC GGCCAACUGACGCCACACACCAAAGCGGUGUACCAACCAA GGGGUGCAUUUGGAGGGAGCGAGAAUGCUGCGAAUCUGU UCUUCUGGAACUGCUUGGUGCAGGAGAGCUGGCACUAA CCAUGCGAAGCAAGAAGCUCUCCCAUCAACGUUACCACCGG GGAAGAACAGCAAGUCAGCCUUGAAUCCGUGGAUGUGUA CUUUCAGGAUGUUUUCGGCACCAUGUGGUGUCACCACGC UGAGAUGCAGAAUCCCGUGUAUCUCAUACCCGAGACUGU ACCCUACAUCAAGUGGGUAUAAUUGCAAUUCAGCGAAUAU UACGGCUGUGGUGAGGGCCAGGGCUUGGACGUGACUCU GCCCUAUCUCUACCUACUUCUGCCCAAGACUCCAUUUC GCGGUCAAGACCGAGAUGCUCGGGAAUGAGAUCGAUAUC GAGUGCAUCAUGGAGGACGGUGAGAUAAAGCCAGGUUCUG CCCGGCGACAACAAGUUCAAUAUCGCGUGUUCUGGGCUAC GAGUCCCAUGUGCCUAGUGGUGGGCAUACUCACAAGUACU UCUCCCGUAGCCACGCCCAUUCUCCGGAACCGGAUACGCCU ACAGUCUGCGUCUGACCCACGGCCUGUGUCCAGAUUCCU GGGUAACAAUAGUAUCUUAUACGUGUUUUAUAGCGGAAA CGGCCCUAAAGCGUCCGGAGGGGACUUAUGUAUUCAGAG UAAUAUCGUUUUCUCUGAUGAGAUUCCUGCCAGUACGGA CAUGCCGACAAACACAACUGAUUUUACCUACGUGGGCGA CAAUGCCACGUAUUCAGUGCCCAUGGUCACGAGCGAGGA CGCCAAUUCACCAAUUGUUGCGGUAACAGCUUUCUGGGC CUGGCCAAUUAACACUGAGACUGACUCAAUUGUAAGUG GACUUUGACCUCUGGAACUCCGUCGGGUUGCGAGAAUAU CAGCGGGGCCUUUGCUUCCAACAGGACUUUCGACAUCAC UGUCUCAGGGCUGGGGACAGCACCGAAGACAUUAAUCAU AACACGGACCGCCACCAACGCCGCGACUACAACCCAUAA GUGAUCUUUUCUAAAGGCACCUAGUCCACCACUACCUCUCC CGACUCUUAACACUACGGGCUUCGUGAUCCCAACACCAC UACGGGGUUGCCUAGCUCGACACAUGUGCCGACGAACCU GACUGCCCCUGCAUCGACCGGGGCCACAGUUUCGACCGCC GAUGUGACAUCACCAACGCCCGCAGGUACAACCUCAGGC GCCAGCCCAGUGACCCCUUCCCCAAGCCCCUGGGUAUAAUG GAACGGAGUCCAAGGCUCCUGAUUAGACUCCUCUACCA GCCCCGUGACUACACCCACUCCCAACGCAACUAGCCCAAC CCCAGCUGUGACGACGCCACCCGAACGCGACAUCUCCC ACACCUGCUGUGACAACCCCAACCCCUAACGCCACUAGCC CUACCCUAGGUAAAGACCAGUCCGACUAGCGCCGUUACAA CCCCUACCCCUAACGCAACCGGCCCGACCGUGGGCGAGAC UCCCCGCAAGCCAAUGCGACAAAUCACACAUUGGGCGG GACCUCUCCUACACCAGUCGUUACAUCUCAGCCUAAGAAC	211

	GCUACCUCCGUGUCACUACCGGACAGCACAACAUCACCA GCUCAAGCACGAGUUCUUGAGCUUGCGGCCGAGCUCAA AUCCCGAGACCCUUAUACCAUCCACAUAGACAACAGUAC UUCACACAUGCCACUCUUGACGAGCGCUCACCCACCGGC GCGGAGAAACUACCCAGGUGACUCCGGCGUCUAAUUC ACCCACCACGUCAGCACGUCGUCUCCCGCACCAGACCAG GGACGACUUCUCAGGCCAGUGGGCCUGGCAACUCCUCUA CAAGCACAAAGCCAGGCGAAGUUAACGUGACAAAGGGAA CGCCUCCCCAGAACGCAACCAGUCCUCAGGCGCCCAGCGG GCAGAAGACUGCGGUGCCAACUGUGACCAGCACCGGUGG CAAGGCCAACUCAACAACUGGAGGCAAGCAUACGACGGG GCACGGCGCCCGGACCUCACUGAACCCACGACCGAUUAC GGAGGUGACAGCACAAACCCGCGGCCACGAUAAUUGCC ACCACUUAUCUGCCACCAUCCACAAGCUCCAAGCUGCGGC CACGGUGGACCUUCACAAGCCCACCCGUGACGACUGCCCA AGCGACGGUGCCAGUGCCACCUACAAGCCAGCCACGCUUC UCCAACCUUAGUAGCUCGUUCUCCAGUGGGCCAGCCUU GCUGUUCUGACCCUCCUCCUGCUGCUGUGAUGGCCGAU UGCGCCUUUAGGAGAAACCUCAGCACUAGCCACACGUAC ACCACGCCGCCCUACGAUGACGCCGAGACUUAACGUC	
3' UTR	UGAUAAUAGGCUUGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGS ENAANLFLELLGAGELALTMRSKKLPINVTTGEEQQVSLESV DVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSAN ITAVVRAQGLDVTPLSLPTSAQDSNFAVKTEMLGNEIDIECI MEDGEISQVLPDGNKFNIACSGYESHVPSGGILTSTSPVATPIP GTGYAYSLRLTPRPVSRFLGNNISILYVFYSGNGPKASGGDYCI QSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDAN SPNVAVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFA SNRTFDITVSGLTAPKTLITRTATNAATTTTHKVIFSKAPESTT TSPTLNTTGFADPNNTTGLPSSTHVPTNLAPASTGPTVSTADV TSPTPAGTTSASPVTSPSPWDNGTESKAPDMTSSTSPVTTPT PNATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTS VTTPTPNATGPTVGETSPQANATNHTLGGTSPTPVVTSQPKNA TSAVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSDNSTSHMPLL TSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGN SSTSTKPGEVNVTKGTPPQATSPQAPSGQKTAVPTVSTGGK ANSTTGKKHTTGHGARTSTEPTTDYGGDSTTPRPRYNATTYL PPSTSSKLRPRWFTSPPVTTAQTVPVPPTSQPRFSNLSMLVL QWASLAVLTLTLLLLVMADCAFRRNLSTSHTYTTPPYDDAETY V	70
PolyA tail	100 nt	
EBV Linked Construct 1 (1723942)		
SEQ ID NO: 212 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 213, and 3' UTR SEQ ID NO:106.		212
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGGUGAGCUUCAAGCAGGUGAGAGUGCCCCUGUUCACC GCCAUCGCCCUGGUGAUCGUGCUGCUGGCCUACUUC UGCCACCCAGAGUGAGAGGCGGCGGCAGAGUGGCCCGCCG CCGCCAUCACCUGGGUGCCCAAGCCCAACGUGGAGGUGU GGCCCGUGGACCCGCCACCUCGCCUGAACUUAACAAGAC CGCCGAGCAGGAGUACGGCGACAAGGAGGUGAAGCUGCC	213

CCACUGGACGCCGACCCUGCACACCUUCCAGGUGCCCCAG AACUACACCAAGGCCAACUGCACCUCACUGCAACACCAGAG AGUACACCUUCAGCUACAAGGGCUGCUGCUUCUACUUA CCAAGAAGAAGCACACCUGGAACGGCUGCUUCCAGGCCU GCGCCGAGCUGUACCCUGCACCUCUUCUACGGCCCCAC CCCAGACAUCCUGCCCGUGGUGACCAGAAACCUGAACGCC AUCGAGAGCCUGUGGGUGGGCGUGUACAGAGUGGGCGAG GGCAACUGGACCAGCCUGGACGGCGGCACCUUCAAGGUG UACCAGAUUCUGGCAGCCACUGCACCUCAGUGAGCAAG UUCAGCACCGUGCCCGUGAGCCACCACGAGUGCAGCUUCC UGAAGCCCUGCCUGUGCGUGAGCCAGAGAAGCAACAGCG GCACUAGCGGCUCUAGCGGAUCAGGCAGCGGAGGGAGUG GAGGCUCAGGAGGGACCAGCGGCAGCAGUGGCUCCGGAA GCGGAGGCAGCCCCUGCUGCCACGUGACCCAGCUGAGAGC CCAGCACCUUGCUGGCCCUGGAGAACAUACAGCGACAUCUAC CUGGUGAGCAACCAGACCUGCGACGGCUUCAGCCUGGCC AGCCUGAACAGCCCCAAGAACGGCAGCAACCAGCUGGUG AUCAGCAGAU GCGCCAACGGCCUGAACGUGGUGAGCUUC UUCAUCAGCAUCCUGAAGAGAAGCAGCAGCGCCUGACC GGCCACCUGAGAGAGCUGCUGACCACCCUGGAGACCCUG UACGGCAGCUUCAGCGUGGAGGACCUGUUCGGCGCCAAC CUGAACAGAUACGCCUGGCACAGAGGCGGCGGAGGAGGU GGCUCCGGUGGAGGUGGCAGCGGAGGAGGAGGCAGUGGU GGCGGAGGCAGCCUUCAGCGAGGUGAAGCUCCACUUGGAC AUCGAGGGCCACGCCAGCCACUACACCAUCCCCUGGACCG AGCUCAUGGCCAAGGUGCCCCGGCCUUCAGCCCCGAGGCCU GUGGCGGGAGGCCAACGUGACCGAGGACCUGGCCAGCAU GCUGAACCGGUACAAGCUGAUUCUACAAGACCAGCGGCAC CCUGGGCAUCGCCCUGGCCGAGCCCGUGGACAUCCCCGCC GUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGCAAGGUG CACCCCGGCGUGAUCAGCGGCCUGAACAGCCCCGCCUGUA UGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCUACUACA UCGGCACCAUGCUGCCCAACACCCGGCCCCACAGCUACGU GUUCUACCAGCUGCGGUGCCACCUGAGCUACGUUGCCCU GAGCAUCAACGGCGACAAGUUCAGUACACCGGCGCCAUC GACCAGCAAGUUCUGAUGGGCACCUACAAGCGGGUCAC CGAGAAGGGCGACGAGCACGUGCUGUCACUGGUGUUCGG CAAGACCAAGGACCUGCCCGACCUGCGGGGCCCCUUCAGC UACCCUAGUUUGACCAGCGCCAGAGCGGCGACUACAGC UUGGUGAUCGUGACCACCUUCGUGCACUACGCCAACUUC CACAACUACUUCGUGCCCAACCUGAAGGACAUGUUCAGC CGGGCCGUGACCAUGACUGCCGCUUCUUCAGCCCCGGUACG UGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGGGCGGCU GCCGGGAGCCCGAGCUGGACACCGAAACACUGACCACCAU GUUCGAGGUGAGCGUGGCCUUCUUCUUAAGGUGGGUACGC GGUGGGCGAAACCGGCAACGGCUGCGUGGACUUCAGCUG GCUGGCCAAGAGCUUCUUCGAGCUGACCGUGCUGAAGGA UAUCAUCGGCAUCUGCUACGGCGCCACCUGAAGGGCAU GCAGAGCUACGGCCUGGAGCGGCUGGCCGCCAUGCUUAU GGCAACAGUGAAGAUGGAGGAGCUGGGACACCUGACAAC AGAGAAGCAGGAGUACGCCUGAGACUGGCCACAGUGGG CUACCCAAAGGCCGCGUGUACAGUGGACUGAUCGGCGG CGCAACCAGCGUGCUGCUAUCCGCUUACAACCGGCACCCG CUGUUCAGCCCCUGCACACCGUGAUGCGGGAAACCCUGU UCAUCGGAAGCCACGUCGUGCUGCGGGAGCUGAGGCUGA ACGUAAACACCCAGGGCCCUAAUCUGGCCUGUAUCAGCU CCUCAGUACCGCCUGUGCAGCGCCCUUGAGAUCGGCGAG GUGCUCAGAGGCCUGGCCUCGGUACCGAGAGCGGCCUC UUCAGCCCAUGCUACUUAAGCCUGCGGUUCGACCUGACCC GGGACAAGUUGCUGAGCAUGGCCCGCAGGAGGCCACAC UGGACCAGGCAGCUGUAUCCAACGCCGUGGACGGCUUCC UGGGCAGACUGUCCUGGAACGGGAGGACCGGGACGCCU	

	GGCACCUGCCUGCCUACAAGUGUGUGGAUCGGCUGGACA AGGUGCUGAUGAUAUCCUCUGAUUAAUGUCACCUUCA UCAUCAGCAGCGACCGGGAGGUGCGGGGAUCCGCCUCU ACGAGGCCAGCACCACCUAUCUGAGCAGCAGCCUGUCCU GUCUCCUGUGAUAUGAACAAGUGCAGCCAGGGCGCCGU GGCCGGCGAGCCCCGGCAGAUCCCCAAGAUCAGAACUUC ACCCGGACCCAGAAGUCUUGCAUCUUCUGCGGCUUCGCC UUUUGUCCUACGACGAGAAGGAGGGCUUGGAGACUACAA CCUACAUCACCAGCCAGGAGGUGCAGAACAGCAUCCUGU CAUCUAAUUAUCUUGGACUUCGACAACCUGCACGUUCAU ACCUGCUCCUACACCAACGGUACCGUCAUGGAAAUCCG CGGACUGUACGAGGAGCGGGCCCAUGUUGUGCUGGCCAU CAUCCUGUACUUCGCUUUCGCACUUGGCAUCUUCU GGUGCACAAGAUCGUGAUGUUCUUCUG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVRGGRVAAA ITWVPKPNVEVWPVDP PPPVNFNKTAEQEYGDKEVKLP HWTPTLHTFQVPQNYTKANCTYCNTRYTFSYKGCFFYFT KKKHTWNGCFQACAELYPCTYFYGPTDILPVVTRNLNA IESLWVG VYRVGEGNWTSLDGGTFKVYQIFGSHCTYVSK FSTVPVSHHECSFLKPCLCVSQRSNSGTSGSSGSGSGG SGSGGTSGSSGSGSGSGSPCCHVTQLRAQHLLALENIS DIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFVDELFG ANLNR YAWHRGGGGGGSGGGGSGGGSGGSGSLSEVKL HLDIEGHASHYTIPWTELMKVPLSPEALWREANVTEDL ASMLNRYKLIYKTSGLGIALAEPVDIPAVSEGSMQV DASKVHPGVISGLNSPACMLSAPLEKQLFYIYGTMLPN TRPHSYV FYQLRCHLSYVALSINGDKFQYTGAMTSKFL MGTYKRVTEKGDEHVLSLVFGKTKDLPDLRGPFSYPSL TSAQSGDYSLVIVTTTFVHYANFNHYFVPNLKDMFSRA VTMTAASYARYVLQKLVLLEMKGKCREPELDTETLTMT FEVSVAFFKVGHAVGETGNVCVDRWLAKSFFELTVLK DIIGICYGATVKGMQSYGLERLAAMLATVKMEELGHLT TEKQEYALRLATVGYPKAGVYSGLIGGATSVLLSAYNR HPLFQPLHTVMRETLFIGSHVVLRELRLNVTQQPNLAL YQLLSTALCSALEIGEVLRGLALGTESGLFSPCYLSL RFDLTRDKLLSMAPQEATLDQAAVSNVAVDGFGLRSL LEREDRDAWHLPAYKCVDRLDKVLMIPLINVTFIISDRE VRGSALYEASTTYLSSSLFLSPVIMNKCSQGA VAGEPR QIPKIQNFRTQKSCIFCGFALLSYDEKEGLETTTYITSQ EVQNSILSSNYFDFDNLVHYLLTTNGTVMEIAGLYEER AHVVLAILLYFIAFALGIFLVHKIVMFFL	214
PolyA tail	100 nt	
EBV Linked Construct 2 (1723941)		
SEQ ID NO: 215 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 216, and 3' UTR SEQ ID NO: 106.		215
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGGUGAGCUUCAAGCAGGUGAGAGUGCCCCUGUUCACC GCCAUCGCCCUGGUGAUCGUGCUGCUGGCCUACUUC UGCCACCCAGAGUGAGAGGCGGCGGCAGAGUGGCCCGCCG CCGCCAUCACCUGGGUGCCCAAGCCCAACGUGGAGGUGU GGCCCGUGGACCCGCCACCUCGUGAACUUAACAAGAC CGCCGAGCAGGAGUACGGCGACAAGGAGGUGAAGCUGCC CCACUGGACGCCGACCCUGCACACCUUCCAGGUGCCCCAG	216

	AACUACACCAAGGCCAACUGCACCUCACUGCAACACCAGAG AGUACACCUUCAGCUACAAGGGCUGCUGCUUCUACUUCA CCAAGAAGAAGCACACCUGGAACGGCUGCUUCCAGGCCU GCGCCGAGCUGUACCCUGCACCUCUUCUACGGCCCCAC CCCAGACAUCCUGCCCGUGGUGACCAGAAACCUGAACGCC AUCGAGAGCCUGUGGGUGGGCGUGUACAGAGUGGGCGAG GGCAACUGGACCAGCCUGGACGGCGGCACCUUCAAGGUG UACCAGAUUCUGGCAGCCACUGCACCUCAGUGAGCAAG UUCAGCACCGUGCCCGUGAGCCACCACGAGUGCAGCUUCC UGAAGCCCUGCCUGUGCGUGAGCCAGAGAAGCAACAGCG GAGGAGGAGGAUCUGGAGGGCGGCGGAAGUGGUGGAGGAG GAAGCGGAGGAGGUGGCAGCGGAGGUGGUGGAAGUGGCG GCGGAGGAAGCCCCUGCUGCCACGUGACCCAGCUGAGAG CCCAGCACCUUGCUGGCCUGGAGAACAUACGCGACAUCUA CCUGGUGAGCAACCAGACCUGCGACGGCUUCAGCCUGGCC AGCCUGAACAGCCCCAAGAACGGCAGCAACCAGCUGGUG AUCAGCAGAU GCGCCAACGGCCUGAACGUGGUGAGCUUC UUCAUCAGCAUCCUGAAGAGAAGCAGCAGCGCCUGACC GGCCACCUGAGAGAGCUGCUGACCACCCUGGAGACCCUG UACGGCAGCUUCAGCGUGGAGGACCUGUUCGGCGCCAAC CUGAACAGAUACGCCUGGCACAGAGGCGGCGGAGGAGGU GGCUCCGGUGGAGGUGGCAGCGGAGGAGGAGGCAGUGGU GGCGGAGGCAGCCUAGCGAGGUGAAGCUCCACUUGGAC AUCGAGGGCCACGCCAGCCACUACACCAUCCCCUGGACCG AGCUCAUGGCCAAGGUGCCCGGCCUAGCCCCGAGGCCCU GUGGCGGGAGGCCAACGUGACCGAGGACCUGGCCAGCAU GCUGAACCGGUACAAGCUGAUCAACAAGACCAGCGGCAC CCUGGGCAUCGCCUGGCCGAGCCCGUGGACAUCCCCGCC GUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGCAAGGUG CACCCCGGCGUGAUACAGCGGCCUGAACAGCCCCGCCUGUA UGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCUACUACA UCGGCACCAUGCUGCCCAACACCCGGCCCCACAGCUACGU GUUCUACCAGCUGCGGUGCCACCUGAGCUACGUUGCCCU GAGCAUCAACGGCGACAAGUUCAGUACACCGGCGCCAU GACCAGCAAGUUCUGAUGGGCACCUACAAGCGGGUCAC CGAGAAGGGCGACGAGCACGUGCUGUCACUGGUGUUCGG CAAGACCAAGGACCUGCCCGACCUGCGGGGCCCCUUCAGC UACCCUAGUUUGACCAGCGCCAGAGCGGCGACUACAGC UUGGUGAUCGUGACCACCUUCGUGCACUACGCCAACUUC CACAACUACUUCGUGCCCAACCUGAAGGACAUGUUCAGC CGGGCCGUGACCAUGACUGCCGCUUCUACGCCCGGUACG UGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGGGCGGCU GCCGGGAGCCCGAGCUGGACACCGAAACACUGACCACCAU GUUCGAGGUGAGCGUGGCCUUCUUCAAGGUGGGUACGC GGUGGGCGAAACCGGCAACGGCUGCGUGGACUUCAGCUG GCUGGCCAAGAGCUUCUUCGAGCUGACCGUGCUGAAGGA UAUCAUCGGCAUCUGCUACGGCGCCACCGUGAAGGGCAU GCAGAGCUACGGCCUGGAGCGGCUGGCCGCCAUGCUUAU GGCAACAGUGAAGAUGGAGGAGCUGGGACACCUGACAAC AGAGAAGCAGGAGUACGCCCUGAGACUGGCCACAGUGGG CUACCCAAAGGCCGCGUGUACAGUGGACUGAUCGGCGG CGCAACCAGCGUGCUGCUAUCCGCUUACAACCGGCACCCG CUGUUCAGCCCCUGCACACCGUGAUGCGGGAAACCCUGU UCAUCGGAAGCCACGUCGUGCUGCGGGAGCUGAGGCUGA ACGUAACCACCCAGGGCCCUAAUCUGGCCUGUAUCAGCU CCUCAGUACCGCCUGUGCAGCGCCCUUGAGAUCGGCGAG GUGCUCAGAGGCCUGGCCUCGGUACCGAGAGCGGCCUC UUCAGCCCAUGCUACUUAAGCCUGCGGUUCGACCUGACCC GGGACAAGUUGCUGAGCAUGGCCCCGCAGGAGGCCACAC UGGACCAGGCAGCUGUAUCCAACGCCGUGGACGGCUUCC UGGGCAGACUGUCCUGGAACGGGAGGACCGGGACGCCU GGCACCUGCCUGCCUACAAGUGUGUGGAUCGGCUGGACA	

	AGGUGCUGAUGAUGAUAUCCUCUGAUUAAUGUCACCUUCA UCAUCAGCAGCGACCGGGAGGUGCGGGGAUCCGCCUCU ACGAGGCCAGCACCACCUAUCUGAGCAGCAGCCUGUCCU GUCUCCUGUGAUGAUGAACAAGUGCAGCCAGGGCGCCGU GGCCGGCGAGCCCCGGCAGAUCCCCAAGAUCCAGAACUUC ACCCGGACCCAGAAGUCUUGCAUCUUCUGCGGCUUCGCC UUUUGUCCUACGACGAGAAGGAGGGCUUGGAGACUACAA CCUACAUCACCAGCCAGGAGGUGCAGAACAGCAUCCUGU CAUCUAAUUAUCUUCGACUUCGACAACCUGCACGUUCAU ACCUGCUCCUACACCACCAACGGUACCGUCAUGGAAAUCCG CGGACUGUACGAGGAGCGGGCCCAUGUUGUGCUGGCCAU CAUCCUGUACUUCAUCGCUUUCGCACUUGGCAUCUCCU GGUGCACAAGAUCGUGAUGUUCUCCUG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVGGGRVAAAAT WVPKPNVEVWPVDPPPPVNFNKTAEQEYGDKEVKLPHWTPT LHTFQVPQNYTKANCTYCNTRYTFSYKGCCFYFTKKKHTW NGCFQACAELYPCTYFYGPTDILPVVTRNLNAIESLWVG VYR VGEWNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPVSHHECSFL KPCLCVSQRSNSGGGSGGGGSGGGGSGGGGSGGGGSGGGG SPCCHVTQLRAQHLLALENISDIYLVSNQTCDFSLASLNSPK NGSNQLVISRCANGLNVVSSFFISILKRSSSALTGHLRELLTLET LYGSFSVEDLFGANLNRYAWHRGGGGGSGGGGSGGGGSGG GGSLSEVKLHLDIEGHASHYTIPWTELMKVPGLSPEALWR EANVTEDLASMLNRYKLIYKTSGLTGIALAEPVDIPAVSEGSM QVDASKVHPGVISGLNSPACMLSAPLEKQLFYIIGTMLPNTRP HSYVFYQLRCHLSYVALSINGDKFQYTGAMTSKFLMGTYKR VTEKGDEHVLSLVFGKTKDLPDLRGPFSSYPSLTSAQSGDYSLV IVTTFVHYANFNHYFVFNKDMFSRAVTMTAASYARYVLQK LVLLEMKGKCREPELDTETLTTFEVSVAFFKVGHAVGETGN GCVDLRWLAKSFFELTVLKDIIICYGATVKGMQSYGLERLA AMLMATVKMEELGHLTTEKQEYALRLATVGYPKAGVYSGLI GGATSVLLSAYNRHPLFQPLHTVMRETLFIGSHVVLRELRLNV TTQGPNLALYQLLSTALCSALEIGEVLRGLALGTESGLFSPCYL SLRFDLTRDKLLSMAPQEATLDQAAVSNVAVDGLGRSLERE DRDAWHLPAYKCVDRDLKVLMIPLINVTFISSDREVRSAL YEASTTYLSSSLFLSPVIMNKCSQGAVAGEPRQIPKIQNFTRTQ KSCIFCGFALLSYDEKEGLETTTYITSQEVQNSILSSNYFDFDN LHVHYLLLTNGTVMEIAGLYEERAHVVLAILYFIAFALGIFL VHKIVMFFL	217
PolyA tail	100 nt	
EBV Linked Construct 3 (1723940)		
SEQ ID NO: 218 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 219, and 3' UTR SEQ ID NO: 106.		218
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUCCUGGCCAUCUGCCUGGUG ACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAUCAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCGUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUCAUCAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCGGCCACCUGAGA	219

	GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUAC GCCUGGCACAGAGGCGGCGGAGGAGGUGGCAGCGGAGGA GGAGGGUCUGGAGGUGGCGGCAGCCUAGCGAGGUGAAG CUCCACUUGGACAUCGAGGGCCACGCCAGCCACUACACCA UCCCCUGGACCGAGCUCAUGGCCAAGGUGCCCGGCCUAG CCCCGAGGCCUGUGGCGGGAGGCCAACGUGACCGAGGA CCUGGCCAGCAUGCUGAACCGGUACAAGCUGAUCUACAA GACCAGCGGCACCCUGGGCAUCGCCCUGGCCGAGCCCGUG GACAUCCCCGCCGUAGCGAAGGCAGCAUGCAGGUGGAC GCCAGCAAGGUGCACCCCGGCGUGAUCAGCGGCCUGAAC AGCCCCGCCUGUAUGUUGAGCGCCCCACUGGAGAAGCAG CUGUUCUACUACAUCGGCACCAUGCUGCCCAACACCCGGC CCCACAGCUACGUGUUCUACCAGCUGCGGUGCCACCUGAG CUACGUUGCCCUGAGCAUCAACGGCGACAAGUUCAGUA CACCGGCGCCAUGACCAGCAAGUUCUGAUGGGCACCUAC AAGCGGGUACCGGAGAAGGGCGACGAGCACGUGCUGUCA CUGGUGUUCGGCAAGACCAAGGACCUGCCCGACCUGCGG GGCCCCUUCAGCUACCCUAGUUGUAGCCAGCGCCAGAGCG GCGACUACAGCUUGGUGAUCGUGACCACCUUCGUGCACU ACGCCAACUCCACAACUACUUCGUGCCCAACCUGAAGGA CAUGUUCAGCCGGGCCGUGACCAUGACUGCCGCUUCUUA CGCCCGGUACGUGCUGCAGAAGCUGGUCCUGCUGGAGAU GAAGGGCGGCGUGCCGGGAGCCCGAGCUGGACACCGAAAC ACUGACCACCAUGUUCGAGGUGAGCGUGGCCUUCUCAA GGUGGGUACGCGGUGGGCGAAACCGGCAACGGCUGCGU GGACUACGCUGGCUGGCCAAGAGCUUCUUCGAGCUGAC CGUGCUGAAGGAUAUCAUCGGCAUCUGCUACGGCGCCAC CGUGAAGGGCAUGCAGAGCUACGGCCUGGAGCGGCUGGC CGCCAUGCUUAUGGCAACAGUGAAGAUGGAGGAGCUGGG ACACCUGACAACAGAGAAGCAGGAGUACGCCUGAGACU GGCCACAGUGGGCUACCCAAAGGCCGGCGUGUACAGUGG ACUGAUCGGCGGCGCAACCAGCGUGCUGCUAUCCGCUUA CAACCGGCACCCGCUUUCAGCCCCUGCACACCGUGAUG CGGGAAACCCUGUUCUACGGAAGCCACGUCGUGCUGCGG GAGCUGAGGCUGAACGUAACCACCCAGGGCCCUAAUCUG GCCUGUAUCAGCUCCUCAGUACCGCCCUGUGCAGCGCCC UUGAGAUCGGCGAGGUGCUCAGAGGCCUGGCCUCGGUA CCGAGAGCGGCCUCUUCAGCCCAUGCUACUUAAGCCUGCG GUUCGACCUGACCCGGGACAAGUUGCUGAGCAUGGCCCC GCAGGAGGCCACACUGGACCAGGCAGCUGUAUCCAACGC CGUGGACGGCUUCCUGGGCAGACUGUCCUGGAACGGGA GGACCGGGACGCCUGGCACCUGCCUGCCUACAAGUGUGU GGAUCGGCUGGACAAGGUGCUGAUGAUAUCCUCUGAU UAAUGUCACCUUCAUCAUCAGCAGCGACCGGGAGGUGCG GGGAUCCGCCUCUACGAGGCCAGCACCAACUUCUGAGC AGCAGCCUGUCCUGUCUCCUGUGAUGAACAAGUGC AGCCAGGGCGCCGUGGCCGGCGAGCCCCGGCAGAUCCCCA AGAUCAGAACUUCACCCGGACCCAGAAGUCUUGCAUCU UCUGCGGCUUCGCCUUCUUGUCCUACGACGAGAAGGAGG GCUUGGAGACUACAACCUACAUCACCAGCCAGGAGGUGC AGAACAGCAUCCUGUAUCUAAUUAUCUUCGACUUCGACA ACCUGCACGUUCAUUAACUGCUCCUACCAACCAACGGUAC CGUCAUGGAAAUCGCCGGACUGUACGAGGAGCGGGCCCA UGUUGUGCUGGCCAUCAUCCUGUACUUAUCGCUUUCGC ACUUGGCAUCUUCUGGUGCACAAGAUCGUGAUGUUCUU CCUG	
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106

Corresponding amino acid sequence	MRAVGVLAICLVTIFVLPTWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFSVEDLFGANLNR YAWHRGGGGGGSGGGGGSGGGGSLSEVKLHLDIEGHASHYTIP WTELMKVPGLSPEALWREANVTEDLASMLNRYKLIYKTS TLGIALAEPVDIPAVSEGSMQVDASKVHPGVISGLNSPACMLS APLEKQLFYIYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDK FQYTGAMTSKFLMGTYKRVTEKGDHVLVSLVFGKTKDLPLD RGPFSPSLTSAQSGDYSLVIVTTTFVHYANFHNYPVNLKDMF SRAVTMTAASYARYVLQKLVLLEMKGKCREPELDTETLTMT FEVSVAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIGI CYGATVKGMQSYGLERLAAMLMA TVKMEELGHLTTEKQEY ALRLATVGYPKAGVYSGLIGGATSVLLSAYNRHPLFQPLHTV MRETLFIGSHVVLRELRLNVTTQGPNLALYQLLSTALCSALEI GEVLRGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLD QAAVSNAVDGFLGRLSLEREDRDAWHLPAYKCVDRDLKVL MIPLINVTFISSDREVRGSALYEASTTYLSSSLFLSPVIMNKCS QGAVAGEPRQIPKIQNFTRTQKSCIFCGFALLSYDEKEGLETTT YITSQEVQNSILSSNYFDFDNLHVHYLLLTNGTVMEIAGLYE ERAHVVLAILLYFIAFALGIFLVHKIVMFFL	220
PolyA tail	100 nt	
EBV Linked Construct 4 (1723939)		
SEQ ID NO: 221 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 222, and 3' UTR SEQ ID NO: 106.		221
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUUCUGGCCAUCUGCCUGGUG ACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAACAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUAUCAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCCGCCACCUGAGA GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUAC GCCUGGCACAGAGGCGGCGGAGGAGGUGGCUCGCGUGGA GGUGGCAGCGGAGGAGGAGGCAGUGGUGGCGGAGGCAGC CUUAGCGAGGUGAAGCUCCACUUGGACAUCGAGGGCCAC GCCAGCCACUACACCAUCCCCUGGACCGAGCUCAUGGCCA AGGUGCCCGGCCUUAAGCCCCGAGGCCUGUGGCGGGAGG CCAACGUGACCGAGGACCUGGCCAGCAUGCUGAACCGGU ACAAGCUGAUCUACAAGACCAGCGGCACCCUGGGCAUCG CCCUGGCCGAGCCCGUGGACAUCCCCGCGGUAGCGAAGG CAGCAUGCAGGUGGACGCCAGCAAGGUGCACCCCGGCGU GAUCAGCGGCCUGAACAGCCCCGCCUGUAUGUUGAGCGC CCCACUGGAGAAGCAGCUGUUCUACUACAUCGGCACCAU GCUGCCCAACACCCGGCCCCACAGCUACGUGUUCUACCAG CUGCGGUGCCACCUGAGCUACGUUGCCCUGAGCAUCAAC GGCGACAAGUUCAGUACACCGGCGCCAUGACCAGCAAG UUCUGAUGGGCACCACAAGCGGGUCACCGAGAAGGGC GACGAGCACGUGCUGUCACUGGUGUUCGGCAAGACCAAG GACCUGCCCGACCUGCGGGGGCCCCUUCAGCUACCCUAGUU UGACCAGCGCCAGAGCGGCGACUACAGCUUGGUGAUCG UGACCACCUUCGUGCACUACGCCAACUCCACAACUACUU CGUGCCCAACCUGAAGGACAUGUUCAGCCGGGGCCGUGAC CAUGACUGCCGCUUCUACGCCCGGUACGUGCUGCAGAA	222

	GCUGGUCCUGCUGGAGAUGAAGGGCGGCUGCCGGGAGCC CGAGCUGGACACCGAAACACUGACCACCAUGUUCGAGGU GAGCGUGGCCUUCUUAAGGUGGGUACGCGGUGGGCGA AACCGGCAACGGCUGCGUGGACUUACGCUGGCUGGCCAA GAGCUUCUUCGAGCUGACCGUGCUGAAGGAUAUCAUCGG CAUCUGCUACGGCGCCACCGUGAAGGGCAUGCAGAGCUA CGGCCUGGAGCGGCUGGCCGCCAUGCUUAUGGCAACAGU GAAGAUGGAGGAGCUGGGACACCUGACAACAGAGAAGCA GGAGUACGCCUGAGACUGGCCACAGUGGGCUACCCAAA GGCCGGCGUGUACAGUGGACUGAUCGGCGGCGCAACCAG CGUGCUGCUAUCCGCUUACAACCGGCACCCGCUGUCCAG CCCCUGCACACCGUGAUGCGGGAAACCCUGUUAUCGGA AGCCACGUCGUGCUGCGGGAGCUGAGGCUGAACGUAACC ACCCAGGGCCCUAAUCUGGCCUGUAUCAGCUCCUCAGUA CCGCCUGUGCAGCGCCCUUGAGAUCGGCGAGGUGCUC GAGGCCUGGCCCUUGGUACCGAGAGCGGCCUCUUCAGCCC AUGCUACUUAAGCCUGCGGUUCGACCUGACCCGGGACAA GUUGCUGAGCAUGGCCCCGCAGGAGGCCACACUGGACCA GGCAGCUGUAUCCAACGCCGUGGACGGCUUCCUGGGCAG ACUGUCCUGGAACGGGAGGACCGGGACGCCUGGCACCU GCCUGCCUACAAGUGUGUGGAUCGGCUGGACAAGGUGCU GAUGAUAUCCUCUGAUUAAUGUCACCUUCAUCAUCAG CAGCGACCGGGAGGUGCGGGGAUCCGCCCUUACGAGGC CAGCACCAACUUCUGAGCAGCAGCCUGUCCUGUCUCCU GUGAUAUGAACAAGUGCAGCCAGGGCGCCUGGCCGGC GAGCCCCGGCAGAUCCCAAGAUCCAGAACUUCACCCGGA CCCAGAAGUCUUGCAUCUUCUGCGGCUUCGCCCUUUGU CCUACGACGAGAAGGAGGGCUUGGAGACUACAACCUACA UCACCAGCCAGGAGGUGCAGAACAGCAUCCUGUCAUCUA AUUACUUCGACUUCGACAACCUGCACGUUCAUUAACUGC UCCUCACCACCAACGGUACCGUCAUGGAAAUCGCCGGACU GUACGAGGAGCGGGCCCAUGUUGUGCUGGCCAUCAUCCU GUACUUAUCGCUUUCGCACUUGGCAUCUCCUGGUGCA CAAGAUCGUGAUGUUCUCCUG	
3' UTR	UGAUAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	106
Corresponding amino acid sequence	MRAVGVFLAICLVITFVLPTWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFSVEDLFGANLNR YAWHRGGGGGGSGGGGSGGGGSGGGGSLSEVKLHLDIEGHA SHYTIPWTELMKVPGLSPEALWREANVTEDLASMLNRYKLI YKTSGLTGIALAEPVDIPAVSEGSMQVDASKVHPGVISGLNSP ACMLSAPLEKQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVAL SINGDKFQYTGAMTSKFLMGTYKRVTEKGDEHVLVSLVFGKT KDLPLDRGPFSSPSLTSAQSGDYSLVIVTTFVHYANFHNYP NLKDMFSRAVTMTAASYARYVLQKLVLLEMKGKCREPELDT ETLTMFEVSVAFFKVGHAVGETGNGCVDLRWLAKSFFELTV LKDIIGICYGATVKGMQSYGLERLAAMLMA TVKMEELGHLT TEKQEYALRLATVGYPKAGVYSGLIGGATSVLLSAYNRHPLF QPLHTVMRETLFIGSHVVLRELRLNVTQGPNLALYQLLSTAL CSALEIGEVLRLGLALGTESGLFSPCYLSLRFDLTRDKLLSMAP QEATLDQAAVSNAVDGFLGRSLEREDRDAWHLPAYKCVDR LDKVLMIPLINVTFISSDREVRGSALYEASTTYLSSSLFLSPVI MNKCSQGAVAGEPRQIPKIQNFRTQKSCIFCGFALLSYDEKE GLETTYITSQEVQNSILSSNYFDNHLVHYLLLTNTNGTVMEI AGLYEERAHVVLAILLYFIAFALGIFLVHKIVMFFL	223
PolyA tail	100 nt	
EBV gH (BXLF2)_RX - UTRB		

SEQ ID NO: 228 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 84, and 3' UTR SEQ ID NO:3		228
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGCAGUUGUUGUGCGUGUUCUGCCUCGUGUACUCUGG GAGGUGGGCGCCGCCAGCCUUAGCGAGGUGAAGCUCCAC UUGGACAUCGAGGGGCCACGCCAGCCACUACACCAUCCCCU GGACCGAGCUCAUGGCCAAGGUGCCCGGCCUUAGCCCCGA GGCCUGUGGGCGGGAGGCCAACGUGACCGAGGACCUGGC CAGCAUGCUGAACCAGGUACAAGCUGAUCUACAAGACCAG CGGCACCCUGGGCAUCGCCCUGGCCGAGCCCGUGGACAUC CCCGCCGUUAGCGAAGGCAGCAUGCAGGUGGACGCCAGC AAGGUGCACCCCGGCGUGAUCAGCGGCCUGAACAGCCCCG CCUGUAUGUUGAGCGCCCCACUGGAGAAGCAGCUGUUCU ACUACAUCGGCACCAUGCUGCCCAACACCCGGCCCCACAG CUACGUGUUCUACCAGCUGCGGUGCCACCUGAGCUACGU UGCCUGAGCAUCAACGGCGACAAGUUCAGUACACCGG CGCAUGACCAGCAAGUUCUGAUGGGCACCUCACAAGCG GGUACCGAGAAGGGCGACGAGCACGUGCUGUCACUGGU GUUCGGCAAGACCAAGGACCUGCCCCGACCUGCGGGGCCCC UUCAGCUACCCUAGUUUGACCAGCGCCAGAGCGGGCGAC UACAGCUUGGUGAUCGUGACCACCUUCGUGCACUACGCC AACUCCACAACUACUUCGUGCCCAACCUGAAGGACAUG UUCAGCCGGGCGGUGACCAUGACUGCCGCUUCUACGCCC GGUACGUGCUGCAGAAGCUGGUCCUGCUGGAGAUGAAGG GCGGCUGCCGGGAGCCCGAGCUGGACACCGAAACACUGA CCACCAUGUUCGAGGUGAGCGUGGCCUUCUUAAGGUGG GUCACGCGGUGGGCGAAACCGGCAACGGCUGCGUGGACU UACGCUGGCUGGCCAAGAGCUUCUUCGAGCUGACCGUGC UGAAGGAUAUCAUCGGCAUCUGCUACGGCGCCACCGUGA AGGGCAUGCAGAGCUACGGCCUGGAGCGGCUGGCCGCCA UGC UUAUGGCAACAGUGAAGAUGGAGGAGCUGGGACACC UGACAACAGAGAAGCAGGAGUACGCCUGAGACUGGCCA CAGUGGGCUACCCAAAGGCCGGCGUGUACAGUGGACUGA UCGGCGGCGCAACCAGCGUGCUGCUAUCCGCUUACAACCG GCACCCGCGUUCAGCCCCUGCACACCGUGAUGCGGGAA ACCCUGUUCUACGGAAGCCACGUCGUGCUGCGGGAGCUG AGGCUGAACGUAACCAACCCAGGGCCCUAAUCUGGCCUG UAUCAGCUCCUCAGUACCGCCCUGUGCAGCGCCCUUGAGA UCGGCGAGGUGCUCAGAGGCCUGGCCCUCCGUACCGAGA GCGGCCUCUUCAGCCCAUGCUACUUAAGCCUGCGGUUCG ACCUGACCCGGGACAAGUUGCUGAGCAUGGCCCCGCAGG AGGCCACACUGGACCAGGCAGCUGUAUCCAACGCCGUGG ACGGCUUCCUGGGCAGACUGUCCUGGAACGGGAGGACC GGGACGCCUGGCACCUGCCUGCCUACAAGUGUGUGGAUC GGCUGGACAAGGUGCUGAUGAUCAUCCUCUGAUUAAUG UCACCUUCAUCAUCAGCAGCGACCGGGAGGUGCGGGGAU CCGCCUCUACGAGGCCAGCACCACCUAUCUGAGCAGCAG CCUGUUCUGUCUCCUGUGAUGAUGAACAAGUGCAGCCA GGGCGCCGUGGCCGGCGAGCCCCGGCAGAUCCCCAAGAUC CAGAACUUCACCCGGACCCAGAAGUCUUGCAUCUUCUGC GGCUUCGCCC UUUUGUCCUACGACGAGAAGGAGGGCUG GAGACUACAACCUACAUCACCAGCCAGGAGGUGCAGAAC AGCAUCCUGUCAUCUAAUUAUCUUCGACUUCGACAACCUG CACGUUCAUUAACCGUCCUACACCAACGGUACCGUCA UGGAAAUCGCCGGACUGUACGAGGAGCGGGCCCAUGUUG UGCUGGCCAUCAUCCUGUACUUAUCGCUUUCGCACUUG GCAUCUUCUGGUGCACAAGAUCGUGAUGUUCUUCUG	84

3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MQLLCVFCLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTE LMAKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGLGI ALAEPVDIPAVSEGSMQVDASKVHPGVISGLNSPACMLSAPLE KQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFQYT GAMTSKFLMGTYKRVTEKGDEHVLSLVFGKTKDLPDLRGPF YPSLTSAQSGDYSLVIVTTFVHYANFNHYFVPNLKDMFSRAV TMTAASYARYVLQKLVLLEMKGCCREPELDTETLTMTFEVS VAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIGICYG ATVKGMQSYGLERLAAMLATVKMEELGHLTTEKQEYALR LATVGYPKAGVYSGLIGGATSVLLSAYNRHPLFQPLHTVMRE TLFIGSHVVLRELRLNVTQGPNLALYQLLSTALCSALEIGEVL RGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAA VSNVVDGFLGRLSLEREDRDWHLPAYKCVDRDLKVLMIPL INVTFISSDREVRGSALYEASTTYLSSSLFLSPVIMNKCSQGAV AGEPRQIPKIQNFTRTQKSCIFCGFALLSYDEKEGLETTTYITSQ EVQNSILSSNYFDFDNLHVHYLLLTNGTVMEIAGLYEERAH VVLAILLYFIAFALGIFLVHKIVMFFL	38
PolyA tail	100 nt	
EBV gL (B95-8) - UTRB		
SEQ ID NO: 229 consists of from 5' end to 3' end: 5' UTR SEQ ID NO: 104, mRNA ORF SEQ ID NO: 85, and 3' UTR SEQ ID NO:3		229
Chemistry	1-methylpseudouridine	
Cap	7mG(5')ppp(5')NlmpNp	
5' UTR	GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUA AGACCCCGGCGCCGCCACC	104
ORF of mRNA Construct (excluding the stop codon)	AUGAGAGCCGUGGGCGUGUCCUGGCCAUCUGCCUGGUG ACCAUCUUCGUGCUGCCCACCUGGGGCAACUGGGCCUACC CCUGCUGCCACGUGACCCAGCUGAGAGCCCAGCACCUGCU GGCCUGGAGAAUCAUCAGCGACAUCUACCUGGUGAGCAA CCAGACCUGCGACGGCUUCAGCCUGGCCAGCCUGAACAGC CCCAAGAACGGCAGCAACCAGCUGGUGAUCAGCAGAUGC GCCAACGGCCUGAACGUGGUGAGCUUCUUAUCAGCAUC CUGAAGAGAAGCAGCAGCGCCUGACCGGCCACCUGAGA GAGCUGCUGACCACCCUGGAGACCCUGUACGGCAGCUUC AGCGUGGAGGACCUGUUCGGCGCCAACCUGAACAGAUAC GCCUGGCACAGAGGCGGC	85
3' UTR	UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCC CCUUGGGCCUCCCCCAGCCCCUCCUCCCCUCCUGCACC CGUACCCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG C	3
Corresponding amino acid sequence	MRAVGVFLLAICLVITFVLPTWGNWAYPCCHVTQLRAQHLLA LENISDIYLVSNQTCDFSLASLNSPKNGSNQLVISRCANGLNV VSFFISILKRSSSALTGHLRELLTTLETLYGSFSVEDLFGANLNR YAWHRGG	36
PolyA tail	100 nt	

What is claimed is:

CLAIMS

1. An Epstein-Barr virus (EBV) vaccine, comprising a ribonucleic acid (RNA) having an open reading frame (ORF) encoding an EBV antigen, wherein intramuscular (IM)
5 administration of a therapeutically effective amount of the vaccine to a subject induces in the subject a neutralizing antibody titer and/or a T cell immune response.
2. The vaccine of claim 1, wherein the neutralizing antibody titer is at least 100 neutralizing units per milliliter (NU/mL).
- 10 3. The vaccine of claim 2, wherein the neutralizing antibody titer is at least 500 NU/mL.
4. The vaccine of claim 3, wherein the neutralizing antibody titer is at least 1000 NU/mL.
- 15 5. The vaccine of any one of claims 1-4, wherein the neutralizing antibody titer is sufficient to reduce EBV infection of B cells by at least 50% relative to a neutralizing antibody titer of an unvaccinated control subject or relative to a neutralizing antibody titer of a subject vaccinated with a live attenuated EBV vaccine, an inactivated EBV vaccine, or a protein subunit EBV vaccine.
- 20 6. The vaccine of any one of claims 1-5, wherein the neutralizing antibody titer is induced in the subject following fewer than three doses of the vaccine.
7. The vaccine of any one of claims 1-6, wherein a single dose is of 10 μ g-100 μ g.
- 25 8. The vaccine of any one of claims 1-7, wherein the neutralizing antibody titer and/or a T cell immune response is sufficient to reduce the rate of symptomatic infectious mononucleosis relative to the neutralizing antibody titer of unvaccinated control subjects.
- 30 9. The vaccine of any one of claims 1-8, wherein the neutralizing antibody titer and/or a T cell immune response is sufficient to reduce the rate of asymptomatic EBV infection relative to the neutralizing antibody titer of unvaccinated control subjects.

10. The vaccine of any one of claims 1-9, wherein the neutralizing antibody titer and/or a T cell immune response is sufficient to prevent EBV latency the subject.
- 5 11. The vaccine of any one of claims 1-10, wherein the neutralizing antibody titer is sufficient to block fusion of EBV with epithelial cells and/or B cells of the subject.
12. The vaccine of any one of claims 1-11, wherein the neutralizing antibody titer is induced within 20 days following a single 10-100 μ g dose of the vaccine.
- 10 13. The vaccine of any one of claims 1-12, wherein the neutralizing antibody titer is induced within 40 days following a second 10-100 μ g dose of the vaccine.
14. The vaccine of any one of claims 1-13, wherein the T cell immune response comprises a CD4⁺ T cell immune response.
- 15 15. The vaccine of any one of claims 1-14, wherein the T cell immune response comprises a CD8⁺ T cell immune response.
16. The vaccine of any one of claims 1-15, wherein the EBV antigen is expressed on the surface of cells of the subject.
- 20 17. The vaccine of any one of claims 1-16, wherein a single 2 μ g dose of the vaccine induces in mice NT₅₀ neutralizing antibody titers of about 100.
- 25 18. The vaccine of claim 17, wherein a 2 μ g booster dose of the vaccine induces in mice NT₅₀ neutralizing antibody titers.
19. The vaccine of any one of claims 1-18, wherein the EBV vaccine comprises
- 30 (a) a ribonucleic acid (RNA) having an open reading frame (ORF) encoding two EBV antigens, or
- (b) two RNAs, each having an ORF encoding an EBV antigen.
20. The vaccine of any one of claims 1-19, wherein the vaccine comprises a RNA having an ORF encoding two EBV antigens formulated in a lipid nanoparticle.

