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(54) **FUSION PROTEIN COMPRISING *GAUSSIA LUCIFERASE*, TRANSLATION INTERRUPTER SEQUENCE, AND INTERFERON AMINO ACID SEQUENCES**

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(51) **Int. Cl.**

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C07K 14/56	(2006.01)
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(52) **U.S. Cl.**

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(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Polynucleotides encoding fusion proteins comprising interferons and luciferases which have biotherapeutic, diagnostic, and quality control applications in biotechnological, medical, and veterinary fields.

33 Claims, 10 Drawing Sheets

Specification includes a Sequence Listing.

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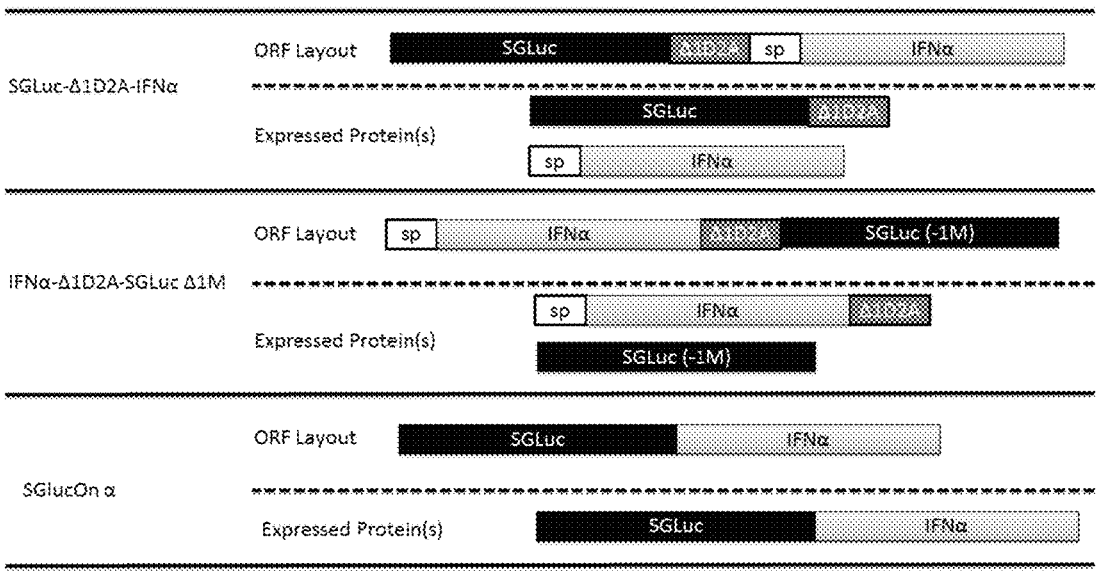
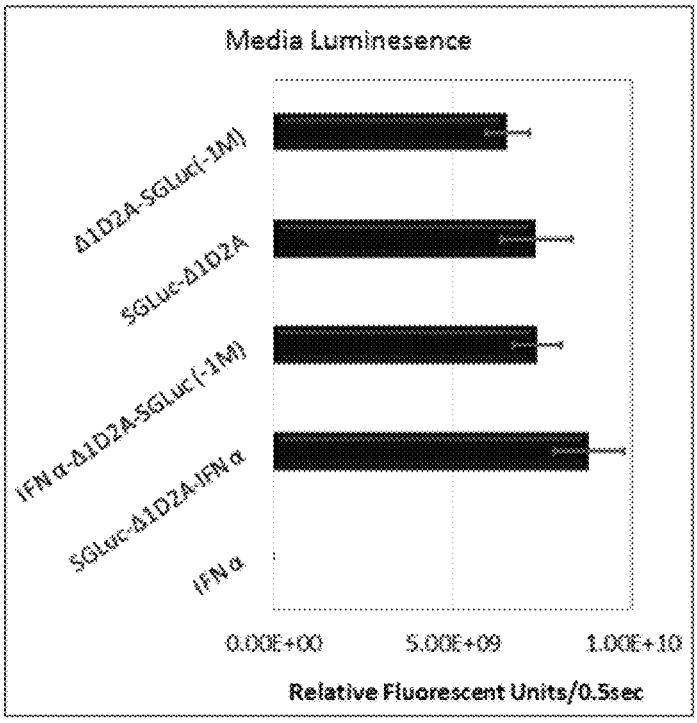
FIG. 1



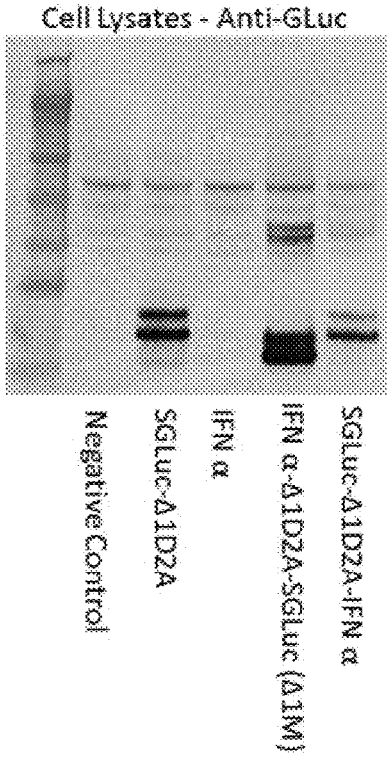
Layout of the three interferon α containing constructs created and evaluated. "sp" = secretion peptide sequence of interferon α.