21. The vaccine of any one of claims 1-19, wherein the vaccine comprises two RNAs, each having an ORF encoding an EBV antigen, wherein the two RNAs are formulated in a single lipid nanoparticle.
- 5
22. The vaccine of any one of claims 1-19, wherein the vaccine comprises two RNAs, each having an ORF encoding an EBV antigen, wherein the each RNAs is formulated in a single lipid nanoparticle.
- 10
23. The vaccine of any one of claims 1-22, further comprising at least one additional RNA having an ORF encoding at least one additional EBV antigen.
24. The vaccine of any one of claims 20-23, wherein the lipid nanoparticle comprises a molar ratio of 20-60% ionizable cationic lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid.
- 15
25. The vaccine of any one of claims 1-24, wherein the EBV antigens are selected from the group consisting of: gp350, gH, gL, gB, gp42, LMP1, LMP2, EBNA1, and EBNA3.
- 20
26. The vaccine of claim 25, wherein the EBV antigens include EBV gp350 antigen, EBV gH antigen, and EBV gL antigen, optionally wherein the EBV gH antigen is linked to the EBV gL antigen, optionally wherein the linker comprises a GGGGS motif, and optionally wherein the linker comprises an amino acid sequence of SEQ ID NO: 224 or SEQ ID NO: 225.
- 25
27. The vaccine of claim 26, wherein the EBV antigens further include EBV gp42 antigen and/or gB antigen.
28. The vaccine of any one of claims 25-27, wherein the EBV gp350 antigen is a wild-type EBV gp350 antigen, a mutated EBV gp350 antigen, or a truncated EBV gp350 antigen.
- 30
29. The vaccine of any one of claims 1-28, wherein the RNA comprises or consists of a sequence selected from the group consisting of SEQ ID NOs: 201, 202, 203, 204, 207, 208, 177, 178, 179, 181, 182, 185, 187, 188, 189, 209, 218, and 221.

30. The vaccine of any one of claims 1-29, wherein the EBV antigens are fused to a scaffold moiety.
- 5 31. The vaccine of claim 30, wherein the scaffold moiety is selected from the group consisting of: ferritin, encapsulin, lumazine synthase, hepatitis B surface antigen, and hepatitis B core antigen.
- 10 32. The vaccine of any one of claims 1-31, wherein the RNA comprises messenger RNA (mRNA).
33. The vaccine of any one of claims 1-32, wherein the RNA further comprises a 5' UTR.
- 15 34. The vaccine of claim 33, wherein the 5' UTR comprises a sequence identified by SEQ ID NO: 1 or SEQ ID NO: 104.
35. The vaccine of any one of claims 1-34, wherein the RNA further comprises a 3' UTR.
- 20 36. The vaccine of claim 35, wherein the 3' UTR comprises a sequence identified by SEQ ID NO: 3 or SEQ ID NO: 106.
37. The vaccine of any one of claims 1-36, wherein the EBV antigen is fused to a signal peptide.
- 25 38. The vaccine of claim 37, wherein the signal peptide is a bovine prolactin signal peptide, optionally comprising SEQ ID NO: 115.
39. The vaccine of any one of claims 1-38, wherein the RNA is unmodified.
- 30 40. The vaccine of any one of claims 1-38, wherein the RNA comprise at least one modified nucleotide.
41. The vaccine of claim 40, wherein at least 80% of the uracil in the ORF comprise 1-methyl-pseudouridine modification.

42. A method comprising administering to a subject the EBV vaccine of any one of claims 1-41 in a therapeutically effective amount to induce in the subject a neutralizing antibody titer and/or a T cell immune response.
- 5
43. The method of claim 42, wherein efficacy of the EBV vaccine is at least 80% relative to unvaccinated control subjects.
44. The method of claim 42 or 43, wherein detectable levels of EBV antigen are produced in the serum of the subject at 1-72 hours post administration of the vaccine.
- 10
45. The method of any one of claims 42-44, wherein a neutralizing antibody titer of at least 100 NU/ml is produced in the serum of the subject at 1-72 hours post administration of the vaccine.
- 15
46. The method of claim 45, wherein a neutralizing antibody titer of at least 500 NU/ml is produced in the serum of the subject at 1-72 hours post administration of the vaccine.
47. The method of claim 46, wherein a neutralizing antibody titer of at least 1000 NU/ml is produced in the serum of the subject at 1-72 hours post administration of the vaccine.
- 20
48. The method of any one of claims 42-47, wherein the therapeutically effective amount is a total dose of 20 µg-200 µg.
- 25
49. The method of claim 48, wherein the therapeutically effective amount is a total dose of 50 µg-100 µg.

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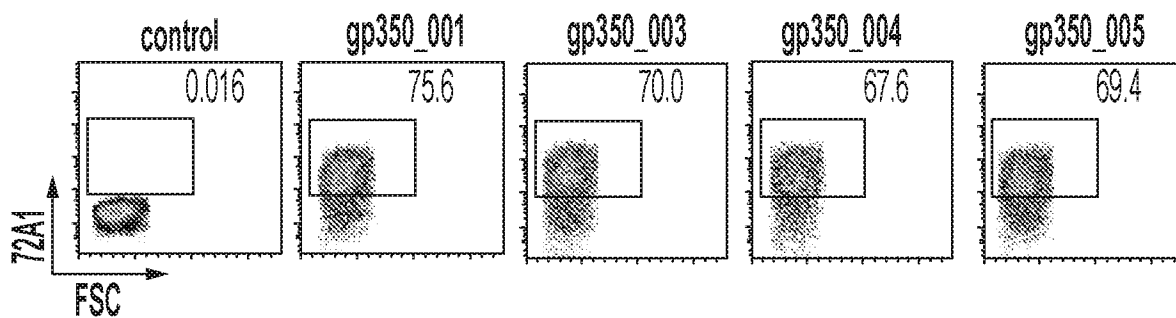


FIG. 1A

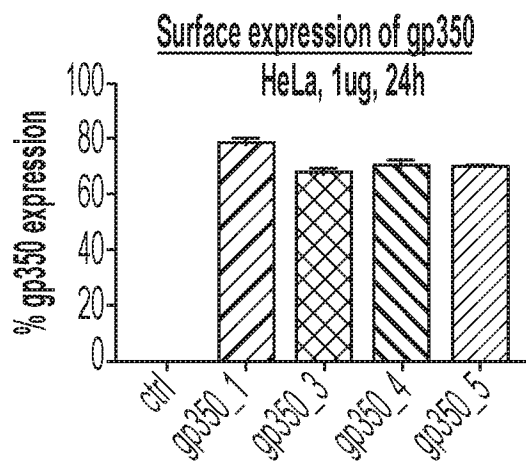


FIG. 1B

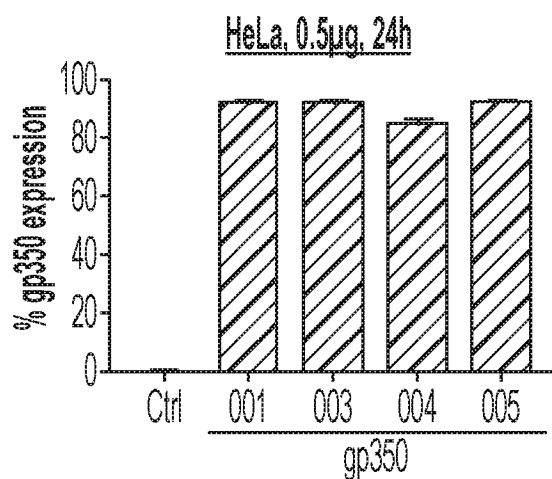


FIG. 1C

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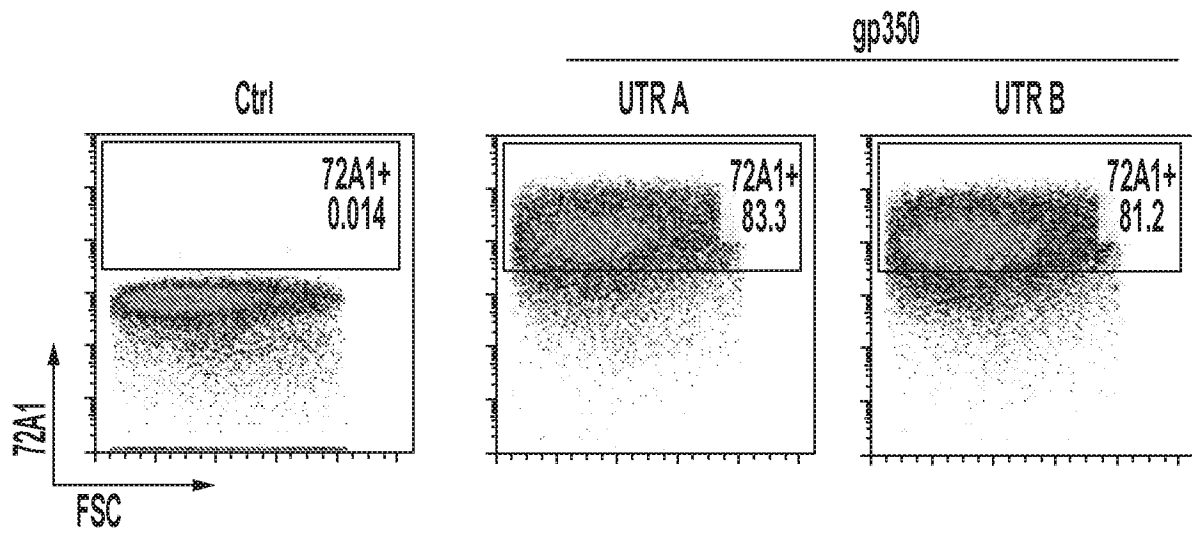


FIG. 2A

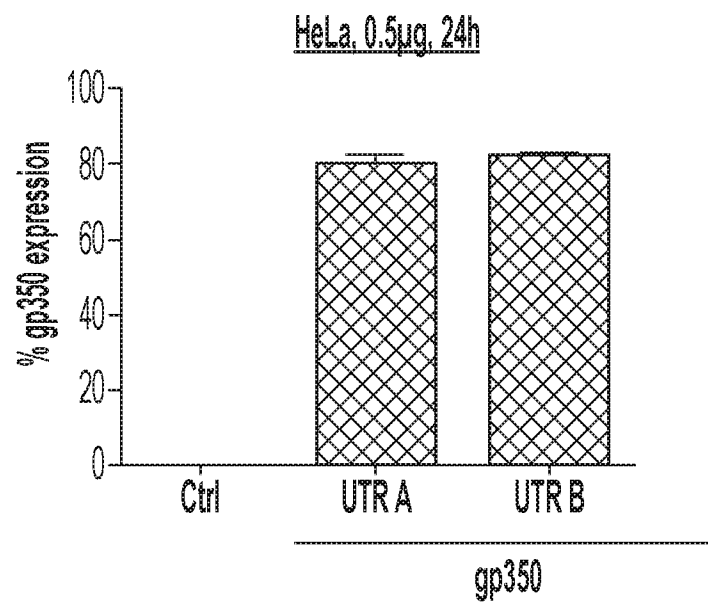


FIG. 2B

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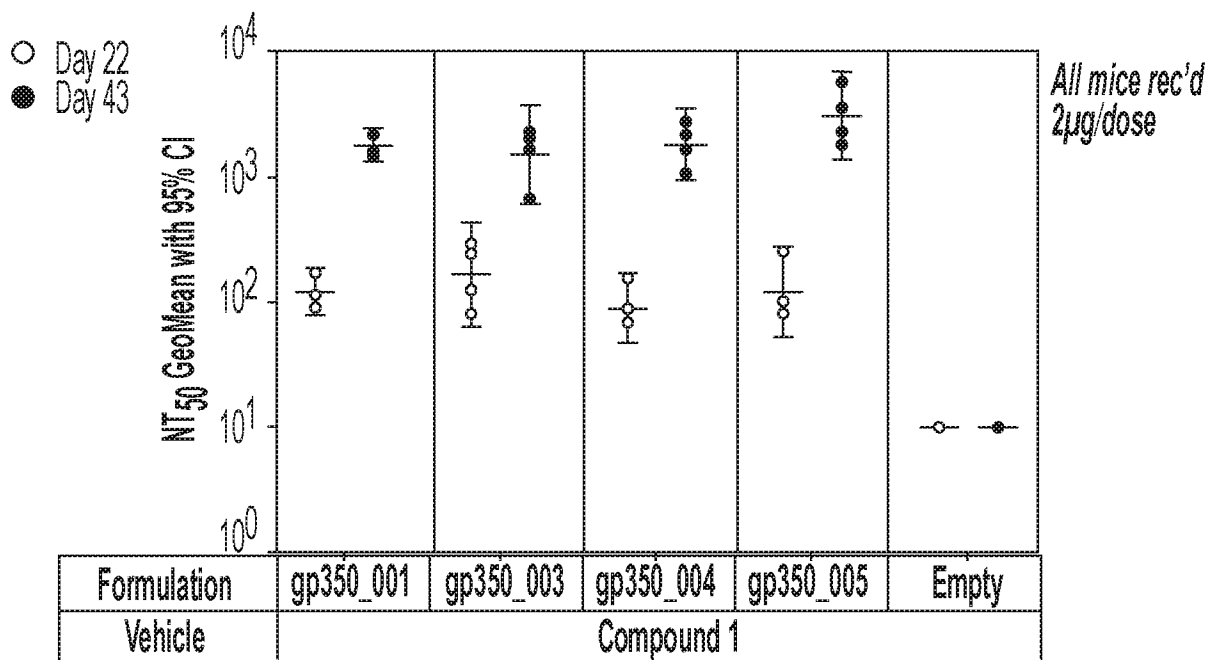


FIG. 3

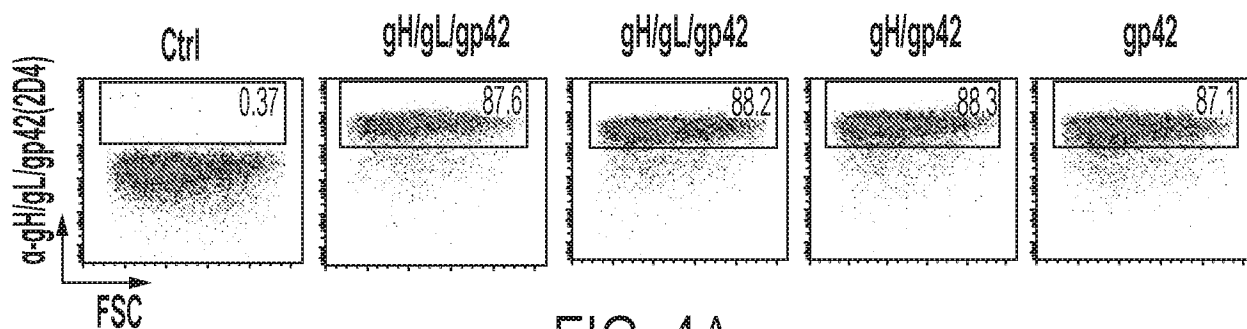


FIG. 4A

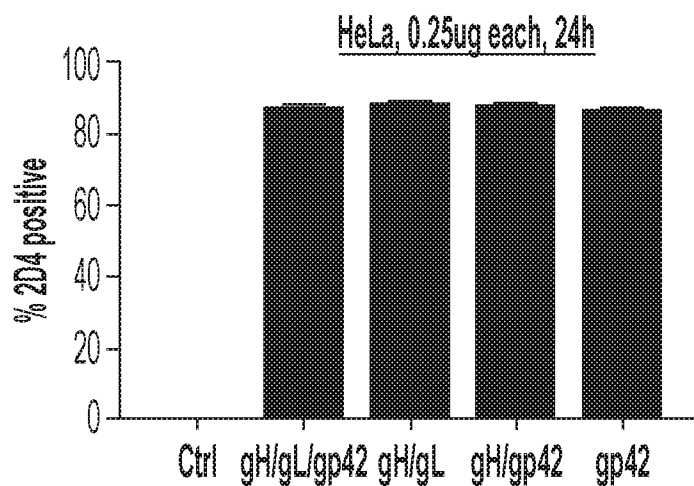


FIG. 4B

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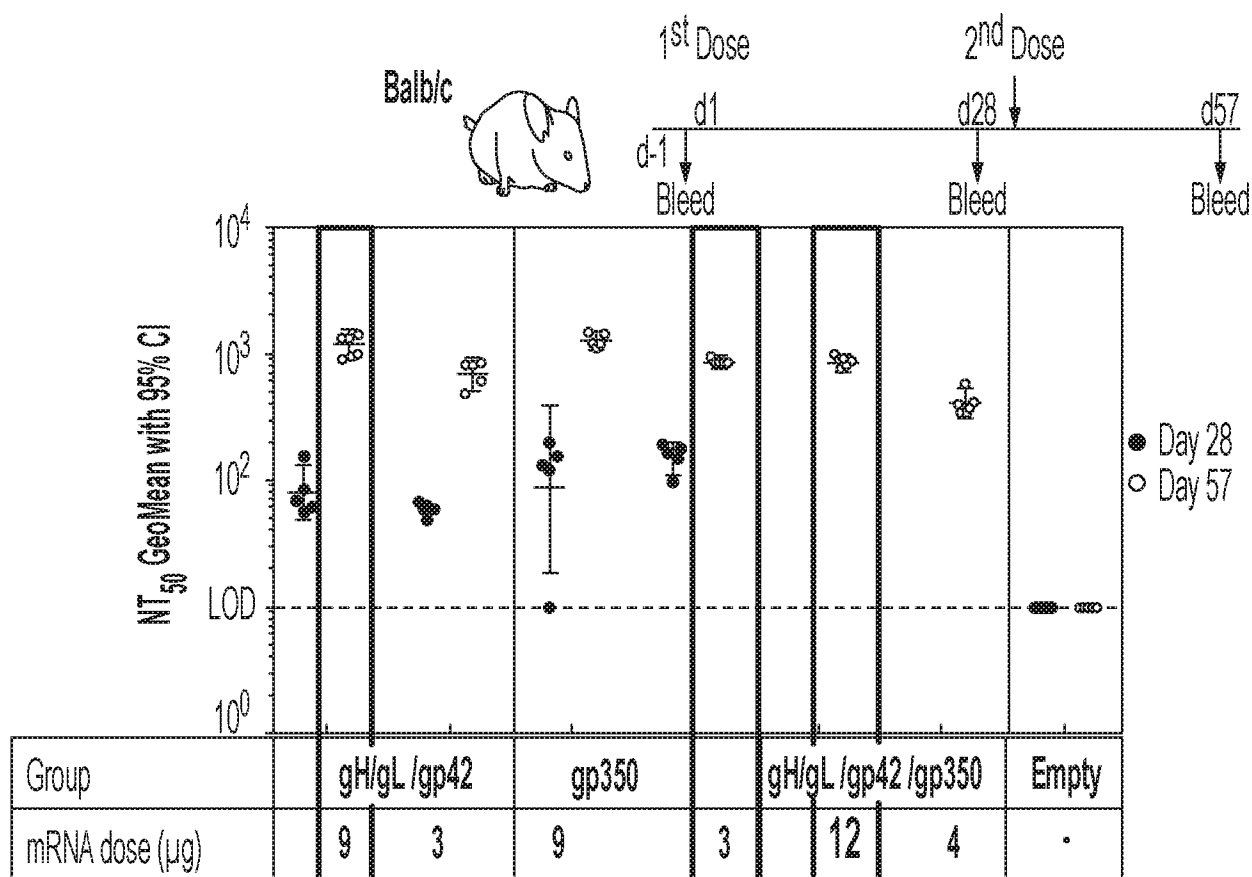


FIG. 5

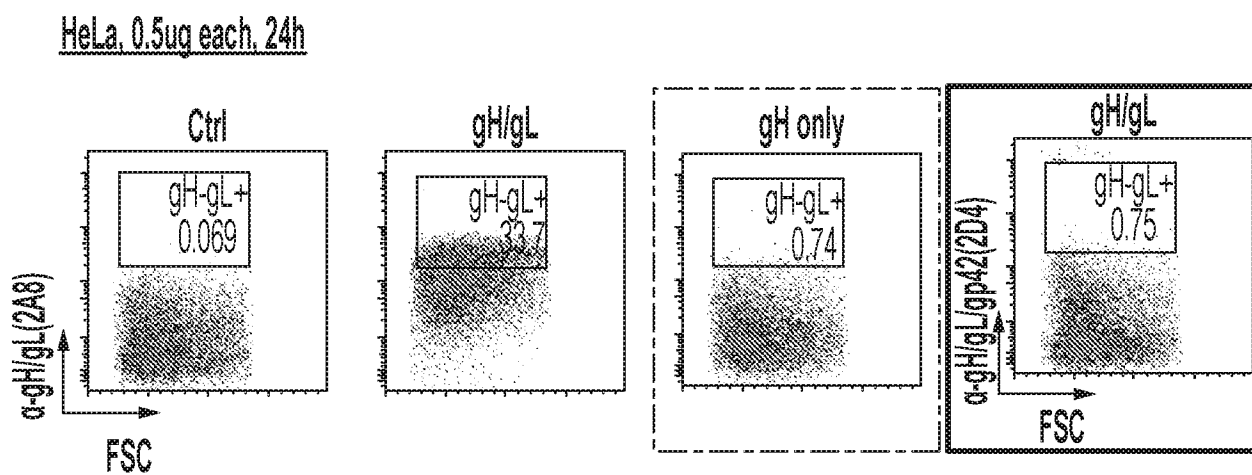


FIG. 6A

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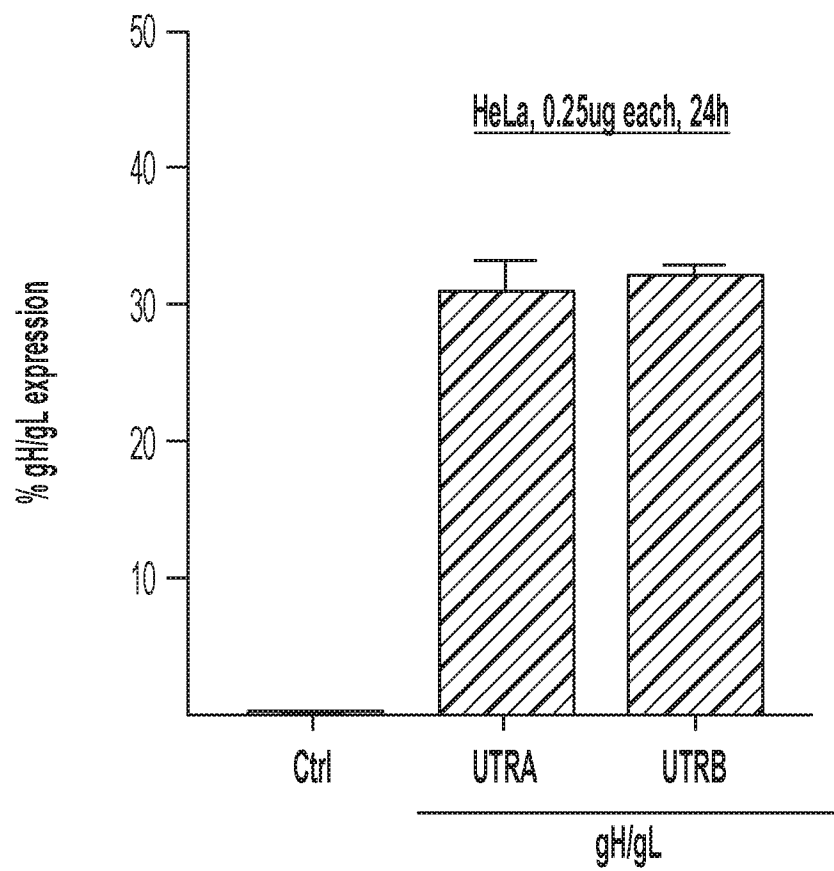


FIG. 6B

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Anti-gH/gL Abs

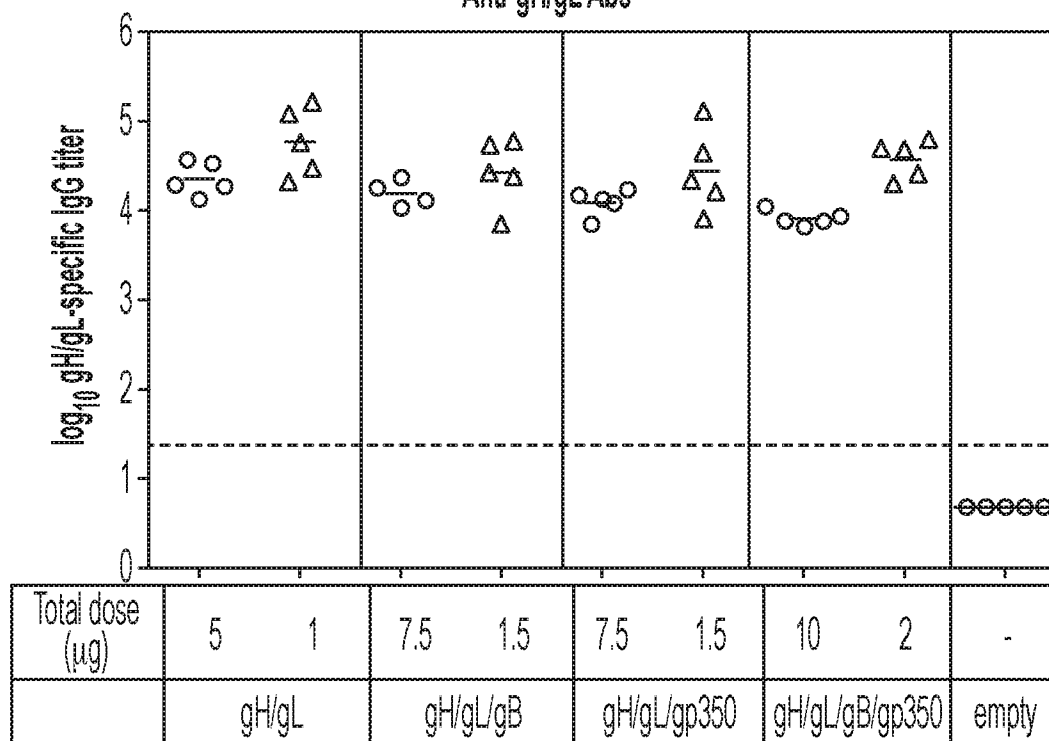


FIG. 7

Anti-gB Abs

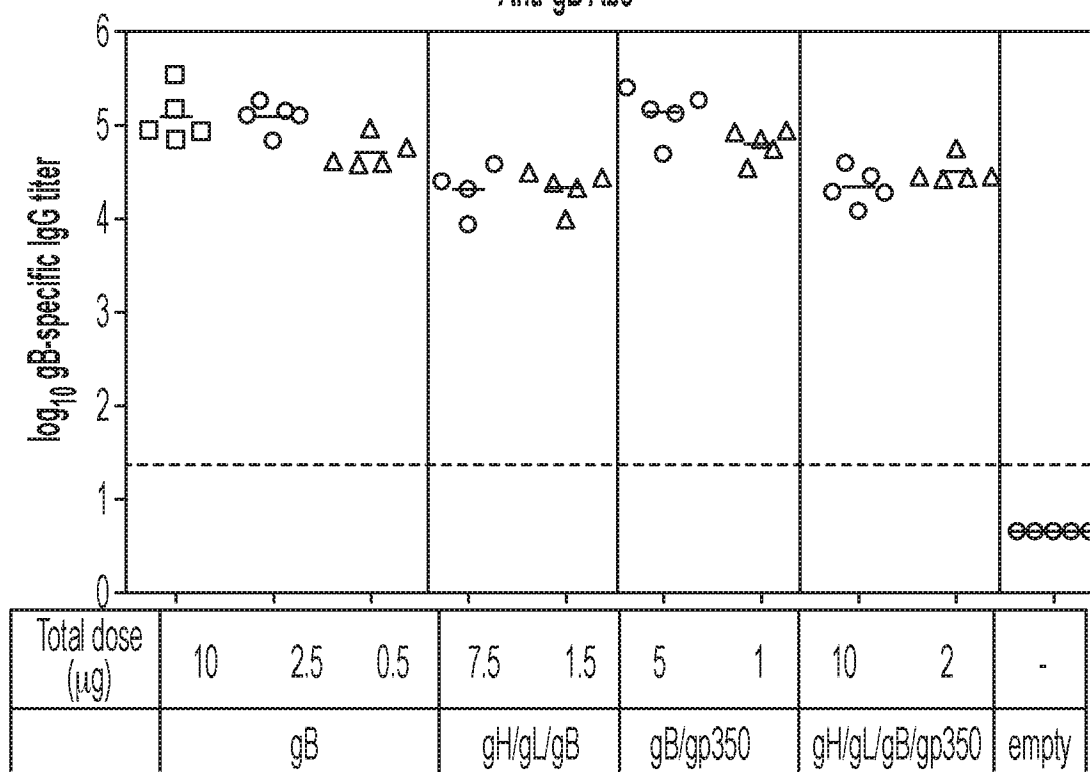


FIG. 8

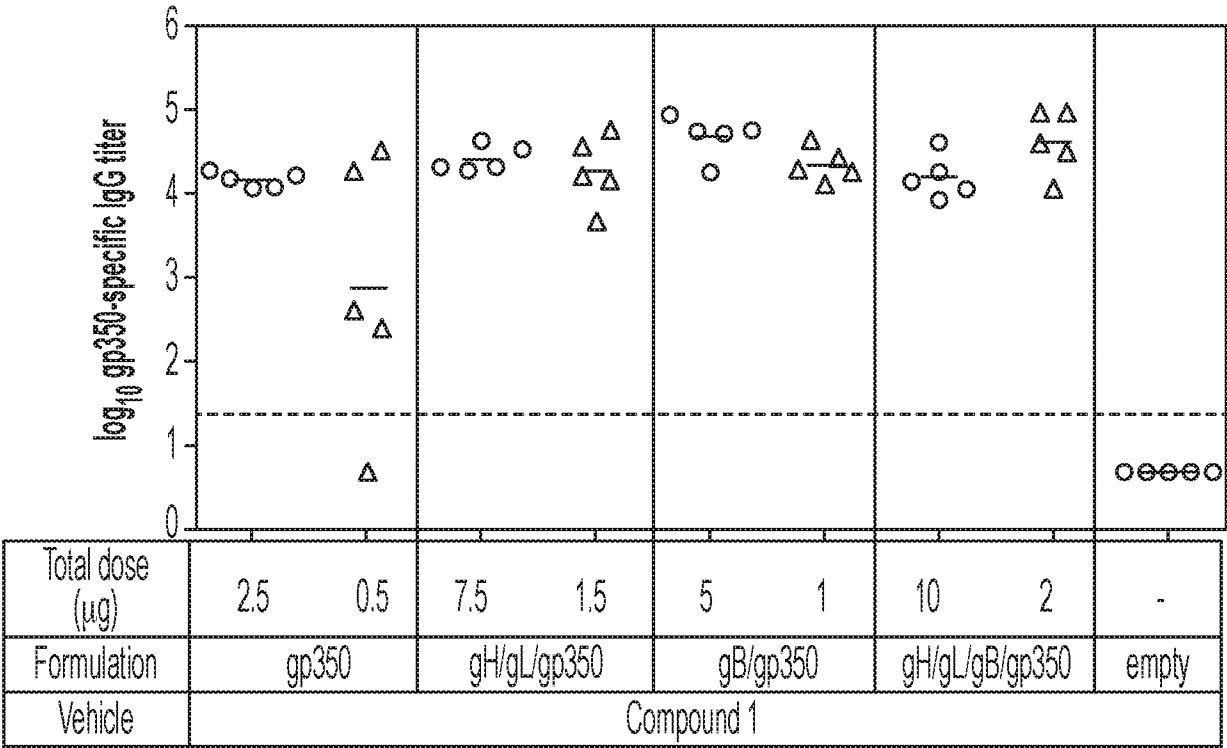


FIG. 9

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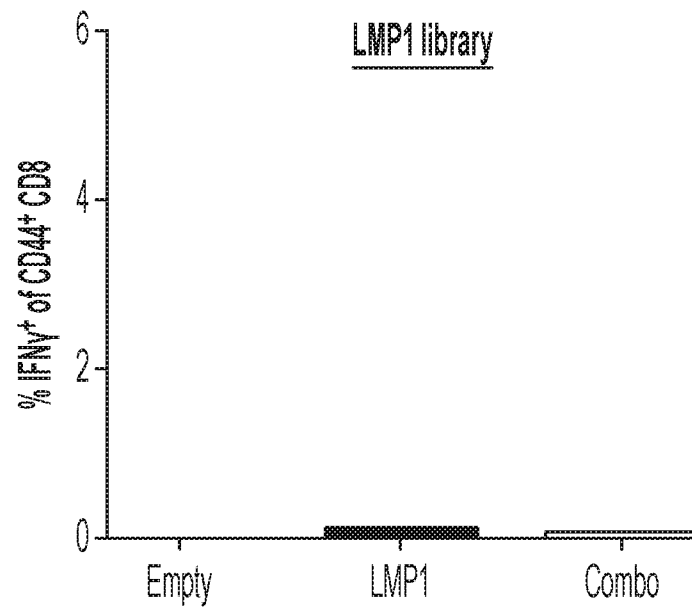


FIG. 10A

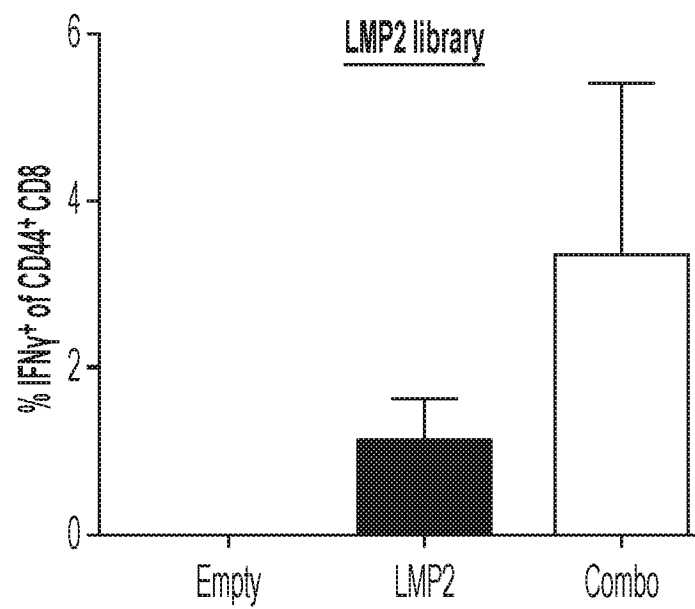


FIG. 10B

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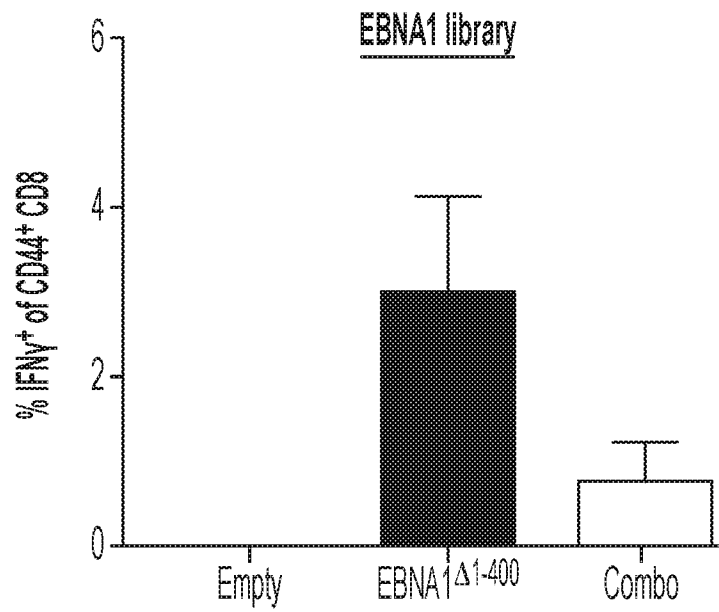


FIG. 10C

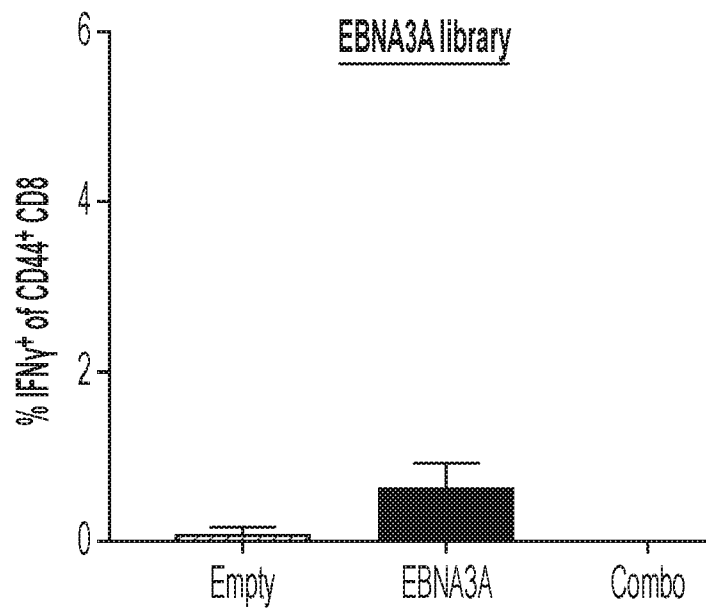


FIG. 10D

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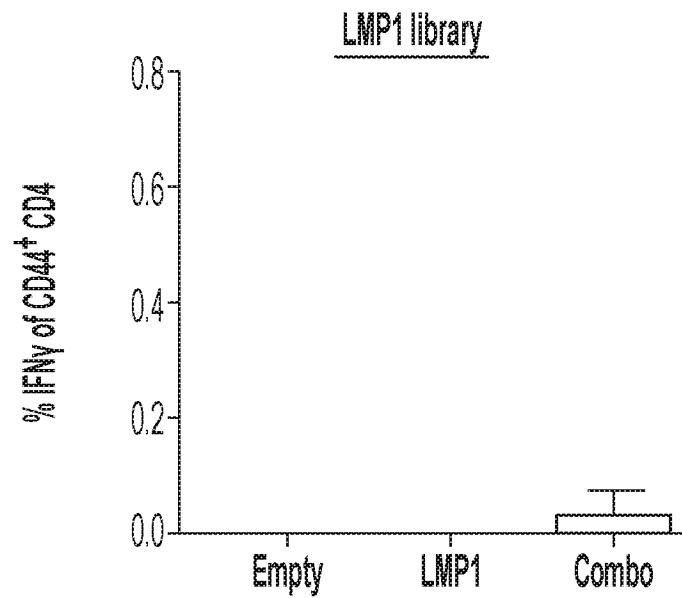


FIG. 11A

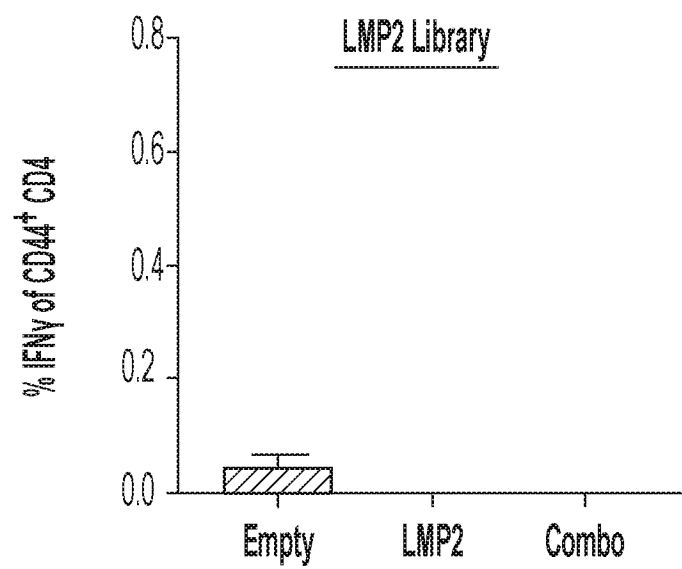


FIG. 11B

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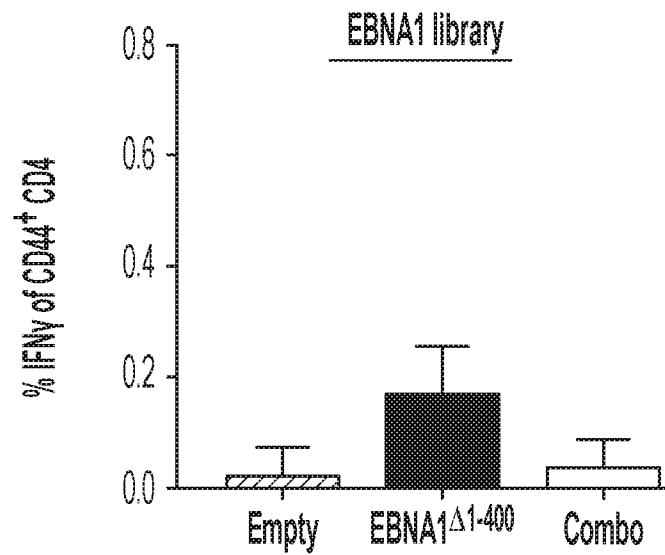


FIG. 11C

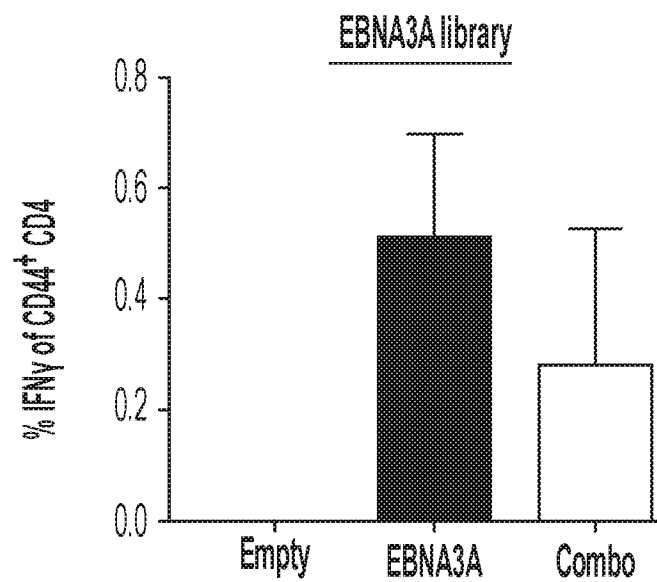


FIG. 11D

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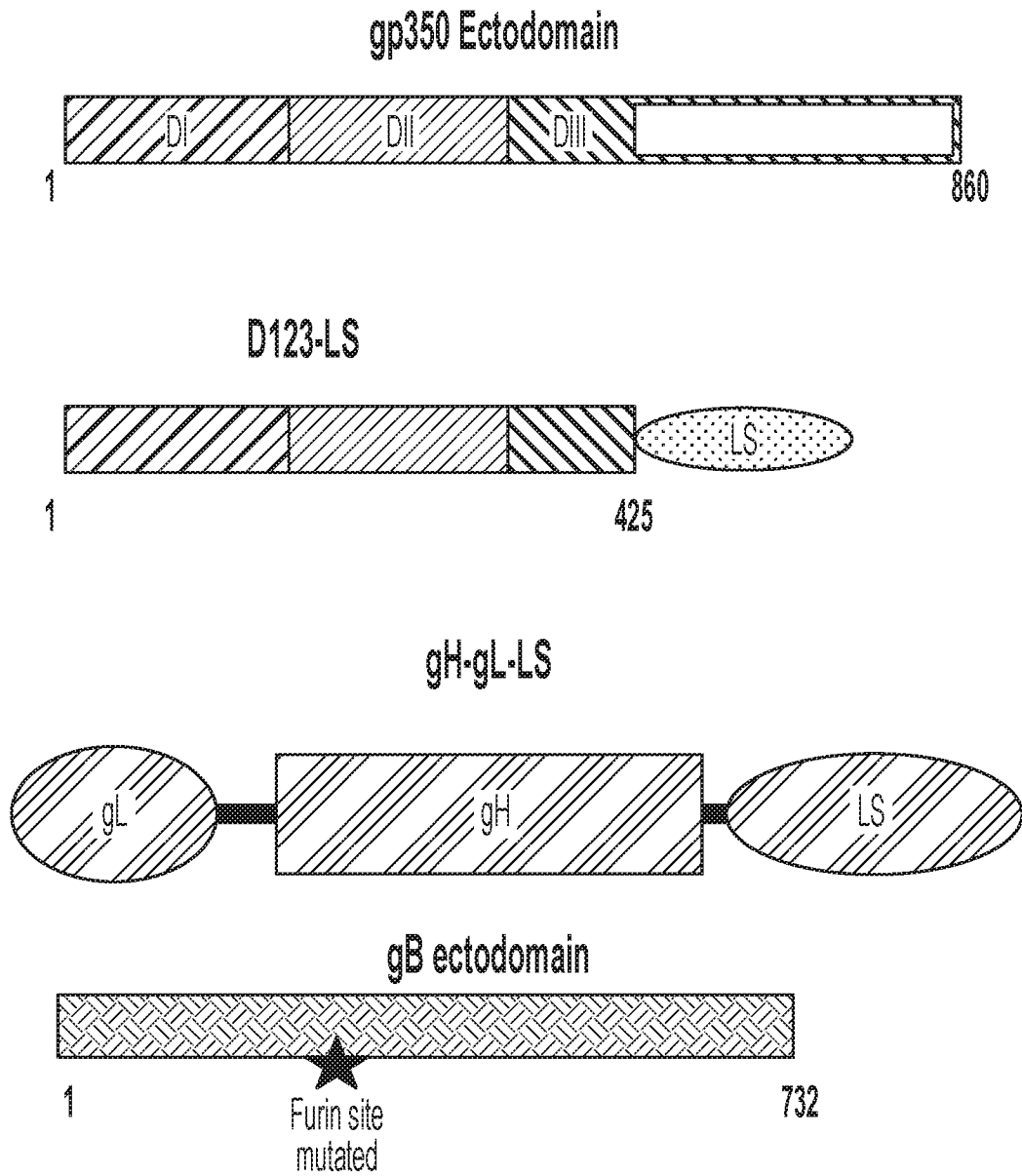