FIG. 2A



Luciferase readings of constructs separated by the Δ1D2A translational interrupter and corresponding controls.

FIG. 2B



Western blots of media harvested off of cells transfected with constructs separated by the Δ1D2A translational interrupter and corresponding controls.

FIG. 3

Porcine IFN α	MAPTSAFLTALVLLSCNAICSLGCDLPQTHSLAHTRALRLLAQMRRISPFSCLDHRRDFG SPHEAFGGNQVQKAQAMALVHEMLQQTFQLFSTEGSAAAWNESLLHQFCTGLDQQ LRDLEACVMQEAGLEGTPLLEEDSILAVRKYFHRLTLYLQEKSYSPCAWEIVRAEVMRSF SSSRNLQDRLRKKE
Porcine IFN β	MANKCILQIALLMCFSTTALSMSYDVLRYQQRSSNLACQKLLGQLPGTPQYCLEDRMN FEVPEEIMQPPQFQKEDAVLIIHEMLQQIFGILRRNFSSTGWNETVIKTILVELDGQMD DLETILEEIMEEENFPRGDMTILHLKKYYLSILQYLKSKEYRSCAWTVVQVEILRNFSFLN RLTDYLRN
Bovine IFN γ	MKYTSYFLALLLCGLLGFSGSYGQGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWK DESDKKIIQSQIVSFYFKLFENLKDNQVIQRSMDIIKQDMFQKFLNGSSEKLEDFKKLIQI PVDDLQIQRKAINELIKVMNDLSPKSNLRKRKRSQNLFRGRRAST
Bovine IFN λ	MAPGCTLVLVLMLTTVALSRTGAVPVPSAPRALPPARGCHVAQFKSLSPQELQAFKTA RDAFEDSFLPKDWDCSTHLFPRTRDLKHLQVWERPVALEAELALTLTVLEAMANSSLG HSLEQPLLTLQNIHSKLQACVPAQPTASSRPRGRLHHWLHRLQEARKESQDCLEASVM FNLLRLLTRDLKCVASGDQCV

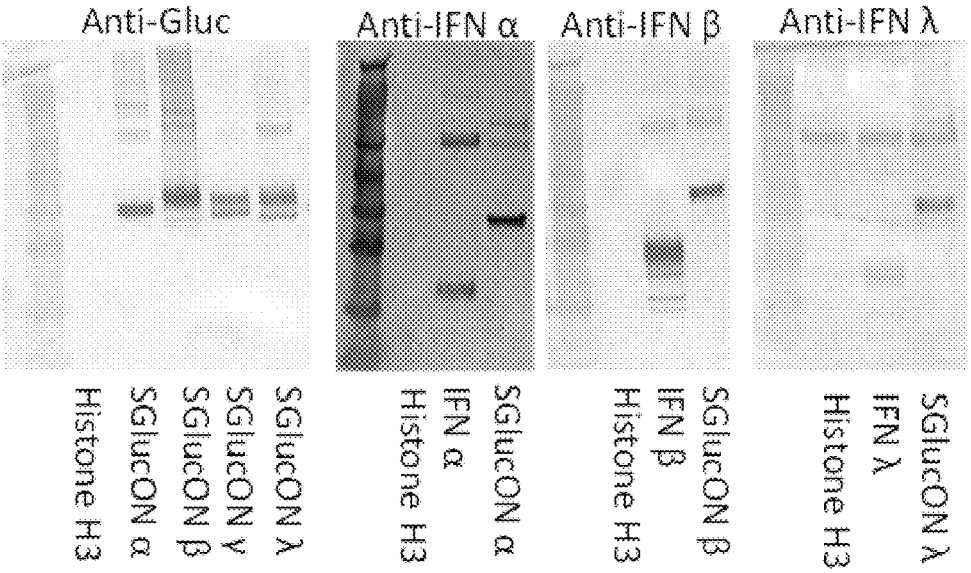
Amino acid sequences for Porcine Interferon α, Porcine Interferon β, Bovine Interferon γ, and Bovine Interferon λ. Underlined letters represent the secretion domains of each interferon sequence.

FIG. 4

SGlucON α	*MGVKVLFALICIAVAEAKPTENNEDFNIVAVASNFATTDLDADRGKLPGKKLPLEVLKEMEAN* *ARKAGCTRGCLICLSHIKCTPKMKKWLPGRCHTYEGDKESAQGGIGEAIVDIPEIPGFKDLEP* *MEQFIAQVDLCVDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQGQVDKIKGAGGDGP* GCDLPQTHSLAHTRALRLLAQMRRISPFSCLDHRRDFGSPHEAFGGNQVQKAQAMALVHE MLQQTFQLFSTEGSAAAWNESLLHQFCTGLDQQLRDLEACVMQEAGLEGTPLLEEDSILAV RKYFHRLTLYLQEKSYSPCAWEIVRAEVMRSFSSSRNLQDRLRKKE
SGlucON β	*MGVKVLFALICIAVAEAKPTENNEDFNIVAVASNFATTDLDADRGKLPGKKLPLEVLKEMEAN* *ARKAGCTRGCLICLSHIKCTPKMKKWLPGRCHTYEGDKESAQGGIGEAIVDIPEIPGFKDLEP* *MEQFIAQVDLCVDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQGQVDKIKGAGGDGP* MSYDVLRYQQRSSNLACQKLLGQLPGTPQYCLEDRMNFEVPEEIMQPPQFQKEDAVLIIHE MLQQIFGILRRNFSSTGWNETVIKTILVELDGQMDDLETILEEIMEEENFPRGDMTILHLKKY YLSILQYLKSKEYRSCAWTVVQVEILRNFSFLNRLTDYLRN
SGlucON γ	*MGVKVLFALICIAVAEAKPTENNEDFNIVAVASNFATTDLDADRGKLPGKKLPLEVLKEMEAN* *ARKAGCTRGCLICLSHIKCTPKMKKWLPGRCHTYEGDKESAQGGIGEAIVDIPEIPGFKDLEP* *MEQFIAQVDLCVDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQGQVDKIKGAGGDGP* QGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWKDESDKKIIQSQIVSFYFKLFENLKDNQ VIQRSMDIIKQDMFQKFLNGSSEKLEDFKKLIQIPVDDLQIQRKAINELIKVMNDLSPKSNLRK RKRSQNLFRGRRAST
SGlucON λ	*MGVKVLFALICIAVAEAKPTENNEDFNIVAVASNFATTDLDADRGKLPGKKLPLEVLKEMEAN* *ARKAGCTRGCLICLSHIKCTPKMKKWLPGRCHTYEGDKESAQGGIGEAIVDIPEIPGFKDLEP* *MEQFIAQVDLCVDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQGQVDKIKGAGGDGP* RTGAVPVPSAPRALPPARGCHVAQFKSLSPQELQAFKTARDAFEDSFLPKDWDCSTHLFPRT RDLKHLQVWERPVALEAELALTLTVLEAMANSSLGHSLEQPLLTLQNIHSKLQACVPAQPTAS SRPRGRLHHWLHRLQEARKESQDCLEASVMFNLLRLLTRDLKCVASGDQCV

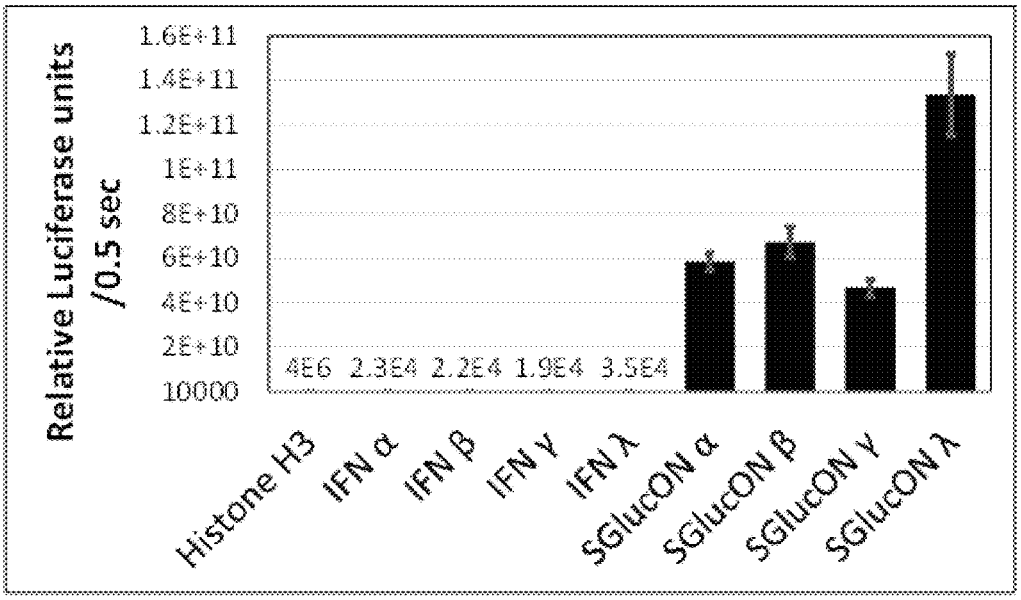
Amino acid sequences for SGLucON α, SGLucON β, SGLucON γ, and SGLucON λ. Italicized white letters with black background represent the *Gaussia* Luciferase amino acids.