FIG. 12

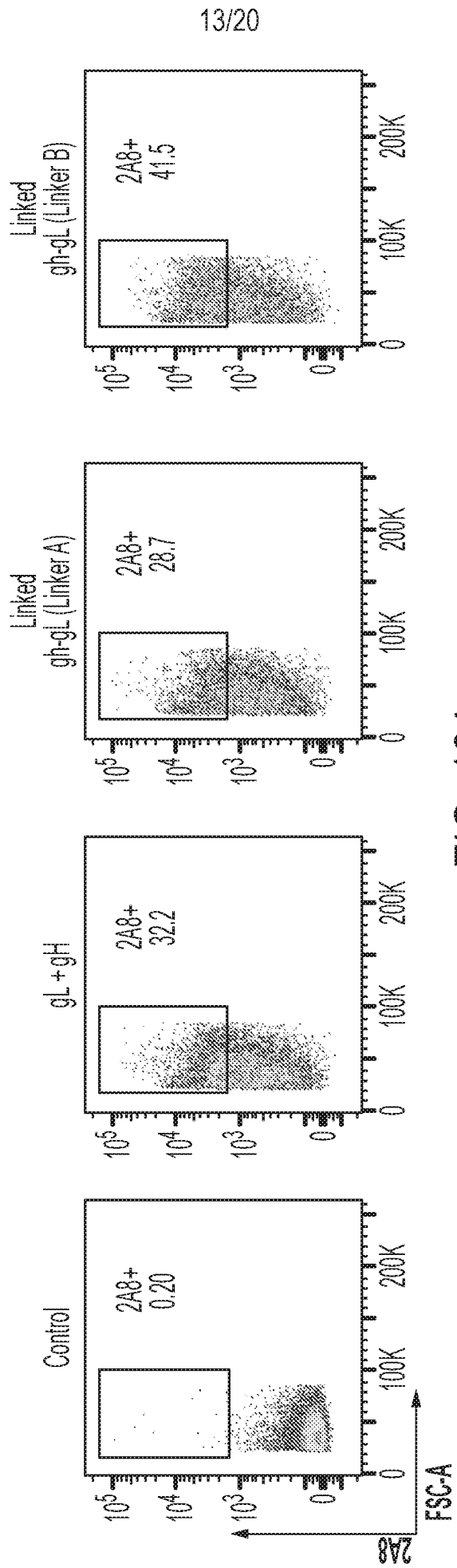


FIG. 13A

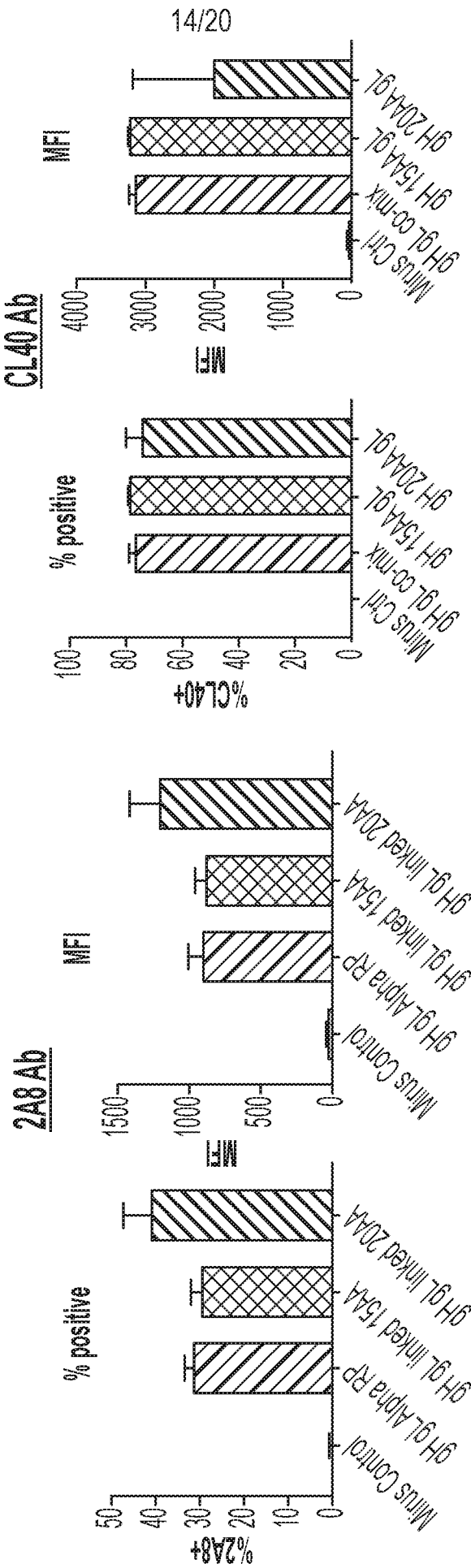


FIG. 13B

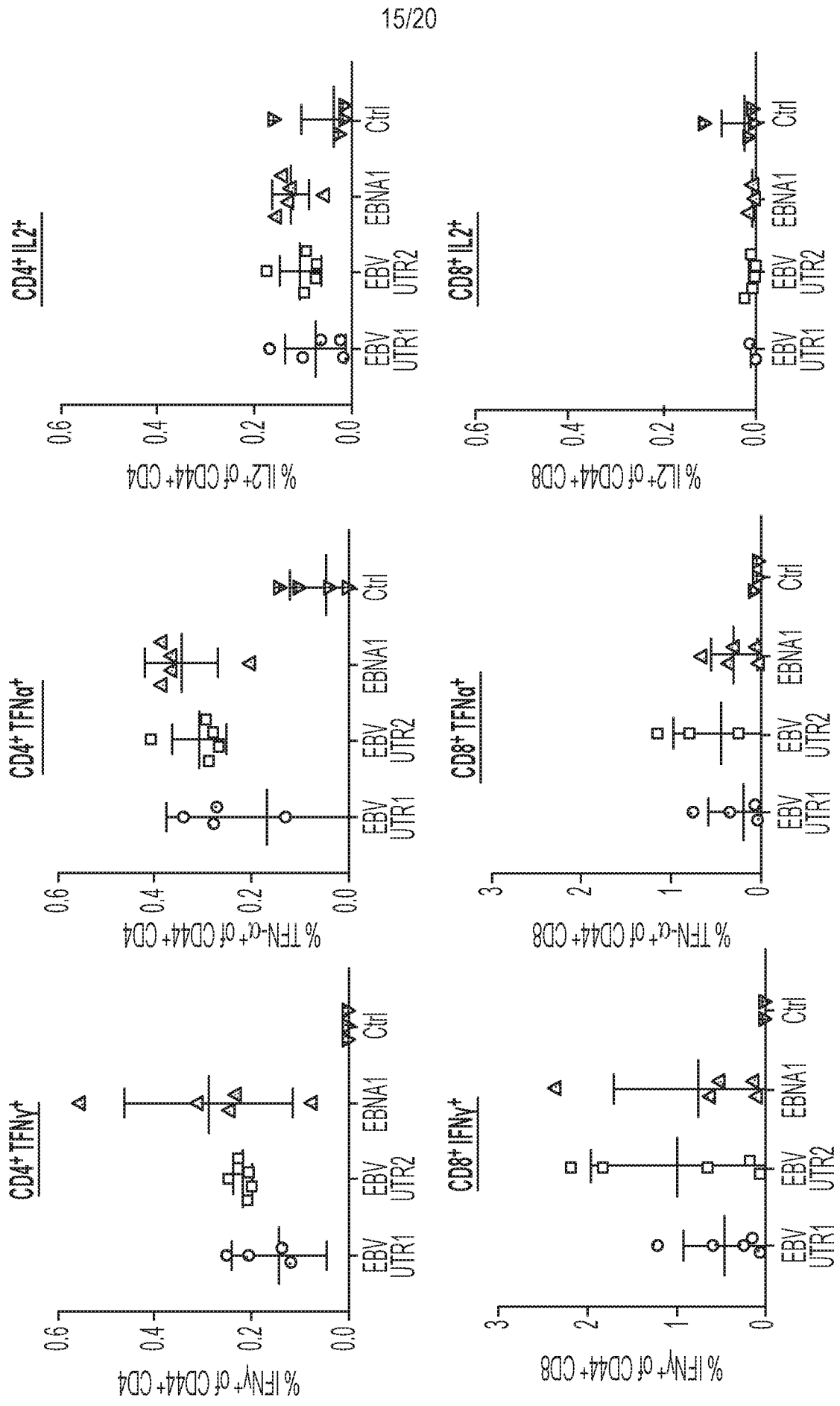


FIG. 14

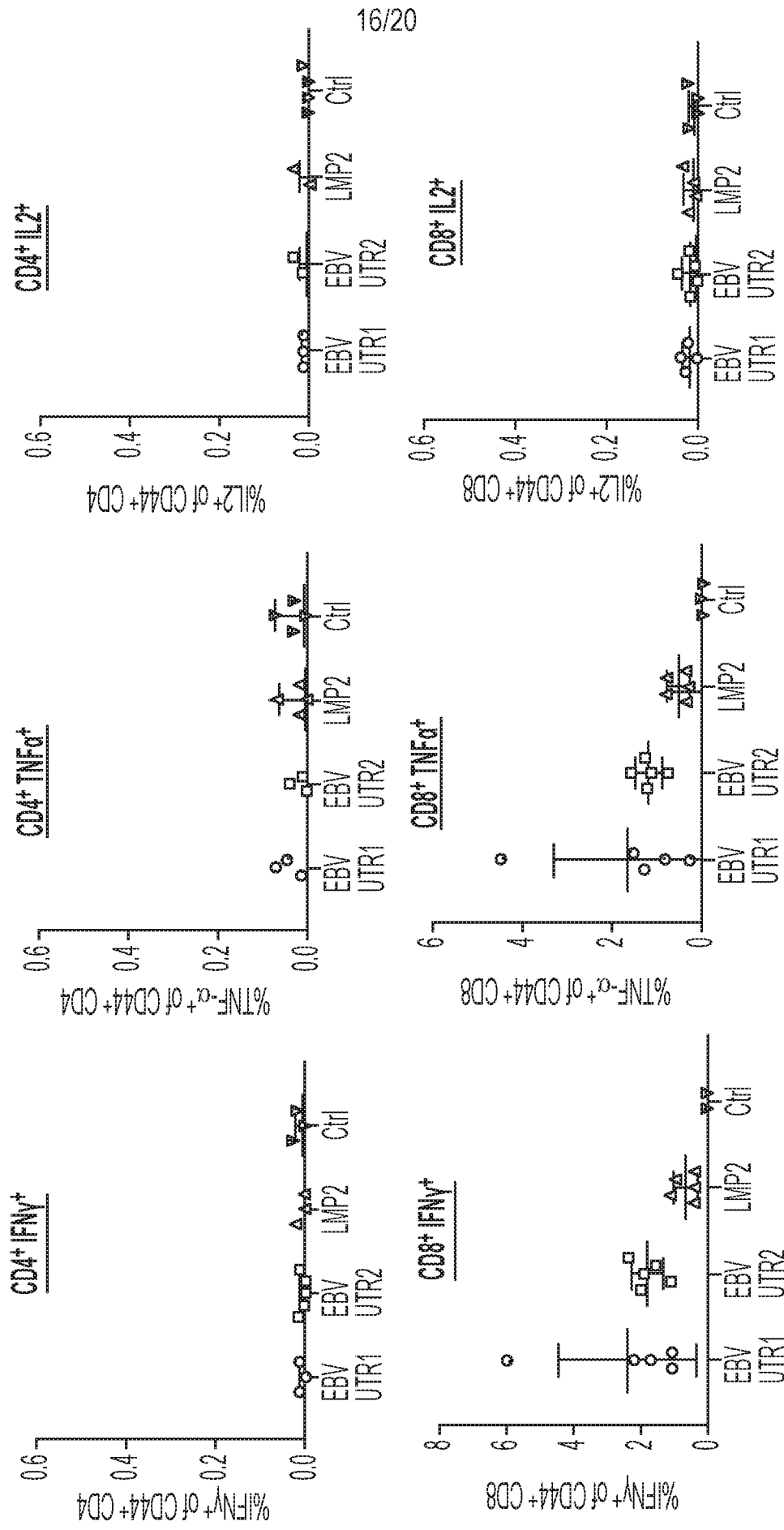


FIG. 15

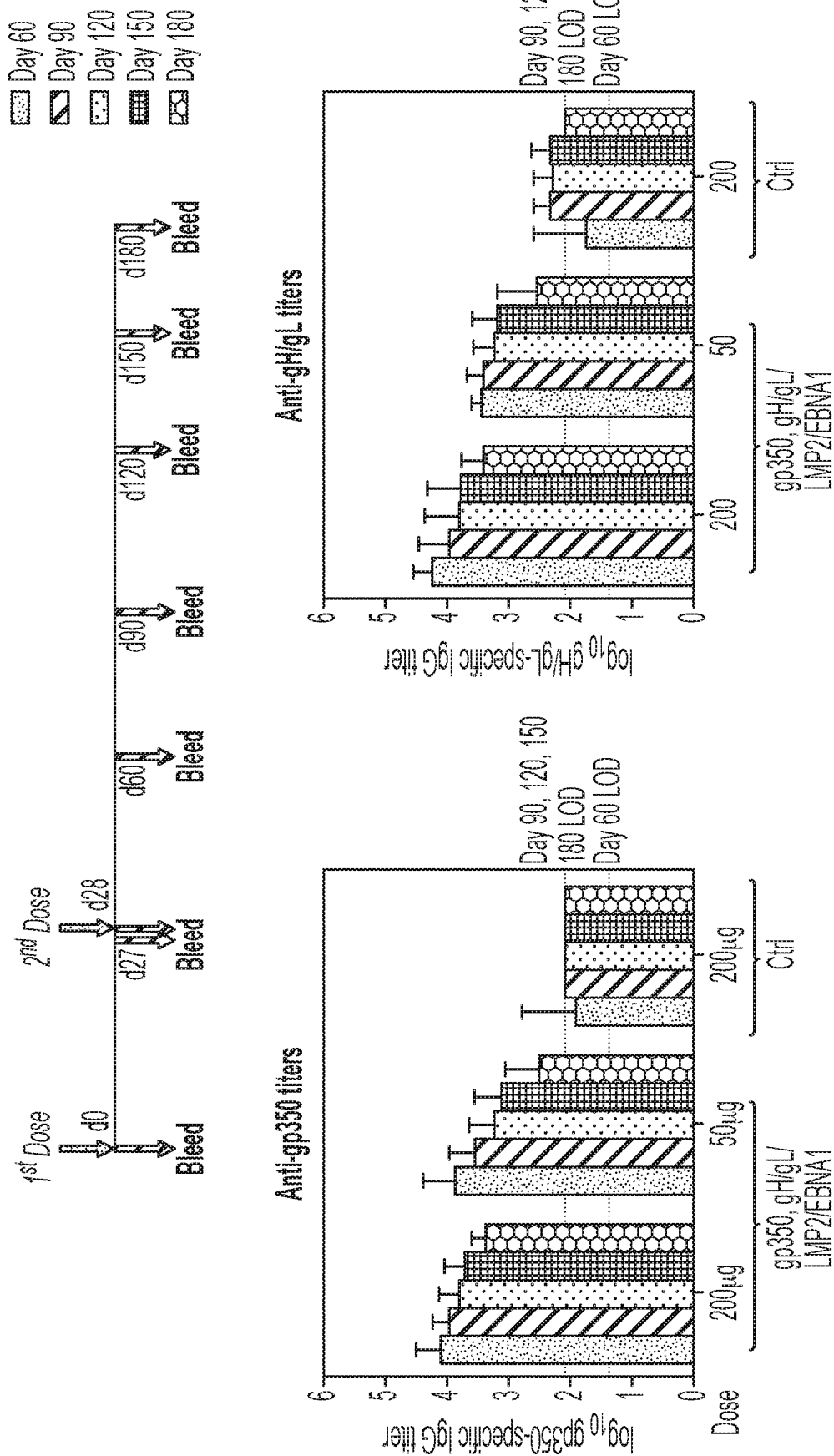


FIG. 16

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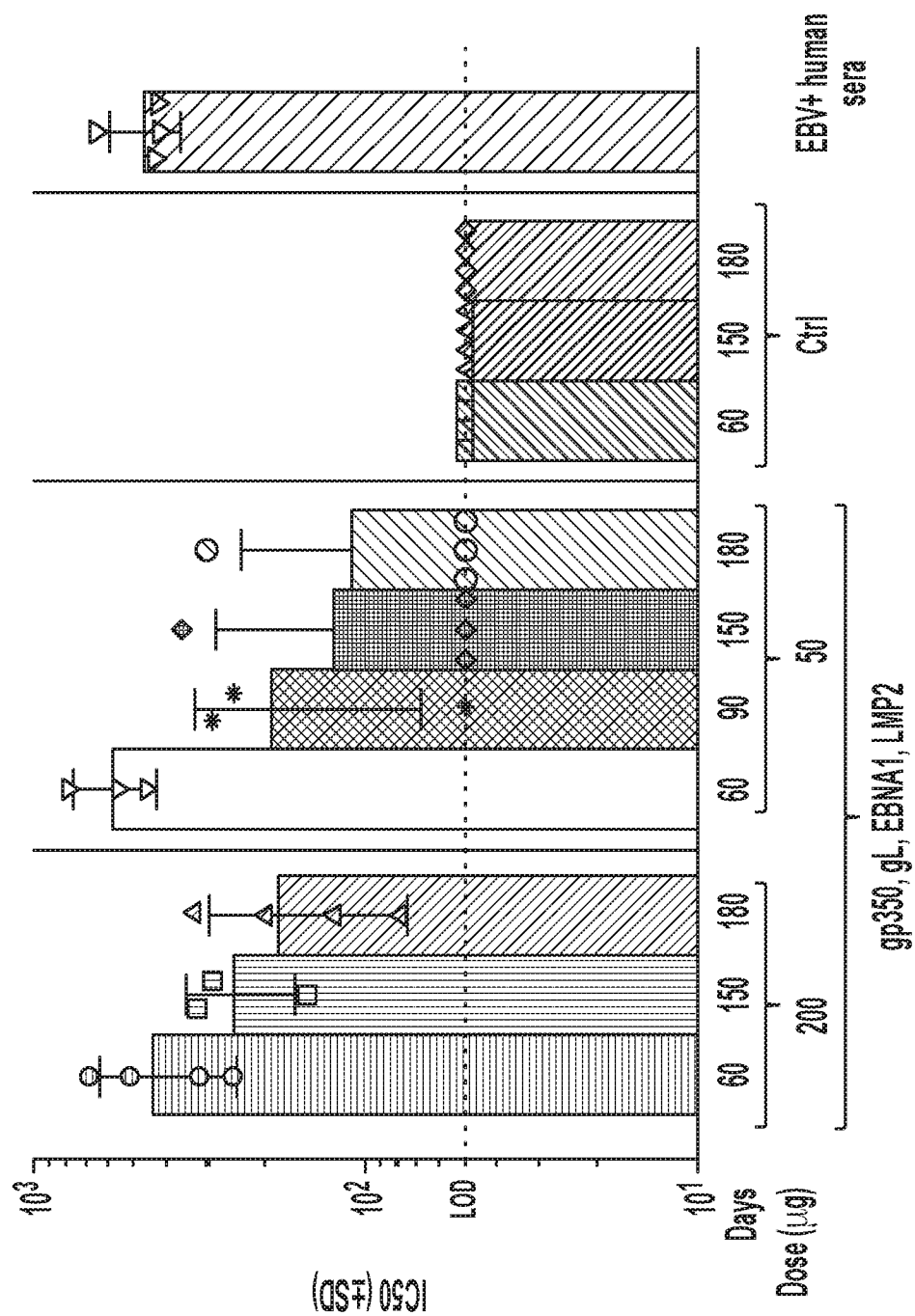


FIG. 17

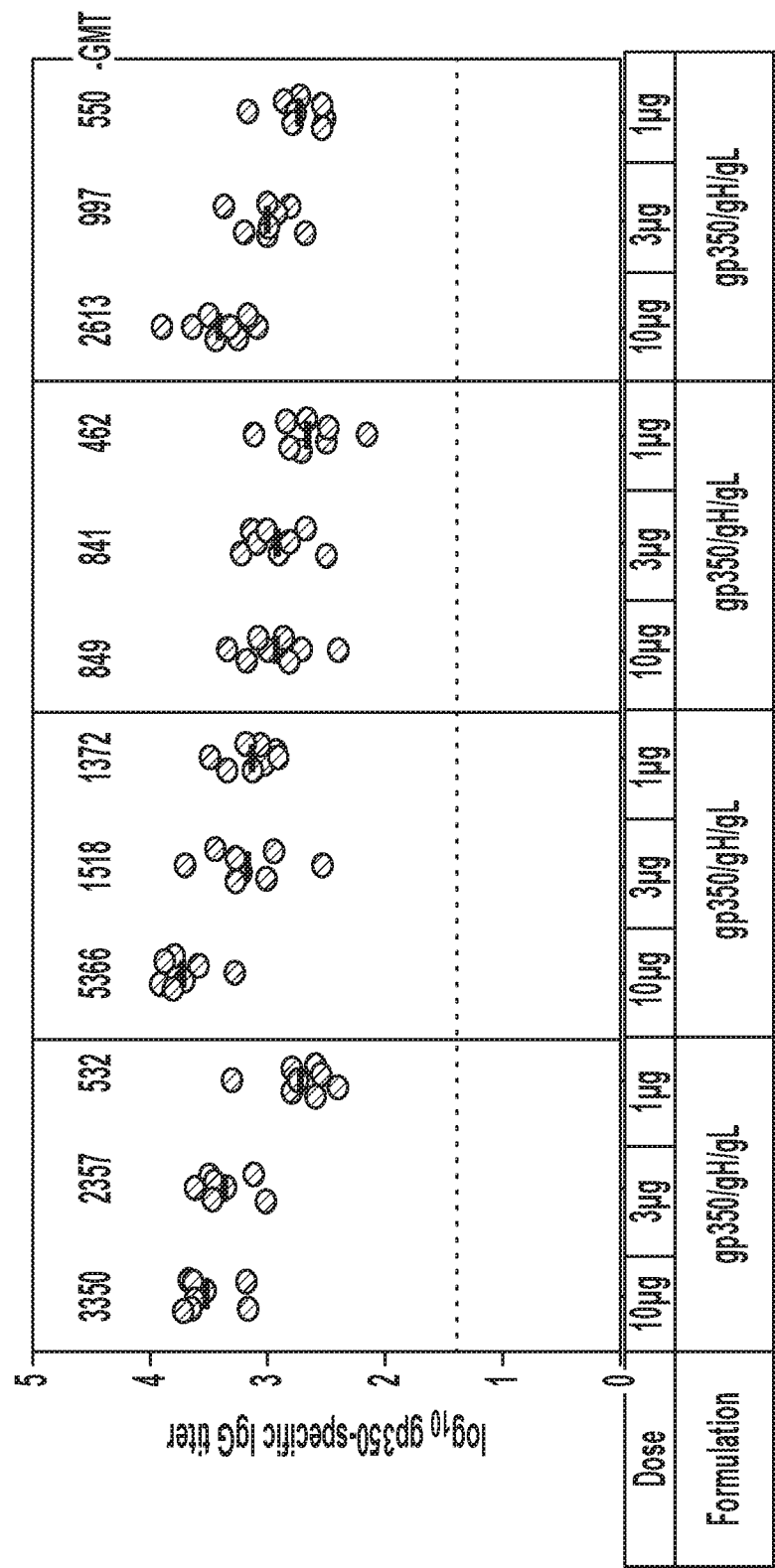


FIG. 18

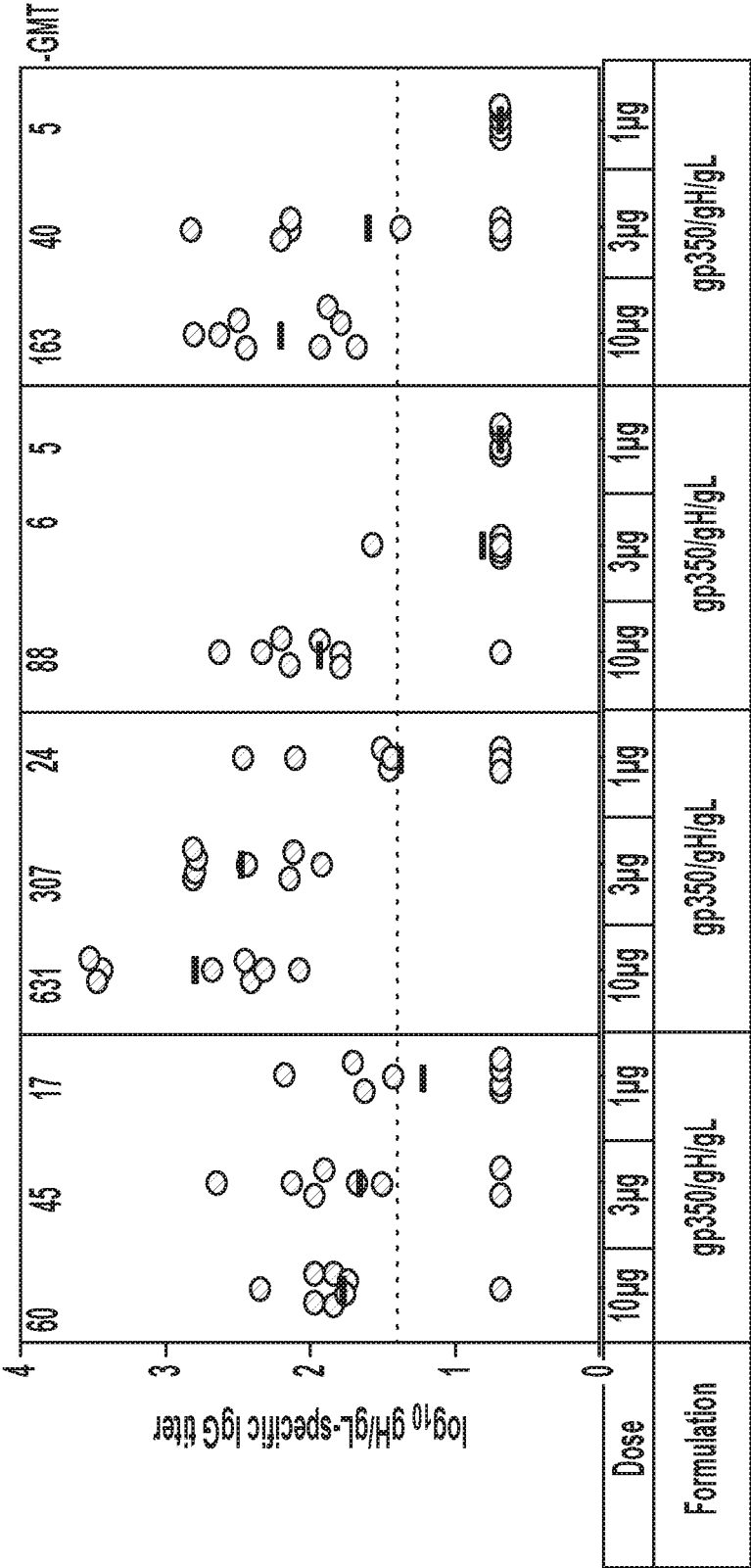


FIG. 19

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<140> Not Yet Assigned

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<160> 229

<170> PatentIn version 3.5

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<220>

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120

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180

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300

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 35 40 45

Arg Gly Gly Gly Arg Pro Gly Ala Pro Gly Gly Ser Gly Ser Gly Pro
 50 55 60

Arg His Arg Asp Gly Val Arg Arg Pro Gln Lys Arg Pro Ser Cys Ile
 65 70 75 80

Gly Cys Lys Gly Thr His Gly Gly Thr Gly Gly Gly Ala Gly Ala Gly
 85 90 95

Gly Ala Arg Gly Arg Gly Gly Ser Gly Gly Arg Gly Arg Gly Gly Ser
 100 105 110

Gly Gly Arg Arg Gly Arg Gly Arg Glu Arg Ala Arg Gly Gly Ser Arg
 115 120 125

Glu Arg Ala Arg Gly Arg Gly Arg Gly Arg Gly Glu Lys Arg Pro Arg
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Ser Pro Ser Ser Gln Ser Ser Ser Ser Gly Ser Pro Pro Arg Arg Pro
 145 150 155 160

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180 185 190

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195 200 205

Ser Thr Gly Pro Arg Gly Gln Gly Asp Gly Gly Arg Arg Lys Lys Gly
210 215 220

Gly Trp Phe Gly Lys His Arg Gly Gln Gly Gly Ser Asn Pro Lys Phe
225 230 235 240

Glu Asn Ile Ala Glu Gly Leu Arg Ala Leu Leu Ala Arg Ser His Val
245 250 255

Glu Arg Thr Thr Asp Glu Gly Thr Trp Val Ala Gly Val Phe Val Tyr
260 265 270

Gly Gly Ser Lys Thr Ser Leu Tyr Asn Leu Arg Arg Gly Thr Ala Leu
275 280 285

Ala Ile Pro Gln Cys Arg Leu Thr Pro Leu Ser Arg Leu Pro Phe Gly
290 295 300

Met Ala Pro Gly Pro Gly Pro Gln Pro Gly Pro Leu Arg Glu Ser Ile
305 310 315 320

Val Cys Tyr Phe Met Val Phe Leu Gln Thr His Ile Phe Ala Glu Val
325 330 335

Leu Lys Asp Ala Ile Lys Asp Leu Val Met Thr Lys Pro Ala Pro Thr
340 345 350

Cys Asn Ile Arg Val Thr Val Cys Ser Phe Asp Asp Gly Val Asp Leu
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gacgaggggca ccuggguggc uggugucuuc guuuauggcg ggagcaagac cucccuguau	840
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aaggauucgg ugaugaccaa gccugcaccu acgugcaua ucagggugac agaugcucc 600
uucgacgacg guguggaccu cccccccugg uucccaccca uggucgaggg ggccgccgcc 660
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caggag 726

<210> 10
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 10

Met Gly Arg Arg Pro Phe Phe His Pro Val Gly Glu Ala Asp Tyr Phe
1 5 10 15

Glu Tyr His Gln Glu Gly Gly Pro Asp Gly Glu Pro Asp Val Pro Pro
20 25 30

Gly Ala Ile Glu Gln Gly Pro Ala Asp Asp Pro Gly Glu Gly Pro Ser
35 40 45

Thr Gly Pro Arg Gly Gln Gly Asp Gly Gly Arg Arg Lys Lys Gly Gly
50 55 60

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Trp Phe Gly Lys His Arg Gly Gln Gly Gly Ser Asn Pro Lys Phe Glu
65 70 75 80

Asn Ile Ala Glu Gly Leu Arg Ala Leu Leu Ala Arg Ser His Val Glu
85 90 95

Arg Thr Thr Asp Glu Gly Thr Trp Val Ala Gly Val Phe Val Tyr Gly
100 105 110

Gly Ser Lys Thr Ser Leu Tyr Asn Leu Arg Arg Gly Thr Ala Leu Ala
115 120 125

Ile Pro Gln Cys Arg Leu Thr Pro Leu Ser Arg Leu Pro Phe Gly Met
130 135 140

Ala Pro Gly Pro Gly Pro Gln Pro Gly Pro Leu Arg Glu Ser Ile Val
145 150 155 160

Cys Tyr Phe Met Val Phe Leu Gln Thr His Ile Phe Ala Glu Val Leu
165 170 175

Lys Asp Ala Ile Lys Asp Leu Val Met Thr Lys Pro Ala Pro Thr Cys
180 185 190

Asn Ile Arg Val Thr Val Cys Ser Phe Asp Asp Gly Val Asp Leu Pro
195 200 205

Pro Trp Phe Pro Pro Met Val Glu Gly Ala Ala Ala Glu Gly Asp Asp
210 215 220

Gly Asp Asp Gly Asp Glu Gly Gly Asp Gly Asp Glu Gly Glu Glu Gly
225 230 235 240

Gln Glu

<210> 11
 <211> 726
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 gacgaccug gcgagggccc uagcaccgga ccuagaggac aaggcgacgg cgggaggaga 180
 aagaaggggg gcugguucgg gaagcaccgc gggcaaggcg gcagcaacc aaaguucgag 240
 aacaucgccg agggguugcg ggcccugcuc gcccguucc acguggagcg gacaaccgac 300
 gaggggaaccu ggguugccgg gguuuuugug uacggcggca guaagaccag ccuguauaac 360
 cucagaagag gaacagcccu ggccaucca cagugcaggc ugacacccu cucccggcug 420
 ccauuuggaa uggcaccgg gccuggacc cagccuggcc cacugcgca gucuauugug 480
 uguuacuuu uggucuuccu gcaaaccac aucuucgcc agguuuuuaa ggaugccauc 540
 aaagaccug ugaugacaaa gcccgcucc accugcaua ucagagugac cguaugcagc 600
 uuugacgac gcguggaccu gccucccugg uucccuccua ugguggaggg cggcgccgca 660
 gaaggggacg acggugacga uggcgaugag ggaggggaug gagacgaagg cgaggagggc 720
 caggag 726

<210> 12
 <211> 726
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 12
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 gagggcgggc ccgacggcga accugacgug ccaccuggcg ccuugaaca aggcccagcc 120

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gacgacccug gggagggccc uagcacaggg cccagggggcc agggagacgg ggguaaggcgu	180
aagaagggag gcugguucgg uaagcaccgc ggccagggug gcagcaaccc uaaauucgag	240
aaauuugccg aaggucugcg agcccucuug gccagaagcc acguggaacg cacuacugau	300
gagggcaccu gggucgccgg aguguucgug uacggcgga gcaaaaccag ucuguacaac	360
cugcgccggg gaaccgcucu ugccaucucc cagugucgcc ugaccccauu guccagacug	420
ccaauuggca uggcccccg ccccgccccc cagcccggcc ccugagggga gagcaucgug	480
ugcuacuuca ugguguuccu gcagaccac auauucgug aggugcugaa ggacgccauu	540
aaggaccugg ugaugaccaa gcccgcuccu accugcaaca uccgcgucac cgucuguagu	600
uucgaugacg gcguggaucu cccaccaugg uuuccuccaa ugguggaggg cgucugcucc	660
gagggggacg acggagacga cggagacgag ggcggggacg gggacgaagg cgaagagggg	720
caagag	726

<210> 13
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 <212> RNA
 <213> Artificial Sequence

<220>
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gacgacccag gagagggacc uagcacugga ccccgagguc agggcgaugg ggggcgaaga	180
aagaagggcg gcugguucgg caaacauagg ggccagggcg ggucuaaccc aaaguucgag	240
aacauagccg agggccugag agcccugcug gcaagaagcc acguggagcg aaccacagau	300
gaaggcaccu ggguggccgg cguguucgug uacgggggca gcaagaccuc ccuguauaac	360
cucagaagag ggaccgccc ggccaucucc cagugccgac ugaccccccu gagcaggcug	420
cccuucggaa uggccccugg ucccggucc caaccgggcc cgcuucggga guccauagug	480

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ugcuacuuca	ugguguuccu	gcagacacac	aucuucgccg	aggugcugaa	ggaugcaauc	540
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uuugaugacg	gcguggaccu	gccaccucgg	uucccgccua	ugguggaggg	cgugcagcc	660
gagggcgacg	acggggacga	cggcgacgag	ggcggagaug	gcgacgaggg	cgaggagggc	720
caggag						726

<210> 14
 <211> 726
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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gacgaccucg	gggagggccc cagcaccggc cccagaggcc agggggacgg gggcaggaga 180
aaaaagggug	gcugguucgg caagcacaga gggcaggggg ggagcaaccc aaaguucgag 240
aacaucgccg	agggcuugag agcacugcug gccagaagcc acguggagag aaccaccgau 300
gaggggaaccu	ggguugcugg cguguucguc uacggcggca gcaagaccag ccuguacaac 360
cuuagaagag	gcaccgccc ggccaucucc cagugccgcc ugacaccgcu gagcagacuc 420
cccuucggca	uggcuuccgg ccccgggccc cagcccgggc ccugagaga gagcaucgug 480
ugcuacuuca	ugguguuucu ucagacgcac aucuucgcug agguccugaa agacgccauu 540
aaggaccugg	ugaugacaaa accagcuccg accugcaaca ucaggguac ugucuguagc 600
uucgacgaug	gcguggaucu cccucccugg uccccccaa ugguggaggg cgugccgcu 660
gagggggacg	acggcgacga cggggaugaa ggcggcgacg gcgacgaggg ggaagagggc 720
caggag	

<210> 15
 <211> 1158
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 15
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 uauauaguca ugucugacug gacaggcgagg gcauuauugg ugcucuacag cuuugcacug 180
 augcucauuu ucauuauucu gauuaucuuu auuuuuagac gggacuugcu cuguccauua 240
 ggcgcgcugu guauuuugcu gcugaugauc acacugcugc ugauugcgcu guggaaccuc 300
 cacggucagg cccuuuuucu cggcaucgug cuguuuauucu uugggugccu cuuggugcuu 360
 gggauuuugga ucuaccuucu cgaaaugua uggcggcucg gcgcuacaau cuggcagcuc 420
 cuggccuucu ucuuagcauu uuuucuggau cugauccugc ugauaaauagc ccuguaccua 480
 caacagaacu gguggacucu gcugguugac cuguuauggc ugcuccuguu ccucgccauu 540
 cucauuugga uguacuacca cgggcagcgu cauucagacg aacaccacca cgaugauagc 600
 cugccgcacc cucaacaagc uacggaugac uccggacacg aguccgauag uaacuccaac 660
 gagggacgcc aucacuugcu ggucucuggg gcuggcgacg ggccuccacu guguagccaa 720
 aaucuggggag cccccggcgg gggcccugau aaugggccuc aggauccuga uaacacggau 780
 gauaacggcc cacaggaucc agauaaauacc gacgauaaug gaccucauga uccucuucca 840
 caggaucccc acaauacaga ugacaauagg cgcaggauc cagacaauac ugacgauaau 900
 ggcccacaug auccccugcc acacagcccc ucagacucag cgggaaauga uggcgggccc 960
 ccacaguuaa ccgaggaagu ggaaaacaaa gggggagauc aggguccucc ccuauagaca 1020
 gauggcgggg gcggccacag ucaugauagu gggcacgggg guggcgaucc acaucucucc 1080
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 caguugagcu auuacgac 1158

<210> 16
 <211> 386
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 16

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 1 5 10 15

Arg Gly Pro Pro Leu Ser Ser Ser Leu Gly Leu Ala Leu Leu Leu Leu
 20 25 30

Leu Leu Ala Leu Leu Phe Trp Leu Tyr Ile Val Met Ser Asp Trp Thr
 35 40 45

Gly Gly Ala Leu Leu Val Leu Tyr Ser Phe Ala Leu Met Leu Ile Ile
 50 55 60

Ile Ile Leu Ile Ile Phe Ile Phe Arg Arg Asp Leu Leu Cys Pro Leu
 65 70 75 80

Gly Ala Leu Cys Ile Leu Leu Leu Met Ile Thr Leu Leu Leu Ile Ala
 85 90 95

Leu Trp Asn Leu His Gly Gln Ala Leu Phe Leu Gly Ile Val Leu Phe
 100 105 110

Ile Phe Gly Cys Leu Leu Val Leu Gly Ile Trp Ile Tyr Leu Leu Glu
 115 120 125

Met Leu Trp Arg Leu Gly Ala Thr Ile Trp Gln Leu Leu Ala Phe Phe
 130 135 140

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Leu Ala Phe Phe Leu Asp Leu Ile Leu Leu Ile Ile Ala Leu Tyr Leu
145 150 155 160

Gln Gln Asn Trp Trp Thr Leu Leu Val Asp Leu Leu Trp Leu Leu Leu
165 170 175

Phe Leu Ala Ile Leu Ile Trp Met Tyr Tyr His Gly Gln Arg His Ser
180 185 190

Asp Glu His His His Asp Asp Ser Leu Pro His Pro Gln Gln Ala Thr
195 200 205

Asp Asp Ser Gly His Glu Ser Asp Ser Asn Ser Asn Glu Gly Arg His
210 215 220

His Leu Leu Val Ser Gly Ala Gly Asp Gly Pro Pro Leu Cys Ser Gln
225 230 235 240

Asn Leu Gly Ala Pro Gly Gly Gly Pro Asp Asn Gly Pro Gln Asp Pro
245 250 255

Asp Asn Thr Asp Asp Asn Gly Pro Gln Asp Pro Asp Asn Thr Asp Asp
260 265 270

Asn Gly Pro His Asp Pro Leu Pro Gln Asp Pro Asp Asn Thr Asp Asp
275 280 285

Asn Gly Pro Gln Asp Pro Asp Asn Thr Asp Asp Asn Gly Pro His Asp
290 295 300

Pro Leu Pro His Ser Pro Ser Asp Ser Ala Gly Asn Asp Gly Gly Pro
305 310 315 320

Pro Gln Leu Thr Glu Glu Val Glu Asn Lys Gly Gly Asp Gln Gly Pro
325 330 335

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Pro Leu Met Thr Asp Gly Gly Gly Gly His Ser His Asp Ser Gly His
340 345 350

Gly Gly Gly Asp Pro His Leu Pro Thr Leu Leu Leu Gly Ser Ser Gly
355 360 365

Ser Gly Gly Asp Asp Asp Asp Pro His Gly Pro Val Gln Leu Ser Tyr
370 375 380

Tyr Asp
385

<210> 17
<211> 1158
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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uacaucguca ugagcgauug gacaggggggu gcucugcugg uguuguacag cuuugcgug 180
auguugauua uuaucauccu gauuauuuu auauuucgaa gggaccuccu uuguccccug 240
ggagcgugcu gcuaucugcu cuuaaugauc acguugcucc ucauugcuuu auggaaucug 300
cacggacagg cucuauuccu cggcaucguu uuauucauuu ucgggugccu ccuugugcug 360
ggaauucugga ucuaucugcu agagaugcug uggcggcucg gcgccaccu uuggcagcuu 420
cuggcauuuu uccuagcguu uuuucuggau cucauccuac uuauuauugc cuuguauuug 480
cagcagaacu gguggacucu ccugguggau cuccuguggc uccuccuguu ccucgccaau 540
uugauaugga uguacuacca cggacagcgc cacagcgacg agcaccacca cgaugauagu 600
cugccucacc cucaacaggc uacagaugac ucaggccacg aaagcgauuc caacucaaau 660
gaaggccggc accacuuguu gguguccgga gccggcgacg ggccaccacu cugcagccag 720

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aaucugggcg cucccggcgg agguccagac aaugggccac aggaccuga uaacacggau	780
gauaacggac cgcaggaucc ugacaauaca gaugacaacg gcccgauga uccacugccu	840
caggauccug auaauacuga cgauaacgga cccaggauc cugauaacac cgacgacaac	900
gggccucacg aucccccuaacc ccauucccca ucugacucug cuggcaacga uggcgggcca	960
ccgcagcuga ccgaagaggu agaaaacaag ggcggggaucc agggcccucc acugaugaca	1020
gacggcggcg ggggacacuc ccaugauucg ggccaugggg gaggggaucc ucaccuuccc	1080
acacucuugc ugggaaguag cggguccggc ggggacgaug augaucccca ugguccaguc	1140
caguugucan auuacgau	1158

<210> 18
 <211> 1158
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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uacaucguua ugucugauug gacaggagga gcucugcugg uucuuuacuc uuucgcgcug	180
augcugauca ucaucaucu gaucauuuuc auuuucagac gagaccuccu uuguccucuc	240
ggagcccugu guauccuccu gcugaugaua acccuucugc ugauugcuuu guggaauucg	300
caugggcaag cucuguuucu uggaauuguc uuauuuauuu uugggugucu gcugguguug	360
ggaauucgga ucuaucuucu ugaaaugcug uggcggcugg gcgccacaau cuggcagcua	420
cucgccuuuu uccuagcuuu cuuuuuggau cugauucugc ugauuauugc ucucuaccug	480
cagcagaauu gguggacccu cuuagucgau cugcuguggc uguugcucu ucucgccauc	540
cugauuugga uguacuauca ugggcagcgc cauagugaug aacaucauca cgaugauucc	600
cugccacauc cucagcaggc cacagaugau ucaggccacg aaucagacag caauagcaau	660

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gagggccgcc accaccugcu gguuucaggg gccggugacg gccuccauu gugcagucag	720
aaccuggggag ccccgggggg uggaccugau aacgggccgc aggauccuga caauacugau	780
gacaacggac cccaggaucc agauaacacu gacgacaug gcccccauga ccccuaccc	840
caggaucccg acaauacaga cgacaacgga ccgcaggacc ccgacaacac ugaugauau	900
gggccacacg auccucugcc ucacucucca ucagacucug ccggaaauga cgguggaccg	960
ccacaguuaa cugaagaagu cgaaaacaag ggcggcgau c aggggccgcc gcucaugaca	1020
gauggcgggg gagguacag ccacgauagc ggacacggag gaggugaccc ucaucugccu	1080
acacuucugu ugguagcuc ugaggaguggg ggggaugacg acgaccuca cggaccuguu	1140
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<210> 19
 <211> 1158
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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uauauuguga uguccgacug gaccggcggc gccugcucg uccuguauag cuuugcuuug	180
augcugauaa uuauuauuu gaucaucuuu auuuuccggc gugauuugcu cuguccucuu	240
ggugcccuuu guauccugcu guuaaugauc acucugcucc ucauugcccu auggaaccuc	300
cacggacaag cccuguuucu uggcaucguu cucuuuauau ucggaugccu cuuagugcuu	360
gggaucugga uauaccuguu ggaaaugcug uggaggcuug gagccacgau auggcaauua	420
uuggcauucu uucuggccuu cuuccuggau cugaucugu ugaauuugc ucuguaccug	480
cagcagaacu gguggacacu acuuguugac cugcucuggc uacuccuguu ccuugcgauc	540
cugauuugga uguacuauca cggacagaga cacuccgacg agcaucauca cgacgauucc	600

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uuaccacacc	cucagcaggc	gacagaugau	ucuggccaug	agagcgauuc	caacagcaac	660
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aacuugggcg	cgcccggcgg	cggggccgau	aacggcccg	aggacccgga	caauaccgac	780
gauaaugggc	cucaagauc	cgacaauacu	gaugacaau	gaccacacga	uccucugcca	840
caggaucccg	acaacacaga	ugacaauagg	ccgcaagacc	ccgacaauac	agacgauaau	900
ggccccacg	accacuacc	acauucucc	ucugacagug	cggggauga	ugguggucc	960
ccacaacuga	ccgaggaggu	ggagaauaag	gggggggacc	aagguccacc	ccucaugacu	1020
gauggaggag	gaggacacuc	gcacgauuca	ggucacggcg	gggggggacc	ucacuugccc	1080
acucugcugc	ugggcagcag	cgguucuggg	ggcgacgaug	augaucccca	cggcccggug	1140
cagcuaaguu	auuacgac					1158

<210> 20
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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 20	
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uggccuugcu	guucuggcuu
	120
uacaucguga	ugagcgacug
gacuggcggg	gcccugcugg
uccucuauag	cuuugcacug
	180
augcugauua	uaaucauauu
gaucaucuuc	aucuuccgac
gggauuuacu	uugccccug
	240
ggggcauuau	guauucuauu
gcugaugaua	acacuucugc
uuauugcuuu	auggaaucua
	300
cacggucagg	cucuuuuucu
gggaaucgug	cucuuauc
uuggaugccu	ucugguacua
	360
ggaauuugga	uauaccucuu
agaaaugcug	uggcggcucg
gcgcaacc	cuggcaacuc
	420
cuugcguuuu	uucucgcguu
uuuccucgac	cugauucugc
uaauaau	cgc
cuuauaccuu	
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cagcagaauu	gguggacacu
ccugguggac	cugcuguggc
uccugcuauu	ccuugcaauc
	540

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cucauuugga uguauuacca uggccagagg cacucugaug agcaccacca cgaugauagu	600
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gaaggaagac accaucuguu ggugucaggg gccggagacg gccccccucu guguagccag	720
aaccucgggg caccaggggg agguccugac aaugggccgc aagaccuga caauacugau	780
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ggcccucacg aucccuuacc ccuucuccg uccgacucug cagggaacga cgggggccc	960
ccucaguuua ccgaagaggu cgaaaauaag gggggagacc agggcccccc auuaugaca	1020
gacgggggcg gcggucacag ucacgacuca ggucacggcg gcggggaccc ccuuugccu	1080
acacugcugu uaggguuuc uggcucaggc ggggacgaug augauccaca cgguccggug	1140
cagcugucau auuaugau	1158

<210> 21

<211> 1491

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 21

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acuccgaccc cuccaaacga cgaggaaagg gaauccaug aggaaccgcc uccaccauau	180
gaggauccgu acugggggaa cggugauagg cacagugacu accagccacu ugggacacaa	240
gaccaaagcc uguaccucgg acuucagcac gaugguaacg acgguuugcc gccucccccu	300
uauagcccua gagaugauag cucccagcau auauacgagg aggcugguag gggcuccaug	360
aauccaguau gcuugcccgu uaucguagcc ccuaccucu ucuggcuugc ggcgaucgca	420
gcuagcuguu uuacagcuuc cgugagcaca gucguaaccg cgacaggacu ggcacugucu	480

M137870089W000-SEQ-HJD.txt

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gaagauccuc cauuuaauag ucuccuguuu gcacugcugg ccgcugcggg cgggcuacaa 660
gggauauaug ugcuaaguau gcucguccua cuuauucugg ccuauaggcg gagguggcgg 720
cgccugacag ugugcggagg gauaanguuc cuagccugug ugcucgugcu cauuguggac 780
gcuguucuac aguugucucc ucugcugggu gcagugacgg uggucucaau gaccucugcug 840
uuacuugccu ucgugcuuug guugucaucu ccaggggggac ugggcacacu gggcgccgcc 900
cuguuaaccc uggcggccgc ucuggcacuc cuggccucac ugauucuggg aacucugaau 960
cucaccacua uguuucuucu gauguuauug uggacuuugg ugguguugcu gauuugcagc 1020
uccugcaguu cuugccccc uuccaaaaa uuacuggcgc ggcuguuccu uuaugcccuc 1080
gccuuacugc ugcucgcuag cgccuuauu gcugggggcu ccuauucuca gaccaacuuu 1140
aaaucccugu ccagcacuga auucauccc aaccuuuuuu gcaugcugcu ccuaaucgug 1200
gcugggauuc uguuuauucu ggccauuuug accgaguggg gcaguggcaa caggaccuac 1260
ggcccugugu ucaugugucu gggggggcuc uuaacgaugg ucgcuggcgc ugucuggcuc 1320
acggugauga guaacacuuu gcucagcgcg uggauccuga cagccggcuu ucucuuuuu 1380
cugauugggu ucgcuuuguu uggagucuu cgguuguucc gcuaugcug uuacuauugu 1440
uugacauugg aguccgagga gaggccacc accccuacc gaaauacggu a 1491

<210> 22
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 22

Met Gly Ser Leu Glu Met Val Pro Met Gly Ala Gly Pro Pro Ser Pro
1 5 10 15

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

M137870089W000-SEQ-HJD.txt

Leu Phe Ala Leu Leu Ala Ala Ala Gly Gly Leu Gln Gly Ile Tyr Val
210 215 220

Leu Val Met Leu Val Leu Leu Ile Leu Ala Tyr Arg Arg Arg Trp Arg
225 230 235 240

Arg Leu Thr Val Cys Gly Gly Ile Met Phe Leu Ala Cys Val Leu Val
245 250 255

Leu Ile Val Asp Ala Val Leu Gln Leu Ser Pro Leu Leu Gly Ala Val
260 265 270

Thr Val Val Ser Met Thr Leu Leu Leu Leu Ala Phe Val Leu Trp Leu
275 280 285

Ser Ser Pro Gly Gly Leu Gly Thr Leu Gly Ala Ala Leu Leu Thr Leu
290 295 300

Ala Ala Ala Leu Ala Leu Leu Ala Ser Leu Ile Leu Gly Thr Leu Asn
305 310 315 320

Leu Thr Thr Met Phe Leu Leu Met Leu Leu Trp Thr Leu Val Val Leu
325 330 335

Leu Ile Cys Ser Ser Cys Ser Ser Cys Pro Leu Ser Lys Ile Leu Leu
340 345 350

Ala Arg Leu Phe Leu Tyr Ala Leu Ala Leu Leu Leu Leu Ala Ser Ala
355 360 365

Leu Ile Ala Gly Gly Ser Ile Leu Gln Thr Asn Phe Lys Ser Leu Ser
370 375 380

Ser Thr Glu Phe Ile Pro Asn Leu Phe Cys Met Leu Leu Leu Ile Val
385 390 395 400

Ala Gly Ile Leu Phe Ile Leu Ala Ile Leu Thr Glu Trp Gly Ser Gly
 405 410 415

Asn Arg Thr Tyr Gly Pro Val Phe Met Cys Leu Gly Gly Leu Leu Thr
 420 425 430

Met Val Ala Gly Ala Val Trp Leu Thr Val Met Ser Asn Thr Leu Leu
 435 440 445

Ser Ala Trp Ile Leu Thr Ala Gly Phe Leu Ile Phe Leu Ile Gly Phe
 450 455 460

Ala Leu Phe Gly Val Ile Arg Cys Cys Arg Tyr Cys Cys Tyr Tyr Cys
 465 470 475 480

Leu Thr Leu Glu Ser Glu Glu Arg Pro Pro Thr Pro Tyr Arg Asn Thr
 485 490 495

Val

<210> 23
 <211> 1491
 <212> RNA
 <213> Artificial Sequence

<220>
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 acaccacccc cccccaacga cgaggagaga gaauccaacg aggagccucc uccccauac 180
 gaagacccuu acugggggaa uggagaccgu cauucugacu aucaaccucu aggcacucag 240
 gaccagucuc uuuaccuagg guuacaacac gaugguaaug augggguugcc cccgccgccc 300

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uauagucccc gggacgacag uagucagcau auauaugagg aagccggcag agguucuaug	360
aaucccguuu gucuaccggu cauugucgcc ccuauuuau ucuggcuugc agccaucgcc	420
gcuucgugcu ucaccgccuc cguguccacg guggugacag cuacagggcu ggcacucucu	480
cugcuacucc uggcugcugu ggccagcucc uacgcagcgg cucagcggaa gcuucucacu	540
ccuguaacug uccucaccgc gguagugacc uuuuuugcca uaugccugac auggaggauu	600
gaggacccac ccuuuaauuc ucugcuguuu gcgcuuuugg ccgcugccgg aggacugcaa	660
gguaauuaug ugcugguaau guugguucua cuuauucucg cauaccggcg acgguggcgg	720
aggcugacug uaugcggggg gauuauguuc cuggcgugug uucugguuuu gaucgucgau	780
gccgugcugc aguugucacc gcugcucggg gcggucaccg uugugaguau gacacugcuu	840
cugcuggcuu ucgugcucug gcuaucuucc cccggggggc ugaggaccuu gggcgucg	900
cuucugacuc uggcagcugc ucuggcccug cuggccucuc uuauucuugg cacacugaau	960
uugacuacca uguuccucuu gauguugcug uggaccuuag uugugcugcu gaucuguucu	1020
uccuguagca gcuguccacu guccaagauu cuccuggcca gguuguuucu guauggccua	1080
gcgcugcugc uguuagcuuc ugcucugaua gccggcggca guauccugca aaccaacuuc	1140
aagagccucu ccagcacaga auucauccu aaucucuuiu gcaugcuacu gcucaucgug	1200
gcaggcauac uguucauucu ugcuauccug acugaauggg gcucuggcaa uagaacauac	1260
gggccagugu ucaugugcuu gggcggccug uugacaaugg uugcuggagc cguguggcug	1320
acgguaaugu ccaacacucu gcugagcgca uggaucuuaa cagccggauu ccugaucuuu	1380
uuauucggau ucgcacucuu cggagugauc cggugcugua gguauuguug uuauuacugc	1440
cugacacucg agucggaaga gaggccccc acaccuacc ggaauacagu u	1491

<210> 24

<211> 1491

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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acgccuacac caccaaacga cgaggagcgg gagucuaacg aggagccucc acccccuac	180
gaggauccuu acugggggaa cggagaucga cauucugacu accagccuuu agggacacag	240
gaucagucuc ucuaucucgg acugcagcau gauggcaacg acggacugcc cccaccaccu	300
uauucuccac gcgacgacag cucacagcac auauacgaag aggccgggcg cgggucuaug	360
aacccgguuu gccugccagu caucgucgca ccuaccucu uuuggcuggc ggccauugcc	420
gcguccuguu ucacagccuc agugucgacu gugguaaccg caacaggguu cgcacucagc	480
cuacugcugc ucgcugccgu cgcguccucu uaugcugcug cccagcgcaa acugcucacc	540
ccaguuacgg ugcucacugc uguuguuacc uuuuucgua uuugucucac cuggagaau	600
gaagacccgc cguucaacag ucuguuuuuu gccucuuagg cugcagcagg cggccuucag	660
ggcaucuaug uccuggugau gcugguccug cucauccugg cuuacaggag aagauggcgu	720
cggcugaccg uguguggugg caucauguuu cucgcgugug uucuggugcu caucgucgau	780
gccgugcuac agcugagccc acugcuugga gccgugacag ucguuagcau gacacuccug	840
cuauuggcuu ucgugcucug gcugaguagc ccaggugggc ucggcacacu uggugccgcg	900
cuuuuaacac uggccgcggc ccucgcacug cuggccucuc uaaucucgg aacauugaac	960
cugacaacca uguuccuccu gaugcuccuc uggacacugg ugguacuguu aaucuguagc	1020
ucuugcucau caugcccacu gagcaagaua cuccuggcga gacuuuuccu auacgccug	1080
gcccugcugc uguuggcauc ggcucugauc gcugggggaa gcauccuua aacaaauuuc	1140
aagagccuua gcaguacuga guuuauaccu aaccuguucu gnaugcuucu gcugauaguc	1200
gcugggauac uuuuuuuuuc ggcaauccua acagaguggg ggucagguaa caggaccuau	1260
gggccuguuu uuauugccu cggaggccuc cucaccaugg uugccggcgc aguuugguug	1320
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M137870089W000-SEQ-HJD.txt

cuaauaggau uugcccuguu ugaggguuau cggugcugcc guuacugcug cuacuauugu	1440
uugacccuug agucugaaga aaggccgccc acccccuaca gaaacacugu a	1491

<210> 25
 <211> 1491
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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acccccacac caccuacga cgaggaacgg gagucuuacg aggaaccccc accgccguac	180
gaggaccan acugggggaa cggggauca cacucagacu accagccucu cggaacgcag	240
gaucaaaagcc uguaccuggg acugcagcac gaugguaacg auggacugcc accaccuccu	300
uacaguccaa gggauagac cagccagcac auuuauaag aagccggccg agguaguaug	360
aauccagugu gucugcccgu gauugucgcc ccuauucucu uuuggcuggc cgccauugcc	420
gccagcuguu ucaccgcguc gguuucaacc guagugaccg ccacaggccu ggcucucagc	480
uuguuacugu uggccgcugu ggcgagcucc uacgccgccg cccagcgcaa gcuacuuacc	540
ccugugacag ugcugacggc ggugguuaca uucuuugcca uuugccugac cuggcgauu	600
gaggauccac cauucuuuuc cuuauuuuu gccuccucg ccgucugcug agggcuccag	660
gguaucuaacg ugcuggugau gcucguuuug cugauauugg cuuaccggcg gcgucggcg	720
cgccuuaccg ucugcggagg aaucuuuuu uuggcaugcg ugcucguucu cauuguggau	780
gcuuuuuugc agcugucacc ccuuugggu gccugacag uuuaaguau gaccucguc	840
cugcucgcau ucugucucug gcugagcucu cccggggggc ugggcacucu cggagcagcu	900
cugcugacac uagccgcagc acuagccuu cuggccaguc uuaucucgg aacgcugaac	960
cugacgacca uguuccuccu gauguugcuc uggaccucg uagucuguu aaauugcucu	1020

M137870089W000-SEQ-HJD.txt

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aagucccuga guucaacaga auucauuccc aaccucuuiu guaugcugcu gcuuaucgug	1200
gccggcaucc ucuuuauccu cgccaucuug acugaguggg gguccggaaa ucgcacauau	1260
ggcccaguuu ucaugugucu gggggggccug cucacgaugg uggccggcgc aguguggcug	1320
acgguaaugu caaacacuuu gcucucugcg uggaucuuga ccgcaggcuu ccugaucuuu	1380
uugaucggcu ucgcccuguu cggugucauc cggugcugca gauacugcug cuacuauugc	1440
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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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accccgaccc caccaaacga cgaagagcgg gagagcaaug aggagcccc acccccuau	180
gaggacccuu acuggggaaa uggcgauca cacagcgauu accagccccu gggcacacag	240
gaucagagcc uguaccuggg cuugcagcau gaugguaacg acgggcuucc gccccacca	300
uacucaccca gagacgauuc aagucagcac aucuacgagg aggcugguag ggguaugaug	360
aauccugugu gucuccugu gaucgucgcc ccuaccuau uuugguuagc ugcgaucgu	420
gccuccugcu ucaccgcuag cgugucaaca gugguuacgg caaccgggcu ggcguuaagu	480
cugcuucugc uugcggcagu ggcaucuuc uaugcagcgg cccagcggaa gcuuuugacc	540
ccugugacag uacugaccgc agugguuacg uuuuuugcga uuugcuugac guggagaaua	600
gaggaucccc cuuuuaacuc acugcucuuu gcacugcucg cggcugcugg gggccugcag	660

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gggauuuacg uccucguuau gcuggugcuc cugaucuuag ccuacagaag gagauggcgc	720
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gccgucuugc agcuuucccc ccugcugggc gcagucaccg ucgugaguau gacucugcug	840
uuacuggccu ucguacugug gcuuagcagc ccuggaggac uaggcacgcu gggcgccgcu	900
uuauugaccc uggcagccgc ccuggcucug cuggccuccc ugauacuggg gacauuaau	960
uuaacaacua uguuucugcu gaugcugcug uggacucuag uugugcucu gauauguucc	1020
uccuguucca gcugcccucu gagcaagauc cuguuggcuc ggcuauuccu guacgcgcug	1080
gcucuccucc ugcuagcuuc agcgcuauu gcaggcgggu cuauucucca gacgaauuu	1140
aagagccuca guagcacuga guuuaucccg aaucuguucu gcauguugcu auugaucguc	1200
gcaggcauuc ucuucauucu ggccauacuu acagaguggg guagcggcaa ccggacuau	1260
ggcccugugu ucaugugcuu ggggggccuu cucacaaugg uggcaggggc gguauggcug	1320
accgugaugu cuaacaccuu guuauagcc uggauccuua ccgccggcuu ccuaauuuuu	1380
cugaucggcu ucgcccucu cggaguaa cgaugcuguc gguacugcug cuacuauugc	1440
cuuacuuugg agagcgaaga gcggccuccc acucccuaua gaaacaccgu u	1491

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<211> 2595

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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guuugcacug cugacgugaa cgugacaauc aauuucgacg ugggaggaaa gaagcaucag	180
cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
gcuuuuggag ggagcgagaa ugcuacaaau cuguuuuuac uggaacugcu uggugcagga	300

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cagcaaguca gccuugaauc cguggaugug uacuuucagg auguuuucgg caccaugugg	420
ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc	480
aagugggaua auugcaauuc aacuaauuu acggcugugg ugagggccca gggcuuggac	540
gugacucugc ccuuauucuc accuacuucu gcccaagacu ccaauuuuuc ugucaagacc	600
gagaugcucg ggaauagau cgauaucgag ugcaucaugg aggacgguga gauaagccag	660
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agugguggca uacucacaag uacuucucc guagccaccc ccauucccg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaaucac caaauuuac uguaacagcu uuuugggccu ggccaaaua cacugagacu	1080
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aaaacauua ucauaacacg gaccgccacc aacgccacga cuacaacca uaaggugauc	1260
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acaaccucag gcgccagccc agugaccccu ucccgaagcc ccugggauaa uggaacggag	1500
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acuagcccaa ccccgacugu gacgaccccc accccgaacg cgacaucucc cacaccugcu	1620
gugacaaccc caaccccuua cgccacuagc ccuacccuag guaagaccag uccgacuagc	1680
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M137870089W000-SEQ-HJD.txt

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ccuaagaacg cuaccuccgc ugucacuacc ggacagcaca acauccaccag cucaagcacg      1860
aguuccauga gcuugcggcc gagcucaaau cccgagaccc uaucaccauc cacaucagac      1920
aacaguacuu cacacaugcc acucuugacg agcgcucacc ccaccggcgg cgagaacauc      1980
acccagguga cuccggcguc uauuuccacc caccacguca gcacgucguc ucccgcaccg      2040
agaccaggga cgacuucua ggccaguggg ccuggcaacu ccucuacaag caaaaacca      2100
ggcgaaguua acgugacaaa aggaacgccc cccagaacg caaccagucc ucaggcccc      2160
agcgggcaga aaacugcggu gccaacugug accagcaccg guggcaaggc caacucaaca      2220
acuggaggga agcauacgac ggggcacggc gcccggaccu ccacugaacc cacgaccgau      2280
uacggaggug acagcacaac accgcggcca cgauauaauug ccaccacuua ucugccacca      2340
uccacaagcu ccaagcugcg gccacggugg accuucacaa gcccaccgu gacgacugcc      2400
caagcgacgg ugccagugcc cccuacaagc cagccacgcu ucuccaaccu uaguaugcuc      2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau      2520
ugcgccuuua ggagaaaccu cagcacuagc cacacguaca ccacgcccc cuacgaugac      2580
gccgagacuu acguc                                                         2595

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<210> 28
 <211> 865
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 28

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Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
1           5           10          15

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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
          20          25          30

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Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
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Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
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M137870089W000-SEQ-HJD.txt

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
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Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

M137870089W000-SEQ-HJD.txt

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
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Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 29
<211> 2595
<212> RNA
<213> Artificial Sequence

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cuggaccugg acuucgggca guuaacaccc cacacaaagg caguuuacca gcccagagga 240
gccuucggcg gaucggagaa ugcaacaaau cuuuuccugc uagaacugcu cggcgccggc 300
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cagcagguca gccucgaaag uguugacguc uauuuccagg augucuugg gacuaugugg 420
ugccaucacg ccgaaaugca gaaucccgug uaccucauuc ccgagacagu acccuauauc 480
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M137870089W000-SEQ-HJD.txt

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gcuuauaguc ugaggcugac ucccaggcca guaucccgau uucuggguaa uaauuccauc	840
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ucuaauauag uguucuccga ugagauuccc gcgagucagg auaugccac caacaccacc	960
gacaucacgu auguugggga uaacgcuacc uauagugugc cgauggugac auccgaggac	1020
gcaaacucuc cuaacguaac cgugaccgcc uuuugggcau ggccaaauaa uaccgaaacc	1080
gauuuuaau gcaaguggac ccugacaucc gggacucccu ccggaugcga aaauauuucu	1140
ggagcuuuug ccagcaaucg gaccuuugau aucacuguga gugguuuagg caccgcccc	1200
aaaacacuga ucauaaccag gacagccaca aaugcgacca caacuacaca caaaguuaa	1260
uuuaguaaag caccugaguc caccacaacu ucuccgacc ucaacacuac cggcuucgcu	1320
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ucgucaauga gccugcggcc gucaaguaau ccagagacuc ugucgccauc uaccucagau	1920
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ggagaggguca augugacuaa ggggacuccc ccccaaaacg cuaccagccc acaggcuccc	2160
ucagggcaga agaccgcugu uccaacaguu acaucuacug ggggcaaggc aaauagcaca	2220
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guccugcagu gggcuuccu cgccgugcug acauuacugu uauugcuggu gauggccgau	2520
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cuggaucuug auuucggcca gcuaacaccu cauaccaagg ccгucuacca accacгcggg	240
гcauuuggcg guucugagaa ugcuacaaac цгуuuccuuu uggaacuccu цggagcaggг	300
gaacuggcac uuacaaugag гaguaagaag цgccccauca acгucaccac gggгgaagaa	360
cagcaggugu ccцuggaguc цгуugaugug uauuuccagg acгуuuucgg гacaaugugg	420
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gaaaugcuug ggaacgagau cgacaucgag uguaucaugg aggaugggga gaucagucag	660
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agaccaggga	ccaccuccca	ggcuagcggc	ccgggcaacu	ccuccacuag	cacgaaacca	2100
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uccggccaga	aaacugcugu	accuacgguc	acuagcacug	gcggaagc	gaauucaacc	2220
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uacgggggug	acucaacgac	cccgaggccc	agguacaacg	caaccaccua	ucuccacca	2340
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cgugacuau	aacuucgaug
ugggggggaa	gaaacaucaa
	180
cuugaucugg	acuuuggcca
gcuuacucc	cacaccaagg
ccguguacca	gccccgcggc
	240
gcauucggug	ggagcgagaa
cgcgacaaa	cuauucuugc
uggaacugcu	gggcgcagga
	300
gagcucgccc	ugacgaugcg
aucuaaaaag	cuucccauca
acguuaccac	uggcgaggag
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cagcaggugu	cccucgaaag
cgucgacguc	uauuuccaag
acgucuucgg	aacaauuggg
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gucacuuugc cacugucacu gcccacauca gccaagaca gcaacuucag cgucaagaca	600
gaaaugcugg gcaacgaaau cgacaucgaa ugcauaaugg aggaugggga aauuucccag	660
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gccuacagcc ugagacugac gccaagacca guuuccaggu uucuggggaa uaacucuauc	840
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gauaucaccu augucgggga caacgccaca uauagcgugc caauggugac cagcgaagau	1020
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acucagguua cccagcuuc uaucucgacu caccaugucu cuacuucuuc cccagcgcca	2040
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ggcgaaguca acguuaccaa gggaacaccc cccagaaug caaccucucc ccaagcuccc	2160
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gucugcacag ccgacguuaa cguuacaauc aauuucgacg ugggcgggaa aaaacaccag	180
cuggaccucg acuuugggca gcugacgccc cacacuaaag ccguuuacca gcccaggggu	240
gcauucggug gaucugaaaa ugcuaaaaac cucuuucugc uugagcugcu uggugcugga	300
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gugaacuuc acaagaccgc cgagcaggag uacggcgaca aggaggugaa gcugccccac	240
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accuucaagg uguaccagau cuucggcagc cacugcaccu acgugagcaa guucagcacc 600
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Gly Gly Gly Arg Val Ala Ala Ala Ala Ile Thr Trp Val Pro Lys Pro
35 40 45

Asn Val Glu Val Trp Pro Val Asp Pro Pro Pro Pro Val Asn Phe Asn
50 55 60

Lys Thr Ala Glu Gln Glu Tyr Gly Asp Lys Glu Val Lys Leu Pro His
65 70 75 80

Trp Thr Pro Thr Leu His Thr Phe Gln Val Pro Gln Asn Tyr Thr Lys
85 90 95

Ala Asn Cys Thr Tyr Cys Asn Thr Arg Glu Tyr Thr Phe Ser Tyr Lys
100 105 110

Gly Cys Cys Phe Tyr Phe Thr Lys Lys Lys His Thr Trp Asn Gly Cys
115 120 125

Phe Gln Ala Cys Ala Glu Leu Tyr Pro Cys Thr Tyr Phe Tyr Gly Pro
130 135 140

Thr Pro Asp Ile Leu Pro Val Val Thr Arg Asn Leu Asn Ala Ile Glu
145 150 155 160

Ser Leu Trp Val Gly Val Tyr Arg Val Gly Glu Gly Asn Trp Thr Ser
165 170 175

Leu Asp Gly Gly Thr Phe Lys Val Tyr Gln Ile Phe Gly Ser His Cys
180 185 190

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

Ser Phe Leu Lys Pro Cys Leu Cys Val Ser Gln Arg Ser Asn Ser
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gcccuggaga acaucagcga caucuaccug gugagcaacc agaccugcga cggcuucagc 180

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20 25 30

Gln Leu Arg Ala Gln His Leu Leu Ala Leu Glu Asn Ile Ser Asp Ile
35 40 45

Tyr Leu Val Ser Asn Gln Thr Cys Asp Gly Phe Ser Leu Ala Ser Leu
50 55 60

Asn Ser Pro Lys Asn Gly Ser Asn Gln Leu Val Ile Ser Arg Cys Ala
65 70 75 80

Asn Gly Leu Asn Val Val Ser Phe Phe Ile Ser Ile Leu Lys Arg Ser
85 90 95

Ser Ser Ala Leu Thr Gly His Leu Arg Glu Leu Leu Thr Thr Leu Glu
100 105 110

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Asn Arg Tyr Ala Trp His Arg Gly Gly
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gugaccgagg accuggccag caugcugaac cgguacaagc ugaucuacaa gaccagcggc 240
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acccggcccc acagcuacgu guucuaccag cugcggugcc accugagcua cguugcccug 480
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M137870089W000-SEQ-HJD.txt

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aacagcaucc ugucaucuaa uuacuucgac uucgacaacc ugcacguuca uuaccugcuc	1980
cucaccacca acgguaccgu cauggaaauc gccggacugu acgaggagcg ggcccauguu	2040
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<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

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 20 25 30

Ala Ser His Tyr Thr Ile Pro Trp Thr Glu Leu Met Ala Lys Val Pro
 35 40 45

Gly Leu Ser Pro Glu Ala Leu Trp Arg Glu Ala Asn Val Thr Glu Asp
 50 55 60

Leu Ala Ser Met Leu Asn Arg Tyr Lys Leu Ile Tyr Lys Thr Ser Gly
 65 70 75 80

Thr Leu Gly Ile Ala Leu Ala Glu Pro Val Asp Ile Pro Ala Val Ser
 85 90 95

Glu Gly Ser Met Gln Val Asp Ala Ser Lys Val His Pro Gly Val Ile
 100 105 110

Ser Gly Leu Asn Ser Pro Ala Cys Met Leu Ser Ala Pro Leu Glu Lys
 115 120 125

Gln Leu Phe Tyr Tyr Ile Gly Thr Met Leu Pro Asn Thr Arg Pro His
 130 135 140

Ser Tyr Val Phe Tyr Gln Leu Arg Cys His Leu Ser Tyr Val Ala Leu
 145 150 155 160

Ser Ile Asn Gly Asp Lys Phe Gln Tyr Thr Gly Ala Met Thr Ser Lys
 165 170 175

M137870089W000-SEQ-HJD.txt

Phe Leu Met Gly Thr Tyr Lys Arg Val Thr Glu Lys Gly Asp Glu His
180 185 190

Val Leu Ser Leu Val Phe Gly Lys Thr Lys Asp Leu Pro Asp Leu Arg
195 200 205

Gly Pro Phe Ser Tyr Pro Ser Leu Thr Ser Ala Gln Ser Gly Asp Tyr
210 215 220

Ser Leu Val Ile Val Thr Thr Phe Val His Tyr Ala Asn Phe His Asn
225 230 235 240

Tyr Phe Val Pro Asn Leu Lys Asp Met Phe Ser Arg Ala Val Thr Met
245 250 255

Thr Ala Ala Ser Tyr Ala Arg Tyr Val Leu Gln Lys Leu Val Leu Leu
260 265 270

Glu Met Lys Gly Gly Cys Arg Glu Pro Glu Leu Asp Thr Glu Thr Leu
275 280 285

Thr Thr Met Phe Glu Val Ser Val Ala Phe Phe Lys Val Gly His Ala
290 295 300

Val Gly Glu Thr Gly Asn Gly Cys Val Asp Leu Arg Trp Leu Ala Lys
305 310 315 320

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

Gly Ala Thr Val Lys Gly Met Gln Ser Tyr Gly Leu Glu Arg Leu Ala
340 345 350

Ala Met Leu Met Ala Thr Val Lys Met Glu Glu Leu Gly His Leu Thr
355 360 365

M137870089W000-SEQ-HJD.txt

Thr Glu Lys Gln Glu Tyr Ala Leu Arg Leu Ala Thr Val Gly Tyr Pro
 370 375 380

Lys Ala Gly Val Tyr Ser Gly Leu Ile Gly Gly Ala Thr Ser Val Leu
 385 390 395 400

Leu Ser Ala Tyr Asn Arg His Pro Leu Phe Gln Pro Leu His Thr Val
 405 410 415

Met Arg Glu Thr Leu Phe Ile Gly Ser His Val Val Leu Arg Glu Leu
 420 425 430

Arg Leu Asn Val Thr Thr Gln Gly Pro Asn Leu Ala Leu Tyr Gln Leu
 435 440 445

Leu Ser Thr Ala Leu Cys Ser Ala Leu Glu Ile Gly Glu Val Leu Arg
 450 455 460

Gly Leu Ala Leu Gly Thr Glu Ser Gly Leu Phe Ser Pro Cys Tyr Leu
 465 470 475 480

Ser Leu Arg Phe Asp Leu Thr Arg Asp Lys Leu Leu Ser Met Ala Pro
 485 490 495

Gln Glu Ala Thr Leu Asp Gln Ala Ala Val Ser Asn Ala Val Asp Gly
 500 505 510

Phe Leu Gly Arg Leu Ser Leu Glu Arg Glu Asp Arg Asp Ala Trp His
 515 520 525

Leu Pro Ala Tyr Lys Cys Val Asp Arg Leu Asp Lys Val Leu Met Ile
 530 535 540

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

M137870089W000-SEQ-HJD.txt

Arg Gly Ser Ala Leu Tyr Glu Ala Ser Thr Thr Tyr Leu Ser Ser Ser
565 570 575

Leu Phe Leu Ser Pro Val Ile Met Asn Lys Cys Ser Gln Gly Ala Val
580 585 590

Ala Gly Glu Pro Arg Gln Ile Pro Lys Ile Gln Asn Phe Thr Arg Thr
595 600 605

Gln Lys Ser Cys Ile Phe Cys Gly Phe Ala Leu Leu Ser Tyr Asp Glu
610 615 620

Lys Glu Gly Leu Glu Thr Thr Thr Tyr Ile Thr Ser Gln Glu Val Gln
625 630 635 640

Asn Ser Ile Leu Ser Ser Asn Tyr Phe Asp Phe Asp Asn Leu His Val
645 650 655

His Tyr Leu Leu Leu Thr Thr Asn Gly Thr Val Met Glu Ile Ala Gly
660 665 670

Leu Tyr Glu Glu Arg Ala His Val Val Leu Ala Ile Ile Leu Tyr Phe
675 680 685

Ile Ala Phe Ala Leu Gly Ile Phe Leu Val His Lys Ile Val Met Phe
690 695 700

Phe Leu
705

<210> 39
<211> 1158
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

M137870089W000-SEQ-HJD.txt

<400> 39

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uacaucguua ugagugacug gacuggagga gccuccuug uccucuauuc cuuugcucuc      180
augcuuauaa uuauauuuu gaucaucuuu aucuucagaa gagaccuucu cuguccacuu      240
ggagcccuuu guauacuccu acugaugauc acccuccugc ucaucgcucu cuggaauuug      300
cacggacagg cauuguuccu uggaauugug cuguucaucu ucgggugcuu acuugucuua      360
gguaucugga ucuacuuauu ggagaugcuc uggcgacuug gugccaccuau cuggcagcuu      420
uuggccuucu uccuagccuu cuuccuagac cucauccugc ucauuauugc ucucuauua      480
caacagaacu gguggacucu auugguugau cuccuuuggc uccuccuguu ucuggcgauu      540
uuaaucugga uguauuacca uggacaacga cacagugaug aacaccacca cgaugacucc      600
cucccgacc cuacaagc uaccgaugau ucuggccaug aaucugacuc uaacuccaac      660
gagggcagac accaccugcu cgugagugga gccggcgacg gaccaccacu cugcucucag      720
aaccuaggcg caccuggagg ugguccugac aauggcccac aggaccuga caacacggau      780
gauaauggcc cacaggaccc ugauaacacu gaugacaauug gccacauga cccgcugccu      840
caagaccag acaauacuga ugacaauaggc ccacaggacc cugacaacac ugaugacaau      900
ggcccgcacg acccguaacc ucauagccu agcgacucug cuggaaauga uggaggccu      960
ccacaauuga cggaagaggu ugagaacaaa ggaggugacc agggcccgcc uuugaugaca     1020
gacggaggcg gcggucuuag ucaugauucc ggccauggcg gcggugauc acaccuuccu     1080
acgcugcugu ugguuucuuc ugguuccggu ggagaugaug acgaccgca cggcccaguu     1140
cagcuaagcu acuaugac                                         1158

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<210> 40

<211> 1491

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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acgcccaccc caccgaacga ugaggaacgu gaaucuaaug aagagccacc accgccuuau	180
gaggacccau auuggggcaa uggcgaccgu cacucggacu aucaaccacu aggaacccaa	240
gaucaaaguc uguacuuggg auugcaacac gacgggaug acgggcuccc uccaccuccc	300
uacucuccac gggaugacuc aucucaacac auauacgaag aagcgggcag aggaaguaug	360
aauccaguau gccugccugu aauguugcg ccuaccucu uuuggcuggc ggcuauugcc	420
gccucguguu ucacggccuc aguuaguacc guugugaccg ccaccggcuu ggcccucua	480
cuucuacucu uggcagcagu ggccagcuca uaugccgcug caciaaggaa acugcugaca	540
ccggugacag ugcuuacugc gguugucacu uucuuugcaa uuugccuaac auggaggauu	600
gaggacccac cuuuuaauuc ucuucuguuu gcuuugcugg ccgcagcugg cggacuacaa	660
ggcauuuacg uucuggugau gcuugugcuc cugauacuag cguacagaag gagauggcgc	720
cguuugacug uuuguggcgg caucauguuc uggcaugug uacuuguccu caucgucgac	780
gcuguuuugc agcugagucc ccuccuugga gcuguaacug ugguuuuccau gacgcugcug	840
cuacuggcuu ucguccucug gcucucuucg ccagguggcc uagguacucu uggugcagcc	900
cuuuuaacau uggcagcagc ucuggcacug cuagcgucac ugauuuuggg cacacuuaac	960
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ucgugcucu cauguccacu gagcaagau cuucuggcac gacuguuccu auaugcucuc	1080
gcacucuugu ugcuaaggcuc cgcgcuaauc gcugguggca guauuuugca aacaaacuuc	1140
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cucauuggcu uugcccucuu ugagggucauu agaucugcc gcuacugcug cuacuacugc 1440

cuuacacugg aaagugagga gcgcccaccg accccaauauc gcaacacugu a 1491

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<211> 726

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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gacgauccug gcgagggggc uuccacaggc ccucgcggcc agggagaugg cggaaggcgg 180

aagaagggcg gcugguuugg caagcauagg ggccagggcg gcuccaaucc caaguucgag 240

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cugagaaggg gcaccgcccc ugccaucccu cagugcagac ucacgccccu gagcaggcuc 420

cccuuuggga uggcuuccug gccaggcccg cagcccgggc ccucaggga aagcaucgug 480

uguuacuuua ugguguuuuc gcagacacac aucuuugcag aaguucugaa agaugcauc 540

aaggauccug ugaugaccaa gccugcaccu acgugcaaua ucagggugac aguaugcucc 600

uucgacgacg guguggaccu cccgcccugg uucccaccca uggucgaggg ugccgccgcc 660

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caggag 726

<210> 42

<211> 2832

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 42

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uugagcgaca gcagcagcga gaaggaggcc gaggacgccc accuggagcc cgcccagaag	180
ggcaccaaga ggaagagggu ggaccacgac gcuggcggaug cugccccugc caggcccaug	240
cugccacccc agcccgaccu gcccggcagg gaggccaucc ugaggagguu cccacuggac	300
cugaggaccc ugcugcaggc caucggcgcc gccgccacca ggau cgacac cagggccauc	360
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uggaggcugc agaccuggc cgccggcugg cccaugggcu accaggccua cagcagcugg	540
auguacagcu acaccgacca ccagaccacu ccgaccuucg ugcaccucca ggcuaccug	600
ggcugcacug gcggucgcag gugccacgug accuucucag cgggcaccuu caagcugccc	660
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cagaguugca accccaggua cagcaucuuc uucgacuaca uggcgauuca caggagccug	780
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gcucaggugc ccgagccacc caccauccau cucgccgcac agggcauggc cuaccacug	1380

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uccauccacg gccgaccuug cccacaggcu ccagaguggc ccguacagga agaaggcggc	2640
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gaguggccag uucaggguga agguggucag aacgugaccg gcccggaaac ccgaagggug	2760
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2832

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 <211> 944
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 43

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Asp Trp Glu Asn Val Leu Ile Glu Leu Ser Asp Ser Ser Ser Glu Lys
 35 40 45

Glu Ala Glu Asp Ala His Leu Glu Pro Ala Gln Lys Gly Thr Lys Arg
 50 55 60

Lys Arg Val Asp His Asp Ala Gly Gly Ser Ala Pro Ala Arg Pro Met
 65 70 75 80

Leu Pro Pro Gln Pro Asp Leu Pro Gly Arg Glu Ala Ile Leu Arg Arg
 85 90 95

Phe Pro Leu Asp Leu Arg Thr Leu Leu Gln Ala Ile Gly Ala Ala Ala
 100 105 110

Thr Arg Ile Asp Thr Arg Ala Ile Asp Gln Phe Phe Gly Ser Gln Ile
 115 120 125

Ser Asn Thr Glu Met Tyr Ile Met Tyr Ala Met Ala Ile Arg Gln Ala
 130 135 140

M137870089W000-SEQ-HJD.txt

Ile Arg Asp Arg Arg Arg Asn Pro Ala Ser Arg Arg Asp Gln Ala Lys
145 150 155 160

Trp Arg Leu Gln Thr Leu Ala Ala Gly Trp Pro Met Gly Tyr Gln Ala
165 170 175

Tyr Ser Ser Trp Met Tyr Ser Tyr Thr Asp His Gln Thr Thr Pro Thr
180 185 190

Phe Val His Leu Gln Ala Thr Leu Gly Cys Thr Gly Gly Arg Arg Cys
195 200 205

His Val Thr Phe Ser Ala Gly Thr Phe Lys Leu Pro Arg Cys Thr Pro
210 215 220

Gly Asp Arg Gln Trp Leu Tyr Val Gln Ser Ser Val Gly Asn Ile Val
225 230 235 240

Gln Ser Cys Asn Pro Arg Tyr Ser Ile Phe Phe Asp Tyr Met Ala Ile
245 250 255

His Arg Ser Leu Thr Lys Ile Trp Glu Glu Val Leu Thr Pro Asp Gln
260 265 270

Arg Val Ser Phe Met Glu Phe Leu Gly Phe Leu Gln Arg Thr Asp Leu
275 280 285

Ser Tyr Ile Lys Ser Phe Val Ser Asp Ala Leu Gly Thr Thr Ser Ile
290 295 300

Gln Thr Pro Trp Ile Asp Asp Asn Pro Ser Thr Glu Thr Ala Gln Ala
305 310 315 320

Trp Asn Ala Gly Phe Leu Arg Gly Arg Ala Tyr Gly Ile Asp Leu Leu
325 330 335

Arg Thr Glu Gly Glu His Val Glu Gly Ala Thr Gly Glu Thr Arg Glu
340 345 350

Glu Ser Glu Asp Thr Glu Ser Asp Gly Asp Asp Glu Asp Leu Pro Cys
355 360 365

Ile Val Ser Arg Gly Gly Pro Lys Val Lys Arg Pro Pro Ile Phe Ile
370 375 380

Arg Arg Leu His Arg Leu Leu Leu Met Arg Ala Gly Lys Arg Thr Glu
385 390 395 400

Gln Gly Lys Glu Val Leu Glu Lys Ala Arg Gly Ser Thr Tyr Gly Thr
405 410 415

Pro Arg Pro Pro Val Pro Lys Pro Arg Pro Glu Val Pro Gln Ser Asp
420 425 430

Glu Thr Ala Thr Ser His Gly Ser Ala Gln Val Pro Glu Pro Pro Thr
435 440 445

Ile His Leu Ala Ala Gln Gly Met Ala Tyr Pro Leu His Glu Gln His
450 455 460

Gly Met Ala Pro Cys Pro Val Ala Gln Ala Pro Pro Thr Pro Leu Pro
465 470 475 480

Pro Val Ser Pro Gly Asp Gln Leu Pro Gly Val Phe Ser Asp Gly Arg
485 490 495

Val Ala Cys Ala Pro Val Pro Ala Pro Ala Gly Pro Ile Val Arg Pro
500 505 510

Trp Glu Pro Ser Leu Thr Gln Ala Ala Gly Gln Ala Phe Ala Pro Val
515 520 525

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Arg Pro Gln His Met Pro Val Glu Pro Val Pro Val Pro Thr Val Ala
530 535 540

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

Ile Ala Met Gln Gly Pro Gly Glu Thr Ser Gly Ile Arg Arg Ala Arg
565 570 575

Glu Arg Trp Arg Pro Ala Pro Trp Thr Pro Asn Pro Pro Arg Ser Pro
580 585 590

Ser Gln Met Ser Val Arg Asp Arg Leu Ala Arg Leu Arg Ala Glu Ala
595 600 605

Gln Val Lys Gln Ala Ser Val Glu Val Gln Pro Pro Gln Leu Thr Gln
610 615 620

Val Ser Pro Gln Gln Pro Met Glu Gly Pro Leu Val Pro Glu Gln Gln
625 630 635 640

Met Phe Pro Gly Ala Pro Phe Ser Gln Val Ala Asp Val Val Arg Ala
645 650 655

Pro Gly Val Pro Ala Met Gln Pro Gln Tyr Phe Asp Leu Pro Leu Ile
660 665 670

Gln Pro Ile Ser Gln Gly Ala Pro Val Ala Pro Leu Arg Ala Ser Met
675 680 685

Gly Pro Val Pro Pro Val Pro Ala Thr Gln Pro Gln Tyr Phe Asp Ile
690 695 700

Pro Leu Thr Glu Pro Ile Asn Gln Gly Ala Ser Ala Ala His Phe Leu
705 710 715 720

M137870089W000-SEQ-HJD.txt

Pro Gln Gln Pro Met Glu Gly Pro Leu Val Pro Glu Gln Trp Met Phe
725 730 735

Pro Gly Ala Ala Leu Ser Gln Ser Val Arg Pro Gly Val Ala Gln Ser
740 745 750

Gln Tyr Phe Asp Leu Pro Leu Thr Gln Pro Ile Asn His Gly Ala Pro
755 760 765

Ala Ala His Phe Leu His Gln Pro Pro Met Glu Gly Pro Trp Val Pro
770 775 780

Glu Gln Trp Met Phe Gln Gly Ala Pro Pro Ser Gln Gly Thr Asp Val
785 790 795 800

Val Gln His Gln Leu Asp Ala Leu Gly Tyr Thr Leu His Gly Leu Asn
805 810 815

His Pro Gly Val Pro Val Ser Pro Ala Val Asn Gln Tyr His Leu Ser
820 825 830

Gln Ala Ala Phe Gly Leu Pro Ile Asp Glu Asp Glu Ser Gly Glu Gly
835 840 845

Ser Asp Thr Ser Glu Pro Cys Glu Ala Leu Asp Leu Ser Ile His Gly
850 855 860

Arg Pro Cys Pro Gln Ala Pro Glu Trp Pro Val Gln Glu Glu Gly Gly
865 870 875 880

Gln Asp Ala Thr Glu Val Leu Asp Leu Ser Ile His Gly Arg Pro Arg
885 890 895

Pro Arg Thr Pro Glu Trp Pro Val Gln Gly Glu Gly Gly Gln Asn Val
900 905 910

Thr Gly Pro Glu Thr Arg Arg Val Val Val Ser Ala Val Val His Met
 915 920 925

Cys Gln Asp Asp Glu Phe Pro Asp Leu Gln Asp Pro Pro Asp Glu Ala
 930 935 940

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 <212> RNA
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<220>
 <223> Synthetic Polynucleotide

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 guuugcacuu acgacgugaa cgugacaau aauuucgacg ugggaggaaa gaagcaucag 180
 cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
 gcuuuuggag ggagcgagaa ugcuaaaaau cuguucuuac uggaacugcu uggugcagga 300
 gagcuggcac uaaccaugcg aagcaagaag cuccccauc acguuaccac cggggaagaa 360
 cagcaaguca gccuugaau cguggaugug uacuucagg auguuucgg caccaugugg 420
 ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc 480
 aagugggaua auugcaauuc aacuaauau acggcugugg ugagggcca gggcuuggac 540
 gugacucugc ccuuaucucu accuacuucu gcccaagacu ccaauuucuc ugucaagacc 600
 gagaugcucg ggaugagau cgauaucgag ugcaucaugg aggacgguga gauaagccag 660
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 gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc 840
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M137870089W000-SEQ-HJD.txt

aguaauaucg uuuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
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acuagcccaa cccagcugu gacgacgcc accccgaacg cgacaucucc cacaccugcu	1620
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 gccgagacuu acguc 2595

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 45

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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
 20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Tyr Asp Val Asn Val
 35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

Gly Pro Lys Ala Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val
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Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
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Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
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Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
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Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
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Val
865

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 guucugcccc gcgacaaca guucaauauc acuuguucug gcuacgaguc ccaugugccu 720
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 aguaauaucg uuuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu 960
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<223> Synthetic Polypeptide

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 20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
 35 40 45

Thr Phe Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
 115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
 130 135 140

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Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
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Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

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Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

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<223> Synthetic Polynucleotide

<400> 48

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cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
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cagcaaguca gccuugaaucc cguggaugug uacuuucagg auguuuucgg caccaugugg	420
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acuagcccaa cccagcugu gacgacgcc accccgaacg cgacaucucc cacaccugcu	1620
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acuggaggca agcauacgac ggggcacggc gcccggaccu ccacugaacc caccgaccgau	2280
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guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau	2520
ugcgccuuua ggagaaaccu cagcacuagc cacacguaca ccacgccgcc cuacgaugac	2580
gccgagacuu acguc	2595

<210> 49
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<223> Synthetic Polypeptide

<400> 49

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			20					25					30		

Phe	Pro	Phe	Tyr	Pro	Thr	Cys	Asn	Val	Cys	Thr	Ala	Asp	Val	Asn	Val
		35					40					45			

Thr	Ile	Asn	Phe	Asp	Val	Gly	Gly	Lys	Lys	His	Gln	Leu	Asp	Leu	Asp
	50					55					60				

Phe	Gly	Gln	Leu	Thr	Pro	His	Thr	Lys	Ala	Val	Tyr	Gln	Pro	Arg	Gly
65					70				75						80

Ala	Phe	Gly	Gly	Ser	Glu	Asn	Ala	Thr	Asn	Leu	Phe	Leu	Leu	Glu	Leu
				85					90					95	

Leu	Gly	Ala	Gly	Glu	Leu	Ala	Leu	Thr	Met	Arg	Ser	Lys	Lys	Leu	Pro
			100					105					110		

Ile	Asn	Val	Thr	Thr	Gly	Glu	Glu	Gln	Gln	Val	Ser	Leu	Glu	Ser	Val
		115				120						125			

Asp	Val	Tyr	Phe	Gln	Asp	Val	Phe	Gly	Thr	Met	Trp	Cys	His	His	Ala
	130					135					140				

Glu	Met	Gln	Asn	Pro	Val	Tyr	Leu	Ile	Pro	Glu	Thr	Val	Pro	Tyr	Ile
145					150					155					160

Lys	Trp	Asp	Asn	Cys	Asn	Ser	Thr	Asn	Ile	Thr	Ala	Val	Val	Arg	Ala
				165					170					175	

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Ile Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 50
<211> 2595
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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gaggaccccc gcuucuuuaa cguggaaauc ccagaguucc cuuucuauc aaccuguaac 120
guuugcacug cugacgugaa cgugacauc aaauucgacg ugggaggaaa gaagcaucag 180

M137870089W000-SEQ-HJD.txt

cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
gcuuuuggag ggagcgagaa ugcuaaaaau cuguucuac uggaacugcu uggugcagga	300
gagcuggcac uaaccaugcg aagcaagaag cuccccaauca acguuaccac cggggaagaa	360
cagcaaguca gccuugaau cugggauug uacuucagg auguuucgg caccaugugg	420
ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc	480
aagugggaua auugcaauuc aacuaauuu acggcugugg ugagggcca gggcuuggac	540
gugacucugc ccuuauucu accuacuucu gccaagacu ccauuucuc ugucaagacc	600
gagaugcucg ggaugagau cgauaucgag ugcaucaugg aggacgguga gaaagccag	660
guucugcccg gcgacaaca guucaauauc acuuguucug gcuacgaguc ccaugugccu	720
agugguggca uacucacaag uacuucucc guagccacgc ccauucccg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguaa caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaauucac caaauuuac uguaacagcu uucugggccu ggccaaauaa cacugagacu	1080
gacuucaau gaaugggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
ggggccuuug cuuccaagac gacuuucgac aucacugucu cagggcuggg gacagcaccg	1200
aagacauuaa ucauaacacg gaccgccacc aacgccacga cuacaaccug gaaggugauc	1260
uuuuccaagg caccugaguc caccacuacc ucccgacuc uuaacacuac gggcuucgcu	1320
gaucccaaca ccacuacggg guugccuagc ucgacacaug ugccgacgaa ccugacugcc	1380
ccugcaucga ccggggccac aguuucgacc gccgauguga caucaccaac gcccgcaggu	1440
acaaccucag gcgccagccc agugacccu uccccaagcc ccugggauaa uggaacggag	1500
uccaaggcuc cugauaugac uuccucuacc agccccguga cuacaccac ucccaacgca	1560
acuagcccaa cccagcugu gacgacgcc accccgaacg cgacaucucc cacaccugcu	1620

M137870089W000-SEQ-HJD.txt

gugacaaccc caaccccuaa cgccacuagc ccuacccuag guaagaccag uccgacuagc	1680
gccguuacaa ccccuacccc uaacgcaacc ggcccgaccg ugggcgagac uuccccgcaa	1740
gccaaugcga caaaucacac auugggcggg accucuccua caccagucgu uacaucucag	1800
ccuaagaacg cuaccuccgc ugucacuacc ggacagcaca acaucaccag cucaagcacg	1860
aguuccauga gcuugcggcc gagcucaaau cccgagaccc uaucaccauc cacaucagac	1920
aacaguacuu cacacaugcc acucuugacg agcgcucacc ccaccggcgg cgagaacauc	1980
accagguga cuccggcguc uauuuccacc caccacguca gcacgucguc ucccgcaccg	2040
agaccaggga cgacuucua ggccaguggg ccuggcaacu ccucuacaag caaaaagcca	2100
ggcgaaguua acgugacaaa gggaacgccu cccagaacg caaccagucc ucaggcgccc	2160
agcgggcaga agacugcggu gccaacugug accagcaccg guggcaaggc caacucaaca	2220
acuggaggca agcauacgac ggggcacggc gcccggaccu ccacugaacc cacgaccgau	2280
uacggaggug acagcacaac accgcggcca cgauauaauug ccaccacuua ucugccacca	2340
uccacaagcu ccaagcugcg gccacggugg accuucacaa gcccacccgu gacgacugcc	2400
caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc	2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau	2520
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gccgagacuu acguc	2595

<210> 51
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 51

Met	Glu	Ala	Ala	Leu	Leu	Val	Cys	Gln	Tyr	Thr	Ile	Gln	Ser	Leu	Ile
1				5					10					15	

M137870089W000-SEQ-HJD.txt

His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

M137870089W000-SEQ-HJD.txt

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

Trp Lys Val Ile Phe Ser Lys Ala Pro Glu Ser Thr Thr Thr Ser Pro
420 425 430

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

M137870089W000-SEQ-HJD.txt

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 52
<211> 2595
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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guuugcacuu acgacgugaa cgugacauuc aauuucgacg ugggaggaaa gaagcaucag 180
cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
gcuuuuggag ggagcgagaa ugcuaaaaau cuguucuuac uggaacugcu uggugcagga 300
gagcuggcac uaaccaugcg aagcaagaag cuccccauc acguuaccac cggggaagaa 360
cagcaaguc gccuugaau cguggaugug uacuucagg auguuucgg caccaugugg 420

M137870089W000-SEQ-HJD.txt

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gugacucugc ccuuauucuc accuacuucg gccaagacu ccaauuucuc ugucaagacc	600
gagauacucg ggaugagau cgauaucgag ugcaucaugg aggacgguga gauaagccag	660
guucugcccg gcgacaaca guucaauauc acuuguucug gcuacgaguc ccaugugccu	720
agugguggca uacucacaag uacuucucc guagccacgc ccuaucccg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaauucac caaauuuac uguaacagcu uucugggccu ggccaaauaa cacugagacu	1080
gacuucuuuu guaaguggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
ggggccuuug cuuccaacag gacuucgac aucacugucu cagggcuggg gacagcaccg	1200
aagacauuaa ucauaacacg gaccgccacc aacgccacga cuacaaccug gaaggugauc	1260
uuuuccaagg caccugaguc caccacuacc ucccgcaguc uuaacacuac gggcuucgcu	1320
gaucccaaca ccacuacggg guugccuagc ucgacacaug ugccgacgaa ccugacugcc	1380
ccugcaucga ccgggcccac aguuucgacc gccgauguga caucaccaac gcccgaggu	1440
acaaccucag gcgccagccc agugaccccu ucccgaagcc ccugggauaa uggaacggag	1500
uccaaggcuc cugauaugac uuccucuacc agccccguga cuacaccac uccaacgca	1560
acuagcccaa cccagcugu gacgacgccc accccgaacg cgacaucucc cacaccugcu	1620
gugacaaccc caaccccuua cgccacuagc ccuacccuag guaagaccag uccgacuagc	1680
gccguuacaa ccccuacccc uaacgcaacc ggcccagacc ugggcgagac uccccgcaa	1740
gccaauugcga caaauacac auugggcggg accucuccua caccagucgu uacaucucag	1800
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M137870089W000-SEQ-HJD.txt