FIG. 5A



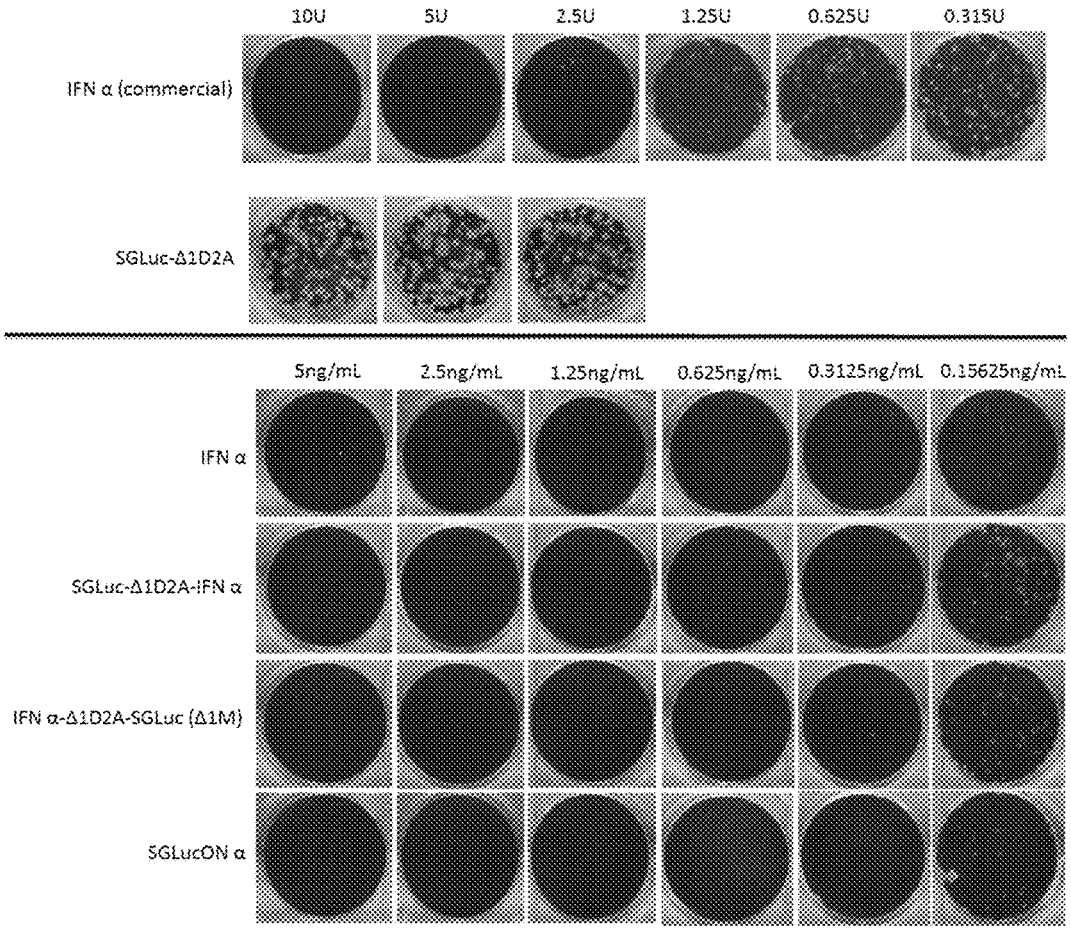
Western blots of media harvested from transfected cells using anti-GLuc, Anti-IFN α, Anti-IFN β, and Anti-IFN λ antibodies.

FIG. 5B



Relative Luciferase Units per half second for IFN and SGLucON α, β, γ, and λ media samples.

FIG. 6



Plaque assay of IFN α, SGLuc-Δ1D2A-IFN α, IFN α-Δ1D2A-SGLuc (Δ1M), and SGLucON α activity against VSV-NJ.

FIG. 7

Sample	Concentration of IFNα ± standard deviation (ng/ml)
IFNα	1239 ± 86
SGLuc-Δ1D2A-IFNα	921 ± 55
IFNα-Δ1D2A-SGLucΔ1M	528 ± 72
Δ1D2A-SGLucΔ1M (IFNα negative control)	<18 (limit of detection at 1:500 dilution)
SGLuc-Δ1D2A (IFNα negative control)	<18 (limit of detection at 1:500 dilution)

Concentration of IFNα in harvested media from cells transfected with pTarget IFNα, pTarget SGLuc-Δ1D2A-IFNα, pTarget IFNα-Δ1D2A-SGLucΔ1M, pTarget Δ1D2A-SGLucΔ1M, and pTarget SGLuc-Δ1D2A. There were 3 replicates per each of 4 dilutions for each sample.

FIG 8.

Sample	Concentration of IFNα in each sample (ng/ml)					
	5	**2.5**	**1.25**	**0.625**	**0.312**	**0.1525**
IFNα	0	0	0	4.5	19	58
SGLuc-Δ1D2A-IFNα	0	0	2	17.5	53.5	116.5
IFNα-Δ1D2A-SGLucΔ1M	0	0	1	11.5	37	91.5
SGLucONα	0	0	0	1.5	9.5	25.5
SGLuc-Δ1D2A (IFNα negative control)	245	230	220.5	ND	ND	ND

Effects of IFNα on growth of Vesicular Stomatitis Virus-NJ (VSV-NJ). IFNα levels produced in growth media harvested from HEK293-T cells transfected with pTarget IFNα, pTarget SGLuc-Δ1D2A-IFNα, pTarget IFNα-Δ1D2A-SGLucΔ1M, mpTarget SGLucONα, or pTarget SGLuc-Δ1D2A (negative control) were measured and adjusted to concentrations listed before samples were exposed to MDBK cells. VSV-NJ was added to the MDBK cells and Plaque Forming Units (PFU) were counted after the growth period; average of 2 replicates are reported. ND, not determined.

FUSION PROTEIN COMPRISING *GAUSSIA LUCIFERASE*, TRANSLATION INTERRUPTER SEQUENCE, AND INTERFERON AMINO ACID SEQUENCES

CROSS-REFERENCE TO RELATED APPLICATIONS

This continuation in part (CIP) application claims priority to U.S. application Ser. No. 15/259,409, filed Sep. 8, 2016, which is incorporated by reference in its entirety.

REFERENCE TO A SEQUENCE LISTING

In accordance with 37 CFR § 1.52(e)(5), the present specification makes reference to a Sequence Listing submitted electronically as a .txt file named "500012us_ST25.txt" on May 1, 2017. The .txt file was generated on Feb. 21, 2017, and is 308 kb in size. The entire contents of the Sequence Listing are herein incorporated by reference.

BACKGROUND OF THE INVENTION

Field of the Invention

The present disclosure generally relates to fusion polynucleotides encoding fusion proteins comprising interferons and luciferases which have biotherapeutic, diagnostic, and quality control uses in both the medical and veterinary fields.

Description of the Related Art

Interferons (IFN) are a class of cytokines that interfere with viral replication. Interferons are divided into three classes, type I, type II, and type III. Type I interferons utilize the IFNAR1-IFNAR2 receptor complex and include IFN α and IFN β. Type II interferons consist of IFN γ and utilize the IFNGR1-IFNGR2 receptor complex. Type III interferons consist of IFN λ, also called interleukin-28A, interleukin-28B, and interleukin-29, the most recently discovered interferon type. Type III interferons utilize the IFNLR1-IL10Rβ receptor complex.

Type I interferons are used to treat a number of medical conditions in humans. Commercially available IFN alpha is used for the treatment of hairy cell leukemia, malignant melanoma, and AIDS-related Kaposi's sarcoma while IFN beta has been used as a treatment for relapsing-remitting and secondary-progressive forms of multiple sclerosis. In a veterinary setting IFN alpha can be used to treat Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, and Canine papilloma virus in companion animals while in livestock both IFN α and IFN β have been found to inhibit Foot-and-Mouth Disease Virus (FMDV). Type III interferon, IFN λ, is also capable of inhibiting FMDV in cattle.

Interferons are naturally secreted, often by specialized cell types, and are comprised of a secretion peptide sequence along with an activity domain. The secretion domain is not essential for protective activity. Protective activity of interferons, and in particular IFN α, is often evaluated using Vesicular Stomatitis Virus (VSV). VSV is a member of the Rhabdoviridea family and is capable of infecting insects, cattle, horses, pigs, and under the right circumstances humans.

Hybrid peptides comprised of interferons and various molecules have been constructed and evaluated for a number of reasons. Previous work has made hybrid molecules comprised of IFN α and portions of placental growth factor-2 to enhance the anti-tumor properties of IFN α. Chimeras of interferons with different reporter molecules such as DsRed2 and GFP as well as with antibodies for immunotherapy have also been previously reported in literature.

Quantification of interferon concentrations is typically dependent upon either an activity assay or antibody based methods such as an ELISA. Measurements obtained by interferon activity assays are related to interferon concentration but not definitively related. For example, addition of placental growth factor-2 can enhance interferon activity resulting in detection of a higher interferon activity. However, this higher interferon activity is not directly related to the absolute concentration of interferon. This raises the potential that undesired and/or unknown contaminations during production can artificially influence determination of a final product concentration.