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accaggguga cuccggcguc uauuuuccacc caccacguca gcacgucguc ucccgcaccg      2040
agaccaggga cgacuucua ggccaguggg ccuggcaacu ccucuacaag caaaaagcca      2100
ggcgaaguua acgugacaaa gggaacgccu cccagaacg caaccagucc ucaggcgccc      2160
agcgggcaga agacugcggu gccaacugug accagcaccg guggcaaggc caacucaaca      2220
acuggaggca agcauacgac ggggcacggc gcccggaccu ccacugaacc cacgaccgau      2280
uacggaggug acagcacaac accgcggcca cgauauaauug ccaccacuua ucugccacca      2340
uccacaagcu ccaagcugcg gccacggugg accuucacaa gcccaccgu gacgacugcc      2400
caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc      2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau      2520
ugcgccuuua ggagaaaccu cagcacuagc cacacguaca ccacgccgcc cuacgaugac      2580
gccgagacuu acguc                                                         2595

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<210> 53
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 53

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His	Leu	Thr	Gly	Glu	Asp	Pro	Gly	Phe	Phe	Asn	Val	Glu	Ile	Pro	Glu
			20					25					30		

Phe	Pro	Phe	Tyr	Pro	Thr	Cys	Asn	Val	Cys	Thr	Tyr	Asp	Val	Asn	Val
		35					40					45			

M137870089W000-SEQ-HJD.txt

Thr Phe Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Ile Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

M137870089W000-SEQ-HJD.txt

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

Trp Lys Val Ile Phe Ser Lys Ala Pro Glu Ser Thr Thr Thr Ser Pro
420 425 430

M137870089W000-SEQ-HJD.txt

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

M137870089W000-SEQ-HJD.txt

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

M137870089W000-SEQ-HJD.txt

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 54
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<212> RNA
<213> Artificial Sequence

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<223> Synthetic Polynucleotide

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cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
gcuuuuggag ggagcgagaa ugcugcgaau cuguucuuac uggaacugcu uggugcagga 300
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ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc 480
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M137870089W000-SEQ-HJD.txt

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gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
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aagacauua ucauaacacg gaccgccacc aacgccgcga cuacaacca uaaggugauc	1260
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acaaccucag gcgccagccc agugaccccu uccccaagcc ccugggauaa uggaacggag	1500
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acuagcccaa cccagcugu gacgacgccc accccgaacg cgacaucucc cacaccugcu	1620
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M137870089W000-SEQ-HJD.txt

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<210> 55
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 55

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Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
          20          25          30

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Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Tyr Asp Val Asn Val
          35          40          45

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Thr Phe Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
          50          55          60

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Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65          70          75          80

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M137870089W000-SEQ-HJD.txt

Ala Phe Gly Gly Ser Glu Asn Ala Ala Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Ala Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ala Val Lys Thr Glu Ile Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

Asp Asn Lys Phe Asn Ile Ala Cys Ser Gly Tyr Glu Ser His Val Pro
225 230 235 240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

M137870089W000-SEQ-HJD.txt

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Ala Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Ala Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
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Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
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M137870089W000-SEQ-HJD.txt

Gly Pro Thr Val Ser Thr Trp Asp Val Thr Ser Pro Thr Pro Ala Gly
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Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
 850 855 860

Val
 865

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 guuugcacug cugacgugaa cguggcgauac aaauucgacg ugggaggaaa gaagcaucag 180
 cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
 gcuuuuggag ggagcgagaa ugcugcgaau cuguucuuac uggaacugcu uggugcagga 300
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 ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc 480
 aagugggaua auugcaauuc agcgaauau gcggcugugg ugagggccca gggcuuggac 540
 gugacucugc ccuuaucucu accuacuucu gcccaagacu ccaauuucgc ggucaagacc 600
 gagaugcucg ggaaugagau cgauaucgag ugcaucaugg aggacgguga gauaagccag 660
 guucugccccg gcgacaacaa guucaauauc gcguguucug gcuacgaguc ccaugugccu 720
 agugguggca uacucacaag uacuucucc guagccacgc ccauucccg aaccggauac 780
 gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caaugcgauc 840
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M137870089W000-SEQ-HJD.txt

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gccaauucac	caaauguugc	gguaacagcu	uucugggccu	ggccaaauaa	cgcgagacu	1080
gacuucaaa	guaaguggac	uuugaccucu	ggaacuccgu	cggguugcga	gaauaucgcg	1140
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uuuuccaagg	caccugaguc	caccacuacc	uccccgacuc	uuaacacugc	gggcuucgcu	1320
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<400> 57

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Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
 35 40 45

Ala Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Ala Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

M137870089W000-SEQ-HJD.txt

Ile Asn Val Ala Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
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Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Ala Asn Ile Ala Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ala Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

Asp Asn Lys Phe Asn Ile Ala Cys Ser Gly Tyr Glu Ser His Val Pro
225 230 235 240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ala Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

M137870089W000-SEQ-HJD.txt

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Ala
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Ala Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Ala Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Ala Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ala Gly Ala Phe Ala
370 375 380

Ser Asn Arg Ala Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Ala Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Ala Gly Phe Ala Asp Pro Asn Thr Ala Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Ala Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
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Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

M137870089W000-SEQ-HJD.txt

Asn Gly Ala Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
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Val Thr Thr Pro Thr Pro Asn Ala Ala Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Ala Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Ala Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Ala Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Ala Asn His Ala Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Ala Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Ala Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Ala Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Ala Gln Val Thr Pro Ala Ser Ile Ser Thr His His
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Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

M137870089W000-SEQ-HJD.txt

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Val Ala Lys Gly Thr Pro Pro Gln Asn Ala Ala Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Ala Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Ala Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ala Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ala
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
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Val
865

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caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc	2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau	2520
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gccgagacuu acguc

2595

<210> 59

<211> 865

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 59

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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
 20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
 35 40 45

Ala Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Ala Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

Ile Asn Val Ala Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
 115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
 130 135 140

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Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
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Lys Trp Asp Asn Cys Asn Ser Ala Asn Ile Ala Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ala Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

Asp Asn Lys Phe Asn Ile Ala Cys Ser Gly Tyr Glu Ser His Val Pro
225 230 235 240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ala Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Ala
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Ala Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Ala Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Ala Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ala Gly Ala Phe Ala
370 375 380

Ser Asn Arg Ala Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Ala Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Ala Gly Phe Ala Asp Pro Asn Thr Ala Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Ala Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
 530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
 545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
 565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
 580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
 595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
 610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
 625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
 645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
 660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
 675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
 690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
 705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 60
<211> 2595
<212> RNA
<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 60

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guuugcacug cugacgugaa cgugacaaucc aaauucgacg ugggaggaaa gaagcaucag	180
cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
gcuuuuggag ggagcgagaa ugcugcgaau cuguucuuac uggaacugcu uggugcagga	300
gagcuggcac uaaccaugcg aagcaagaag cuccccaauca acguuaccac cggggaagaa	360
cagcaaguca gccuugaaucc cguggaugug uacuuucagg auguuuucgg caccaugugg	420
ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc	480
aagugggaua auugcaauuc aacuaauauu acggcugugg ugagggccca gggcuuggac	540
gugacucugc ccuuauucuc accuacuucg gcccaagacu ccaauuucuc ugucaagacc	600
gagaugcucg ggaugagau cgauaucgag ugcaucaugg aggacgguga gauaagccag	660
guucugccccg gcgacaacaa guucaauauc acuuguucug gcuacgaguc ccaugugccu	720
aguggguggca uacucacaag uacuucuccc guagccacgc ccuuucccg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaaauccac caaauuuac uguaacagcu uucugggccu ggccaaauaa cacugagacu	1080
gacuucuuu gaauguggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
ggggccuuug cuuccaacag gacuucgac aucacugucu cagggcuggg gacagcaccg	1200
aagacauuaa ucauaacacg gaccgccacc aacgccacga cuacaacca uaaggugauc	1260
uuuuccaagg caccugaguc caccacuacc uccccgacuc uuaacacuac gggcuucgcu	1320
gaucccaaca ccacuacggg guugccuagc ucgacacaug ugccgacgaa ccugacugcc	1380

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acaaccucag gcgccagccc agugaccccu uccccaagcc ccugggauaa uggaacggag	1500
uccaaggcuc cugauaugac uuccucuacc agccccguga cuacaccac ucccaacgca	1560
acuagcccaa cccagcugu gacgacgcc accccgaacg cgacaucucc cacaccugcu	1620
gugacaaccc caaccccuaa cgccacuagc ccuacccuag guaagaccag uccgacuagc	1680
gccguuacaa ccccuacccc uaacgcaacc ggcccgaccg ugggcgagac uccccgcaa	1740
gccaaugcga caaaucacac auugggcggg accucuccua caccagucgu uacaucucag	1800
ccuaagaacg cuaccuccgc ugucacuacc ggacagcaca acauccaccag cucaagcacg	1860
aguuccauga gcuugcggcc gagcuaaaau cccgagaccc uaucaccauc cacaucagac	1920
aacaguacuu cacacaugcc acucuugacg agcgcucacc ccaccggcgg cgagaacauc	1980
accagguga cuccggcguc uauuuccacc caccacguca gcacgucguc ucccgaccg	2040
agaccaggga cgacuucua ggccaguggg ccuggcaacu ccucuacaag caaaaagcca	2100
ggcgaaguua acgugacaaa gggaacgccu cccagaacg caaccagucc ucaggcgccc	2160
agcgggcaga agacugcggu gccaacugug accagcaccg guggcaaggc caacucaaca	2220
acuggaggca agcauacgac ggggcacggc gcccggaccu ccacugaacc caccgaccgau	2280
uacggaggug acagcacaac accgcggcca cgauauaauug ccaccacuua ucugccacca	2340
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caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc	2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau	2520
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gccgagacuu acguc	2595

<210> 61
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 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 61

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His	Leu	Thr	Gly	Glu	Asp	Pro	Gly	Phe	Phe	Asn	Val	Glu	Ile	Pro	Glu
			20					25					30		

Phe	Pro	Phe	Tyr	Pro	Thr	Cys	Asn	Val	Cys	Thr	Ala	Asp	Val	Asn	Val
		35					40					45			

Thr	Ile	Asn	Phe	Asp	Val	Gly	Gly	Lys	Lys	His	Gln	Leu	Asp	Leu	Asp
	50					55					60				

Phe	Gly	Gln	Leu	Thr	Pro	His	Thr	Lys	Ala	Val	Tyr	Gln	Pro	Arg	Gly
65					70					75					80

Ala	Phe	Gly	Gly	Ser	Glu	Asn	Ala	Ala	Asn	Leu	Phe	Leu	Leu	Glu	Leu
				85					90					95	

Leu	Gly	Ala	Gly	Glu	Leu	Ala	Leu	Thr	Met	Arg	Ser	Lys	Lys	Leu	Pro
			100					105					110		

Ile	Asn	Val	Thr	Thr	Gly	Glu	Glu	Gln	Gln	Val	Ser	Leu	Glu	Ser	Val
		115					120					125			

Asp	Val	Tyr	Phe	Gln	Asp	Val	Phe	Gly	Thr	Met	Trp	Cys	His	His	Ala
	130					135					140				

Glu	Met	Gln	Asn	Pro	Val	Tyr	Leu	Ile	Pro	Glu	Thr	Val	Pro	Tyr	Ile
145					150					155					160

Lys	Trp	Asp	Asn	Cys	Asn	Ser	Thr	Asn	Ile	Thr	Ala	Val	Val	Arg	Ala
				165					170					175	

M137870089W000-SEQ-HJD.txt

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

M137870089W000-SEQ-HJD.txt

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 62
<211> 2595
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<213> Artificial Sequence

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M137870089W000-SEQ-HJD.txt

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gagcuggcac uaaccaugcg aagcaagaag cuccccauca acguuaccac cggggaagaa	360
cagcaaguca gccuugaauc cguggaugug uacuuucagg auguuuucgg caccaugugg	420
ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc	480
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guucugcccg gcgacaaca guucaauauc acuuguucug gcuacgaguc ccaugugccu	720
agugguggca uacucacaag uacuucucc guagccacgc ccuuucccg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguaa caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaauucac caaauuuac uguaacagcu uucugggccu ggccaaauaa cacugagacu	1080
gacuucaau gaaugggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
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M137870089W000-SEQ-HJD.txt

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<400> 63

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M137870089W000-SEQ-HJD.txt

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Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Ala Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
 210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
 245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
 260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
 275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
 305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
 325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
 340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
 355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
 370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
 385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
 595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
 610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
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Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
 645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
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Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
 675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
 690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
 705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
 725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
 740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
 755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
 770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
 785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
 805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
 820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
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Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
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Val
 865

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 guuugcacug cugacgugaa cgugacaaua aauuucgacg ugggaggaaa gaagcaucag 180
 cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
 gcauuuggag ggagcgagaa ugcuaaaaau cuguucuuac uggaacugcu uggugcagga 300
 gagcuggcac uaaccaugcg aagcaagaag cuccccaaua acguuaccac cggggaagaa 360
 cagcaaguca gccuugaaua cguggaugug uacuuucagg auguuuucgg caccaugugg 420

M137870089W000-SEQ-HJD.txt

ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc	480
aaguggggaug auugcaauuc aacuaauauu acggcugugg ugagggccca gggcuuggac	540
gugacucugc ccuuaucucu accuacuucu gcccagacu ccaauuucgc ggucaagacc	600
gagaugcucg ggaugagau cgauaucgag ugcaucaugg aggacgguga gauaagccag	660
guucugcccg gcgacaaca guucaauauc acuuguucug gcuacgaguc ccaugugccu	720
agugguggca uacucacaag uacuucucc guagccacgc ccuaucccg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaaucac caaauuuac uguaacagcu uucugggccu ggccaaaua cacugagacu	1080
gacuucuuu gaaugggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
ggggccuuug cuuccaacag gacuucgac aucacugucu cagggcuggg gacagcaccg	1200
aagacauua ucauaacacg gaccgccacc aacgccacga cuacaacca uaaggugauc	1260
uuuuccaagg caccugaguc caccacuacc ucccgcaguc uuaacacuac gggcuucgcu	1320
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acaaccucag gcgccagccc agugacccu ucccgaagcc ccugggauua uggaacggag	1500
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acuagcccaa cccagcugu gacgacgccc accccgaacg cgacaucucc cacaccugcu	1620
gugacaaccc caaccccuua cgccacuagc ccuacccuag guaagaccag uccgacuagc	1680
gccguuacaa ccccuacccc uaacgcaacc ggcccagacc ugggcgagac uccccgcaa	1740
gccaaugcga caaauacac auugggcggg accucuccua caccagucgu uacaucucag	1800
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M137870089W000-SEQ-HJD.txt

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aguuccauga gcuugcggcc gagcucaaau cccgagaccc uaucaccauc cacaucagac      1920
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accaggguga cuccggcguc uauuuuccacc caccacguca gcacgucguc ucccgcaccg      2040
agaccaggga cgacuucua ggccaguggg ccuggcaacu ccucuacaag cacaaagcca      2100
ggcgaaguua acgugacaaa gggaacgccu cccagaacg caaccagucc ucaggcgccc      2160
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caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc      2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau      2520
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gccgagacuu acguc                                                         2595

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<210> 65
 <211> 865
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 65

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Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
1           5           10           15

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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
20           25           30

```

```

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
35           40           45

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M137870089W000-SEQ-HJD.txt

Thr	Ile	Asn	Phe	Asp	Val	Gly	Gly	Lys	Lys	His	Gln	Leu	Asp	Leu	Asp	50	55	60	
Phe	Gly	Gln	Leu	Thr	Pro	His	Thr	Lys	Ala	Val	Tyr	Gln	Pro	Arg	Gly	65	70	75	80
Ala	Phe	Gly	Gly	Ser	Glu	Asn	Ala	Thr	Asn	Leu	Phe	Leu	Leu	Glu	Leu	85	90	95	
Leu	Gly	Ala	Gly	Glu	Leu	Ala	Leu	Thr	Met	Arg	Ser	Lys	Lys	Leu	Pro	100	105	110	
Ile	Asn	Val	Thr	Thr	Gly	Glu	Glu	Gln	Gln	Val	Ser	Leu	Glu	Ser	Val	115	120	125	
Asp	Val	Tyr	Phe	Gln	Asp	Val	Phe	Gly	Thr	Met	Trp	Cys	His	His	Ala	130	135	140	
Glu	Met	Gln	Asn	Pro	Val	Tyr	Leu	Ile	Pro	Glu	Thr	Val	Pro	Tyr	Ile	145	150	155	160
Lys	Trp	Asp	Asn	Cys	Asn	Ser	Thr	Asn	Ile	Thr	Ala	Val	Val	Arg	Ala	165	170	175	
Gln	Gly	Leu	Asp	Val	Thr	Leu	Pro	Leu	Ser	Leu	Pro	Thr	Ser	Ala	Gln	180	185	190	
Asp	Ser	Asn	Phe	Ala	Val	Lys	Thr	Glu	Met	Leu	Gly	Asn	Glu	Ile	Asp	195	200	205	
Ile	Glu	Cys	Ile	Met	Glu	Asp	Gly	Glu	Ile	Ser	Gln	Val	Leu	Pro	Gly	210	215	220	
Asp	Asn	Lys	Phe	Asn	Ile	Thr	Cys	Ser	Gly	Tyr	Glu	Ser	His	Val	Pro	225	230	235	240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

M137870089W000-SEQ-HJD.txt

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
 820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
 835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
 850 855 860

Val
 865

<210> 66
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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 guuugcacug cugacgugaa cgugacaaua aauuucgacg ugggaggaaa gaagcaucag 180
 cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
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 gugacucugc ccuuaucucu accuacuucu gcccaagacu ccaauuucuc ugucaagacc 600
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M137870089W000-SEQ-HJD.txt

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gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
uuauacgugu uuuaugcgg aaacggcccu aaagcguccg gaggggacua uuguauucag	900
aguaauaucg uuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
gccaaucac caaauuuac uguaacagcu uucugggccu ggccaaauaa cacugagacu	1080
gacuucaaa uuaaguggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
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gccguuacaa ccccuacccc uaacgcaacc ggcccgaccg ugggcgagac uucccgcaa	1740
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aacaguacuu cacacaugcc acucuugacg agcgcucacc ccaccggcgg cgagaacauc	1980
acccagguga cuccggcguc uauuuccacc caccacguca gcacgucguc ucccgaccg	2040
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M137870089W000-SEQ-HJD.txt

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guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau 2520
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gccgagacuu acguc 2595

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<210> 67
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 <212> PRT
 <213> Artificial Sequence

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 <223> Synthetic Polypeptide

<400> 67

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```

```

His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
          20          25          30

```

```

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
          35          40          45

```

```

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
          50          55          60

```

```

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65          70          75          80

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M137870089W000-SEQ-HJD.txt

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

Asp Asn Lys Phe Asn Ile Ala Cys Ser Gly Tyr Glu Ser His Val Pro
225 230 235 240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

M137870089W000-SEQ-HJD.txt

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
 465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
 485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
 500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
 515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
 530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
 545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
 565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
 580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
 595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
 610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
 625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
 645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
 660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
 675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
 690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
 705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
 725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
 740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
 755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
 770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
 785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
 805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
 820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
 835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
 850 855 860

Val
 865

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 <211> 2595
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 <213> Artificial Sequence

<220>
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 guuugcacug cugacgugaa cgugacaaucc aaauucgacg ugggaggaaa gaagcaucag 180
 cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
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 cagcaaguca gccuugaaucc cguggaugug uacuucagg auguuucgg caccaugugg 420
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 agugguggca uacucacaag uacuucucc guagccacgc ccauucccg aaccggauac 780
 gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc 840
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gccaauucac caaauguugc gguaacagcu uucugggccu ggccaaauaa cacugagacu	1080
gacuucaaa uuaaguggac uuugaccucu ggaacuccgu cggguugcga gaauaucagc	1140
ggggccuuug cuuccaacag gacuucgac aucacugucu cagggcuggg gacagcaccg	1200
aagacauuaa ucauaacacg gaccgccacc aacgccacga cuacaacca uaaggugauc	1260
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ccuaagaacg cuaccuccgc ugucacuacc ggacagcaca acaucaccag cucaagcacg	1860
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acccagguga cuccggcguc uauuuccacc caccacguca gcacgucguc ucccgacccg	2040
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guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau	2520
ugcgccuuua ggagaaaccu cagcacuagc cacacguaca ccacgccgcc cuacgaugac	2580
gccgagacuu acguc	2595

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<220>
 <223> Synthetic Polynucleotide

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guuugcacug cugacugaa cgugacaau aauuucgacg ugggaggaaa gaagcaucag	180
cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
gcauuuggag ggagcgagaa ugcuaaaaau cuguucuuac uggaacugcu uggugcagga	300
gagcuggcac uaaccaugcg aagcaagaag cuccccauc acguuaccac cggggaagaa	360
cagcaaguca gccuugaau cguggaugug uacuuucagg auguuuucgg caccaugugg	420
ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc	480
aagugggaua auugcaauuc aacuaauuu acggcugugg ugagggccca gggcuuggac	540
gugacucugc ccuuaucucu accuacuucu gcccaagacu ccauuucuc ugucaagacc	600
gagaugcucg ggaauagau cgauaucgag ugcaucaugg aggacgguga gauaagccag	660
guucugccccg gcgacaacaa guucaauauc acuuguucug gcuacgaguc ccaugugccu	720
agugguggca uacucacaag uacuucucc guagccacgc ccuuuccgg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840

M137870089W000-SEQ-HJD.txt

uuauacgugu	uuuauagcgg	aaacggcccu	aaagcguccg	gaggggacua	uuguauucag	900
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gauauuaccu	acgugggcga	caaugccacg	uauucagugc	ccauggucac	gagcgaggac	1020
gccaaauucac	caaauuguuac	uguaacagcu	uucugggccu	ggccaaaaua	cacugagacu	1080
gacuucaaaau	guaaguggac	uuugaccucu	ggaacuccgu	cggguugcga	gaauaucagc	1140
ggggccuuug	cuuccaacag	gacuucgac	aucacugucu	cagggcuggg	gacagcaccg	1200
aagacauuaa	ucauaacacg	gaccgccacc	aacgccgcga	cuacaacca	uaaggugauc	1260
uuuuccaagg	caccugaguc	caccacuacc	uccccgacuc	uuaacacuac	gggcuucgcu	1320
gaucccaaca	ccacuacggg	guugccuagc	ucgacacaug	ugccgacgaa	ccugacugcc	1380
ccugcaucga	ccggggccac	aguuucgacc	gccgauguga	caucaccaac	gcccgcaggu	1440
acaaccucag	gcgccagccc	agugaccccu	uccccaagcc	ccugggauaa	uggaacggag	1500
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acuagcccaa	ccccagcugu	gacgacgccc	accccgaacg	cgacaucucc	cacaccugcu	1620
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gccguuacaa	ccccuacccc	uaacgcaacc	ggcccgaaccg	ugggcgagac	uuccccgcaa	1740
gccaaugcga	caaaucacac	auugggcggg	accucuccua	caccagucgu	uacaucucag	1800
ccuaagaacg	cuaccuccgc	ugucacuacc	ggacagcaca	acaucaccag	cucaagcacg	1860
aguuccauga	gcuugcggcc	gagcucaaau	cccgaagacc	uauaccauc	cacaucagac	1920
aacaguacuu	cacacaugcc	acucuugacg	agcgcucacc	ccaccggcgg	cgagaacauc	1980
acccagguga	cuccggcguc	uauuuccacc	caccacguca	gcacgucguc	ucccgacaccg	2040
agaccaggga	cgacuucuca	ggccaguggg	ccuggcaacu	ccucuacaag	cacaaagcca	2100
ggcgaaguua	acgugacaaa	gggaacgccu	ccccagaacg	caaccagucc	ucaggcgccc	2160
agcgggcaga	agacugcggu	gccaacugug	accagcaccg	guggcaaggc	caacucaaca	2220
acuggaggga	agcauacgac	ggggcacggc	gcccggaccu	ccacugaacc	cacgaccgau	2280

M137870089W000-SEQ-HJD.txt

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caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc 2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau 2520
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gccgagacuu acguc 2595

<210> 70
<211> 865
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 70

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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

M137870089W000-SEQ-HJD.txt

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

M137870089W000-SEQ-HJD.txt

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
 305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
 325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
 340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
 355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
 370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
 385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Ala Thr Thr Thr
 405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
 435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
 450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
 465 470 475 480

M137870089W000-SEQ-HJD.txt

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

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Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

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<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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 gccaucaccu gggugcccaa gcccaacgug gagguguggc ccguggaccc cccaccccc 180
 gugaacuuca acaagaccgc cgagcaggag uacggcgaca aggaggugaa gcugccccac 240
 uggaccccca cccugcacac cuuccaggug cccagaacu acaccaaggc caacugcacc 300
 uacugcaaca ccagagagua cacuucagc uacaagggcu gcugcuucua cuucaccaag 360
 aagaagcaca ccuggaacgg cugcuuccag gccugcgccg agcuguaccc cugcaccuac 420
 uucuacggcc ccacccccga cauccugccc guggugacca gaaaccugaa cgccaucgag 480
 agccuguggg ugggcgugua cagagugggc gagggcaacu ggaccagccu ggacggcggc 540
 accuuaagg uguaccagau cuucggcagc cacugcaccu acgugagcaa guucagcacc 600
 gugcccguga gccaccacga gugcagcuuc cugaagcccu gccugugcgu gagccagaga 660
 agcaacagc 669

<210> 72
<211> 2832
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 72
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M137870089W000-SEQ-HJD.txt

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ggcaccaaga	ggaagagggg	ggaccacgac	gcuggcggau	cugccccugc	caggcccaug	240
cugccacccc	agcccgaccu	gcccggcagg	gaggccaucc	ugaggagguu	cccacuggac	300
cugaggaccc	ugcugcaggc	caucggcgcc	gccgccacca	ggaucgacac	cagggccauc	360
gaccaguucu	ucggcagcca	gaucagcaac	accgagaugu	acaucaugua	cgccauggcc	420
aucagacaag	caauuagggg	ucgacgcaga	aauccugcca	gcaggaggga	ccaggccaag	480
uggaggcugc	agaccucggc	cgccggcugg	cccaugggcu	accaggccua	cagcagcugg	540
auguacagcu	acaccgacca	ccagaccacu	ccgaccuucg	ugcaccucca	ggcuaccucg	600
ggcugcacug	gcggucgcag	gugccacgug	accuucucag	cgggcaccuu	caagcugccc	660
aggugcacac	cuggcgacag	gcaguggcug	uacgugcaga	gcagcguggg	caacauuguu	720
cagaguugca	accccaggua	cagcaucuuc	uucgacuaca	uggcgauuca	caggagccug	780
accaagaucu	gggaggaagu	ccugaccccu	gaccagaggg	ugagcuucau	ggaguuccug	840
ggcuuccugc	agaggaccga	ccugagcuac	aucaagagcu	ucgugagcga	cgcccugggc	900
accaccagca	uccagacucc	uuggaucgac	gauaaccua	gcaccgaaac	cgcccaggcc	960
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gugcccaagc	cgcuuccuga	agucccgcag	agugaugaga	cagcgacuag	ccauggcagu	1320
gcucaggugc	ccgagccacc	caccauccau	cucgccgcac	agggcauggc	cuaccacug	1380
cacgagcagc	acggcauggc	gcccugcccc	guggcccagg	cuccuccaac	cccgcuuccu	1440
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ccaguuccug caccagcagg cccaauugug aggcccuggg agcccuccu aaccagggcg	1560
gcaggucagg ccuucgcucc aguuagacca cagcacaugc ccguggaacc ggugccagug	1620
ccuacggugg cgcuggagag gcccuguuac ccaaagccug ugcgaccugc gccuccuaag	1680
aucgccaugc aaggcccggg cgagacuagc gguaucaggc gggccaggga gagguggcgc	1740
ccggcaccgu ggacucccaa cccaccaagg ucaccuaguc agaugagcgu gcgugauagg	1800
cuggcacggc uucgggcaga ggcucaggua aagcaggcca guguggaggu gcagccacca	1860
cagcugacuc agguguccc gcagcagccc auggagggcc cacuggugcc ggaacagcag	1920
auguuccccg gcgccccguu cagccaggug gccgacgugg uuagggcucc uggcgugccu	1980
gcuauhcagc cucaguacuu cgaccuaccg cugauccagc ccaucaguca aggugcccca	2040
guggccccac ugagggcuag caugggcccg gucccuccug uuccagccac ccagccucaa	2100
uauuucgaca uuccucugac cgagccuaua aaccagggcg cgucugcggc ccacuuccug	2160
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cugagccaau cagugaggcc gggaguugcc cagagccagu auuucgaucu cccuuugaca	2280
cagccuauca aucacggagc accugccgcu cacuuccuuc accagccucc gauggaaggu	2340
ccuuggguuc cagagcaaug gauguuccaa ggugcgccac caucucaggg cacagacgug	2400
guccagcauc agcuggacgc gcuuggcuac acucuacacg gccugaacca cccgggcguu	2460
ccagugaguc cagccgugaa ccaguaccu cucucucagg cugccuucgg ccugcccauu	2520
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uccauccacg gccgaccuug cccacaggcu ccagaguggc ccguacagga agaaggcggc	2640
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gaguggccag uucaggguga agguggucag aacgugaccg gcccggaaac ccgaagggug	2760
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 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 gacgauccug gcgagggggc uuccacaggc ccucgcggcc agggagaugg cggaaggcgg 180
 aagaagggcg gcugguuugg caagcauagg ggccagggcg gcuccaaucc caaguucgag 240
 aaauauggcg agggggcuccg ggcucugcug gcccggucgc acgucgaacg uaccacugac 300
 gaggggacgu ggguggccgg cgucuuugug uacggaggau ccaagaccuc ccuguacaac 360
 cugagaaggg gcaccgcccc ugccaucucu cagugcagac ucacgccccu gagcaggcuc 420
 cccuuuggga uggcuccugg gccaggcccc cagcccgggc ccucaggga aagcaucgug 480
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 aaggauccug ugaugaccaa gccugcaccu acgugcaaua ucagggugac aguaugcucc 600
 uucgacgacg guguggaccu cccgcccugg uucccaccca uggucgaggg ugccgccgcc 660
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 caggag 726

<210> 74
 <211> 1158
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 74
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ggagcccuuu guauacuccu acugaugauc acccuccugc ucaucgcucu cuggaauuug	300
cacggacagg cauuguuccu uggaauugug cuguucaucu ucgggugcuu acuugucuua	360
gguaucugga ucuacuauuu ggagaugcuc uggcgacuug gugccaccuau cuggcagcuu	420
uuggccuucu uccuagccuu cuuccuagac cucauccugc ucauuauugc ucucuaucua	480
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uuaaucugga uguauuacca uggacaacga cacagugaug aacaccacca cgaugacucc	600
cucccgacacc cucaacaagc uaccgaugau ucuggccaug aaucugacuc uaacuccaac	660
gagggcagac accaccugcu cgugagugga gccggcgacg gaccaccacu cugcucucag	720
aaccuaggcg caccuggagg ugguccugac aauggcccac aggaccuga caacacggau	780
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caagaccag acaauacuga ugacaauggc ccacaggacc cugacaacac ugaugacaau	900
ggcccgacg acccgauacc ucauagcccu agcgacucug cuggaaauga uggaggcccu	960
ccacaauuga cggaagaggu ugagaacaaa ggaggugacc agggcccgcc uuugaugaca	1020
gacggaggcg gcggucuuag ucaugauucc ggccauggcg gcggugauc acaccuuccu	1080
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<210> 75

<211> 1491

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 75

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M137870089W000-SEQ-HJD.txt

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acgcccaccc caccgaacga ugaggaacgu gaaucaaug aagagccacc accgccuuau	180
gaggaccgau auuggggcaa uggcgaccgu cacucggacu aucaaccacu aggaacccaa	240
gaucaaaguc uguacuuggg auugcaacac gacgggaug acgggcuccc uccaccuccc	300
uacucuccac gggaugacuc aucucaacac auauacgaag aagcgggcag aggaaguaug	360
aauccaguau gccugccugu aauguugcg cccuaccucu uuuggcuggc ggcuaaugcc	420
gccucguguu ucacggccuc aguuaguacc guugugaccg ccaccggcuu ggcccucuca	480
cuucuacucu uggcagcagu ggccagcuca uauccgcug cacaaggaa acugcugaca	540
ccggugacag ugcuuacugc gguugucacu uucuuugcaa uuugccuac auggaggauu	600
gaggaccac cuuuuaauuc ucuucuguuu gcauugcugg ccgcagcugg cggacuacaa	660
ggcauuuacg uucuggugau gcuugucuc cugauacuag cguacagaag gagauggcgc	720
cguuugacug uuuguggcgg caucauguu uuggcaugug uacuuguccu caucgucgac	780
gcuguuuugc agcugagucc ccuccuugga gcuguaacug ugguuuccau gacgcugcug	840
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cuuuuaacau uggcagcagc ucuggcacug cuagcgucac ugauuuuggg cacacuuaac	960
uugacuacaa uguuccuucu caugcuccua uggacacuug ugguucuccu gauuugcucu	1020
ucgugcucu cauguccacu gagcaagau cuucuggcac gacuguuccu auaugcucuc	1080
gcacucuugu ugcuaaggcuc cgcgcuaauc gcugguggca guauuuugca aacaaacuuc	1140
aagaguuaa gcagcacuga auuuauacc aaauuguucu gcauguuau acugauuguc	1200
gcuggcauac ucuucauucu ugcuauccug accgauggg gcaguggaaa uagaacauac	1260
gguccagucu uuaugugccu cgguggccug cucaccaugg uagccggcgc uguguggcug	1320
acggugaugu cuaacacgcu uuugucugcc uggauucuua cagcaggauu ccugauuuuc	1380
cucuuuggcu uugcccucu uggggucuu agaugcugcc gcuacugcug cuacuacugc	1440
cuuacacugg aaagugagga gcgcccaccg accccauauc gcaacacugu a	1491

<210> 76
 <211> 1491
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 acgcccaccc caccgaacga ugaggaacgu gaaucaaag aagagccacc accgccuuau 180
 gaggaccgau auuggggcaa uggcgaccgu cacucggacu aucaaccacu aggaacccaa 240
 gaucaaaguc uguacuuggg auugcaacac gacgggaug acgggcuccc uccaccuccc 300
 uacucuccac gggaugacuc aucucaacac auauacgaag aagcgggcag aggaaguaug 360
 aauccaguau gccugccugu aauguugcg ccuaccucu uuuggcuggc ggcuauugcc 420
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 cuucuacucu uggcagcagu ggccagcuca uaugccgcug caciaaggaa acugcugaca 540
 ccggugacag ugcuuacugc gguugucacu uucuuugcaa uuugccuaac auggaggauu 600
 gaggaccac cuuuuaauuc ucuucuguuu gcauugcugg ccgcagcugg cggacuacaa 660
 ggcauuuacg uucuggugau gcuugugcuc cugauacuag cguacagaag gagauggcgc 720
 cguuugacug uuuguggcgg caucauguuc uuggcaugug uacuuguccu caucgucgac 780
 gcuguuuugc agcugagucc ccuccuugga gcuguaacug ugguuuccau gacgcugcug 840
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 cuuuuaacau uggcagcagc ucuggcacug cuagcgucac ugauuuuggg cacacuuaac 960
 uugacuacaa uguuccuucu caugcuccua uggacacuug ugguucuccu gauuugcucu 1020
 ucgugcucu cauguccacu gagcaagau cuucuggcac gacuguuccu auaugcucuc 1080
 gcacucuugu ugcuagccuc cgcgcuaauc gcugguggca guauuuugca aacaaacuuc 1140

M137870089W000-SEQ-HJD.txt

aagaguuuuaa gcagcacuga auuuauaccc aauuuguucu gcauguuauu acugauuguc	1200
gcuggcatauac ucuucauucu ugcuauccug accgaauagg gcaguggaaa uagaacauac	1260
gguccagucu uuauuguccu cggugggccug cucaccaugg uagccggcgc uguguggcug	1320
acggugaugu cuaacacgcu uuugucugcc uggauucuua cagcaggauu ccugauuuuc	1380
cucauuggcu uugcccucuu uggggucuuu agaugcugcc gcuacugcug cuacuacugc	1440
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 <213> Artificial Sequence

<220>
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guguguacug ccgacguuaa cguuacuauu aacuuugacg ugggcgga aa gaagcaccag	180
cuggaucuug auuucggcca gcuaacaccu cauaccaagg ccgucuacca accacgcggg	240
gcauuuggcg guucugagaa ugcuacaaac cuguuccuuu uggaacuccu cggagcaggg	300
gaacuggcac uuacaauag gaguaagaag cugcccauca acgucaccac gggugaagaa	360
cagcaggugu cccuggaguc cguugaugug uauuuccagg acguuuucgg gacaauugg	420
ugucaucaug ccgaaaugca gaauccggug uaucucauuc cugagaccgu gcccuauuu	480
aaaugggaua acuguaauuc gacaaacaua acugccguag ugcgugcca gggucuggau	540
guaacuuugc cucucuccu ucccacuuc gcccaggacu ccaauuuc agugaagacc	600
gaaaugcuug ggaacgagau cgacaucgag uguaucaugg aggaugggga gaucagucag	660
guguugccug gugacaauaa guuuauaua acauguuccg gcuaugaau acauguucca	720
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M137870089W000-SEQ-HJD.txt

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gacauuacau acgucgguga uaacgccacu uauucagucc cuauggucac auccgaggac	1020
gcgaacucac ccaauguuac cguuaccgca uucugggcgu ggcccaauaa uacggaaaca	1080
gacuucaaa uuaaguggac ccugaccagu ggcacccuu cuggcugcga gaauuaagc	1140
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acaagcccua cgccagccgu gaccacccu acgcccuaug ccaccagccc aacaccgcu	1620
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gcuguaacca cgccacacc aaacgcuacc gggccaaccg uuggcgaaac cucgccccag	1740
gccaaugcga caaaccacac ccuuggcggg acuucucca cuccuguggu gacuucacaa	1800
ccgaagaacg cgacgucggc cguuacgacc gggcagcaca auaucaccuc guccuccacg	1860
ucguccaugu ccuugcggcc uuccaguaac ccagagacac ugucuccuag uaccagugac	1920
aacagcaccu cucacaugcc auuacugacu uccgcccacc caaccggcgg agagaacau	1980
acucagguga cgcccgauc uauuuacuacc caccacguga gcacuagcag cccggcacca	2040
agaccaggga ccaccucca ggcuagcggc ccgggcaacu ccuccacuag cacgaaacca	2100
ggagagguga acgugacaa gggcacaccg ccacagaug caacuuccc acaggcgccc	2160
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M137870089W000-SEQ-HJD.txt

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uccacaucuu ccaagcucag gccucguugg acuuucaccu ccccgccugu gacuacagcg 2400
caggccacag ugccagugcc uccaacguca cagccgcggu uuagcaaucu cuccaugcug 2460
guccugcagu gggcaucucu ggcaguccug acacugcuuc uuuugcucgu gauggccgau 2520
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gcagagacuu augug 2595

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<212> PRT
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<220>
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<400> 78

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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

M137870089W000-SEQ-HJD.txt

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
 305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
 325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
 340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
 355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
 370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
 385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
 405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
 435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
 450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
 465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
 485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
 500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
 515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
 530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
 545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
 565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
 580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
 595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
 610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
 625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
 645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
 660 665 670

M137870089W000-SEQ-HJD.txt

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

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<212> RNA
<213> Artificial Sequence

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gugaccgagg accuggccag caugcugaac cgguacaagc ugaucuacaa gaccagcggc 240
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cagguggacg ccagcaaggu gcaccccggc gugaucagcg gccugaacag ccccgccugu 360
auguugagcg ccccacugga gaagcagcug uucuacuaca ucggcaccac gcugcccaac 420
acccggcccc acagcuacgu guucuaccag cugcggugcc accugagcua cguugcccug 480
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accaaggacc ugcccgaccu gcggggcccc uucagcuacc cuaguuugac cagcgcccag 660
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uacuucgugc ccaaccugaa ggacauguuc agccgggccc ugaccaugac ugccgcuucu 780
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cccgagcugg acaccgaaac acugaccacc auguucgagg ugagcguggc cuucuuaag 900
gugggucacg cggugggcga aaccggcaac ggcugcgugg acuuacgcug gcuggccaag 960
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M137870089W000-SEQ-HJD.txt

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gugggcuacc caaaggccgg cguguacagu ggacugaucg gcggcgcaac cagcgugcug	1200
cuauccgcuu acaaccggca cccgcuguuc cagccccugc acaccgugau gcgggaaacc	1260
cuguucaucg gaagccacgu cgugcugcgg gagcugaggc ugaacguaac caccagggc	1320
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cucaccacca acgguaccgu cauggaaauc gccggacugu acgaggagcg ggcccauguu	2040
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<210> 80

<211> 411

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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 gcccuggaga acaucagcga caucuaccug gugagcaacc agaccugcga cggcuucagc 180
 cuggccagcc ugaacagccc caagaacggc agcaaccagc uggugaucag cagaugcgcc 240
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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu 240
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 gagcuggcac uaaccaugcg aagcaagaag cuccccauc acguuaccac cggggaagaa 360
 cagcaaguca gccuugaau cugggaugug uacuuucagg auguuuucgg caccaugugg 420
 ugucaccacg cugagaugca gaaucccgug uaucucauac ccgagacugu acccuacauc 480
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 gugacucugc ccuuaucucu accuacuucu gccaagacu ccaauuucuc ugucaagacc 600
 gagaugcucg ggaugagau cgauaucgag ugcaucaugg aggacgguga gaaagccag 660
 guucugcccc gcgacaacaa guucaaua acuuuguucg gcuacgaguc ccaugugccu 720

M137870089W000-SEQ-HJD.txt

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aguaauaucg uuuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
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agaccaggga cgacuucua ggccaguggg ccuggcaacu ccucuacaag caaaaagcca	2100
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M137870089W000-SEQ-HJD.txt

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caagcgacgg ugccagugcc accuacaagc cagccacgcu ucuccaaccu uaguaugcuc	2460
guucuccagu gggccagccu ugcuguucug acccuccucc ugcugcucgu gauggccgau	2520
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gccgagacuu acguc	2595

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 <212> RNA
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<220>
 <223> Synthetic Polynucleotide

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uguauacucc uauugaugau caccuccuc cucaucgcuc ucuggaauuu gcacggacag	180
gcuuuguucc uuggaaugu gcuguuauu uucgggugcu uacuugucuu agguaucugg	240
aucuacuuau uggagaugcu cuggcgacuu ggugccacca ucuggcagcu uuuggccuuc	300
uuccuagcgu ucuuccucga ccucauucua cucauuauug cucucuaucu acaacagaac	360
ugguggacuc uauugguuga ucuccuuugg cuccuccugu uucuggcgau uuuaaucugg	420
augauuuacc auggacaacg acacagugau gaacaccacc acgaugacuc ccuccgcac	480
ccucaacaag cuaccgauga uucuggccau gaaucugacu cuaacuccaa cgagggcaga	540
caccaccugc ucgugagugg agccggcgac ggaccaccac ucugcucuca gaaccuaggc	600
gcaccuggag gugguccuga caauggccca caggaccug acaacacgga ugauaacggu	660

M137870089W000-SEQ-HJD.txt

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 gacccguuac cucauagccc uagcgacucu gcuggaaaug auggaggccc uccacaauug 840
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 ggcggucaua gucaugauuc cggccauggc ggaggagau c cacaccuucc uacgcugcug 960
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 uacuaugac 1029

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 <212> PRT
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<220>
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<400> 83

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 20 25 30

Leu Leu Cys Pro Leu Gly Ala Leu Cys Ile Leu Leu Leu Met Ile Thr
 35 40 45

Leu Leu Leu Ile Ala Leu Trp Asn Leu His Gly Gln Ala Leu Phe Leu
 50 55 60

Gly Ile Val Leu Phe Ile Phe Gly Cys Leu Leu Val Leu Gly Ile Trp
 65 70 75 80

Ile Tyr Leu Leu Glu Met Leu Trp Arg Leu Gly Ala Thr Ile Trp Gln
 85 90 95

M137870089W000-SEQ-HJD.txt

Leu Leu Ala Phe Phe Leu Ala Phe Phe Leu Asp Leu Ile Leu Leu Ile
 100 105 110

Ile Ala Leu Tyr Leu Gln Gln Asn Trp Trp Thr Leu Leu Val Asp Leu
 115 120 125

Leu Trp Leu Leu Leu Phe Leu Ala Ile Leu Ile Trp Met Tyr Tyr His
 130 135 140

Gly Gln Arg His Ser Asp Glu His His His Asp Asp Ser Leu Pro His
 145 150 155 160

Pro Gln Gln Ala Thr Asp Asp Ser Gly His Glu Ser Asp Ser Asn Ser
 165 170 175

Asn Glu Gly Arg His His Leu Leu Val Ser Gly Ala Gly Asp Gly Pro
 180 185 190

Pro Leu Cys Ser Gln Asn Leu Gly Ala Pro Gly Gly Gly Pro Asp Asn
 195 200 205

Gly Pro Gln Asp Pro Asp Asn Thr Asp Asp Asn Gly Pro Gln Asp Pro
 210 215 220

Asp Asn Thr Asp Asp Asn Gly Pro His Asp Pro Leu Pro Gln Asp Pro
 225 230 235 240

Asp Asn Thr Asp Asp Asn Gly Pro Gln Asp Pro Asp Asn Thr Asp Asp
 245 250 255

Asn Gly Pro His Asp Pro Leu Pro His Ser Pro Ser Asp Ser Ala Gly
 260 265 270

Asn Asp Gly Gly Pro Pro Gln Leu Thr Glu Glu Val Glu Asn Lys Gly
 275 280 285

Gly Asp Gln Gly Pro Pro Leu Met Thr Asp Gly Gly Gly Gly His Ser
290 295 300

His Asp Ser Gly His Gly Gly Gly Asp Pro His Leu Pro Thr Leu Leu
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Leu Gly Ser Ser Gly Ser Gly Gly Asp Asp Asp Asp Pro His Gly Pro
325 330 335

Val Gln Leu Ser Tyr Tyr Asp
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aucgugaugu ucuuccug 2118

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 cuggccagcc ugaacagccc caagaacggc agcaaccagc uggugaucag cagaugcgcc 240
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 gaggaccugu ucggcgccaa ccugaacaga uacgccuggc acagaggcgg c 411

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<220>
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agccuguggg ugggcgugua cagagugggc gagggcaacu ggaccagccu ggacggcggc	540
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<210> 87

<211> 1881

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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guggugaggg cccagggcuu ggacgugacu cugcccuuau cucuaccuac uucugcccaa	660
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<211> 627

<212> PRT

<213> Artificial Sequence

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<400> 88

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 35 40 45

Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu Phe Pro Phe Tyr
 50 55 60

Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val Thr Ile Asn Phe
 65 70 75 80

Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp Phe Gly Gln Leu
 85 90 95

Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly Ala Phe Gly Gly
 100 105 110

Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu Leu Gly Ala Gly
 115 120 125

Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro Ile Asn Val Thr
 130 135 140

Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val Asp Val Tyr Phe
 145 150 155 160

Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala Glu Met Gln Asn
 165 170 175

Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile Lys Trp Asp Asn
 180 185 190

Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala Gln Gly Leu Asp
195 200 205

Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln Asp Ser Asn Phe
210 215 220

Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp Ile Glu Cys Ile
225 230 235 240

Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly Asp Asn Lys Phe
245 250 255

Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro Ser Gly Gly Ile
260 265 270

Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro Gly Thr Gly Tyr
275 280 285

Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser Arg Phe Leu Gly
290 295 300

Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn Gly Pro Lys Ala
305 310 315 320

Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val Phe Ser Asp Glu
325 330 335

Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr Asp Ile Thr Tyr
340 345 350

Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val Thr Ser Glu Asp
355 360 365

Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp Ala Trp Pro Asn
370 375 380

Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu Thr Ser Gly Thr
 385 390 395 400

Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala Ser Asn Arg Thr
 405 410 415

Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro Lys Thr Leu Ile
 420 425 430

Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr His Lys Val Ile
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Phe Ser Lys Ala Pro Gly Ser Gly Ser Ala Gly Ser Ala Ser Gly Gly
 450 455 460

Ala Ser Ser Gly Ser Gly Gly Ala Ser Met Gln Ile Tyr Glu Gly Lys
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Leu Thr Ala Glu Gly Leu Arg Phe Gly Ile Val Ala Ser Arg Phe Asn
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His Ala Leu Val Asp Arg Leu Val Glu Gly Ala Ile Asp Ala Ile Val
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Arg His Gly Gly Arg Glu Glu Asp Ile Thr Leu Val Arg Val Pro Gly
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Ser Trp Glu Ile Pro Val Ala Ala Gly Glu Leu Ala Arg Lys Glu Asp
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Ile Asp Ala Val Ile Ala Ile Gly Val Leu Ile Arg Gly Ala Thr Pro
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His Phe Asp Tyr Ile Ala Ser Glu Val Ser Lys Gly Leu Ala Asp Leu
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Ser Leu Glu Leu Arg Lys Pro Ile Thr Phe Gly Val Ile Thr Ala Asp
580 585 590

Thr Leu Glu Gln Ala Ile Glu Arg Ala Gly Thr Lys His Gly Asn Lys
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Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile His Leu Thr Gly
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Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu Phe Pro Phe Tyr
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Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val Thr Ile Asn Phe
 65 70 75 80

Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp Phe Gly Gln Leu
 85 90 95

Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly Ala Phe Gly Gly
 100 105 110

Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu Leu Gly Ala Gly
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Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro Ile Asn Val Thr
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Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val Asp Val Tyr Phe
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Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala Gln Gly Leu Asp
 195 200 205

Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln Asp Ser Asn Phe
 210 215 220

Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp Ile Glu Cys Ile
 225 230 235 240

Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly Asp Asn Lys Phe
 245 250 255

Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro Ser Gly Gly Ile
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Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro Gly Thr Gly Tyr
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Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser Arg Phe Leu Gly
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Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn Gly Pro Lys Ala
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Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val Phe Ser Asp Glu
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Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu Thr Ser Gly Thr
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Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala Ser Asn Arg Thr
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Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro Lys Thr Leu Ile
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Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr His Lys Val Ile
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Phe Ser Lys Ala Pro Gly Ser Gly Ser Ala Gly Ser Ala Ser Gly Gly
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Ala Ser Ser Gly Ser Gly Gly Ala Ser Met Glu Asn Ile Ala Ser Gly
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Leu Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr
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Lys Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu
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Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly
580 585 590

Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Phe Pro
595 600 605

Ser Cys Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro
610 615 620

Ile Pro Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Glu Trp Ala Ser
625 630 635 640

Val Arg Phe Ser Trp Leu Ser Leu Leu Ala Pro Phe Val Gln Trp Phe
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Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp
660 665 670

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<223> Synthetic Polynucleotide

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gaaauuccug ccagucagga caugccgaca aacacaacug auauuaccua cgugggcgac	1800
aaugccacgu auucagugcc cauggucacg agcgaggacg ccaauucacc aaauguuacu	1860
guaacagcuu ucugggccug gccaaauaac acugagacug acuucaaaug uaaguggacu	1920
uugaccucug gaacuccguc gggguugcgag aaauacagcg gggccuuugc uucaaacagg	1980
acuuucgaca ucacugucuc agggcugggg acagcaccga agacauuaau cauaacacgg	2040
accgccacca acgccacgac uacaaccuau aaggugaucu uuuccaaggc accuggaucc	2100
ggacugggugg ucaacuauugu gaauacaaau augggccuca agauuaggca gcuccuauug	2160
uucauauuu ccugcuuaac uuucgguagg gaaacugucc uggaauaucu cguuagcuuc	2220
ggagugugga uucggacucc uccugccuac agaccaccua acgcuccaau ucugucaacu	2280
cucccagaga cgacuguggu cagaaggagg ggcaggagcc ccagacggcg gacaccaagc	2340
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ugc	2403

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 <211> 801
 <212> PRT
 <213> Artificial Sequence

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 <223> Synthetic Polypeptide

<400> 92

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 20 25 30

Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro
 35 40 45

Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala Ala
 50 55 60

Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His
 65 70 75 80

Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu
 85 90 95

Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu
 100 105 110

Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu
 115 120 125

Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu
 130 135 140

Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr
 145 150 155 160

Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val
 165 170 175

Val Gly Ser Gly Ser Ala Gly Ser Ala Ser Gly Gly Ala Ser Ser Gly
 180 185 190

M137870089W000-SEQ-HJD.txt

Ser Gly Gly Ala Ser Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr
195 200 205

Val Glu Leu Leu Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg
210 215 220

Asp Leu Leu Asp Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser
225 230 235 240

Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu
245 250 255

Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Gly
260 265 270

Ser Gly Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu
275 280 285

Ile His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro
290 295 300

Glu Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn
305 310 315 320

Val Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu
325 330 335

Asp Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg
340 345 350

Gly Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu
355 360 365

Leu Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu
370 375 380

M137870089W000-SEQ-HJD.txt

Pro Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser
385 390 395 400

Val Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His
405 410 415

Ala Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr
420 425 430

Ile Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg
435 440 445

Ala Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala
450 455 460

Gln Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile
465 470 475 480

Asp Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro
485 490 495

Gly Asp Asn Lys Phe Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val
500 505 510

Pro Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile
515 520 525

Pro Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val
530 535 540

Ser Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly
545 550 555 560

Asn Gly Pro Lys Ala Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile
565 570 575

Val Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr
 580 585 590

Thr Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met
 595 600 605

Val Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe
 610 615 620

Trp Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr
 625 630 635 640

Leu Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe
 645 650 655

Ala Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala
 660 665 670

Pro Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr
 675 680 685

Thr His Lys Val Ile Phe Ser Lys Ala Pro Gly Ser Gly Leu Val Val
 690 695 700

Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu Trp
 705 710 715 720

Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu Tyr
 725 730 735

Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro
 740 745 750

Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val Arg
 755 760 765

Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg
 770 775 780

Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln
 785 790 795 800

Cys

<210> 93
 <211> 2538
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 cagucgcuca uucaucuaac aggcgaggac cccggcuucu uuaacgugga aaucccagag 180
 uucccuuucu auccaaccug uaacguuugc acugccgacg ugaacgugac aaucuuuuc 240
 gacgugggag gaaagaagca ucagcuugau cuggauuucg gccaacugac gccacacacc 300
 aaagcggugu accaaccaag gggugcauuu ggagggagcg agaaugcuac aaucuguuuc 360
 uuacuggaac ugcuuuggugc aggagagcug gcacuaacca ugcgaagcaa gaagcucucc 420
 aucaacguua ccaccgggga agaacagcaa gucagccuug aauccgugga uguguacuuu 480
 caggauguuu ucggcaccau guggugucac cacgcugaga ugcagaaucc cguguaucuc 540
 auacccgaga cuguaccua caucaagugg gauaaugca auucaacuaa uauuacggcu 600
 guggugaggg cccagggcuu ggacgugacu cugcccuau cucuaccuac uucugcccaa 660
 gacuccaauu ucucugucaa gaccgagaug cucgggaug agaucgauau cgagugcauc 720
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M137870089W000-SEQ-HJD.txt

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agauuccugg guaacaauag uaucuuauac guguuuuaua gcggaaacgg cccuaaagcg	960
uccggagggg acuaauuguau ucagaguaau aucguuuucu cugaugagau uccagccagu	1020
caggacaugc cgacaaacac aacugauauu accuacgugg gcgacaaugc cacguauuca	1080
gugcccaugg ucacgagcga ggacgccauu ucacaaaug uuacuguaac agcuuucugg	1140
gccuggccaa auaacacuga gacugacuuc aaauguaagu ggacuuugac cucuggaacu	1200
ccgucggguu gcgagaauau cagcggggcc uuugcuucca acaggacuuu cgacaucacu	1260
gucucagggc uggggacagc accgaagaca uuaaucauaa cacggaccgc caccaacgcc	1320
acgacuacaa cccauaaggu gaucuuuucc aaggcaccug aguccaccac uaccuccccg	1380
acucuuuaca cuacgggcuu cgcugauccc aaauacuacua cuggguugcc uagcucgaca	1440
caugugccga cgaaccugac ugccccugca ucgaccgggc ccacaguuuu gaccgccgau	1500
gugacaagcc cuacggccgc agguacaacc ucaggcgcca gcccagugac cccuucccca	1560
agccccuggg acaacggaac ggaguccaag gcuccugaua ugacuuccuc uaccagcccc	1620
gugacuacac ccacucccaa cgcaacuagc ccaaccccag cugugacgac gcccaccccg	1680
aacgcgacau cuccacacc ugcugugaca accccuaccc cuaacgccac uagcccuacc	1740
cuagguaaga ccaguccgac uagcgccguu acuacaccga ccccuaaugc aaccggcccg	1800
acugucggcg agacuuccc gcaagccaau gcgacaaauc acacauuggg cgggaccucu	1860
ccuacaccag ucguuacauc ucagccuaag aacgcuaccu ccgcugucac uaccggccag	1920
cacaacauca caagcucaag cacgaguucc augagcuugc ggccgagcuc aaaucccag	1980
acacuaucac cauccacauc agacaacagu acuucacaca ugccacucuu gacgagcgcu	2040
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gucagcacgu cgucuccgc accacggcca gggacgacuu cucaggccag cggcccagga	2160
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accuccacug aaccacgac cgauuacgga ggugauagua ccaccccgcg gccacgauau 2400
aaugccacca cuuauugcc accuagcacu uccuccaagc uccggccacg guggaccuuc 2460
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cgcuucucca accuuagu 2538

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<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 94

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20 25 30

Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile His Leu Thr Gly
35 40 45

Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu Phe Pro Phe Tyr
50 55 60

Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val Thr Ile Asn Phe
65 70 75 80

Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp Phe Gly Gln Leu
85 90 95

M137870089W000-SEQ-HJD.txt

Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly Ala Phe Gly Gly
 100 105 110

Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu Leu Gly Ala Gly
 115 120 125

Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro Ile Asn Val Thr
 130 135 140

Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val Asp Val Tyr Phe
 145 150 155 160

Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala Glu Met Gln Asn
 165 170 175

Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile Lys Trp Asp Asn
 180 185 190

Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala Gln Gly Leu Asp
 195 200 205

Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln Asp Ser Asn Phe
 210 215 220

Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp Ile Glu Cys Ile
 225 230 235 240

Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly Asp Asn Lys Phe
 245 250 255

Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro Ser Gly Gly Ile
 260 265 270

Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro Gly Thr Gly Tyr
 275 280 285

M137870089W000-SEQ-HJD.txt

Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser Arg Phe Leu Gly
290 295 300

Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn Gly Pro Lys Ala
305 310 315 320

Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val Phe Ser Asp Glu
325 330 335

Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr Asp Ile Thr Tyr
340 345 350

Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val Thr Ser Glu Asp
355 360 365

Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp Ala Trp Pro Asn
370 375 380

Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu Thr Ser Gly Thr
385 390 395 400

Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala Ser Asn Arg Thr
405 410 415

Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro Lys Thr Leu Ile
420 425 430

Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr His Lys Val Ile
435 440 445

Phe Ser Lys Ala Pro Glu Ser Thr Thr Thr Ser Pro Thr Leu Asn Thr
450 455 460

Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu Pro Ser Ser Thr
465 470 475 480

M137870089W000-SEQ-HJD.txt

His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr Gly Pro Thr Val
485 490 495

Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly Thr Thr Ser Gly
500 505 510

Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp Asn Gly Thr Glu
515 520 525

Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro Thr Pro
545 550 555 560

Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro Thr Pro Asn Ala
565 570 575

Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser Ala Val Thr Thr
580 585 590

Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu Thr Ser Pro Gln
595 600 605

Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser Pro Thr Pro Val
610 615 620

Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val Thr Thr Gly Gln
625 630 635 640

His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser Leu Arg Pro Ser
645 650 655

Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp Asn Ser Thr Ser
660 665 670

M137870089W000-SEQ-HJD.txt

His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly Gly Glu Asn Ile
675 680 685

Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His Val Ser Thr Ser
690 695 700

Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala Ser Gly Pro Gly
705 710 715 720

Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn Val Thr Lys Gly
725 730 735

Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro Ser Gly Gln Lys
740 745 750

Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys Ala Asn Ser Thr
755 760 765

Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg Thr Ser Thr Glu
770 775 780

Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro Arg Pro Arg Tyr
785 790 795 800

Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser Lys Leu Arg Pro
805 810 815

Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala Gln Ala Thr Val
820 825 830

Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn Leu Ser
835 840 845

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<211> 3057

<212> RNA

<213> Artificial Sequence

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<223> Synthetic Polynucleotide

<400> 95

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gugacaaucu uuguguugcc gaccuggggc aacuggggccu accccugcug ccacgugacc	180
cagcugagag cucaacaccu gcuugcccug gagaacauca gcgacauca ccuuguaagc	240
aaccagacau gcgacggcuu cagucuggcc agccugaaca gcccgaagaa cggcucaaac	300
cagcuaguga ucagccggug cgcuaacggu cugaacguug ugagcuucuu caucagcauc	360
uugaagagaa guaguagcgc gcugaccggc caccugagag agcugcugac cacucucgag	420
acacucuaug gcagcuucag cguggaggac cuguucggcg caaaccugaa ccgcuacgcc	480
uggcacagag gcggcggaag cgguagcgcu ggcagcgcca gcggaggcg uucauccgga	540
uccggcgggcg caagcagccu uucugaggug aagcuccacu uggacaucga aggccacgcc	600
agccauuaca ccuaccaug gaccgagcug auggcaaagg ugcccggccu uagcccagaa	660
gcccuguggc gagaggccaa cguuaccgaa gacuuggcua guauguuaaa cagguacaaa	720
cuuaucuaca agacuagcgg caccugggc aucgcauuag ccgagcccgu ggacaucccc	780
gccguuagcg agggcagcau gcagguggac gccagcaagg uucaccugg uguaaauagu	840
ggccucaaca gccagccug uauguugagc gcccacugg agaagcagcu guuuuacuau	900
aucgggacca uguugcccaa uaccggcca cacaguacg uguucuacca gcugcggugu	960
caccugagcu acguggcccu gucuaucaac ggcgacaagu uccaguacac cggcgccaug	1020
accagcaagu uccugauggg caccuacaag cgggucaccg agaaggcgga cgagcacgug	1080
cugucacuug uguucgguaa gaccaaggac cugcccgacc uucggggccc cuuuuacauac	1140
ccuaguuuga ccagcgccca aaguggcgac uacagccuug ugauagugac caccuucgug	1200
cauuacgcca acuuccaaa cuacuucgug cccaaccuga aggacauguu cagccgggcg	1260
guaaccauga cggccgcuuc uuaugcccgg uaugugcugc agaagcuggu ccugcuggag	1320

M137870089W000-SEQ-HJD.txt

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guuagcgugg ccuucuuaa ggugggucac gcggugggcg aaaccggcaa uggaugcgug	1440
gacuuacgcu ggcuggccaa gaguuucuuu gagcuuaccg ugcugaagga uaucaucggc	1500
aucugcuacg gcgccaccgu aaagggaug cagagcuauug ggcuggagag acugccgcc	1560
augcucaugg cuaccgugaa gauggaggag cugggacacc ugacaacaga gaagcaggag	1620
uacgcccuga gacuggccac cgugggcuac ccuaaggccg gcguguacag uggacucaua	1680
ggcggagcua ccagcgugcu ccuauccgcu uauaacagac accccuuuu ucagccccug	1740
cacacaguga ugcgggagac uuuaaucauc ggaucucacg ucguacugcg ggaguugcgg	1800
cugaacguua ccaccagggg ccuaauuuu gcacuuuau agcugcucag uacugcccug	1860
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cuguuuucuc caugcuaccu uagccugcgg uuugaucuga ccagagacaa guugcugagc	1980
auggcuccuc aagaggcgac ccuugaccag gcagccgugu caaacgccgu ggacggauuc	2040
cugggcagac ugucucugga acgggaagac cgggaugcuu ggcaccuucc ugccuauaag	2100
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ggcaucgugg cuuccagauu caaccacgca cugguggaca ggcuggugga gggcgccauc	2700
gacgcaaucg ugcgccacgg cggcaggag gaggacauca ccucguaag agucccuggu	2760

M137870089W000-SEQ-HJD.txt

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guuucaaagg gacucgccga cuuaagucug gagcugagga agcccaucac cuuuggcgug 2940
aucaccgccg acaccugga gcaggccauc gagcgcgccg gcaccaagca cgggaacaag 3000
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<210> 96
<211> 1019
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 96

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20 25 30

Gly Val Phe Leu Ala Ile Cys Leu Val Thr Ile Phe Val Leu Pro Thr
35 40 45

Trp Gly Asn Trp Ala Tyr Pro Cys Cys His Val Thr Gln Leu Arg Ala
50 55 60

Gln His Leu Leu Ala Leu Glu Asn Ile Ser Asp Ile Tyr Leu Val Ser
65 70 75 80

Asn Gln Thr Cys Asp Gly Phe Ser Leu Ala Ser Leu Asn Ser Pro Lys
85 90 95

Asn Gly Ser Asn Gln Leu Val Ile Ser Arg Cys Ala Asn Gly Leu Asn
100 105 110

M137870089W000-SEQ-HJD.txt

Val Val Ser Phe Phe Ile Ser Ile Leu Lys Arg Ser Ser Ser Ala Leu
115 120 125

Thr Gly His Leu Arg Glu Leu Leu Thr Thr Leu Glu Thr Leu Tyr Gly
130 135 140

Ser Phe Ser Val Glu Asp Leu Phe Gly Ala Asn Leu Asn Arg Tyr Ala
145 150 155 160

Trp His Arg Gly Gly Gly Ser Gly Ser Ala Gly Ser Ala Ser Gly Gly
165 170 175

Ala Ser Ser Gly Ser Gly Gly Ala Ser Ser Leu Ser Glu Val Lys Leu
180 185 190

His Leu Asp Ile Glu Gly His Ala Ser His Tyr Thr Ile Pro Trp Thr
195 200 205

Glu Leu Met Ala Lys Val Pro Gly Leu Ser Pro Glu Ala Leu Trp Arg
210 215 220

Glu Ala Asn Val Thr Glu Asp Leu Ala Ser Met Leu Asn Arg Tyr Lys
225 230 235 240

Leu Ile Tyr Lys Thr Ser Gly Thr Leu Gly Ile Ala Leu Ala Glu Pro
245 250 255

Val Asp Ile Pro Ala Val Ser Glu Gly Ser Met Gln Val Asp Ala Ser
260 265 270

Lys Val His Pro Gly Val Ile Ser Gly Leu Asn Ser Pro Ala Cys Met
275 280 285

Leu Ser Ala Pro Leu Glu Lys Gln Leu Phe Tyr Tyr Ile Gly Thr Met
290 295 300

M137870089W000-SEQ-HJD.txt

Leu Pro Asn Thr Arg Pro His Ser Tyr Val Phe Tyr Gln Leu Arg Cys
305 310 315 320

His Leu Ser Tyr Val Ala Leu Ser Ile Asn Gly Asp Lys Phe Gln Tyr
325 330 335

Thr Gly Ala Met Thr Ser Lys Phe Leu Met Gly Thr Tyr Lys Arg Val
340 345 350

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

Lys Asp Leu Pro Asp Leu Arg Gly Pro Phe Ser Tyr Pro Ser Leu Thr
370 375 380

Ser Ala Gln Ser Gly Asp Tyr Ser Leu Val Ile Val Thr Thr Phe Val
385 390 395 400

His Tyr Ala Asn Phe His Asn Tyr Phe Val Pro Asn Leu Lys Asp Met
405 410 415

Phe Ser Arg Ala Val Thr Met Thr Ala Ala Ser Tyr Ala Arg Tyr Val
420 425 430

Leu Gln Lys Leu Val Leu Leu Glu Met Lys Gly Gly Cys Arg Glu Pro
435 440 445

Glu Leu Asp Thr Glu Thr Leu Thr Thr Met Phe Glu Val Ser Val Ala
450 455 460

Phe Phe Lys Val Gly His Ala Val Gly Glu Thr Gly Asn Gly Cys Val
465 470 475 480

Asp Leu Arg Trp Leu Ala Lys Ser Phe Phe Glu Leu Thr Val Leu Lys
485 490 495

Asp Ile Ile Gly Ile Cys Tyr Gly Ala Thr Val Lys Gly Met Gln Ser
 500 505 510

Tyr Gly Leu Glu Arg Leu Ala Ala Met Leu Met Ala Thr Val Lys Met
 515 520 525

Glu Glu Leu Gly His Leu Thr Thr Glu Lys Gln Glu Tyr Ala Leu Arg
 530 535 540

Leu Ala Thr Val Gly Tyr Pro Lys Ala Gly Val Tyr Ser Gly Leu Ile
 545 550 555 560

Gly Gly Ala Thr Ser Val Leu Leu Ser Ala Tyr Asn Arg His Pro Leu
 565 570 575

Phe Gln Pro Leu His Thr Val Met Arg Glu Thr Leu Phe Ile Gly Ser
 580 585 590

His Val Val Leu Arg Glu Leu Arg Leu Asn Val Thr Thr Gln Gly Pro
 595 600 605

Asn Leu Ala Leu Tyr Gln Leu Leu Ser Thr Ala Leu Cys Ser Ala Leu
 610 615 620

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Ile Gln Asn Phe Thr Arg Thr Gln Lys Ser Cys Ile Phe Cys Gly Phe
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Thr Phe Gly Val Ile Thr Ala Asp Thr Leu Glu Gln Ala Ile Glu Arg
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Ile Pro Tyr Ser Phe Lys Val Arg Ser Tyr Thr Lys Ile Val Thr Asn
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Thr Thr Val Asn Cys Leu Ile Thr Asp Met Met Ala Lys Ser Asn Ser
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Ser Phe His Val Arg Thr Asn Tyr Lys Ile Val Asp Tyr Asp Asn Arg
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Tyr Thr Leu Ser Trp Lys Leu Glu Asn Arg Thr Ala Tyr Cys Pro Leu
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Gln His Trp Gln Thr Phe Asp Ser Thr Ile Ala Thr Glu Thr Gly Lys
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Val Leu Arg Gly Ser Gly Ser Ala Gly Ser Ala Ser Gly Gly Ala Ser
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Ser Gly Ser Gly Gly Ala Ser Ala Gly Asn Ala Thr Thr Pro Val Pro
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Pro Thr Ala Pro Gly Lys Ser Leu Gly Thr Leu Asn Asn Pro Ala Thr
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Met Leu Gly Asp Leu Ala Arg Ala Trp Cys Leu Glu Gln Lys Arg Gln
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His Val Tyr Asn Asp Tyr His His Phe Lys Thr Ile Glu Leu Asp Gly
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Gln Ala Gln Asn Ile Ala Gly Leu Arg Lys Asp Leu Asp Asn Ala Val
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Glu Gly Leu Arg Phe Gly Ile Val Ala Ser Arg Phe Asn His Ala Leu
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Val Asp Arg Leu Val Glu Gly Ala Ile Asp Ala Ile Val Arg His Gly
805 810 815