Antibody-based detection assays, such as ELISA, can be inaccurate because antibodies used to detect interferon can bind to more than one type of interferon or can exhibit different affinities for interferon under different conditions. Antibody binding affinities are dependent upon recognition of structural elements such as linear and conformational epitopes in the target substrate such as interferon. Amino acid sequence differences or conformation differences between or among interferon molecules in a sample can cause antibodies to exhibit different binding affinities. This leads to inaccuracies in determining the absolute concentration of an interferon, or a particular interferon, in a sample. As a result the usage of ELISA to determine the absolute concentrations of molecules with different amino acid sequences is not always a reliable option. Antibody-based detection assays also carry a high cost associated with the need to produce a consistent antibody amongst different production batches. The usage of antibodies also contributes to a limited shelf life.

In view of these problems, the inventors developed novel chimeric proteins that fuse a luciferase reporter with an interferon or enzyme of interest. The resulting chimeric proteins allow for easy and accurate determination of absolute concentrations for interferons and other biologically active molecules.

BRIEF SUMMARY OF THE INVENTION

The inventors disclose herein chimeric proteins fusing a *Gaussia* Luciferase (GLuc) or Super-luminescent *Gaussia* Luciferase (SGLuc) reporter to different kinds of interferons.

GLuc is a 185 amino acid naturally secreted luciferase isolated from *Gaussia princeps*. Mutations to GLuc which enhance luciferase output may include, but are not limited to, the 8990 mutant also identified as SGLuc.

GLuc and SGLuc constructs with 2A or 2A-like protein sequences such as, for example, a Δ1D2A translational interrupter, retained both luciferase activity and secretion, which make them viable biomarkers for expression in a single open reading frame.

Several types of such chimeric fusion proteins are exemplified. In one or more embodiments, three different chimeric molecules were created using IFN α sequence, as exemplified in FIG. **1**. As a first example, SGLuc-Δ1D2A-IFNα is a SGLuc-Δ1D2A fused to a complete IFN α sequence on the C-terminus. This translated construct expresses two separate proteins—SGLuc-Δ1D2A and IFN α. As a second example, IFNα-Δ1D2A-SGLuc Δ1M, is a complete IFN α sequence with a Δ1D2A-SGLuc Δ1M fused on the C-ter-

minus. This translated construct expresses two separate proteins IFNα-A1D2A and SGLuc Δ1M. As a third example, SGLucON α is a SGLuc sequence with just the activity domain of IFN α fused to the C-terminus. This translated construct expresses a single protein SGLucON α which is comprised of both SGLuc and just the activity domain of IFNα.

SGLucON α was used as a template to create three additional chimeric molecules based off of porcine IFN β, bovine IFN γ, and bovine IFN λ. For the creation of these constructs each IFN sequence was examined and the secretion domains identified, FIG. **3**. Chimeric molecules were constructed by making chimeras only of SGLuc with the resulting non-secretion related amino acid sequences, FIG. **4**. The resulting chimeras are identified as SGLucON β, SGLucON γ, and SGLucON λ.

Utilization of chimeric molecules of GLuc or SGLuc with interferons or a protein of interest provides a simple and fast method to substantially quantify an absolute concentration of a particular kind of interferon or protein of interest. When utilizing a construct containing the Δ1D2A translational interrupter the resulting product is two proteins and concentration is determined of the luciferase as a correlate to concentration of interferon or a protein of interest. When utilizing fused protein like SGLucON α, the concentration can be measured directly using the resulting luciferase activities of the chimeric protein.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** depicts the layout of the three interferon α containing construct open reading frames.

FIG. **2**A describes luciferase readings of constructs separated by the Δ1D2A translational interrupter and corresponding controls.

FIG. **2**B depicts Western blots of media harvested off of cells transfected with constructs separated by the Δ1D2A translational interrupter and corresponding controls.

FIG. **3** describes amino acid sequences for Porcine Interferon α (SEQ ID NO: 24), Porcine Interferon β (SEQ ID NO: 66), Bovine Interferon γ (SEQ ID NO: 75), and Bovine Interferon λ, (SEQ ID NO: 84). Underlined residues represent the secretion domains of each interferon sequence.

FIG. **4** describes amino acid sequences for SGLucON α (SEQ ID NO: 48), SGLucON β (SEQ ID NO: 70), SGLucON γ (SEQ ID NO: 111), and SGLucON λ (SEQ ID NO: 113). Underlined residues represent the *Gaussia* Luciferase amino acids.

FIG. **5**A depicts Western blots of media harvested from transfected cells using anti-GLuc, Anti-IFN α, Anti-IFN β, and Anti-IFN λ, antibodies.

FIG. **5**B describes relative Luciferase Units per half second for IFN and SGLucON α, β, γ, and λ, media samples.

FIG. **6** depicts a plaque assay of IFN α, SGLuc-Δ1D2A-IFN α, IFN α-Δ1D2A-SGLuc (Δ1M), and SGLucON α activity against Vesicular Stomatitis Virus-NJ.