Gly Arg Glu Glu Asp Ile Thr Leu Val Arg Val Pro Gly Ser Trp Glu
820 825 830

Ile Pro Val Ala Ala Gly Glu Leu Ala Arg Lys Glu Asp Ile Asp Ala
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Val Ile Ala Ile Gly Val Leu Ile Arg Gly Ala Thr Pro His Phe Asp
850 855 860

Tyr Ile Ala Ser Glu Val Ser Lys Gly Leu Ala Asp Leu Ser Leu Glu
865 870 875 880

Leu Arg Lys Pro Ile Thr Phe Gly Val Ile Thr Ala Asp Thr Leu Glu
885 890 895

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cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
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<212> RNA

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guuugcacug cugacgugaa cgugacaauc aauuucgacg ugggaggaaa gaagcaucag      180
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accaaggccg uguaccagcc caggggcgcc uucggcggca gcgagaacgc caccaaccug	360
uuccugcugg agcugcuggg cgccggcgag cuggcccuga ccaugagguc caagaagcug	420
cccaucaaug ugaccacagg agaggagcag caggugagcc uggagagcgu ggacguguac	480
uuccaggacg uguucggcac cauguggugc caccacgccg agaugcagaa cccaguuuac	540
uugauuccug agacagugcc cuacaucaag ugggacaacu gcaacagcac caacaucacc	600
gccgugguga gggcccaggg ccuggacgug acccugcccc ugagccugcc caccagcgcc	660
caggauagca acuucagcgu gaagaccgaa augcugggca acgagaucga caucgagugc	720
aucauggagg acggcgagau cagccaggug cugcccggcg acaacaaguu caacauuacc	780
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gccacuccga uccccggcac cggcuacgcc uacagccugc gucugacacc uaggcccug	900
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gcuuccggcg gcgacuacug uauucaauca aacaucgugu ucagcgacga gauaccagcc	1020
agccaggaca ugccuacuaa caccaccgac aucaccuaug ugggagacaa ugcuaauac	1080
agcgugccca uggugaccag cgaggacgcc aacagcccaa augucaccgu gaccgccuuc	1140
ugggccuggc ccaacaacac ugagacagac uucaagugca aguggacccu cacaucggc	1200
accccuagcg gaugcgagaa caucagcgga gcguucgcca gcaacaggac cuucgauua	1260
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gcaacuacua cuacacacaa ggugaucuuu agcaaggcuc cggaaucaca agugaggcag	1380
caguucuaa aggauaucga gaagcuucug aacgagcaag uuaacaagga aaugcagagc	1440
aguaaucucu acaugagcau gagcagcugg ugcuaacccc acucccugga cggagcaggc	1500
cucuuccugu ucgaccacgc agccgaggag uacgagcacg cuaagaaguu gaucauuuuc	1560
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M137870089W000-SEQ-HJD.txt

gagggccuga cccagaucuu ccagaaggcc uacgaacacg aacagcacau cuccgagagc 1680
 aucaacaaua uuguggauca cgcuaucaag uccaaggacc acgcuaccuu caacuuccug 1740
 cagugguacg uggccgagca acaugaggag gaggugcugu ucaaggacau ccuggacaag 1800
 aucgagcuga ucgguaauga gaaucacggc cuguaccugg ccgaccagua cgugaagggc 1860
 aucgccaaga gccggaaguc a 1881

<210> 111
 <211> 627
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 111

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
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Leu Val Val Ser Asn Leu Leu Leu Pro Gln Gly Val Val Gly Glu Ala
 20 25 30

Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile His Leu Thr
 35 40 45

Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu Phe Pro Phe
 50 55 60

Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val Thr Ile Asn
 65 70 75 80

Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp Phe Gly Gln
 85 90 95

Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly Ala Phe Gly
 100 105 110

M137870089W000-SEQ-HJD.txt

Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu Leu Gly Ala
115 120 125

Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro Ile Asn Val
130 135 140

Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val Asp Val Tyr
145 150 155 160

Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala Glu Met Gln
165 170 175

Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile Lys Trp Asp
180 185 190

Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala Gln Gly Leu
195 200 205

Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln Asp Ser Asn
210 215 220

Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp Ile Glu Cys
225 230 235 240

Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly Asp Asn Lys
245 250 255

Phe Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro Ser Gly Gly
260 265 270

Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro Gly Thr Gly
275 280 285

Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser Arg Phe Leu
290 295 300

M137870089W000-SEQ-HJD.txt

Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn Gly Pro Lys
305 310 315 320

Ala Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val Phe Ser Asp
325 330 335

Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr Asp Ile Thr
340 345 350

Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val Thr Ser Glu
355 360 365

Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp Ala Trp Pro
370 375 380

Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu Thr Ser Gly
385 390 395 400

Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala Ser Asn Arg
405 410 415

Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro Lys Thr Leu
420 425 430

Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr His Lys Val
435 440 445

Ile Phe Ser Lys Ala Pro Glu Ser Gln Val Arg Gln Gln Phe Ser Lys
450 455 460

Asp Ile Glu Lys Leu Leu Asn Glu Gln Val Asn Lys Glu Met Gln Ser
465 470 475 480

Ser Asn Leu Tyr Met Ser Met Ser Ser Trp Cys Tyr Thr His Ser Leu
485 490 495

Asp Gly Ala Gly Leu Phe Leu Phe Asp His Ala Ala Glu Glu Tyr Glu
500 505 510

His Ala Lys Lys Leu Ile Ile Phe Leu Asn Glu Asn Asn Val Pro Val
515 520 525

Gln Leu Thr Ser Ile Ser Ala Pro Glu His Lys Phe Glu Gly Leu Thr
530 535 540

Gln Ile Phe Gln Lys Ala Tyr Glu His Glu Gln His Ile Ser Glu Ser
545 550 555 560

Ile Asn Asn Ile Val Asp His Ala Ile Lys Ser Lys Asp His Ala Thr
565 570 575

Phe Asn Phe Leu Gln Trp Tyr Val Ala Glu Gln His Glu Glu Glu Val
580 585 590

Leu Phe Lys Asp Ile Leu Asp Lys Ile Glu Leu Ile Gly Asn Glu Asn
595 600 605

His Gly Leu Tyr Leu Ala Asp Gln Tyr Val Lys Gly Ile Ala Lys Ser
610 615 620

Arg Lys Ser
625

<210> 112
<211> 1884
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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60

M137870089W000-SEQ-HJD.txt

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auccagagcc ucauccaccu caccggcgag gaccucggcu ucuucaacgu ggagaucccu	180
gaguucccuu ucuacccuac cugcaacgug ugcaccgccg acgugaacgu gaccaucaac	240
uucgacgugg gcggcaagaa gcaccagcug gaccuggacu ucggccagcu gacccucac	300
accaaggccg uguaccagcc uagaggcgcc uucggcggca gcgagaacgc caccaaccug	360
uuccugcugg agcugcuggg cgccggcgag cuggcccuga ccaugagaag uaagaagcug	420
ccuaucaacg ucacuacugg cgaggagcag caggugagcc uggagagcgu ggacguguac	480
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cugaucccag aaaccgugcc uuacaucaag ugggacaacu gcaacagcac caacaucacc	600
gcugugguga gagcccaggg ccuggacgug acccugccuc ugagccugcc uaccagcgcc	660
caagacagua acuucagcgu gaagacggag augcugggca acgagaucga caucgagugc	720
aucauggagg acggcgagau cagccaggug cugccuggcg acaacaaguu caacauaaca	780
ugcagcggcu acgagagcca cgugccuagc ggcggaucc ugaccuccac cagcccugug	840
gccacccua ucccuggcac cggcuacgcc uacagccuga gacucacgcc aagaccugug	900
agcagauucu uaggaaaca cagcauccug uacguguucu acagcggcaa cggcccuaag	960
gccuccggcg gugacuacug uauccagucu acaucgugu ucagcgacga aauccagcc	1020
agccaggaca ugccuacaaa caccaccgac aucacuuaug ucggcgacaa ugcgacauac	1080
agcgugccua uggugaccag cgaggacgcc aacagccua acguaaccgu gaccgccuuc	1140
ugggccuggc cuaacaacac cgaaaccgac uucaagugca aguggacuuu aacuaguggc	1200
accccuucug gcugcgagaa caucagcggc gcauucgcca gcaacagaac cuucgauauc	1260
accgugagcg gccugggcac cgccccuaag acccugauca ucaccagaac cgcaacuaau	1320
gcaacuacaa caaccacaa ggugaucuuc agcaaggccc cuggcuccgg cucugccggc	1380
aguggcagcg caggcagugg auccgccggu ucagguuccg ccaugcagau cuacgagggc	1440
aagcugaccg ccgagggccu gagauucggc aucguggcca gcagguucaa ccacgccug	1500

M137870089W000-SEQ-HJD.txt

guggacagac ugguggaggg cgccaucgac gccaucguga gacacggagg aagagaggag 1560
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 gcaagaaagg aggacaucga ugcggugauc gccaucggcg ugcugauccg cggugcaacu 1680
 ccacacuucg acuacaucgc cucugaagug ucaaagggcc uugcggaccu gucccucgaa 1740
 cucagaaaagc cuaucacauu cggagugauu acugcagaua cccuggagca ggccaucgag 1800
 agagccggca ccaagcacgg caacaagggc ugggaagccg cgcugucugc cauagaaaug 1860
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<210> 113
 <211> 628
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 113

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
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Leu Val Val Ser Asn Leu Leu Leu Pro Gln Gly Val Val Gly Glu Ala
 20 25 30

Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile His Leu Thr
 35 40 45

Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu Phe Pro Phe
 50 55 60

Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val Thr Ile Asn
 65 70 75 80

Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp Phe Gly Gln
 85 90 95

Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly Ala Phe Gly
 100 105 110

Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu Leu Gly Ala
 115 120 125

Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro Ile Asn Val
 130 135 140

Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val Asp Val Tyr
 145 150 155 160

Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala Glu Met Gln
 165 170 175

Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile Lys Trp Asp
 180 185 190

Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala Gln Gly Leu
 195 200 205

Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln Asp Ser Asn
 210 215 220

Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp Ile Glu Cys
 225 230 235 240

Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly Asp Asn Lys
 245 250 255

Phe Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro Ser Gly Gly
 260 265 270

Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro Gly Thr Gly
 275 280 285

Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser Arg Phe Leu
 290 295 300

Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn Gly Pro Lys
 305 310 315 320

Ala Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val Phe Ser Asp
 325 330 335

Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr Asp Ile Thr
 340 345 350

Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val Thr Ser Glu
 355 360 365

Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp Ala Trp Pro
 370 375 380

Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu Thr Ser Gly
 385 390 395 400

Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala Ser Asn Arg
 405 410 415

Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro Lys Thr Leu
 420 425 430

Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr His Lys Val
 435 440 445

Ile Phe Ser Lys Ala Pro Gly Ser Gly Ser Ala Gly Ser Gly Ser Ala
 450 455 460

Gly Ser Gly Ser Ala Gly Ser Gly Ser Ala Met Gln Ile Tyr Glu Gly
 465 470 475 480

Lys Leu Thr Ala Glu Gly Leu Arg Phe Gly Ile Val Ala Ser Arg Phe
485 490 495

Asn His Ala Leu Val Asp Arg Leu Val Glu Gly Ala Ile Asp Ala Ile
500 505 510

Val Arg His Gly Gly Arg Glu Glu Asp Ile Thr Leu Val Arg Val Pro
515 520 525

Gly Ser Trp Glu Ile Pro Val Ala Ala Gly Glu Leu Ala Arg Lys Glu
530 535 540

Asp Ile Asp Ala Val Ile Ala Ile Gly Val Leu Ile Arg Gly Ala Thr
545 550 555 560

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

Leu Ser Leu Glu Leu Arg Lys Pro Ile Thr Phe Gly Val Ile Thr Ala
580 585 590

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

Lys Gly Trp Glu Ala Ala Leu Ser Ala Ile Glu Met Ala Asn Leu Phe
610 615 620

Lys Ser Leu Arg
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<210> 114

<211> 865

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 114

Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
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His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
 20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
 35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
 115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
 130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
 145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
 165 170 175

M137870089W000-SEQ-HJD.txt

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Ala Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

M137870089W000-SEQ-HJD.txt

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
 370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
 385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
 405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
 435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
 450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
 465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
 485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
 500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
 515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
 530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
 545 550 555 560

M137870089W000-SEQ-HJD.txt

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

M137870089W000-SEQ-HJD.txt

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 115
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 115

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
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Leu Val Val Ser Asn Leu Leu Leu Pro Gln Gly Val Val Gly
20 25 30

<210> 116
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 116

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15

His Ser

<210> 117
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 117

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly
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<210> 118
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 118

M137870089W000-SEQ-HJD.txt

Met Leu Gly Ser Asn Ser Gly Gln Arg Val Val Phe Thr Ile Leu Leu
1 5 10 15

Leu Leu Val Ala Pro Ala Tyr Ser
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<210> 119
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 119

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

Ala

<210> 120
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 120

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

<210> 121
<211> 10
<212> RNA
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<220>
<223> Synthetic Polynucleotide

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 <223> n is a or g

<400> 121
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<210> 122
 <211> 11
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 122
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<210> 123
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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 <223> n is u or a

<400> 123
 uuauuuann 9

<210> 124
 <211> 2595
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

M137870089W000-SEQ-HJD.txt

<400> 124

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gugugcacgg	cugacgucaa	cgugacuauc	aacuucgaug	ugggagggaa	gaaacaucaa	180
cuugaucugg	acuuuggcca	gcuuacuccc	cacaccaagg	ccguguacca	gccccgcggc	240
gcuuucggug	ggagcgagaa	cgcgacaaa	cuauucuugc	uggaacugcu	gggcgcagga	300
gagcucgccc	ugacgaugcg	aucuaagaag	cuucccauca	acguuaccac	uggcgaggag	360
cagcaggugu	cccucgaaag	cgucgacguc	uauuuccaag	acgucuucgg	aacaugugg	420
ugccaccacg	cugagaugca	gaaccccgua	uauuuuuuc	ccgaaaccgu	gccauacauc	480
aagugggaca	acugcaacuc	aacuaacauc	acugcaguag	ugcgcgccca	gggacuggac	540
gucacuuugc	cacugucacu	gcccacauca	gcccagaca	gcaacuucag	cgucaagaca	600
gaaaugcugg	gcaacgaaau	cgacaucgaa	ugcauaaugg	aggaugggga	aaauucccag	660
guccuccccg	gugauaacia	guuuauuuu	acuuguucug	gauaugaauc	ccaugugccg	720
ucugguggua	uacugacgag	uacaucgcca	guggcuaccc	caauccccgg	gacaggcuau	780
gccuacagcc	ugagacugac	gccaagacca	guuuccaggu	uucuggggaa	uaacucuauc	840
cuguaugugu	uuuauucugg	uaacggaccc	aaggcauccg	gcgguugaua	uuguauccag	900
agcaauauag	uguucucuga	ugagauuccg	gccucccagg	auaugccaac	caacacgaca	960
gauaucaccu	augucgggga	caacgccaca	uauagcgugc	caauggugac	cagcgaagau	1020
gccaauucuc	ccaacgucac	agugacagcc	uuuugggcgu	ggccuaauaa	cacagaaacu	1080
gacuuuaaa	gcaaauggac	ucuaaccuca	ggcaccccau	cuggcugcga	gaacauaagc	1140
ggcgcguuug	caucgaacag	aacuuuugau	auuacaguau	cuggguuggg	cacugcgccc	1200
aagacucuaa	uaauuacacg	gacggccacu	aacgccacca	cgacgacuca	caaggugauc	1260
uucagcaaag	cucccgaauc	uacuacuacc	ucgccgacac	ugaauacgac	aggauucgcc	1320
gacccaaa	cuacgaccgg	ccuucccagc	ucgacacaug	ugccuacaaa	cuuaacggcg	1380
cccgccagua	ccggccccac	cgugagcacc	gcugacguca	ccucuccuac	cccugccggg	1440

M137870089W000-SEQ-HJD.txt

acuacaagug gugcuucccc aguuacuccc agcccuagcc cuugggacaa cggcacugag	1500
agcaaagcuc cggacaugac cagcaguacc aguccaguga caacuccgac acccaaugcg	1560
acgucccca cucccgccgu gaccacgcca acaccaaauug ccacgucacc uacuccagcg	1620
gucaccaccc caacgccaaa cgcuacuagu cccacucuag gcaagacauc ucccaccucc	1680
gcugucacca ccccuacacc caaugcuacc ggucccacgg ugggugagac uagcccacag	1740
gccaacgcaa cuaaucauac auuggguggc acaagcccaa cgcccgucgu cacuagccag	1800
ccuaagaacg ccacaagcgc uguaacuacc ggccagcaca auauaacaag uuccaguacu	1860
agcaguaugu cucugagacc cagcucaaau ccugaaaccc ucucgcccuc uacgucggau	1920
aacuccacgu cccacaugcc ucuacucaca agcgcgcacc cuaccggagg agagaauauc	1980
acucagguua cccagcuuc uaucucgacu caccaugucu cuacuucuuc cccagcgcca	2040
cggcccgga cuaccagcca ggcuagcggg ccagguaauu ccuccacuag cacuaaaccu	2100
ggcgaaguca acguuaccaa gggaacaccu cccagaaug caaccucgcc ccaagcuccc	2160
ucuggacaga agacagccgu cccuaccguc acaagcaccg gugggaaggc gaauucuacg	2220
acaggcggga agcacacuac cggacacgga gcaaggacau ccacugagcc cacgaccgac	2280
uacgguggcg acuccaccac gcccagaccc agguacaauug cgacuaccua ccugccgccu	2340
uccacuucca gcaaacugag gccucguugg acuuucacuu cuccaccagu caccaccgcu	2400
caggcuaccg ugccuguccc gccgaccucu cagccccggu uuucaaaauu gaguaugcuc	2460
gugcugcagu gggccagccu ggcagugcuu acccuccugc ucuugcuggu uauggcugac	2520
ugcgccuucc gacguaacuu auccaccagu cauacuua cuacaccucc uuaugacgac	2580
gcggagaccu acgug	2595

<210> 125

<211> 865

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 125

Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
 1 5 10 15

His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
 20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
 35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
 115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
 130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
 145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
 165 170 175

M137870089W000-SEQ-HJD.txt

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
 180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
 195 200 205

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
 210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
 245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
 260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
 275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
 305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
 325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
 340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
 355 360 365

M137870089W000-SEQ-HJD.txt

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
 370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
 385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
 405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
 435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
 450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
 465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
 485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
 500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
 515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
 530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
 545 550 555 560

M137870089W000-SEQ-HJD.txt

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
740 745 750

M137870089W000-SEQ-HJD.txt

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
770 775 780

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 126
<211> 2595
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 126
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gaggacccgg gguucuucaa cgucgaauc cccgaauucc caucuauc caccuguaac 120
gucugcacag ccgacguuaa cguuacauc aaauucgacg ugpgcgaggaa gaaacaccag 180
cuggaccucg acuuugggca gcugacgccc cacacuaaag ccguuuacca gcccaggggu 240

M137870089W000-SEQ-HJD.txt

gc <u>au</u> ucggug gaucugagaa ugcuacaaac cucuuucugc uugagcugcu uggugcugga	300
gagcuggccc ugacaau <u>gc</u> g cagcaagaag uugccaauca augugaccac aggugaagaa	360
cagcaggugu cc <u>cu</u> agaau <u>c</u> cguggaugug uacuuccagg acguuuucgg cacaau <u>g</u> gg	420
ugccaucacg cagagaugca gaauccggug uaccuuaucc ccgaaacagu gccguacauu	480
aaauggg <u>au</u> a auuguaacuc caca <u>aa</u> cauc acggcagugg ugcgcgcuca ggggcuggac	540
gugacacucc cgcuuu <u>cc</u> uu accaacaagu gcucaagauu ccaacuuuuc ugugaagacc	600
gagaugcugg gcaacgagau ugauauugaa ugcaucaugg aggauggcga gauuagccag	660
guguugccc <u>g</u> gcgacaauaa auuu <u>aa</u> uuuu accuguuccg gcuaugaguc acacgugcca	720
aguggaggca uucucacgag caccucuccc guugcaacac cc <u>au</u> uccugg gacaggg <u>ua</u> c	780
gc <u>au</u> auaguc ucaggcugac accgagaccg guaucgcgc <u>u</u> ucuuagguaa caauuccauc	840
uuguaugugu uu <u>u</u> acagcgg aaacgggcca aaggccucag gaggagacua cugcauccag	900
agcaauauag uc <u>uuu</u> agcga cgaga <u>u</u> ccu gccucacaag acaugcccac caacaccacc	960
gacauacg <u>u</u> acgucgguga uaaugccacu uacagcgugc cuauggugac cucugaagac	1020
gca <u>aa</u> uucac ccaau <u>g</u> ucac gguuaccgca uucugggcuu ggccaa <u>ua</u> a cacugaaacc	1080
gacu <u>u</u> caagu guaaauggac ccuaaccagc ggcaccc <u>ca</u> u cagggu <u>gc</u> ga gaauaucagc	1140
ggggccuucg ccagcaaccg gacauucgac aucaccgugu caggacuagg gacugcucca	1200
aagacau <u>ua</u> a uuauuacacg gacagcaacu aacgcuacga cuacgacuca caaagugaua	1260
uuuagca <u>aa</u> g cgcccga <u>u</u> c gacuacuacg agcccga <u>cc</u> uaaacaccac cgguuucgcc	1320
gauc <u>cc</u> aa <u>ca</u> caacuacugg ucucccaucu ucgacccaug uu <u>cc</u> aacgaa ucugacagcu	1380
ccagcaagua cggggcc <u>cc</u> ac ugugaguaca gccgacguua cuagcccaac uccgcg <u>gg</u> u	1440
acgacuagug gcgcgucucc agugaccc <u>cu</u> ucgccuucuc cgugggauaa uggaaccgag	1500
uca <u>aa</u> ggcuc cugauaugac cagcuccacc agucccguaa caacgccaac gccc <u>aa</u> ugca	1560
acgaguccaa cuccggcggu uaccacuccg acac <u>aa</u> acg ccaccucgcc cacgccugca	1620
guuacuacgc ccaccc <u>cu</u> aa ugcuacguca cccacucugg gaaagaccuc accaaccucu	1680

M137870089W000-SEQ-HJD.txt

gccgugacua cuccuacacc uaaugccaca ggacccacag uuggggaaac cagcccacag	1740
gcuaacgcaa cuaaucauac gcuuggcgagg accucuccca cgcccguggu cacuucacag	1800
ccuaagaauug ccacaagcgc ugugacuaca ggccagcaua auauaaccag caguucaacc	1860
aguagcaugu cccugcgucc uucauccaau ccugagacuc ugagccccag cacuagugac	1920
aacucaacuu cucacaugcc guugcgagacc uccgcgcauc ccacgggcgg ugagaauauc	1980
acacagguga caccgcguc uauuagcaca caucacguga guacguccuc gcccgacccc	2040
cgcccaggca caaccucaca agcaucaggu ccggggaaau gcagcacaag uaccaagccu	2100
ggcgaaguga auguaaccaa gggcacgcca ccgcagaacg ccacaucucc ucaagcccca	2160
uccggccaga agaccgcugu acccaccgug acaucaacug gggggaaagc gaacucaacu	2220
accgguggga agcauacaac agggcacggu gccagaacuu cuacagagcc aaccacggac	2280
uacggagggg acagcacaac gccagaccg cgguacaauug cgaccacaua ccugccuccc	2340
ucaacuucga guaagcugcg acccagaugg accuuuacuu cuccuccugu caccaccgcu	2400
caagccaccg ucccggaucc accuacuucc cagccuagau ucuccaauu gagcaugcuu	2460
guccuacagu gggcaucacu cgcgguacua accuugcugc uacuguuggu gauggcggac	2520
ugcgcguuuc gccgcaacuu auccaccucc cacacguaca caacaccucc cuaugaugac	2580
gcugagacuu acguc	2595

<210> 127
 <211> 865
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 127

Met	Glu	Ala	Ala	Leu	Leu	Val	Cys	Gln	Tyr	Thr	Ile	Gln	Ser	Leu	Ile
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M137870089W000-SEQ-HJD.txt

His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
 20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
 35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
 50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
 65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
 85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
 100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
 115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
 130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
 145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
 165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
 180 185 190

Asp Ser Asn Phe Ser Val Lys Thr Glu Met Leu Gly Asn Glu Ile Asp
 195 200 205

M137870089W000-SEQ-HJD.txt

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
 210 215 220

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

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
 245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
 260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
 275 280 285

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

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr
 305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
 325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
 340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
 355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
 370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
 385 390 395 400

M137870089W000-SEQ-HJD.txt

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

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

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Gly Pro Thr Val Gly Glu
565 570 575

Thr Ser Pro Gln Ala Asn Ala Thr Asn His Thr Leu Gly Gly Thr Ser
580 585 590

M137870089W000-SEQ-HJD.txt

Pro Thr Pro Val Val Thr Ser Gln Pro Lys Asn Ala Thr Ser Ala Val
 595 600 605

Thr Thr Gly Gln His Asn Ile Thr Ser Ser Ser Thr Ser Ser Met Ser
 610 615 620

Leu Arg Pro Ser Ser Asn Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp
 625 630 635 640

Asn Ser Thr Ser His Met Pro Leu Leu Thr Ser Ala His Pro Thr Gly
 645 650 655

Gly Glu Asn Ile Thr Gln Val Thr Pro Ala Ser Ile Ser Thr His His
 660 665 670

Val Ser Thr Ser Ser Pro Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala
 675 680 685

Ser Gly Pro Gly Asn Ser Ser Thr Ser Thr Lys Pro Gly Glu Val Asn
 690 695 700

Val Thr Lys Gly Thr Pro Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro
 705 710 715 720

Ser Gly Gln Lys Thr Ala Val Pro Thr Val Thr Ser Thr Gly Gly Lys
 725 730 735

Ala Asn Ser Thr Thr Gly Gly Lys His Thr Thr Gly His Gly Ala Arg
 740 745 750

Thr Ser Thr Glu Pro Thr Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro
 755 760 765

Arg Pro Arg Tyr Asn Ala Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser
 770 775 780

M137870089W000-SEQ-HJD.txt

Lys Leu Arg Pro Arg Trp Thr Phe Thr Ser Pro Pro Val Thr Thr Ala
785 790 795 800

Gln Ala Thr Val Pro Val Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn
805 810 815

Leu Ser Met Leu Val Leu Gln Trp Ala Ser Leu Ala Val Leu Thr Leu
820 825 830

Leu Leu Leu Leu Val Met Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser
835 840 845

Thr Ser His Thr Tyr Thr Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr
850 855 860

Val
865

<210> 128
<211> 2571
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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cgccagcaga ccuccuucc cuuccgcguc ugcgagcucu ccuccacgg cgaccucuuc 180
cgcuucuccu ccgacaucca gugccccucc uucggcacc gcgagaacca caccgagggc 240
cuccucaugg ucuucaagga caacaucauc ccuacuucc ucaagguccg cuccuacacc 300
aagaucguca ccaacauccu caucuacaac ggcugguacg ccgacucugu gacuaaucgc 360
cacgaggaga aguucuccgu cgacuccuac gagacugacc agauggacac caucuaccag 420
ugcuacaacg ccgucaagau gaccaaggac ggccucaccc gcgucuacgu cgaccgcgac 480

M137870089W000-SEQ-HJD.txt

ggcgucaaca ucaccgucaa ccucaagccu acaggcggcc ugcccaacgg cguccgccgc	540
uacgccuccc agaccgagcu cuacgacgcc ccuggcuggc ucaucuggac cuaccgcacc	600
aggaccacug ucaauugccu caucaccgac augauggcca aguccaacuc cccuuucgac	660
uucuucguga ccaccacagg ccagaccguc gagaugucgc cauucuauga cggcaagaac	720
aaggagacuu uccacgagag agcggacucu uucaugucc gcaccaacua caagauuguc	780
gacuacgaca accgcggcac caauccacag ggcgagcgcc gcgccuuccu cgacaagggc	840
accuacaccc ucuccuggaa gcucgagaac cgcaccgccu acuguccucu ccagcacugg	900
cagaccuucg auuccaccau cgccaccgag acuggcaagu ccauccauuu cgucaccgac	960
gaaggaacau cuucauucgu cacaaauaca accgugggca ucgagcuccc cgacgccuuc	1020
aagugcaucg aggagcaggu caacaagacc augcacgaga aguacgaggc cguccaggac	1080
cggauuacaa agggccagga ggccaucacc uacuucauca ccagcggagg ucugcuucuc	1140
gccuggcuuc cacucacacc ucgcucccug gccacaguga agaaccucac ugaguugacc	1200
acccaacaa guuccccacc uaguaguuccu agcccuccug cuccuuccgc cgcccgccgc	1260
uccacgccug ccgccguccu gcggagacgg agaagggacg ccggcaacgc uaccacuccu	1320
gugccgccga cagccccugg aaagucccua gguaccuca acaaccagc gacaguucag	1380
auccaguucg ccuacgacuc ucucaggcgc cagaucaacc gcaugcuugg ugaccuugcc	1440
cgcgccuggu gccucgagca gaagcgccag aacauggugc uucgugaacu aacaaagauu	1500
aauccuacua cagugauguc cuccaucuaac ggcaaggccg ucgccgcca gcgccucggc	1560
gacgucaucu ccgucucca gugcgucca gugaaccagg cuaccgugac ccucaggaag	1620
uccaugagag ugccaggcuc cgagacaauug ugcuaucucc gcccacucgu cuccuucucc	1680
uucaucaacg acacaaagac cuacgagggc caguuaggca cugacaacga gaucuucuug	1740
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M137870089W000-SEQ-HJD.txt

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uuccgcgagu acaacuucca ggcacagaac auagccggcc uccguaagga ucuggacaau 2040
gccgugucca acggccgcaa ccaguucguc gacgguuugg gugaacucau ggacucucug 2100
ggcuccgucg gccaguccau aacuaacuua gucucuacgg ugggaggccu auucagcagc 2160
cuggugagcg gcuucaucuc uuucuucaag aaccccuucg gcggcaugcu cauccucguc 2220
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cuccacgagc agaaccagga acagaagcgg gccgccagc gagcugccgg cccuccguc 2460
gccaguaggg cacuacaagc cgcccgggac cgcuucccag gccugagaag gaggagauac 2520
cacgacccag agacagccgc ugcccuccuu ggcgaagcag aaaccgaguu c 2571

<210> 129
<211> 857
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 129

Met Thr Arg Arg Arg Val Leu Ser Val Val Val Leu Leu Ala Ala Leu
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Ala Cys Arg Leu Gly Ala Gln Thr Pro Glu Gln Pro Ala Pro Pro Ala
20 25 30

Thr Thr Val Gln Pro Thr Ala Thr Arg Gln Gln Thr Ser Phe Pro Phe
35 40 45

Arg Val Cys Glu Leu Ser Ser His Gly Asp Leu Phe Arg Phe Ser Ser
50 55 60

Asp Ile Gln Cys Pro Ser Phe Gly Thr Arg Glu Asn His Thr Glu Gly
65 70 75 80

Leu Leu Met Val Phe Lys Asp Asn Ile Ile Pro Tyr Ser Phe Lys Val
85 90 95

Arg Ser Tyr Thr Lys Ile Val Thr Asn Ile Leu Ile Tyr Asn Gly Trp
100 105 110

Tyr Ala Asp Ser Val Thr Asn Arg His Glu Glu Lys Phe Ser Val Asp
115 120 125

Ser Tyr Glu Thr Asp Gln Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ala
130 135 140

Val Lys Met Thr Lys Asp Gly Leu Thr Arg Val Tyr Val Asp Arg Asp
145 150 155 160

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

Gly Val Arg Arg Tyr Ala Ser Gln Thr Glu Leu Tyr Asp Ala Pro Gly
180 185 190

Trp Leu Ile Trp Thr Tyr Arg Thr Arg Thr Thr Val Asn Cys Leu Ile
195 200 205

Thr Asp Met Met Ala Lys Ser Asn Ser Pro Phe Asp Phe Phe Val Thr
210 215 220

Thr Thr Gly Gln Thr Val Glu Met Ser Pro Phe Tyr Asp Gly Lys Asn
225 230 235 240

Lys Glu Thr Phe His Glu Arg Ala Asp Ser Phe His Val Arg Thr Asn
245 250 255

Tyr Lys Ile Val Asp Tyr Asp Asn Arg Gly Thr Asn Pro Gln Gly Glu
 260 265 270

Arg Arg Ala Phe Leu Asp Lys Gly Thr Tyr Thr Leu Ser Trp Lys Leu
 275 280 285

Glu Asn Arg Thr Ala Tyr Cys Pro Leu Gln His Trp Gln Thr Phe Asp
 290 295 300

Ser Thr Ile Ala Thr Glu Thr Gly Lys Ser Ile His Phe Val Thr Asp
 305 310 315 320

Glu Gly Thr Ser Ser Phe Val Thr Asn Thr Thr Val Gly Ile Glu Leu
 325 330 335

Pro Asp Ala Phe Lys Cys Ile Glu Glu Gln Val Asn Lys Thr Met His
 340 345 350

Glu Lys Tyr Glu Ala Val Gln Asp Arg Tyr Thr Lys Gly Gln Glu Ala
 355 360 365

Ile Thr Tyr Phe Ile Thr Ser Gly Gly Leu Leu Leu Ala Trp Leu Pro
 370 375 380

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

Thr Pro Thr Ser Ser Pro Pro Ser Ser Pro Ser Pro Pro Ala Pro Ser
 405 410 415

Ala Ala Arg Gly Ser Thr Pro Ala Ala Val Leu Arg Arg Arg Arg Arg
 420 425 430

Asp Ala Gly Asn Ala Thr Thr Pro Val Pro Pro Thr Ala Pro Gly Lys
 435 440 445

M137870089W000-SEQ-HJD.txt

Ser Leu Gly Thr Leu Asn Asn Pro Ala Thr Val Gln Ile Gln Phe Ala
450 455 460

Tyr Asp Ser Leu Arg Arg Gln Ile Asn Arg Met Leu Gly Asp Leu Ala
465 470 475 480

Arg Ala Trp Cys Leu Glu Gln Lys Arg Gln Asn Met Val Leu Arg Glu
485 490 495

Leu Thr Lys Ile Asn Pro Thr Thr Val Met Ser Ser Ile Tyr Gly Lys
500 505 510

Ala Val Ala Ala Lys Arg Leu Gly Asp Val Ile Ser Val Ser Gln Cys
515 520 525

Val Pro Val Asn Gln Ala Thr Val Thr Leu Arg Lys Ser Met Arg Val
530 535 540

Pro Gly Ser Glu Thr Met Cys Tyr Ser Arg Pro Leu Val Ser Phe Ser
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565 570 575

Glu Ile Phe Leu Thr Lys Lys Met Thr Glu Val Cys Gln Ala Thr Ser
580 585 590

Gln Tyr Tyr Phe Gln Ser Gly Asn Glu Ile His Val Tyr Asn Asp Tyr
595 600 605

His His Phe Lys Thr Ile Glu Leu Asp Gly Ile Ala Thr Leu Gln Thr
610 615 620

Phe Ile Ser Leu Asn Thr Ser Leu Ile Glu Asn Ile Asp Phe Ala Ser
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Leu Glu Leu Tyr Ser Arg Asp Glu Gln Arg Ala Ser Asn Val Phe Asp
645 650 655

Leu Glu Gly Ile Phe Arg Glu Tyr Asn Phe Gln Ala Gln Asn Ile Ala
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Gly Leu Arg Lys Asp Leu Asp Asn Ala Val Ser Asn Gly Arg Asn Gln
675 680 685

Phe Val Asp Gly Leu Gly Glu Leu Met Asp Ser Leu Gly Ser Val Gly
690 695 700

Gln Ser Ile Thr Asn Leu Val Ser Thr Val Gly Gly Leu Phe Ser Ser
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Leu Val Ser Gly Phe Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met
725 730 735

Leu Ile Leu Val Leu Val Ala Gly Val Val Ile Leu Val Ile Ser Leu
740 745 750

Thr Arg Arg Thr Arg Gln Met Ser Gln Gln Pro Val Gln Met Leu Tyr
755 760 765

Pro Gly Ile Asp Glu Leu Ala Gln Gln His Ala Ser Gly Glu Gly Pro
770 775 780

Gly Ile Asn Pro Ile Ser Lys Thr Glu Leu Gln Ala Ile Met Leu Ala
785 790 795 800

Leu His Glu Gln Asn Gln Glu Gln Lys Arg Ala Ala Gln Arg Ala Ala
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Gly Pro Ser Val Ala Ser Arg Ala Leu Gln Ala Ala Arg Asp Arg Phe
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ccggcggggg cccugauaau gggccucagg auccugauaa cacggaugau aacggcccac	840
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M137870089W000-SEQ-HJD.txt

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gccacaguca ugauaguggg cacgggggug gcgauccaca ucuccccaca cugcugcuag	1140
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<220>
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gcgauuggac aggggggugcu cugcuggugu uguacagcuu ugcgcuugaug uugauuuua	240
ucauccugau uaucuuuuaa uuucgaaggg accuccuug uccccuggga gcgcugugca	300
uacugcucuu aaugaucacg uugcuccuca uugcuuuuug gaaucugcac ggacaggcuc	360
uauuccucgg caucguuuua uucauuuucg ggugccuccu ugugcuggga aucuggaucu	420
aucugcuaga gaugcugugg cggcucggcg ccaccauuug gcagcuucug gcuuuuuucc	480
uagcguuuuu ucuggaucuc auccuacuua uuaucgccuu guauuugcag cagaacuggu	540
ggacucuccu gguggaucuc cuguggcucc uccuguuccu cgccauauug auauuggaugu	600
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M137870089W000-SEQ-HJD.txt

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cccuaccca uuccccauc gacucugcug gcaacgaugg cggcccaccg cagcugaccg	1020
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ugggacuggc acugcugcug uugcuucugg ccucguguu cuggcuguac aucguuaugu	180
cugauuggac aggaggagcu cugcugguuc uuuacucuuu cgcgcuugaug cugaucauca	240
ucaucuugau cauuuucuu uucagacgag accuccuuug uccucucgga gccugugua	300
uccuccugcu gaugauaacc cuucgcuga uugcuuugug gaucugcau gggcaagcuc	360
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M137870089W000-SEQ-HJD.txt

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M137870089W000-SEQ-HJD.txt

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uccugcuguu aaugaucacu cugcuccuca uugcccuaug gaaccuccac ggacaagccc	360
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acgacugaua auaggcugga gccucggugg ccaugcuucu ugccccuugg gccucgggg	1260
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cggc	1324

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<220>

<223> Synthetic Polynucleotide

<400> 144

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uagggcuggc auugcuccug cuccuccugg ccuugcuguu cuggcuuuac aucgugauga	180
gcgacuggac uggcggggcc cugcuggucc ucuauagcuu ugcacugaug cugauuauaa	240
ucauauugau caucuuauc uuccgacggg auuuacuug ccccguggg gcauuangua	300
uucuauugcu gaugauaaca cuucugcuu uugcuuuug gaaucuacac ggucaggcuc	360
uuuuucuggg aaucgugcuc uuuaucuuug gaugccuucu gguacuagga auuuggauau	420
accucuuaga aaugcugugg cggcucggcg caaccaucug gcaacuccuu gcguuuuuuc	480
ucgcguuuuu ccucgaccug auucugcuua uaaucgccuu auaccuucag cagaauuggu	540
ggacacuccu gguggaccug cuguggcucc ugcuaauccu ugcaauccuc auuuggaugu	600
auuaccaugg ccagaggcac ucugaugagc accaccacga ugauagucua ccucauccac	660
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gucacaguca cgacucaggu cacggcggcg gggaccccca uuugccuaca cugcuguuag	1140
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<220>
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 ggggaaaauaa cucgcaauau cccucagccu caggcucauc ggguaauacu ccgaccccuc 180
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 ggggggaacgg ugauaggcac agugacuacc agccacuugg gacacaagac caaagccugu 300
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ccgaggagag gccaccacc ccuaccgaa auacgguaug auaauaggcu ggagccucgg	1560
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ccgccuccgu guccacggug gugacagcua cagggcuggc acucucucug cuacuccugg	540
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<211> 1657

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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<220>
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<210> 149
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 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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accugggcuu gcagcaugau gguaacgacg ggcuuccgcc cccaccauac ucaccagag	360
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M137870089W000-SEQ-HJD.txt

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agaugcaaaa uccgguguac cuuauccccg aaacagugcc guacauuaaa ugaggauaaau	540
guaacuccac aaacaucacg gcaguggugc gcgcucaggg gcuggacgug acacuccccc	600
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acaauaaaau uaauuuuacc uguuccggcu augagucaca cgugccaagu ggaggcauuc	780
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ggcugacacc gagaccggua ucgcgcuucu uagguaacaa uuccaucuug uauguguuuu	900
acagcggaaa cgggccaaag gccucaggag gagacuacug cauccagagc aaauaguuuu	960
uuagcgacga gaucccugcc ucacaagaca ugcccaccaa caccaccgac aucacguacg	1020
ucggugauaa ugccacuuac agcgugccua uggugaccuc ugaagacgca aaucaccca	1080
augucacggu uaccgcauuc ugggcuuggc caaauaacac ugaaaccgac uucaagugua	1140
aauggacccu aaccagcggc accccaucag ggugcgagaa uaucagcggg gccuucgcca	1200
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cuacuggucu cccaucuuug acccauguuc caacgaauuc gacagcucca gcaaguacgg	1440
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cgucuccagu gaccccuucg ccuucuccgu gggauaaugg aaccgaguca aaggcuccug	1560
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cggcgguuac cacuccgaca ccaaacgcca ccucacccac gccugcaguu acuacgccc	1680
ccccuaaugc uacgucaccc acucugggaa agaccucacc aaccucugcc gugacuacuc	1740
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aucauacgcu ugggggggacc ucucccacgc ccguggucac uucacagccu aagaaugcca	1860
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ugcguccuuc auccaauccu gagacucuga gccccagcac uagugacaac ucaacuucuc	1980
acaugccguu gcugaccucc gcgcauccca cgggcgguga gaauaucaca caggugacac	2040
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ccucacaagc aucagguccg gggaacagca gcacaaguac caagccuggc gaagugaaug	2160
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cggauccacc uacuucccag ccuagauucu ccaaucugag caugcuuguc cuacaguggg	2520
caucacucgc gguacuaacc uugcugcuac uguuggugau ggcgagacugc gcguuucgcc	2580
gcaacuuauc caccucccac acguacaaa caccuccua ugaugacgcu gagacuuaag	2640
ucugauaaua ggcuggagcc ucgguggcca ugcuuucugc cccuugggcc uccccccagc	2700
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 <213> Artificial Sequence

<220>
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M137870089W000-SEQ-HJD.txt

acuuccugcc cccagagug agaggcggcg gcagaguggc cgccgccgcc aucaccuggg	180
ugcccaagcc caacguggag guguggcccg uggaccccc acccccgug aacuucaaca	240
agaccgccga gcaggaguac ggcgacaagg aggugaagcu gcccacugg accccaccc	300
ugcacaccuu ccaggugccc cagaacuaca ccaaggccaa cugcaccuac ugcaacacca	360
gagaguacac cuucagcuac aagggcugcu gcuucuacuu caccaagaag aagcacaccu	420
ggaacggcug cuuccaggcc ugcgccgagc uguacccug caccuacuuc uacggcccca	480
cccccacau ccugcccgug gugaccagaa accugaacgc caucgagagc cugugggugg	540
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accagaucuu cggcagccac ugcaccuacg ugagcaaguu cagcaccgug cccgugagcc	660
accacgagug cagcuuccug aagcccugcc ugugcgugag ccagagaagc aacagcugau	720
aauaggcugg agccucggug gccaugcuuc uugcccuug gccuccccc cagccccucc	780
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<210> 156

<211> 577

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 156

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ccuaccccgug cugccacgug acccagcuga gagcccagca ccugcuggcc cuggagaaca	180
ucagcgacau cuaccuggug agcaaccaga ccugcgacgg cuucagccug gccagccuga	240
acagcccca gaacggcagc aaccagcugg ugaucagcag augcgccaac ggccugaacg	300
uggugagcuu cuucaucagc auccugaaga gaagcagcag cgcccugacc ggccaccuga	360
gagagcugcu gaccaccug gagaccugu acggcagcuu cagcguggag gaccuguucg	420

M137870089W000-SEQ-HJD.txt

gcgccaaccu gaacagauac gccuggcaca gaggcggcug auaauaggcu ggagccucgg	480
uggccaugcu ucuugccccc ugggccuccc cccagccccc ccuccccuuc cugcaccggu	540
acccccgugg ucuuuugaaua aagucugagu gggcggc	577

<210> 157
 <211> 2284
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 157	
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uccacuugga caucgagggc cacgccagcc acuacaccau cccugggacc gagcucaugg	180
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cacuggagaa gcagcuguuc uacuacaucg gcaccaugcu gccaacacc cggccccaca	480
gcuacguguu cuaccagcug cggugccacc ugagcuacgu ugcccugagc aucaacggcg	540
acaaguucca guacaccggc gccaugacca gcaaguuccu gaugggcacc uacaagcggg	600
ucaccgagaa gggcgacgag cacgugcugu cacugguguu cggcaagacc aaggaccugc	660
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M137870089W000-SEQ-HJD.txt

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aggccggcgu guacagugga cugaucggcg gcgcaaccag cgugcugcua uccgcuuaca	1260
accggcaccc gcuguuccag cccucgcaca ccgugaugcg ggaaaccug uucaucggaa	1320
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gccuggcccu cgguaccgag agcggccucu ucagcccaug cuacuuaagc cugcgguucg	1500
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ucuacgaggc cagcaccacc uaucugagca gcagccuguu ccugucuccu gugaucauga	1800
acaagugcag ccaggcgcc guggccggcg agccccggca gauccccaag auccagaacu	1860
ucacccggac ccagaagucu ugcaucuucu gcggcuucgc ccuuuugucc uacgacgaga	1920
aggagggcuu ggagacuaca accuacauca ccagccagga ggugcagaac agcauccugu	1980
caucuaauua cuucgacuuc gacaaccugc acguucaua ccugcuccuc accaccaacg	2040
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uccuguacuu caucgcuuc gcacuuggca ucuuccuggu gcacaagauc gugauguucu	2160
uccugugaua auaggcugga gccucggugg ccaugcuucu ugccccuugg gccuuccccc	2220
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cggc	2284

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 uaggccuugc ucuccuucuc cuccucuugg cgcuacuguu uggcuguac aucguuauga 180
 gugacuggac uggaggagcc cuccuugucc ucuauuccuu ugcucucaug cuuauaauua 240
 uaauuuugau caucuuauc uucagaagag accuucucug uccacuugga gcccuuugua 300
 uacuccuacu gaugaucacc cuccugcuca ucgcucucug gaauuugcac ggacaggcau 360
 uguuccuugg aaauugucug uucaucuucg ggugcuuacu ugucuuaaggu aucuggaucu 420
 acuuauugga gaugcucugg cgacuuggug ccaccaucug gcagcuuuug gccuucuucc 480
 uagccuucuu ccuagaccuc auccugcuca uuauugcucu cuaucuacaa cagaacuggu 540
 ggacucuaau gguugaucuc cuuuggcucc uccuguuucu ggcgauuuua aucuggaugu 600
 auuaccaugg acaacgacac agugaugaac accaccacga ugacucccuc ccgcaccuc 660
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 cuggaggugg uccugacaau ggcccacagg acccugacaa cacggaugau aauggcccac 840
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augacugaua auaggcugga gccucggugg ccaugcuucu ugcccuugg gccucucccc	1260
agccuccuccu ccccuuccug caccgguacc cccguggucu uugaauaaag ucugaguggg	1320
cggc	1324

<210> 159
 <211> 1657
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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gcggaaacaa cucccaauau ccaucugcuu cuggcucuuc uggaacacg cccacccac	180
cgaacgauga ggaacgugaa ucuaaugaag agccaccacc gccuuaugag gaccacauuu	240
ggggcaauagg cgaccgucac ucggacuau aaccacuagg aaccaagau caaagucugu	300
acuugggauu gcaacacgac gggaugacg ggcuccucc accuccuac ucuccacggg	360
augacucauc ucaacacaua uacgaagaag cgggcagagg aaguaugaau ccaguaugcc	420
ugccuguaau uguugcgccc uaccucuuuu ggcuggcggc uauugccgcc ucguguuua	480
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gugaggagcg cccaccgacc ccuaucgca acacuguaug auaauaggcu ggagccucgg	1560
uggccaugcu ucuugcccu ugggccuccc cccagcccu ccucccuuc cugcaccgcu	1620
acccccgugg ucuuugaaua aagucugagu gggcggc	1657

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<211> 892

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 160

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acggcgagcc cgacgugccu ccaggcgcca ucgaacaggg ccccgugac gauccuggcg	180
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M137870089W000-SEQ-HJD.txt

ccgccc <u>u</u> gc caucccucag ugcagacuca cgccc <u>c</u> ugag caggcu <u>cccc</u> uuuggg <u>au</u> gg	480
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gcgacgacgg ugaugaggg <u>u</u> ggagacggag augaaggcga ggagggg <u>c</u> ag gagugaua <u>au</u>	780
aggcu <u>gg</u> agc cucggugg <u>cc</u> augcuuc <u>u</u> g ccccu <u>ggg</u> c cu <u>cccccc</u> ag cccu <u>ccu</u> cc	840
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 <212> RNA
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<220>
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gcagcgagaa ggaggccgag gacgcccacc uggagcccg cccagaagggc accaagagga	240
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M137870089W000-SEQ-HJD.txt

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gauaaauaggc uggagccucg guggccaugc uucuugcccc uugggccucc cccagcccc	2940
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<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 162

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M137870089W000-SEQ-HJD.txt

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ccaugcgaag caagaagcuc cccaaucaacg uuaccaccgg ggaagaacag caagucagcc	420
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gcaauucaac uaauauuacg gcugugguga gggcccaggg cuuggacgug acucugcccu	600
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M137870089W000-SEQ-HJD.txt

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<223> Synthetic Polynucleotide

<400> 163

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acgugaacgu gacauucaau uucgacgugg gaggaaagaa gcaucagcuu gaucuggauu	240
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<220>

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<212> RNA

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M137870089W000-SEQ-HJD.txt

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M137870089W000-SEQ-HJD.txt

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<220>
<223> Synthetic Polynucleotide

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acgugaacgu gacaaucaau uucgacgugg gaggaaagaa gcaucagcuu gaucuggauu 240
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<211> 2761

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 173

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aucacacauu gggcgggacc ucuccuacac cagucguuac aucucagccu aagaacgcua	1860
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<212> RNA

<213> Artificial Sequence

<220>

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<400> 175

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 acuuccugcc ccccagagug agaggcggcg gcagaguggc cgccgccgcc aucaccuggg 180
 ugcccaagcc caacguggag guguggcccg uggaccccc acccccgug aacuucaaca 240
 agaccgccga gcaggaguac ggcgacaagg aggugaagcu gcccacugg accccaccc 300
 ugcacaccuu ccaggugccc cagaacuaca ccaaggccaa cugcaccuac ugcaacacca 360
 gagaguacac cuucagcuac aagggcugcu gcuucuacuu caccaagaag aagcacaccu 420
 ggaacggcug cuuccaggcc ugcgccgagc uguacccug caccuacuuc uacggcccca 480
 ccccgacau ccugcccug gugaccagaa accugaacgc caucgagagc cugugggugg 540
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 accagaucuu cggcagccac ugcaccuacg ugagcaaguu cagcaccgug cccgugagcc 660
 accacgagug cagcuuccug aagcccugcc ugugcgugag ccagagaagc aacagcugau 720
 aauaggcugg agccucggug gccaugcuuc uugcccuug gccuccccc cagccccucc 780
 ucccuuccu gcacccguac ccccgugguc uuugaauaaa gucugagugg gcggc 835

<210> 177
 <211> 2998
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 177
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gcagcgagaa	ggaggccgag	gacgcccacc	uggagcccg	ccagaagggc	accaagagga	240
agaggguuga	ccacgacgu	ggcggaucug	ccccugccag	gcccAugcug	ccaccccagc	300
ccgaccugcc	cggcagggag	gccauccuga	ggagguucc	acuggaccug	aggaccucg	360
ugcaggccau	cggcgccg	gccaccagga	ucgacaccag	ggccaucgac	caguucuucg	420
gcagccagau	cagcaacacc	gagauguaca	ucauguacgc	cauggccauc	agacaagcaa	480
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cccuggccgc	cggcuggccc	augggcuacc	aggccuacag	cagcuggaug	uacagcuaca	600
ccgaccacca	gaccacuccg	accuucgugc	accuccaggc	uaccucgggc	ugcacuggcg	660
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ggaccgaccu	gagcuacauc	aagagcuucg	ugagcgacgc	ccugggcacc	accagcaucc	960
agacuccuug	gaucgacgau	aacccuagca	ccgaaaccgc	ccaggccugg	aacgccgguu	1020
uccugagggg	cagggccuac	ggcaucgacc	ugcuccggac	cgagggcgag	cacguggagg	1080
gcgccaccgg	cgagacuagg	gaggagagcg	aggacacuga	gagcgacggc	gacgacgagg	1140
aucugccgug	caucgugagc	aggggcggcc	ccaaggugaa	gaggccucc	aucuuc	1200
ggaggcuuca	caggcugcug	cugaugaggg	ccggcaagcg	uacugaacag	ggcaaggagg	1260
uacuggagaa	ggccaggggc	agcacauaug	gcaccccuag	accgccugug	cccaagccgc	1320
guccugaagu	cccgcagagu	gaugagacag	cgacuagcca	uggcagugcu	caggugccc	1380
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gcccgggcga gacuagcggu aucaggcggg ccaggagag guggcgcccc gcaccgugga	1800
cucccaaccc accaaggua ccuagucaga ugagcgugcg ugauaggcug gcacggcuuc	1860
gggcagaggc ucagguaaag caggccagug uggaggugca gccaccacag cugacucagg	1920
ugucggcgca gcagcccaug gaggggcccac uggugccgga acagcagaug uucggcgcg	1980
ccccguucag ccagguggcc gacgugguua gggcuccugg cgugccugcu augcagccuc	2040
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agggugaagg uggucagaac gugaccggcc cggaaacccg aaggguugguc guguccgcug	2820
uuguccacau gugucaggau gacgaauucc cagaucugca agauccaccc gacgaggccu	2880
gauaaauaggc uggagccucg guggccaugc uucuuugccc ugggcccucc cccagcccc	2940

uccuccccuu ccugcacccg uacccccgug gucuuugaau aaagucugag ugggcggc 2998

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<211> 892

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 178

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acggcgagcc cgacgugccu ccaggcgcca ucgaacaggg ccccgugac gauccuggcg 180

aggggccuuc cacaggcccu cgcgccagg gagauggcgg aaggcggaag aaggcgggcu 240

gguuuggcaa gcuaaggggc caggcgggcu ccaauccaa guucgagaau aucgccagg 300

ggcuccgggc ucugcuggcc cggucgcacg ucgaacguac cacugacgag gggacuggg 360

uggccggcgu cuuuguguac ggaggaucca agaccuccu guacaaccug agaaggggca 420

ccgcccugc caucccucag ugcagacuca cgccccugag caggcucccc uuugggaug 480

cuccugggcc agggccgcag cccgggcccc ucagggaag caucgugugu uacuuuauug 540

uguuucugca gacacacauc uuugcagaag uucugaaaga ugcaaucaag gaucugguga 600

ugaccaagcc ugcaccuacg ugcaauauca gggugacagu augcuuccu gacgacggug 660

uggaccucc gcccuuguuc ccaccaaug ucgagggugc cgccgccgag ggagacgaug 720

gcgacgacgg ugaugagggg ggagacggag augaaggcga ggaggggcag gagugauaau 780

aggcuggagc cucgguggcc augcuucuug ccccuugggc cccccccag cccuccucc 840

ccuuccugca cccguacccc cguggucuuu gaauaaaguc ugagugggcg gc 892

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<211> 1324

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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uaggccuugc ucuccuucuc cuccucuugg cgcuacuguu uuggcuguac aucguuauga	180
gugacuggac uggaggagcc cuccuugucc ucuauuccuu ugcucucaug cuuauaaaua	240
uaauuuugau caucuuauc uucagaagag accuucucug uccacuugga gcccuuugua	300
uacuccuacu gaugaucacc cuccugcuca ugcucucug gaauuugcac ggacaggcau	360
uguuccuugg aaauugugcug uucaucuucg ggugcuuacu ugucuuaaggu aucuggaucu	420
acuuauugga gaugcucugg cgacuuggug ccaccaucug gcagcuuuug gccuucuucc	480
uagccuucuu ccuagaccuc auccugcuca uuauugcucu cuaucuacaa cagaacuggu	540
ggacucuaau gguugaucuc cuuuggcucc uccuguuucu ggcgauuuua aucuggaugu	600
auuaccaugg acaacgacac agugaugaac accaccacga ugacucccuc ccgcaccuc	660
aacaagcuac cgaugauucu ggccaugaau cugacucuaa cuccaacgag ggcagacacc	720
accugcucgu gaguggagcc ggcgacggac caccacucug cucucagaac cuaggcgcac	780
cuggaggugg uccugacaau ggcccacagg acccugacaa cacggaugau aauggcccac	840
aggaccuga uaacacugau gacaauggcc cacaugaccc gcugccucaa gaccagaca	900
auacugauga caauggccca caggaccug acaacacuga ugacaauggc ccgcacgacc	960
cguuaccuca uagcccuagc gacucugcug gaaauaugg aggccucca caauugacgg	1020
aagagguuga gaacaaagga ggugaccagg gcccgccuuu gaugacagac ggaggcggcg	1080
gucauaguca ugauuccggc cauggcggcg gugauccaca ccuuccuacg cugcuguugg	1140
guucuucugg uuccggugga gaugaugacg acccgcacgg ccagauucag cuaagcuacu	1200
augacugaua auaggcugga gccucggugg ccaugcuucu ugccccuugg gccuccccc	1260
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cggc 1324

<210> 180
 <211> 1657
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 gcggaaaaca cucccaauau ccaucugcuu cuggcucuuc uggaacacg cccacccac 180
 cgaacgauga ggaacgugaa ucuaugaag agccaccacc gccuuaugag gaccacauuu 240
 ggggcaaugg cgaccgucac ucggacuau aaccacuagg aaccaagau caaagucugu 300
 acuugggauu gcaacacgac gggaugacg ggcuccucc accuccuac ucuccacggg 360
 augacucauc ucaacacaua uacgaagaag cgggcagagg aaguagau ccaguaugcc 420
 ugccuguaau uguugcgccc uaccucuuuu ggcuggcggc uauugccgc ucguguuua 480