FIG. **7** depicts concentration of IFNα in harvested media from cells transfected with pTarget IFNα, pTarget SGLuc-Δ1D2A-IFNα, pTarget IFNα-Δ1D2A-SGLucΔ1M, pTarget Δ1D2A-SGLuc Δ1M, and pTarget SGLuc-Δ1D2A. There were 3 replicates per each of 4 dilutions for each sample.

FIG. **8** depicts effects of IFNα on growth of VSV-NJ. IFNα levels produced in growth media harvested from HEK293-T cells transfected with pTarget IFNα, pTarget SGLuc-Δ1D2A-IFNα, pTarget IFNα-Δ1D2A-SGLuc Δ1M, mpTarget SGLucONα, or pTarget SGLuc-Δ1D2A (negative control) were measured and adjusted to concentrations listed before samples were exposed to MDBK cells. VSV-NJ was added to the MDBK cells and Plaque Forming Units (PFU) were counted after the growth period; average of 2 replicates are reported. ND, not determined.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

The term "fusion protein" or "chimeric protein" refers to a polypeptide containing polypeptides or segments of polypeptides from different sources, such as a segment of a luciferase from *Gaussia princeps* and a biologically active segment of an interferon. A fusion protein may be produced by joining two or more polynucleotides that originally coded for the separate proteins or protein segments into a single fusion polynucleotide. Besides the polynucleotide sequences encoding for the separate proteins, a fusion polynucleotide may comprise other polynucleotide sequences such as those encoding translation interrupter sequences or those encoding amino acid sequences which otherwise traffic or process an expressed protein. In some embodiments, the term "fusion protein" will refer to an intact fusion protein, such as a fusion between a luciferase and interferon sequence. In other embodiments, this term may refer to separate polypeptides derived from translation of a fusion polynucleotide, for example, can encompass separate polypeptides produced from a fusion construct containing a translation interrupter sequence.

Translation of the fusion polynucleotide results in a single or multiple polypeptides with functional properties derived from each of the original proteins. A single fusion protein may be expressed from a fusion polynucleotide. Such a single fusion protein may be processed into one, two or more polypeptides depending on the design of the fusion polynucleotide and the host cell expressing it. A fusion polynucleotide can express more than one polypeptide depending on its design, for example, depending on the presence of translation interrupters, stop codons, or other regulatory elements.

A polypeptide encoded by a fusion polynucleotide need not exactly correspond to all the residues of the original protein, for example, it may contain fewer or more amino acid residues than a full-length source protein, but contain an active site or functional domain of the source protein, for example, it may be a fragment of interferon that retains at least one interferon activity. A fusion polynucleotide may also be engineered to encode modified forms of a source protein, such as those having at least 70, 80, 90, 95 or 99% sequence identity or similarly with a source protein or with a functional segment thereof.

The term "fragment thereof," as applied to a polypeptide component of a fusion polypeptide described herein, refers to a polypeptide comprising any portion of the amino acid sequence of the polypeptide, wherein the fragment substantially retains at least one function of the full-length polypeptide from which it was derived. For example, a fragment of a luciferase may emit light or be processed and/or secreted in a manner similar to the full-length luciferase; a fragment of a translation interruption or interrupter sequence can retain the ability to interrupt translation, and a fragment of a biologically active molecule, such as interferon, can retain at least one physiological, pharmacodynamics, pharmacokinetic or immunological activity of the full-length molecule and/or an ability to be processed, trafficked or

secreted in a way similar to the native biologically active molecule from which it was derived.

The term "derivative thereof" or "modified sequence" as applied to the polypeptide components disclosed herein, refers to a polypeptide consisting of an amino acid sequence that is at least 70, 80, 90, 95, or 99% identical or similar to the amino acid sequence of a biologically active molecule such as a luciferase, translation interruption or interrupter sequence, or interferon, wherein the polypeptide derivative substantially retains the ability to induce the secretion of a target polypeptide to which it is fused. In some embodiments, the derivative comprises an amino acid sequence that is at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of a native or previously engineered sequence. The derivative may comprise additions, deletions, substitutions, post-translational modifications, chemical modifications, or a combination thereof to the amino acid sequence of a native or previously engineered molecule. A derivative may include a mutant polypeptide with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11-15, 16-20, 21-25, or 26-30 additions, substitutions, post-translational modifications, chemical modifications, or deletions. Additions or substitutions also include the use of non-naturally occurring amino acids or modified amino acids.

BLASTN may be used to identify a polynucleotide sequence having at least 70%, 75%, 80%, 85%, 87.5%, 90%, 92.5%, 95%, 97.5%, 98%, 99% sequence identity to a reference polynucleotide. A representative BLASTN setting optimized to find highly similar sequences uses an Expect Threshold of 10 and a Wordsize of 28, max matches in query range of 0, match/mismatch scores of 1/−2, and linear gap cost. Low complexity regions may be filtered or masked. Default settings of a Standard Nucleotide BLAST are described by and incorporated by reference to blast.ncbi.nlm.nih.gov/_Blast.cgi?PROGRAM=blastn&BLAST_PROGRAMS=megaBlast&PA GE_TYPE=BlastSearch&SHOW_DEFAULTS=on&LINK_LOC=blasthome (last accessed Feb. 4, 2016).