 cggccucagu uaguaccguu gugaccgcca ccggcuuggc ccucucacuu cuacucuugg 540
 cagcaguggc cagcucauau gccgcugcac aaaggaaacu gcugacaccg gugacagugc 600
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 uuaauucucu ucuguuugca uugcuggccg cagcuggcgg acuacaaggc auuuacguuc 720
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guccacugag caagauccuu cuggcacgac uguuccuaua ugcucucgca cucuuguugc 1140
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 acacgcuuuu gucugccugg auucuuacag caggauuccu gauuuuccuc auuggcuuug 1440
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 gugaggagcg cccaccgacc ccuaucgca acacuguaug auaauaggcu ggagccucgg 1560
 uggccaugcu ucuugcccu ugggccuccc cccagcccu ccucuccuuc cugcaccgcu 1620
 acccccgugg ucuuugaaua aagucugagu gggcggc 1657

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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 gcggaaacaa cuccaauau ccaucugcuu cuggcucuuc uggaacacg cccacccac 180
 cgaacgauga ggaacgugaa ucuaugaag agccaccacc gccuuauagag gacccauauu 240
 ggggcaaugg cgaccgucac ucggacuauc aaccacuagg aaccaagau caaagucugu 300
 acuugggauu gcaacacgac gggaugacg ggcuccucc accuccuac ucuccacggg 360
 augacucauc ucaacacaua uacgaagaag cgggcagagg aaguaugaau ccaguaugcc 420
 ugccuguaau uguugcgccc uaccuuuuu ggcuggcggc uauugccgcc ucguguuua 480
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uccuucucau gcuccuauugg acacuugugg uucuccugau uugcucuucg ugcucuucan	1080
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gcacugaaau uauacccau uuguucugca uguuauuacu gauugucgcu ggcauacucu	1260
ucauucuugc uauccugacc gaauggggca guggaaauag aacauacggc ccagucuuua	1320
ugugccucgg uggccugcuc accaugguag ccggcgcugu guggcugacg gugaugucua	1380
acacgcuuuu gucugccugg auucuuacag caggauuccu gauuuuccuc auuggcuuug	1440
cccucuuggg ggucuuuaga ugcugccgcu acugcugcua cuacugccuu acacuggaaa	1500
gugaggagcg cccaccgacc ccuaucgca acacuguaug auauaaggcu ggagccucgg	1560
uggccaugcu ucuugccccc ugggccuccc cccagccccc ccuccccuuc cugcaccgcu	1620
acccccgugg ucuuugaaua aagucugagu gggcggc	1657

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<211> 2761

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 182

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ucuuuaacgu ggagauucca gaauucccuu ucuauccaac uuguaacgug uguacugccg	180
acguuaacgu uacuauuaac uuugacgugg gcggaaagaa gcaccagcug gaucuugauu	240
ucggccagcu aacaccucau accaaggccg ucuaccaacc acgcggggca uuuggcgguu	300
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guaauucgac aaacauaacu gccguagugc gugcccaggg ucuggaugua acuuugccuc	600
ucucccuucc cacuucugcc caggacucca auuucucagu gaagaccgaa augcuuggga	660
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acaauaaguu uaauauaaca uguuccggcu augaaucaca uguuccaagc ggagguauuc	780
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cagaaucaac uacaaccagu ccgacccuua auaccacagg cuucgcagac ccgaacacaa	1380
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cgcccaacgc uacuucucca acgcuaggaa agacauacc caccucagcu guaaccacgc	1740
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ugcggccuuc caguaacca gagacacugu cuccuaguac cagugacaac agcaccucuc	1980
acaugccauu acugacuucc gcccaccaa ccggcggaga gaacauacu caggugacgc	2040
ccgcaucua uucuaccac cacgugagca cuagcagccc ggcaccaaga ccagggacca	2100
ccucccaggc uagcggcccg ggcaacuccu ccacuagcac gaaaccagga gaggugaacg	2160
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 ccaaggugcc cggccuuagc cccgaggccc uguggcggga ggccaacgug accgaggacc 240
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 cacuggagaa gcagcuguuc uacuacaucg gcaccaugcu gcccacacc cggccccaca 480
 gcuacguguu cuaccagcug cggugccacc ugagcuacgu ugcccugagc aucaacggcg 540
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 ucaccgagaa gggcgacgag cacgugcugu cacugguguu cggcaagacc aaggaccugc 660
 ccgaccugcg gggcccuuc agcuaccua guuugaccag cgcccagagc ggcgacuaca 720
 gcuuggugau cgugaccacc uucgugcacu acgccaacuu ccacaacuac uucgugccca 780
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 ccgaaacacu gaccaccaug uucgagguga gcguggccuu cuucaaggug ggucacgcgg 960
 ugggcgaaac cggcaacggc ugcguggacu uacgcuggcu ggccaagagc uucuucgagc 1020
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 gcuacggccu ggagcggcug gccgccaugc uuauggcaac agugaagaug gaggagcugg 1140
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M137870089W000-SEQ-HJD.txt

aggccggcgu guacagugga cugaucggcg gcgcaaccag cgugcugcua uccgcuuaca	1260
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gccacgucgu gcugcgggag cugaggcuga acguaaccac ccagggcccu aaucuggccc	1380
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gccuggcccu cgguaccgag agcggccucu ucagcccag cuacuuaagc cugcggguucg	1500
accugacccg ggacaaguug cugagcaugg ccccgagga ggccacacug gaccaggcag	1560
cuguauccea cgccguggac ggcuuccugg gcagacuguc ccuggaacgg gaggaccggg	1620
acgccuggca ccugccugcc uacaagugug uggaucggcu ggacaaggug cugaugauca	1680
ucccucugau uaaugucacc uucaucauca gcagcgaccg ggaggugcgg ggauccgccc	1740
ucuacgaggc cagcaccacc uaucugagca gcagccuguu ccugucuccu gugaucauga	1800
acaagugcag ccaggcgcc guggccggcg agccccggca gauccccaag auccagaacu	1860
ucacccggac ccagaagucu ugcaucuucu gcggcuucgc cccuuugucc uacgacgaga	1920
aggagggcuu ggagacuaca accuacauca ccagccagga ggugcagaac agcauccugu	1980
caucuaauua cuucgacuuc gacaaccugc acguucaua ccugcuccuc accaccaacg	2040
guaccgucau ggaaaucgcc ggacuguacg aggagcgggc ccauguugug cuggccauca	2100
uccuguacuu caucgcuuc gcacuuggca ucuuccuggu gcacaagauc gugauguucu	2160
uccugugaua auaggcugga gccucggugg ccaugcuucu ugccccuugg gccucggccc	2220
agccccuccu ccccuuccug caccguacc ccguggucu uugaauaaag ucugaguggg	2280
cggc	2284

<210> 184

<211> 577

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

M137870089W000-SEQ-HJD.txt

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 ccuacccug cugccacgug acccagcuga gagcccagca ccugcuggcc cuggagaaca 180
 ucagcgacau cuaccuggug agcaaccaga ccugcgacgg cuucagccug gccagccuga 240
 acagcccca gaacggcagc aaccagcugg ugaucagcag augcgccaac ggccugaacg 300
 uggugagcuu cuucaucagc auccugaaga gaagcagcag cgccugacc ggccaccuga 360
 gagagcugcu gaccaccug gagaccugu acggcagcuu cagcguggag gaccuguucg 420
 gcgccaaccu gaacagauac gccuggcaca gagggcgugc auaauaggcu ggagccucgg 480
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 acccccgugg ucuuugaaua aagucugagu gggcggc 577

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 <213> Artificial Sequence

<220>
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 acgugaacgu gacaaucau uucgacgugg gaggaaagaa gcaucagcuu gaucuggauu 240
 ucggccaacu gacgccacac accaaagcgg uguaccaacc aaggggugca uuuggaggga 300
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 ccaugcgaag caagaagcuc cccaauaacg uuaccaccgg ggaagaacag caagucagcc 420
 uugaauccgu ggauguguac uuucaggaug uuuucggcac cauguggugu caccacgcug 480
 agaugcagaa ucccguuau cucauaccg agacuguacc cuacaucaag ugggaaauu 540

M137870089W000-SEQ-HJD.txt

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augagaucga uaucgagugc aucauggagg acggugagau aagccagguu cugcccggcg	720
acaacaaguu caauaucacu uguucuggcu acgaguccca ugugccuagu gguggcauac	780
ucacaaguac uucucccgua gccacgcca uucccggaac cggauacgcc uacagucugc	840
gucugacccc acggccugug uccagauucc ugguuaacaa uaguaucuua uacguguuuu	900
auagcggaaa cggcccuaaa gcguccggag gggacuauug uauucagagu aaauucguuu	960
ucucugauga gauuccugcc agucaggaca ugccgacaaa cacaacugau auuaccuacg	1020
ugggcgacaa ugccacguau ucagugccca ugguacagag cgaggacgcc aaucaccaa	1080
auguuacugu aacagcuuuc ugggccuggc caaauaacac ugagacugac uucaaugua	1140
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cuacgggguu gccuagcucg acacaugugc cgacgaaccu gacugcccu gcaucgaccg	1440
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cuaccccuua cgcaaccggc ccgaccgugg gcgagacuuc cccgcaagcc aaugcgacaa	1800
aucacacauu gggcgggacc ucuccuacac cagucguuac aucucagccu aagaacgcua	1860
ccuccgcugu cacuaccgga cagcacaaca ucaccagcuc aagcacgagu uccaugagcu	1920
ugcggccgag cuaaaucc gagacccuau caccauccac aucagacaac aguacuucac	1980

M137870089W000-SEQ-HJD.txt

acaugccacu cuugacgagc gcucacccca ccggcggcga gaacaucacc caggugacuc	2040
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cuucucaggc cagugggccu ggcaacuccu cuacaagcac aaagccaggc gaaguuacg	2160
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cugcggugcc aacugugacc agcaccggug gcaaggccaa cuacaacu ggaggcaagc	2280
auacgacggg gcacggcgcc cggaccucca cugaaccac gaccgauuac ggaggugaca	2340
gcacaacacc gcggccacga uauaauagcca ccacuauuc gccaccaucc acaagcucca	2400
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cagugccacc uacaagccag ccacgcuuc ccaaccuag uaugcucguu cuccaguggg	2520
ccagccuugc uguucugacc cuccuccugc ugcucgugau ggccgauugc gccuuuagga	2580
gaaaccucag cacuagccac acguacacca cgccgccua cgaugacgcc gagacuuacg	2640
ucugauaaua ggcuggagcc ucgguggcca ugcuuucugc cccuugggcc uccccccagc	2700
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 <211> 1195
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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uaauuuuuau cuucagacgg gaccuucucu guccacuugg agcccuugu auacuccuau	180
ugaugaucac ccuccuccuc aucgcucucu ggaauuugca cggacaggca uuguuccuug	240
gaauugugcu guucaucuuc gggugcuuac uugucuuagg uaucuggauc uacuauuugg	300

M137870089W000-SEQ-HJD.txt

agaugcucug gcgacuuggu gccaccaucu ggcagcuuuu ggccuucuuc cuagcguucu	360
uccucgaccu cauucuacuc auuauugcuc ucuaucuaca acagaacugg uggacucuau	420
ugguugaucu ccuuuggcuc cuccuguuuu uggcgauuuu aaucuggaug uauuaccaug	480
gacaacgaca cagugaugaa caccaccacg augacuccu cccgcacccu caacaagcua	540
ccgaugauuc uggccaugaa ucugacucua acuccaacga gggcagacac caccugcucg	600
ugaguggagc cggcgacgga ccaccacucu gcucucagaa ccuaggcgca ccuggaggug	660
guccugacaa uggcccacag gaccugaca acacggauga uaacggucca caagaccag	720
auaacacuga cgacaaugga ccgcaugacc cgcugccuca ggauccugau aacacagacg	780
acaacggccc acaagaucg gacaauaccg acgauaacgg accgcacgac ccguuaccuc	840
auagcccuag cgacucugcu ggaaaugaug gagggccucc acaauugacg gaagagguug	900
agaacaaagg aggugaccag ggcccgccuu ugaugacaga cggaggcggc ggucauaguc	960
augauuccgg ccauggcgga ggagauccac accuuccuac gcugcuguug gguucuucug	1020
guuccggugg agaugaugac gaccgcacg gcccaguuca gcuaagcuac uaugacugau	1080
aaauaggcugg agccucggug gccaugcuuc uugcccuug ggccuccccc cagccccucc	1140
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<210> 187

<211> 2284

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 187

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uccacuugga caucgagggc cacgccagcc acuacaccau cccuuggacc gagcucaugg	180
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M137870089W000-SEQ-HJD.txt

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cccuggccga gcccguggac aucccccgcg uuagcgaagg cagcaugcag guggacgcc	360
gcaaggugca ccccggcgug aucagcggcc ugaacagccc cgccuguaug uugagcgccc	420
cacuggagaa gcagcuguuc uacuacaucg gcaccaugcu gcccacacc cggccccaca	480
gcuacguguu cuaccagcug cggugccacc ugagcuacgu ugcccugagc aucaacggcg	540
acaaguucca guacaccggc gccaugacca gcaaguuccu gaugggcacc uacaagcggg	600
ucaccgagaa gggcgacgag cacgugcugu cacugguguu cggcaagacc aaggaccugc	660
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gcuuggugau cgugaccacc uucgugcacu acgccaacu ccacaacuac uucgugccca	780
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ccgaaacacu gaccaccaug uucgagguga gcguggccuu cuucaaggug ggucacgcgg	960
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cuguauccaa cgccguggac ggcuuccugg gcagacuguc ccuggaacgg gaggaccggg	1620
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M137870089W000-SEQ-HJD.txt

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ucacccggac ccagaagucu ugcaucuucu gcggcuucgc cccuuugucc uacgacgaga	1920
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caucuaauua cuucgacuuc gacaaccugc acguucaua ccugcuccuc accaccaacg	2040
guaccgucau ggaaaucgcc ggacuguacg aggagcgggc ccauguugug cuggccauca	2100
uccuguacuu caucgcuuc gcacuuggca ucuuccuggu gcacaagauc gugauguucu	2160
uccugugaua auaggcugga gccucggugg ccaugcuucu ugcccuugg gccuc(ccccc	2220
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cggc	2284

<210> 188

<211> 577

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 188

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ccuaccccug cugccacgug acccagcuga gagcccagca ccugcuggcc cuggagaaca	180
ucagcgacau cuaccuggug agcaaccaga ccugcgacgg cuucagccug gccagccuga	240
acagcccca gaacggcagc aaccagcugg ugaucagcag augcgccaac ggccugaacg	300
uggugagcuu cuucaucagc auccugaaga gaagcagcag cggccugacc ggccaccuga	360
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gcgccaaccu gaacagauac gccuggcaca gaggcggcug auaauaggcu ggagccucgg	480

uggccaugcu ucuugccccc ugggccuccc cccagccccc ccuccccuuc cugcaccgcu 540

acccccgugg ucuuugaaua aagucugagu gggcggc 577

<210> 189

<211> 835

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 189

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acuuccugcc cccagagug agaggcggcg gcagaguggc cgccgccgcc aucaccuggg 180

ugcccaagcc caacguggag guguggcccg uggaccccc accccccgug aacuucaaca 240

agaccgccga gcaggaguac ggcgacaagg aggugaagcu gccccacugg acccccaccc 300

ugcacaccuu ccaggugccc cagaacuaca ccaaggccaa cugcaccuac ugcaacacca 360

gagaguacac cuucagcuac aagggcugcu gcuucuacuu caccaagaag aagcacaccu 420

ggaacggcug cuuccaggcc ugcgccgagc uguaccccug caccuacuuc uacggcccca 480

cccccgacau ccugcccug gugaccagaa accugaacgc caucgagagc cugugggugg 540

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accagaucuu cggcagccac ugcaccuacg ugagcaaguu cagcaccgug cccgugagcc 660

accacgagug cagcuuccug aagcccugcc ugugcgugag ccagagaagc aacagcugau 720

aauaggcugg agccucggug gccaugcuuc uugcccuug gccuccccc cagccccucc 780

uccccuuccu gcacccguac ccccgugguc uuugaauaaa gucugagugg gcggc 835

<210> 190

<211> 2047

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 190

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cccagggcggu gguggaggca gcacuccucg ucugccagua uacaauccag ucgcucauuc	180
auuugacagg cgaggacccc ggcuucuuua acguggaaaau cccagaguuc ccuucuauc	240
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agaagcauca gcuugaucug gauuucggcc aacugacgcc acacacaaa gcgguguacc	360
aaccaagggg ugcauuugga gggagcgaga augcuacaaa ucuguucuua cuggaacugc	420
uuggugcagg agagcuggca cuaaccaugc gaagcaagaa gcuccccauc aacguuacca	480
ccggggaaga acagcaaguc agccuugaau ccguggaugu guacuucag gauguuuucg	540
gcaccaugug gugucaccac gcugagaugc agaaucccgu guaucucaua cccgagacug	600
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acaauaguau cuuauacgug uuuuauagcg gaaacggccc uaaagcgucc ggaggggacu	1020
auuguauuca gaguaauauc guuuucucug augagaucac ugccagucag gacaugccga	1080
caaacacaac ugauauuacc uacgugggcg acaaugccac guauucagug cccaugguca	1140
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acacugagac ugacuucaaa uguaagugga cuuugaccuc uggaacuccg ucggguugcg	1260
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M137870089W000-SEQ-HJD.txt

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<210> 191
<211> 2263
<212> RNA
<213> Artificial Sequence

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<220>
<223> Synthetic Polynucleotide

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cccagggcgu gguggaggca gcacuccucg ucugccagua uacaauccag ucgcucauuc 180
auuugacagg cgaggacccc ggcuucuuua acguggaaau cccagaguuc ccuuucuauc 240
caaccuguaa cguuugcacg gcagacguga acgugacaau caauuucgac gugggaggaa 300
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ccggggaaga acagcaaguc agccuugaau ccguggaugu guacuuucag gauguuuucg	540
gcaccaugug gugucaccac gcugagaugc agaaucccg uauaucuaua cccgagacug	600
uacccuacau caagugggau aauugcauu caacuaauau uacggcugua gugagggccc	660
agggcuugga cgugacucug cccuuaucuc uaccuacuuc ugccaagac uccaauuucu	720
cugucaagac cgagaugcuc gggaugaga ucgauaucga gugcaucag gaggacggug	780
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cccaugugcc uagugguggc auacucacaa guacuucucc cguagccacg cccauucccg	900
gaaccggaua cgccuacagu cugcgucuga cccacggcc uguguccaga uuccugggua	960
acaauaguau cuuauacgug uuuuauagcg gaaacggccc uaaagcgucc ggaggggacu	1020
auuguauuca gaguaauauc guuuucucug augagauucc agccagucag gacaugccga	1080
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gcucaagcac	gaguuccaug	agcuugcggc	cgagcucaaa	ucccgagaca	cuaucaccau	2040
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M137870089W000-SEQ-HJD.txt

gucugacccc acggccugug uccagauucc uggguaacaa uaguaucuaa uacguguuuu	900
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ucucugauga gauuccugcc agucaggaca ugccgacaaa cacaacugau auuaccuacg	1020
ugggcgacaa ugccacguau ucagugccca uggucacgag cgaggacgcc aaaucaccaa	1080
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aguggacuuu gaccucugga acuccgucgg guugcgagaa uaucagcggg gccuuugcuu	1200
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ccuccgcugu cacuaccgga cagcacaaca ucaccagcuc aagcacgagu uccaugagcu	1920
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M137870089W000-SEQ-HJD.txt

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M137870089W000-SEQ-HJD.txt

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2761

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<223> Synthetic Polynucleotide

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ggcaacuggg ccuaccccug cugccacgug acccagcuga gagcccagca ccugcuggcc      180
cuggagaaca ucagcgacau cuaccuggug agcaaccaga ccugcgacgg cuucagccug      240
gccagccuga acagcccca gaacggcagc aaccagcugg ugaucagcag augcgccaac      300
ggccugaacg uggugagcuu cuucaucagc auccugaaga gaagcagcag cgcccugacc      360
ggccaccuga gagagcugcu gaccaccug gagaccugu acggcagcuu cagcguggag      420
gaccuguucg gcgccaaccu gaacagauac gccuggcaca gaggcggcug auaauaggcu      480
ggagccucgg uggccuagcu ucuugcccu ugggccuccc cccagcccu ccucccuuc      540
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cugcuggccu acuuccugcc acccagagug agaggcggcg gcagaguggc cgccgccgcc      180
aucaccuggg ugccaagcc caacguggag guguggccc uggaccgcc accuccgug      240
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acgccgacc ugcacaccuu ccaggugccc cagaacuaca ccaaggcca cugcaccuac      360
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aagcacaccu ggaacggcug cuuccaggcc ugcgccgagc uguaccccug caccuacuuc 480
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cugugggugg gcguguacag agugggcgag ggcaacugga ccagccugga cggcggcacc 600
uucaaggugu accagaucuu cggcagccac ugcaccuacg ugagcaaguu cagcaccgug 660
cccgugagcc accacgagug cagcuuccug aagcccugcc ugugcgugag ccagagaagc 720
aacagcugau aaauaggcugg agccucggug gccuagcuuc uugcccuug gccuccccc 780
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gcggc 845

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ugcacugcug acgugaacgu gacaaucau uucgacgugg gaggaaagaa gcaucagcuu 240
gaucuggauu ucggccaacu gacgccacac accaaagcgg uguaccaacc aaggggugca 300
uuuggaggga gcgagaauGC uacaaucug uucuuacugg aacugcuugg ugcaggagag 360
cuggcacuaa ccaugcgaag caagaagcuc cccaucaacg uuaccaccgg ggaagaacag 420
caagucagcc uugaauccgu ggauguguac uuucaggaug uuuucggcac cauguggugu 480
caccacgcug agaugcagaa ucccguuau cucauaccg agacuguacc cuacaucaag 540
ugggauauu gcaauucaac uaauuuacg gcugugguga gggcccaggg cuuggacgug 600
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gguggcauac ucacaaguac uucucuccgua gccacgcca uucccggaac cggauacgcc	840
uacagucugc gucugacccc acggccugug uccagauucc ugguuaaca uaguaucua	900
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aaauaucguu ucucugauga gauuccugcc agucaggaca ugccgacaaa cacaacugau	1020
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uccaugagcu ugcggccgag cucaaaucc gagaccuau caccauccac aucagacaac	1980
aguacuucac acaugccacu cuugacgagc gcucaccca ccggcggcga gaacauacc	2040
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ggaggcaagc auacgacggg gcacggcgcc cggaccucca cugaaccac gaccgauuac	2340
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gccuuuagga gaaaccucag cacuagccac acguacacca cgccgccua cgaugacgcc	2640
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gacgugggcg gcaagaagca ccagcuggac cuggacuucg gccagcugac cccgcacacc	360
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gagcugaucg guaaugagaa ucacggccug uaccuggccg accaguacgu gaagggcauc	1920
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aaccuuuua agucccuuag augauauag gcuggagccu cgguggccua gcuucuugcc	1980
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ccagccuggc agugcuuacc cuccugcucu ugcugguuau ggugacugc gccuuccgac	2580
guaacuuauc caccagucac acuuacacua caccuccua uGACGACGCG gagaccuacg	2640
ugugauaaua ggcuggagcc ucgguggcca ugcuuuugc cccuugggcc ucccccagc	2700
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c	2761

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 <213> Artificial Sequence

<220>
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 ucuucaacgu cgaaaucucc gaauucccau ucuaucacac cuguaacguc ugcacagccg 180
 acguuaacgu uacaaucaau uucgacgugg gcgggaagaa acaccagcug gaccucgacu 240
 uugggcagcu gacgccccac acuaaagccg uuuaccagcc caggggugca uucgguggau 300
 cugagaaugc uacaaaccuc uuucugcuug agcugcuugg ugcuggagag cuggcccuga 360
 caaugcgag caagaaguug ccaaucaug ugaccacagg ugaagaacag cagguguccc 420
 uagaauccgu ggauguguac uuccaggacg uuuucggcac aauguggugc caucacgcag 480
 agaugcagaa uccgguguac cuuaucuccg aaacagugcc guacauuaaa ugggauaau 540
 guaacuccac aaacaucacg gcaguggugc gcgcucaggg gcuggacgug acacucccg 600
 uuuccuuacc aacaagugcu caagauucca acuuuucugu gaagaccgag augcugggca 660
 acgagauuga uauugaaugc aucauggagg auggcgagau uagccaggug uugcccggcg 720
 acaauaaaau uaauuuuacc uguuccggcu augagucaca cgugccaagu ggaggcauuc 780
 ucacgagcac cucuccguu gcaacacca uuccugggac aggguacgca uauagucuca 840
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 ucggugauaa ugccacuuac agcgugccua uggugaccuc ugaagacgca aaucaccca 1080
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M137870089W000-SEQ-HJD.txt

aauggacccu aaccagcggc accccaucag ggugcgagaa uaucagcggg gccuucgcca	1200
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uuacacggac agcaacuaac gcuacgacua cgacucacaa agugauauuu agcaaagcgc	1320
ccgaaucgac uacuacgagc ccgaccuaa acaccaccgg uuucgccgau cccaacacaa	1380
cuacuggucu cccaucuucg acccauguuc caacgaauuc gacagcucca gcaaguacgg	1440
ggcccacugu gaguacagcc gacguuacua gccaacucc cgcgguuacg acuaguggcg	1500
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cggcgguuac cacuccgaca ccaaacgcc ccucgcccac gccugcaguu acuacgcca	1680
ccccuaaugc uacgucaccc acucugggaa agaccucacc aaccucugcc gugacuacuc	1740
cuacaccuaa ugccacagga cccacaguug gggaaaccag cccacaggcu aacgcaacua	1800
aucauacgcu uggcgggacc ucuccacgc ccguggucac uucacagccu aagaauGCCa	1860
caagcgcugu gacuacaggc cagcauaaua uaaccagcag uucaaccagu agcauguccc	1920
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acaugccguu gcugaccucc gcgcauccca cgggcgguga gaauaucaca caggugacac	2040
ccgcgucua uagcacacau cacgugagua cguccucgcc cgcaccccgcc ccaggcacia	2100
ccucacaagc aucagguccg gggauuagca gcacaaguac caagccuggc gaagugaauG	2160
uaaccaaggG cagccaccg cagaacgcc caucuccuca agccccaucc ggccagaaga	2220
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auacaacagg gcacggugcc agaacuucua cagagccaac cacggacuac ggaggggaca	2340
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cgguuacc uacuuccag ccuagauuc ccaaucugag caugcuuguc cuacaguggg	2520
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M137870089W000-SEQ-HJD.txt

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c						2761

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<220>
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cggagcagcc	cgcuccucc	gccaccacc	uccagcccac	cgccacccgc	cagcagaccu	180
ccuuccccuu	ccgcgucug	gagcucucc	cccacggcga	ccucuuccgc	uucuccuccg	240
acauccagug	ccccuccuuc	ggcaccgcg	agaaccacac	cgagggccuc	cucauggucu	300
ucaaggacaa	caucauucc	uacuccuuc	agguccgcuc	cuacaccaag	aucgucacca	360
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ucuccgucga	cuccuacgag	acugaccaga	uggacaccau	cuaccagugc	uacaacgccg	480
ucaagaugac	caaggacgg	cucacccgc	ucuacgucga	ccgcgacggc	gucaacauca	540
ccgucaaccu	caagccuaca	ggcggccuc	ccaacggcgu	ccgccgcuac	gccucccaga	600
ccgagcucua	cgcgccccu	ggcuggcuca	ucuggaccua	ccgcaccagg	accacuguca	660
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ccacaggcca	gaccgucgag	augucgccau	ucuaugacgg	caagaacaag	gagacuuucc	780
acgagagagc	ggacucuuuc	cauguccgca	ccaacuacaa	gauugucgac	uacgacaacc	840
gcggcaccaa	uccacagggc	gagcgccgc	ccuuccucga	caagggcacc	uacaccucuc	900

M137870089W000-SEQ-HJD.txt

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cauucgucac aaauacaacc gugggcaucg agcucuccga cgccuucag ugcaucgagg	1080
agcaggucua caagaccaug cacgagaagu acgaggccgu ccaggaccgg uauacaaagg	1140
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ccccuggaaa gucccuaggu acccucaaca acccagcgac aguucagauc caguucgccu	1440
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ucgagcagaa gcgccagaac auggugcuuc gugaacuaac aaagauuaau ccuacuacag	1560
ugauguccuc caucuacggc aaggccgucg ccgccaaagcg ccucggcgac gucaucuccg	1620
ucucccagug cgucccagug aaccaggcua ccgugacccu caggaagucc augagagugc	1680
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cugagguaug ccaggcaacu ucucaauacu acuuccaguc uggaaaugag auccacguau	1860
auaacgacua ccaccacuuc aagacuauug aacucgacgg aaugccacc cuccaaacau	1920
ucaucucacu gaauaccucc cucaucgaga acaucgacuu cgccuccuc gagcuguaua	1980
gcagagacga gcagcgcgcc uccaacgucu ucgaccucga gggcaucuuc cgcgaguaca	2040
acuuccaggc acagaacaua gccggccucc guaaggauu ggacaaugcc guguccaacg	2100
gccgcaacca guucgucgac gguuugggug aacucaugga cucucugggc uccgucggcc	2160
aguccauaac uaacuuaguc ucuacggugg gaggccuauu cagcagccug gugagcggcu	2220
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M137870089W000-SEQ-HJD.txt

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accaggaaca	gaagcgggcc	gcccagcgag	cugccggccc	cuccgucgcc	aguagggcac	2520
uacaagccgc	ccgggaccgc	uucccaggcc	ugagaaggag	gagauaccac	gacccagaga	2580
cagccgcugc	ccuccuuggc	gaagcagaaa	ccgaguucug	auaaauaggcu	ggagccucgg	2640
uggccaugcu	ucuugccccc	ugggccucucc	cccagccccc	ccuccccuuc	cugcacccgu	2700
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ccaguauaca	
auccagucgc	
ucauucaucu	
gacaggcgag	
gacccccggcu	
ucuuuaacgu	180
ggaaauccca	
gaguucccuu	
ucuauccaac	
cuguaacguu	
ugcacugcug	
acgugaacgu	240
gacaaucaau	
uucgacgugg	
gaggaaagaa	
gcaucagcuu	
gaucuggauu	
ucggccaacu	300
gacgccacac	
accaaagcgg	
uguaccaacc	
aaggggugca	
uuuggagggga	
gcgagaaugc	360
ugcgaaucug	
uucuuacugg	
aacugcuugg	
ugcaggagag	
cuggcacuaa	
ccaugcgaag	420
caagaagcuc	
cccaucaacg	
uuaccaccgg	
ggaagaacag	
caagucagcc	
uugaauccgu	480
ggauguguac	
uuucaggau	
uuuucggcac	
cauguggugu	
caccacgcug	
agaugcagaa	540
ucccguguau	
cucauacccg	
agacuguacc	
cuacaucaag	
ugggauaauu	
gcaauucagc	600
gaauauuacg	
gcugugguga	
gggcccagg	
cuuggacgug	
acucugcccu	
uauucuuacc	660
uacuucugcc	
caagacucca	
auuucgcgg	
caagaccgag	
augcucggga	
augagaucga	720
uaucgagugc	
aucauggagg	
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aagccagguu	
cugcccggcg	

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gucugacccc acggccugug uccagauucc ugguuaacaa uaguaucuua uacguguuuu	900
auagcggaaa cggcccuaaa gcguccggag gggacuauug uauucagagu aaauaucguu	960
ucucugauga gauuccugcc agucaggaca ugccgacaaa cacaacugau auuaccuacg	1020
ugggcgacaa ugccacguau ucagugccc uggucacgag cgaggacgcc aaauacacaa	1080
auguugcggu aacagcuuuc ugggccuggc caaauaacac ugagacugac uucaaaugua	1140
aguggacuuu gaccucugga acuccgucgg guugcgagaa uaucagcggg gccuuugcuu	1200
ccaacaggac uuucgacauc acugucucag ggcuggggac agcaccgaag acauuauca	1260
uaacacggac cgccaccaac gccgcgacua caaccacuaa ggugaucuuu uccaaggcac	1320
cugaguccac cacuaccucc ccgacucuua acacuacggg cuucgcugau cccaacacca	1380
cuacgggguu gccuagcucg acacaugugc cgacgaaccu gacugcccu gcaucgaccg	1440
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aucacacauu gggcgggacc ucuccuacac cagucguuac aucucagccu aagaacgcua	1860
ccuccgcugu cacuaccgga cagcacaaca ucaccagcuc aagcacgagu uccaugagcu	1920
ugcggccgag cuaaaucucc gagaccuau caccauccac aucagacaac aguacuucac	1980
acaugccacu cuugacgagc gcucaccca ccggcggcga gaacauacc caggugacuc	2040
cggcgucuau uuccaccac cacgucagca cgucgucucc cgcaccgaga ccagggacga	2100
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ugacaaaggg aacgccuccc cagaacgcaa ccaguccuca ggcgcccagc gggcagaaga	2220
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auacgacggg gcacggcgcc cggaccucca cugaaccac gaccgauuac ggaggugaca	2340
gcacaacacc gcggccacga uauaaugcca ccacuauucu gccaccaucc acaagcucca	2400
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ccagccuugc uguucugacc cuccuccugc ugcucgugau ggccgauugc gccuuuagga	2580
gaaaccucag cacuagccac acguacacca cgccgcccua cgaugacgcc gagacuuacg	2640
ucugauaaua ggcuggagcc ucgguggcca ugcuucuugc cccuugggcc uccccccagc	2700
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c	2761

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cuugaucugg auuucggcca acugacgcca cacaccaaag cgguguacca accaaggggu	240
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cagcaaguca gccuugauc cguggaugug uacuuucagg auguuuucgg caccaugugg	420
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gagaugcucg ggaaugagau cgauaucgag ugcaucaugg aggacgguga gauaagccag	660
guucugcccc gcgacaacaa guucaauauc gcguguucug gcuacgaguc ccaugugccu	720
agugguggca uacucacaag uacuucuccc guagccacgc ccuauuccgg aaccggauac	780
gccuacaguc ugcgucugac cccacggccu guguccagau uccuggguua caauaguauc	840
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aguaauaucg uuuucucuga ugagauuccu gccagucagg acaugccgac aaacacaacu	960
gauauuaccu acgugggcga caaugccacg uauucagugc ccauggucac gagcgaggac	1020
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Lys Thr Ala Glu Gln Glu Tyr Gly Asp Lys Glu Val Lys Leu Pro His
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Trp Thr Pro Thr Leu His Thr Phe Gln Val Pro Gln Asn Tyr Thr Lys
85 90 95

Ala Asn Cys Thr Tyr Cys Asn Thr Arg Glu Tyr Thr Phe Ser Tyr Lys
100 105 110

Gly Cys Cys Phe Tyr Phe Thr Lys Lys Lys His Thr Trp Asn Gly Cys
115 120 125

Phe Gln Ala Cys Ala Glu Leu Tyr Pro Cys Thr Tyr Phe Tyr Gly Pro
130 135 140

Thr Pro Asp Ile Leu Pro Val Val Thr Arg Asn Leu Asn Ala Ile Glu
145 150 155 160

Ser Leu Trp Val Gly Val Tyr Arg Val Gly Glu Gly Asn Trp Thr Ser
165 170 175

Leu Asp Gly Gly Thr Phe Lys Val Tyr Gln Ile Phe Gly Ser His Cys
180 185 190

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

Ser Phe Leu Lys Pro Cys Leu Cys Val Ser Gln Arg Ser Asn Ser Gly
210 215 220

Thr Ser Gly Ser Ser Gly Ser Gly Ser Gly Gly Ser Gly Gly Ser Gly
225 230 235 240

Gly Thr Ser Gly Ser Ser Gly Ser Gly Ser Gly Gly Ser Pro Cys Cys
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His Val Thr Gln Leu Arg Ala Gln His Leu Leu Ala Leu Glu Asn Ile
260 265 270

Ser Asp Ile Tyr Leu Val Ser Asn Gln Thr Cys Asp Gly Phe Ser Leu
275 280 285

Ala Ser Leu Asn Ser Pro Lys Asn Gly Ser Asn Gln Leu Val Ile Ser
290 295 300

Arg Cys Ala Asn Gly Leu Asn Val Val Ser Phe Phe Ile Ser Ile Leu
305 310 315 320

Lys Arg Ser Ser Ser Ala Leu Thr Gly His Leu Arg Glu Leu Leu Thr
325 330 335

Thr Leu Glu Thr Leu Tyr Gly Ser Phe Ser Val Glu Asp Leu Phe Gly
340 345 350

Ala Asn Leu Asn Arg Tyr Ala Trp His Arg Gly Gly Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Leu Ser Glu Val Lys Leu His Leu Asp Ile Glu Gly His Ala Ser His
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Tyr Thr Ile Pro Trp Thr Glu Leu Met Ala Lys Val Pro Gly Leu Ser
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Met Leu Asn Arg Tyr Lys Leu Ile Tyr Lys Thr Ser Gly Thr Leu Gly
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Ile Ala Leu Ala Glu Pro Val Asp Ile Pro Ala Val Ser Glu Gly Ser
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Met Gln Val Asp Ala Ser Lys Val His Pro Gly Val Ile Ser Gly Leu
 465 470 475 480

Asn Ser Pro Ala Cys Met Leu Ser Ala Pro Leu Glu Lys Gln Leu Phe
 485 490 495

Tyr Tyr Ile Gly Thr Met Leu Pro Asn Thr Arg Pro His Ser Tyr Val
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Phe Tyr Gln Leu Arg Cys His Leu Ser Tyr Val Ala Leu Ser Ile Asn
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Gly Asp Lys Phe Gln Tyr Thr Gly Ala Met Thr Ser Lys Phe Leu Met
 530 535 540

Gly Thr Tyr Lys Arg Val Thr Glu Lys Gly Asp Glu His Val Leu Ser
 545 550 555 560

Leu Val Phe Gly Lys Thr Lys Asp Leu Pro Asp Leu Arg Gly Pro Phe
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Ser Tyr Pro Ser Leu Thr Ser Ala Gln Ser Gly Asp Tyr Ser Leu Val
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Ile Val Thr Thr Phe Val His Tyr Ala Asn Phe His Asn Tyr Phe Val
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Pro Asn Leu Lys Asp Met Phe Ser Arg Ala Val Thr Met Thr Ala Ala
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660 665 670

Thr Gly Asn Gly Cys Val Asp Leu Arg Trp Leu Ala Lys Ser Phe Phe
675 680 685

Glu Leu Thr Val Leu Lys Asp Ile Ile Gly Ile Cys Tyr Gly Ala Thr
690 695 700

Val Lys Gly Met Gln Ser Tyr Gly Leu Glu Arg Leu Ala Ala Met Leu
705 710 715 720

Met Ala Thr Val Lys Met Glu Glu Leu Gly His Leu Thr Thr Glu Lys
725 730 735

Gln Glu Tyr Ala Leu Arg Leu Ala Thr Val Gly Tyr Pro Lys Ala Gly
740 745 750

Val Tyr Ser Gly Leu Ile Gly Gly Ala Thr Ser Val Leu Leu Ser Ala
755 760 765

Tyr Asn Arg His Pro Leu Phe Gln Pro Leu His Thr Val Met Arg Glu
770 775 780

Thr Leu Phe Ile Gly Ser His Val Val Leu Arg Glu Leu Arg Leu Asn
785 790 795 800

Val Thr Thr Gln Gly Pro Asn Leu Ala Leu Tyr Gln Leu Leu Ser Thr
805 810 815

Ala Leu Cys Ser Ala Leu Glu Ile Gly Glu Val Leu Arg Gly Leu Ala
 820 825 830

Leu Gly Thr Glu Ser Gly Leu Phe Ser Pro Cys Tyr Leu Ser Leu Arg
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Phe Asp Leu Thr Arg Asp Lys Leu Leu Ser Met Ala Pro Gln Glu Ala
 850 855 860

Thr Leu Asp Gln Ala Ala Val Ser Asn Ala Val Asp Gly Phe Leu Gly
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Arg Leu Ser Leu Glu Arg Glu Asp Arg Asp Ala Trp His Leu Pro Ala
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Tyr Lys Cys Val Asp Arg Leu Asp Lys Val Leu Met Ile Ile Pro Leu
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Ile Asn Val Thr Phe Ile Ile Ser Ser Asp Arg Glu Val Arg Gly Ser
 915 920 925

Ala Leu Tyr Glu Ala Ser Thr Thr Tyr Leu Ser Ser Ser Leu Phe Leu
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Ser Pro Val Ile Met Asn Lys Cys Ser Gln Gly Ala Val Ala Gly Glu
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Pro Arg Gln Ile Pro Lys Ile Gln Asn Phe Thr Arg Thr Gln Lys Ser
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Cys Ile Phe Cys Gly Phe Ala Leu Leu Ser Tyr Asp Glu Lys Glu Gly
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Leu Ser Ser Asn Tyr Phe Asp Phe Asp Asn Leu His Val His Tyr
 1010 1015 1020

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 1025 1030 1035

Tyr Glu Glu Arg Ala His Val Val Leu Ala Ile Ile Leu Tyr Phe
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gccaacuucc acaacuacuu cgugcccaac cugaaggaca uguucagccg ggccgugacc	1860
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ggcggcugcc gggagcccga gcuggacacc gaaacacuga ccaccauguu cgaggugagc	1980
guggccuucu ucaagguggg ucacgcggug ggcgaaaccg gcaacggcug cguggacuua	2040
cgcuggcugg ccaagagcuu cuucgagcug accgugcuga aggauaucu cggaucugc	2100
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gcccuugaga ucggcgaggu gcucagaggc cuggcccucg guaccgagag cggccucuuc	2520
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M137870089W000-SEQ-HJD.txt

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 gaucggcugg acaaggugcu gaugaucauc ccucugauua augucaccuu caucaucagc 2760
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 agccaggagg ugcagaacag cauccugua ucuaauuacu ucgacuucga caaccugcac 3060
 guucauuacc ugcuccucac caccaacggu accgucaugg aaaucgccgg acuguacgag 3120
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 <213> Artificial Sequence

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 <223> Synthetic Polypeptide

<400> 217

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Leu Val Ile Val Leu Leu Leu Ala Tyr Phe Leu Pro Pro Arg Val Arg
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Gly Gly Gly Arg Val Ala Ala Ala Ala Ile Thr Trp Val Pro Lys Pro
 35 40 45

Asn Val Glu Val Trp Pro Val Asp Pro Pro Pro Val Asn Phe Asn
 50 55 60

M137870089W000-SEQ-HJD.txt

Lys Thr Ala Glu Gln Glu Tyr Gly Asp Lys Glu Val Lys Leu Pro His
65 70 75 80

Trp Thr Pro Thr Leu His Thr Phe Gln Val Pro Gln Asn Tyr Thr Lys
85 90 95

Ala Asn Cys Thr Tyr Cys Asn Thr Arg Glu Tyr Thr Phe Ser Tyr Lys
100 105 110

Gly Cys Cys Phe Tyr Phe Thr Lys Lys Lys His Thr Trp Asn Gly Cys
115 120 125

Phe Gln Ala Cys Ala Glu Leu Tyr Pro Cys Thr Tyr Phe Tyr Gly Pro
130 135 140

Thr Pro Asp Ile Leu Pro Val Val Thr Arg Asn Leu Asn Ala Ile Glu
145 150 155 160

Ser Leu Trp Val Gly Val Tyr Arg Val Gly Glu Gly Asn Trp Thr Ser
165 170 175

Leu Asp Gly Gly Thr Phe Lys Val Tyr Gln Ile Phe Gly Ser His Cys
180 185 190

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

Ser Phe Leu Lys Pro Cys Leu Cys Val Ser Gln Arg Ser Asn Ser Gly
210 215 220

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Pro Cys Cys
245 250 255

His Val Thr Gln Leu Arg Ala Gln His Leu Leu Ala Leu Glu Asn Ile
 260 265 270

Ser Asp Ile Tyr Leu Val Ser Asn Gln Thr Cys Asp Gly Phe Ser Leu
 275 280 285

Ala Ser Leu Asn Ser Pro Lys Asn Gly Ser Asn Gln Leu Val Ile Ser
 290 295 300

Arg Cys Ala Asn Gly Leu Asn Val Val Ser Phe Phe Ile Ser Ile Leu
 305 310 315 320

Lys Arg Ser Ser Ser Ala Leu Thr Gly His Leu Arg Glu Leu Leu Thr
 325 330 335

Thr Leu Glu Thr Leu Tyr Gly Ser Phe Ser Val Glu Asp Leu Phe Gly
 340 345 350

Ala Asn Leu Asn Arg Tyr Ala Trp His Arg Gly Gly Gly Gly Gly Gly
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Leu Ser Glu Val Lys Leu His Leu Asp Ile Glu Gly His Ala Ser His
 385 390 395 400

Tyr Thr Ile Pro Trp Thr Glu Leu Met Ala Lys Val Pro Gly Leu Ser
 405 410 415

Pro Glu Ala Leu Trp Arg Glu Ala Asn Val Thr Glu Asp Leu Ala Ser
 420 425 430

Met Leu Asn Arg Tyr Lys Leu Ile Tyr Lys Thr Ser Gly Thr Leu Gly
 435 440 445

M137870089W000-SEQ-HJD.txt

Ile Ala Leu Ala Glu Pro Val Asp Ile Pro Ala Val Ser Glu Gly Ser
450 455 460

Met Gln Val Asp Ala Ser Lys Val His Pro Gly Val Ile Ser Gly Leu
465 470 475 480

Asn Ser Pro Ala Cys Met Leu Ser Ala Pro Leu Glu Lys Gln Leu Phe
485 490 495

Tyr Tyr Ile Gly Thr Met Leu Pro Asn Thr Arg Pro His Ser Tyr Val
500 505 510

Phe Tyr Gln Leu Arg Cys His Leu Ser Tyr Val Ala Leu Ser Ile Asn
515 520 525

Gly Asp Lys Phe Gln Tyr Thr Gly Ala Met Thr Ser Lys Phe Leu Met
530 535 540

Gly Thr Tyr Lys Arg Val Thr Glu Lys Gly Asp Glu His Val Leu Ser
545 550 555 560

Leu Val Phe Gly Lys Thr Lys Asp Leu Pro Asp Leu Arg Gly Pro Phe
565 570 575

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

Ile Val Thr Thr Phe Val His Tyr Ala Asn Phe His Asn Tyr Phe Val
595 600 605

Pro Asn Leu Lys Asp Met Phe Ser Arg Ala Val Thr Met Thr Ala Ala
610 615 620

Ser Tyr Ala Arg Tyr Val Leu Gln Lys Leu Val Leu Leu Glu Met Lys
625 630 635 640

Gly Gly Cys Arg Glu Pro Glu Leu Asp Thr Glu Thr Leu Thr Thr Met
645 650 655

Phe Glu Val Ser Val Ala Phe Phe Lys Val Gly His Ala Val Gly Glu
660 665 670

Thr Gly Asn Gly Cys Val Asp Leu Arg Trp Leu Ala Lys Ser Phe Phe
675 680 685

Glu Leu Thr Val Leu Lys Asp Ile Ile Gly Ile Cys Tyr Gly Ala Thr
690 695 700

Val Lys Gly Met Gln Ser Tyr Gly Leu Glu Arg Leu Ala Ala Met Leu
705 710 715 720

Met Ala Thr Val Lys Met Glu Glu Leu Gly His Leu Thr Thr Glu Lys
725 730 735

Gln Glu Tyr Ala Leu Arg Leu Ala Thr Val Gly Tyr Pro Lys Ala Gly
740 745 750

Val Tyr Ser Gly Leu Ile Gly Gly Ala Thr Ser Val Leu Leu Ser Ala
755 760 765

Tyr Asn Arg His Pro Leu Phe Gln Pro Leu His Thr Val Met Arg Glu
770 775 780

Thr Leu Phe Ile Gly Ser His Val Val Leu Arg Glu Leu Arg Leu Asn
785 790 795 800

Val Thr Thr Gln Gly Pro Asn Leu Ala Leu Tyr Gln Leu Leu Ser Thr
805 810 815

Ala Leu Cys Ser Ala Leu Glu Ile Gly Glu Val Leu Arg Gly Leu Ala
820 825 830

Leu Gly Thr Glu Ser Gly Leu Phe Ser Pro Cys Tyr Leu Ser Leu Arg
835 840 845

Phe Asp Leu Thr Arg Asp Lys Leu Leu Ser Met Ala Pro Gln Glu Ala
850 855 860

Thr Leu Asp Gln Ala Ala Val Ser Asn Ala Val Asp Gly Phe Leu Gly
865 870 875 880

Arg Leu Ser Leu Glu Arg Glu Asp Arg Asp Ala Trp His Leu Pro Ala
885 890 895

Tyr Lys Cys Val Asp Arg Leu Asp Lys Val Leu Met Ile Ile Pro Leu
900 905 910

Ile Asn Val Thr Phe Ile Ile Ser Ser Asp Arg Glu Val Arg Gly Ser
915 920 925

Ala Leu Tyr Glu Ala Ser Thr Thr Tyr Leu Ser Ser Ser Leu Phe Leu
930 935 940

Ser Pro Val Ile Met Asn Lys Cys Ser Gln Gly Ala Val Ala Gly Glu
945 950 955 960

Pro Arg Gln Ile Pro Lys Ile Gln Asn Phe Thr Arg Thr Gln Lys Ser
965 970 975

Cys Ile Phe Cys Gly Phe Ala Leu Leu Ser Tyr Asp Glu Lys Glu Gly
980 985 990

Leu Glu Thr Thr Thr Tyr Ile Thr Ser Gln Glu Val Gln Asn Ser Ile
995 1000 1005

Leu Ser Ser Asn Tyr Phe Asp Phe Asp Asn Leu His Val His Tyr
1010 1015 1020

Leu Leu Leu Thr Thr Asn Gly Thr Val Met Glu Ile Ala Gly Leu
 1025 1030 1035

Tyr Glu Glu Arg Ala His Val Val Leu Ala Ile Ile Leu Tyr Phe
 1040 1045 1050

Ile Ala Phe Ala Leu Gly Ile Phe Leu Val His Lys Ile Val Met
 1055 1060 1065

Phe Phe Leu
 1070

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 <213> Artificial Sequence

<220>
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 ggcaacuggg ccuaccccug cugccacgug acccagcuga gagcccagca ccugcuggcc 180
 cuggagaaca ucagcgacau cuaccuggug agcaaccaga ccugcgacgg cuucagccug 240
 gccagccuga acagcccca gaacggcagc aaccagcugg ugaucagcag augcgccaac 300
 ggccugaacg uggugagcuu cuucaucagc auccugaaga gaagcagcag cgcccugacc 360
 ggccaccuga gagagcugcu gaccaccug gagaccugu acggcagcuu cagcguggag 420
 gaccuguucg gcgccaaccu gaacagauac gccuggcaca gaggcggcgg aggagguggc 480
 agcggaggag gagggucugg agguggcggc agccuuagcg aggugaagcu ccacuuggac 540
 aucgagggcc acgccagcca cuacaccauc ccuggaccg agcucauggc caaggugccc 600
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cccggcguga ucagcggccu gaacagcccc gccuguaugu ugagcgcccc acuggagaag	840
cagcuguucu acuacaucgg caccaugcug cccaacaccc ggccccacag cuacguguuc	900
uaccagcugc ggugccaccu gagcuacguu gcccugagca ucaacggcga caaguuccag	960
uacaccggcg ccaugaccag caaguuccug augggcaccu acaagcgggu caccgagaag	1020
ggcgacgagc acgugcuguc acugguguuc ggcaagacca aggaccugcc cgaccugcgg	1080
ggcccccua gcuacccuag uuugaccagc gccagagcg gcgacuacag cuuggugauc	1140
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uacaguggac ugaucggcgg cgcaaccagc gugcugcuau ccgcuuacaa ccggcacccg	1680
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cugcgggagc ugaggcugaa cguaaccacc cagggcccuu aucuggcccu guaucagcuc	1800
cucaguaccg cccugugcag cgcccuugag aucggcgagg ugcucagagg ccuggcccuc	1860
gguaccgaga gcggccucuu cagccccaugc uacuuaagcc ugcgguucga ccugacccgg	1920
gacaaguugc ugagcauggc cccgcaggag gccacacugg accaggcagc uguauccaac	1980
gccguggacg gcuuccuggg cagacugucc cuggaacggg aggaccggga cgccuggcac	2040
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M137870089W000-SEQ-HJD.txt

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cagggcgccg uggccggcga gccccggcag auccccaaga uccagaacuu cacccgacc	2280
cagaagucuu gcaucuucug cggcuucgcc cuuuuguccu acgacgagaa ggaggguug	2340
gagacuacaa ccuacaucac cagccaggag gugcagaaca gcauccuguc aucuaauuac	2400
uucgacuucg acaaccugca cguucauuac cugcuccuca ccaccaacgg uaccgucaug	2460
gaaaucgccg gacuguacga ggagcgggcc cauguugugc uggccaucan ccuguacuuc	2520
aucgcuuucg cacuuggcau cuuccuggug cacaagaucg ugauguucuu ccugugauaa	2580
uaggcuggag ccucgguggc cuagcuucuu gcccuuggg ccucgggga gcccuuccuc	2640
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<223> Synthetic Polynucleotide

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gcccuggaga acaucagcga caucuaccug gugagcaacc agaccugcga cggcuucagc	180
cuggccagcc ugaacagccc caagaacggc agcaaccagc uggugaucag cagaugcgcc	240
aacggccuga acguggugag cuucucauc agcauccuga agagaagcag cagcgcccug	300
accggccacc ugagagagcu gcugaccacc cuggagaccc uguacggcag cuucagcgug	360
gaggaccugu ucggcgccaa ccugaacaga uacgccuggc acagaggcgg cggaggaggu	420
ggcagcggag gaggaggguc uggagguggc ggcagccua gcgaggugaa gcuccacuug	480
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M137870089W000-SEQ-HJD.txt

cccgcccuua gccccgaggc ccuguggcgg gaggccaacg ugaccgagga ccuggccagc	600
augcugaacc gguacaagcu gaucuacaag accagcggca cccuggggcau cgcccuggcc	660
gagcccuggg acauccccgc cguuagcgaa ggcagcaugc agguggacgc cagcaaggug	720
caccccggcg ugauacgagg ccugaacagc cccgccugua uguugagcgc cccacuggag	780
aagcagcugu ucuacuacau cggcaccaug cugcccaaca cccggcccca cagcuacgug	840
uucuaccagc ugcggugcca ccugagcuac guugcccuga gcaucaacgg cgacaaguuc	900
caguacaccg gcgccaugac cagcaaguuc cugaugggca ccuacaagcg ggucaccgag	960
aagggcgacg agcacgugcu gucacuggug uucggcaaga ccaaggaccu gcccgaccug	1020
cggggccccc ucagcuaccc uaguuugacc agcgcccaga gcggcgacua cagcuuggug	1080
aucgugacca ccuucgugca cuacgccaac uuccacaacu acuucgugcc caaccugaag	1140
gacauguuca gccgggcccgu gaccaugacu gccgcuucuu acgcccggua cgugcugcag	1200
aagcuggucc ugcuggagau gaagggcggc ugccgggagc ccgagcugga caccgaaaca	1260
cugaccacca uguucgaggu gagcguggcc uucucaagg ugggucacgc ggugggcgaa	1320
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acaacagaga agcaggagua cgcccugaga cuggccacag ugggcuaccc aaaggccggc	1560
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cucgguaccg agagcggccu cuucagccca ugcuaauaa gccugcgguu cgaccugacc	1860
cgggacaagu ugcugagcau ggccccgcag gaggccacac uggaccaggc agcuguauc	1920
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M137870089W000-SEQ-HJD.txt

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 gccagcacca ccuauugag cagcagccug uuccugucuc cugugaucu gaacaagugc 2160
 agccagggcg ccguggccgg cgagccccgg cagaucacca agauccagaa cuucacccgg 2220
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 uuggagacua caaccuacau caccagccag gaggugcaga acagcauccu gucaucuaau 2340
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 uucaucgcuu ucgcacuugg caucuuccug gugcacaaga ugcugauguu cuuccug 2517

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 20 25 30

Gln Leu Arg Ala Gln His Leu Leu Ala Leu Glu Asn Ile Ser Asp Ile
 35 40 45

Tyr Leu Val Ser Asn Gln Thr Cys Asp Gly Phe Ser Leu Ala Ser Leu
 50 55 60

Asn Ser Pro Lys Asn Gly Ser Asn Gln Leu Val Ile Ser Arg Cys Ala
 65 70 75 80

M137870089W000-SEQ-HJD.txt

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

Thr Leu Tyr Gly Ser Phe Ser Val Glu Asp Leu Phe Gly Ala Asn Leu
115 120 125

Asn Arg Tyr Ala Trp His Arg Gly Gly Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Leu Ser Glu Val Lys Leu His Leu
145 150 155 160

Asp Ile Glu Gly His Ala Ser His Tyr Thr Ile Pro Trp Thr Glu Leu
165 170 175

Met Ala Lys Val Pro Gly Leu Ser Pro Glu Ala Leu Trp Arg Glu Ala
180 185 190

Asn Val Thr Glu Asp Leu Ala Ser Met Leu Asn Arg Tyr Lys Leu Ile
195 200 205

Tyr Lys Thr Ser Gly Thr Leu Gly Ile Ala Leu Ala Glu Pro Val Asp
210 215 220

Ile Pro Ala Val Ser Glu Gly Ser Met Gln Val Asp Ala Ser Lys Val
225 230 235 240

His Pro Gly Val Ile Ser Gly Leu Asn Ser Pro Ala Cys Met Leu Ser
245 250 255

Ala Pro Leu Glu Lys Gln Leu Phe Tyr Tyr Ile Gly Thr Met Leu Pro
260 265 270

M137870089W000-SEQ-HJD.txt

Asn Thr Arg Pro His Ser Tyr Val Phe Tyr Gln Leu Arg Cys His Leu
 275 280 285

Ser Tyr Val Ala Leu Ser Ile Asn Gly Asp Lys Phe Gln Tyr Thr Gly
 290 295 300

Ala Met Thr Ser Lys Phe Leu Met Gly Thr Tyr Lys Arg Val Thr Glu
 305 310 315 320

Lys Gly Asp Glu His Val Leu Ser Leu Val Phe Gly Lys Thr Lys Asp
 325 330 335

Leu Pro Asp Leu Arg Gly Pro Phe Ser Tyr Pro Ser Leu Thr Ser Ala
 340 345 350

Gln Ser Gly Asp Tyr Ser Leu Val Ile Val Thr Thr Phe Val His Tyr
 355 360 365

Ala Asn Phe His Asn Tyr Phe Val Pro Asn Leu Lys Asp Met Phe Ser
 370 375 380

Arg Ala Val Thr Met Thr Ala Ala Ser Tyr Ala Arg Tyr Val Leu Gln
 385 390 395 400

Lys Leu Val Leu Leu Glu Met Lys Gly Gly Cys Arg Glu Pro Glu Leu
 405 410 415

Asp Thr Glu Thr Leu Thr Thr Met Phe Glu Val Ser Val Ala Phe Phe
 420 425 430

Lys Val Gly His Ala Val Gly Glu Thr Gly Asn Gly Cys Val Asp Leu
 435 440 445

Arg Trp Leu Ala Lys Ser Phe Phe Glu Leu Thr Val Leu Lys Asp Ile
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M137870089W000-SEQ-HJD.txt

Ile Gly Ile Cys Tyr Gly Ala Thr Val Lys Gly Met Gln Ser Tyr Gly
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Leu Glu Arg Leu Ala Ala Met Leu Met Ala Thr Val Lys Met Glu Glu
485 490 495

Leu Gly His Leu Thr Thr Glu Lys Gln Glu Tyr Ala Leu Arg Leu Ala
500 505 510

Thr Val Gly Tyr Pro Lys Ala Gly Val Tyr Ser Gly Leu Ile Gly Gly
515 520 525

Ala Thr Ser Val Leu Leu Ser Ala Tyr Asn Arg His Pro Leu Phe Gln
530 535 540

Pro Leu His Thr Val Met Arg Glu Thr Leu Phe Ile Gly Ser His Val
545 550 555 560

Val Leu Arg Glu Leu Arg Leu Asn Val Thr Thr Gln Gly Pro Asn Leu
565 570 575

Ala Leu Tyr Gln Leu Leu Ser Thr Ala Leu Cys Ser Ala Leu Glu Ile
580 585 590

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

Ser Pro Cys Tyr Leu Ser Leu Arg Phe Asp Leu Thr Arg Asp Lys Leu
610 615 620

Leu Ser Met Ala Pro Gln Glu Ala Thr Leu Asp Gln Ala Ala Val Ser
625 630 635 640

Asn Ala Val Asp Gly Phe Leu Gly Arg Leu Ser Leu Glu Arg Glu Asp
645 650 655

Arg Asp Ala Trp His Leu Pro Ala Tyr Lys Cys Val Asp Arg Leu Asp
660 665 670

Lys Val Leu Met Ile Ile Pro Leu Ile Asn Val Thr Phe Ile Ile Ser
675 680 685

Ser Asp Arg Glu Val Arg Gly Ser Ala Leu Tyr Glu Ala Ser Thr Thr
690 695 700

Tyr Leu Ser Ser Ser Leu Phe Leu Ser Pro Val Ile Met Asn Lys Cys
705 710 715 720

Ser Gln Gly Ala Val Ala Gly Glu Pro Arg Gln Ile Pro Lys Ile Gln
725 730 735

Asn Phe Thr Arg Thr Gln Lys Ser Cys Ile Phe Cys Gly Phe Ala Leu
740 745 750

Leu Ser Tyr Asp Glu Lys Glu Gly Leu Glu Thr Thr Thr Tyr Ile Thr
755 760 765

Ser Gln Glu Val Gln Asn Ser Ile Leu Ser Ser Asn Tyr Phe Asp Phe
770 775 780

Asp Asn Leu His Val His Tyr Leu Leu Leu Thr Thr Asn Gly Thr Val
785 790 795 800

Met Glu Ile Ala Gly Leu Tyr Glu Glu Arg Ala His Val Val Leu Ala
805 810 815

Ile Ile Leu Tyr Phe Ile Ala Phe Ala Leu Gly Ile Phe Leu Val His
820 825 830

Lys Ile Val Met Phe Phe Leu
835

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 <223> Synthetic Polynucleotide

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 ggcaacuggg ccuaccccug cugccacgug acccagcuga gagcccagca ccugcuggcc 180
 cuggagaaca ucagcgacau cuaccuggug agcaaccaga ccugcgacgg cuucagccug 240
 gccagccuga acagcccaa gaacggcagc aaccagcugg ugaucagcag augcgccaac 300
 ggccugaacg uggugagcuu cuucaucagc auccugaaga gaagcagcag cgcccugacc 360
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Gln Leu Arg Ala Gln His Leu Leu Ala Leu Glu Asn Ile Ser Asp Ile
 35 40 45

Tyr Leu Val Ser Asn Gln Thr Cys Asp Gly Phe Ser Leu Ala Ser Leu
 50 55 60

Asn Ser Pro Lys Asn Gly Ser Asn Gln Leu Val Ile Ser Arg Cys Ala
 65 70 75 80

Asn Gly Leu Asn Val Val Ser Phe Phe Ile Ser Ile Leu Lys Arg Ser
 85 90 95

Ser Ser Ala Leu Thr Gly His Leu Arg Glu Leu Leu Thr Thr Leu Glu
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Thr Leu Tyr Gly Ser Phe Ser Val Glu Asp Leu Phe Gly Ala Asn Leu
 115 120 125

M137870089W000-SEQ-HJD.txt

Asn Arg Tyr Ala Trp His Arg Gly Gly Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Ser Glu
145 150 155 160

Val Lys Leu His Leu Asp Ile Glu Gly His Ala Ser His Tyr Thr Ile
165 170 175

Pro Trp Thr Glu Leu Met Ala Lys Val Pro Gly Leu Ser Pro Glu Ala
180 185 190

Leu Trp Arg Glu Ala Asn Val Thr Glu Asp Leu Ala Ser Met Leu Asn
195 200 205

Arg Tyr Lys Leu Ile Tyr Lys Thr Ser Gly Thr Leu Gly Ile Ala Leu
210 215 220

Ala Glu Pro Val Asp Ile Pro Ala Val Ser Glu Gly Ser Met Gln Val
225 230 235 240

Asp Ala Ser Lys Val His Pro Gly Val Ile Ser Gly Leu Asn Ser Pro
245 250 255

Ala Cys Met Leu Ser Ala Pro Leu Glu Lys Gln Leu Phe Tyr Tyr Ile
260 265 270

Gly Thr Met Leu Pro Asn Thr Arg Pro His Ser Tyr Val Phe Tyr Gln
275 280 285

Leu Arg Cys His Leu Ser Tyr Val Ala Leu Ser Ile Asn Gly Asp Lys
290 295 300

Phe Gln Tyr Thr Gly Ala Met Thr Ser Lys Phe Leu Met Gly Thr Tyr
305 310 315 320

Lys Arg Val Thr Glu Lys Gly Asp Glu His Val Leu Ser Leu Val Phe
325 330 335

Gly Lys Thr Lys Asp Leu Pro Asp Leu Arg Gly Pro Phe Ser Tyr Pro
340 345 350

Ser Leu Thr Ser Ala Gln Ser Gly Asp Tyr Ser Leu Val Ile Val Thr
355 360 365

Thr Phe Val His Tyr Ala Asn Phe His Asn Tyr Phe Val Pro Asn Leu
370 375 380

Lys Asp Met Phe Ser Arg Ala Val Thr Met Thr Ala Ala Ser Tyr Ala
385 390 395 400

Arg Tyr Val Leu Gln Lys Leu Val Leu Leu Glu Met Lys Gly Gly Cys
405 410 415

Arg Glu Pro Glu Leu Asp Thr Glu Thr Leu Thr Thr Met Phe Glu Val
420 425 430

Ser Val Ala Phe Phe Lys Val Gly His Ala Val Gly Glu Thr Gly Asn
435 440 445

Gly Cys Val Asp Leu Arg Trp Leu Ala Lys Ser Phe Phe Glu Leu Thr
450 455 460

Val Leu Lys Asp Ile Ile Gly Ile Cys Tyr Gly Ala Thr Val Lys Gly
465 470 475 480

Met Gln Ser Tyr Gly Leu Glu Arg Leu Ala Ala Met Leu Met Ala Thr
485 490 495

Val Lys Met Glu Glu Leu Gly His Leu Thr Thr Glu Lys Gln Glu Tyr
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Ala Leu Arg Leu Ala Thr Val Gly Tyr Pro Lys Ala Gly Val Tyr Ser
515 520 525

Gly Leu Ile Gly Gly Ala Thr Ser Val Leu Leu Ser Ala Tyr Asn Arg
530 535 540

His Pro Leu Phe Gln Pro Leu His Thr Val Met Arg Glu Thr Leu Phe
545 550 555 560

Ile Gly Ser His Val Val Leu Arg Glu Leu Arg Leu Asn Val Thr Thr
565 570 575

Gln Gly Pro Asn Leu Ala Leu Tyr Gln Leu Leu Ser Thr Ala Leu Cys
580 585 590

Ser Ala Leu Glu Ile Gly Glu Val Leu Arg Gly Leu Ala Leu Gly Thr
595 600 605

Glu Ser Gly Leu Phe Ser Pro Cys Tyr Leu Ser Leu Arg Phe Asp Leu
610 615 620

Thr Arg Asp Lys Leu Leu Ser Met Ala Pro Gln Glu Ala Thr Leu Asp
625 630 635 640

Gln Ala Ala Val Ser Asn Ala Val Asp Gly Phe Leu Gly Arg Leu Ser
645 650 655

Leu Glu Arg Glu Asp Arg Asp Ala Trp His Leu Pro Ala Tyr Lys Cys
660 665 670

Val Asp Arg Leu Asp Lys Val Leu Met Ile Ile Pro Leu Ile Asn Val
675 680 685

Thr Phe Ile Ile Ser Ser Asp Arg Glu Val Arg Gly Ser Ala Leu Tyr
690 695 700

Glu Ala Ser Thr Thr Tyr Leu Ser Ser Ser Leu Phe Leu Ser Pro Val
705 710 715 720

Ile Met Asn Lys Cys Ser Gln Gly Ala Val Ala Gly Glu Pro Arg Gln
725 730 735

Ile Pro Lys Ile Gln Asn Phe Thr Arg Thr Gln Lys Ser Cys Ile Phe
740 745 750

Cys Gly Phe Ala Leu Leu Ser Tyr Asp Glu Lys Glu Gly Leu Glu Thr
755 760 765

Thr Thr Tyr Ile Thr Ser Gln Glu Val Gln Asn Ser Ile Leu Ser Ser
770 775 780

Asn Tyr Phe Asp Phe Asp Asn Leu His Val His Tyr Leu Leu Leu Thr
785 790 795 800

Thr Asn Gly Thr Val Met Glu Ile Ala Gly Leu Tyr Glu Glu Arg Ala
805 810 815

His Val Val Leu Ala Ile Ile Leu Tyr Phe Ile Ala Phe Ala Leu Gly
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Ile Phe Leu Val His Lys Ile Val Met Phe Phe Leu
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<212> RNA

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