BLASTP can be used to identify an amino acid sequence having at least 70%, 75%, 80%, 85%, 87.5%, 90%, 92.5%, 95%, 97.5%, 98%, 99% sequence identity, or similarity to a reference amino acid using a similarity matrix such as BLOSUM45, BLOSUM62 or BLOSUM80 where BLOSUM45 can be used for closely related sequences, BLOSUM62 for midrange sequences, and BLOSUM80 for more distantly related sequences. Unless otherwise indicated a similarity score will be based on use of BLOSUM62. When BLASTP is used, the percent similarity is based on the BLASTP positives score and the percent sequence identity is based on the BLASTP identities score. BLASTP "Identities" shows the number and fraction of total residues in the high scoring sequence pairs which are identical; and BLASTP "Positives" shows the number and fraction of residues for which the alignment scores have positive values and which are similar to each other. Amino acid sequences having these degrees of identity or similarity or any intermediate degree of identity or similarity to the amino acid sequences disclosed herein are contemplated and encompassed by this disclosure. A representative BLASTP setting that uses an Expect Threshold of 10, a Word Size of 3, BLOSUM 62 as a matrix, and Gap Penalty of 11 (Existence) and 1 (Extension) and a conditional compositional score matrix adjustment. Other default settings for BLASTP are described by and incorporated by reference to the disclosure available at: blast.ncbi.nlm.nih.gov/_Blast.cgi?PROGRAM= blastp&PAGE_TYPE=BlastSearch& LINK_LOC= blasthome (last accessed Jun. 29, 2016). Derivatives, analogs or modified versions of any of the polynucleotide or amino acid sequences specifically described herein or in the sequence listing having the above-mentioned ranges of sequence identity or similarly are specifically contemplated.

A "biologically active" or "active" interferon or other polypeptide of interest will exhibit at least one activity of the native molecule, such as an ability to modulate the immune system, treat an autoimmune disease, induce humoral or cellular immunity, interfere with virus replication, treat a tumor or microbial infection, contain diagnostically or immunologically useful epitopes, or any other function of the native molecule. These functions will depend on the nature of the native polypeptide of interest.

A "biotherapeutic" or a composition containing a fusion protein or cleavage product(s) of such a fusion protein, as described herein, including living cells which express or contain such a fusion protein or fusion protein fragments, may be formulated by any of the methods known in the art.

It can be typically prepared as an injectable (e.g. subcutaneous, intradermal and intramuscular injection, jet injections) or as a formulation for oral administration, intranasal administration (e.g. aerosol inhalation or instillation), topical administration to the eye, electroporation, gene gun, transfection, liposome-mediated delivery or combinations thereof, either as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid prior to injection or other administration may also be prepared. The preparation may also be emulsified or encapsulated in liposomes. Suitable excipients include but are not limited to water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In a further embodiment, example diluents include, but are not limited to, water, physiological saline solution, human serum albumin, oils, polyethylene glycols, glycerin, propylene glycol or other synthetic solvents, antibacterial agents such as benzyl alcohol, antioxidants such as ascorbic acid or sodium bisulfite, chelating agents, such as ethylene diamine-tetra-acetic acid, buffers such as acetates, citrates or phosphates and agents for adjusting osmolarity, such as sodium chloride or dextrose. In a further embodiment, example carriers include, but are not limited to, liquid carriers (e.g., water, saline, culture medium, saline, aqueous dextrose, aqueous glycols) and solid carriers (e.g., carbohydrates such as starch, glucose, lactose, sucrose, dextrans; anti-oxidants such as ascorbic acid and glutathione, hydrolyzed proteins). In a further embodiment, pharmaceutically acceptable salts, include but are not limited to, the acid addition salts (formed with free amino groups of the peptide) which are formed with inorganic acids (e.g., hydrochloric acid or phosphoric acids) and organic acids (e.g., acetic, oxalic, tartaric, or maleic acid). Salts formed with the free carboxyl groups may also be derived from inorganic bases (e.g., sodium, potassium, ammonium, calcium, or ferric hydroxides), and organic bases (e.g., isopropylamine, trimethylamine, 2-ethylaminoethanol, histidine, and procaine). In a further embodiment, the biotherapeutic or other compositions according to the invention may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or other agents, which enhance the effectiveness of the vaccine. Examples of agents which may be effective include, but are not limited to: aluminum hydroxide; N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetyl muramyl-L-alanyl-D-isoglutaminy 1-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethyl amine (CGP

19835A, referred to as MTP-PE); and RIBI, which contains three components extracted from bacteria: monophosphoryl lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion.

In one or more embodiments, the biotherapeutics and compositions described herein may be administered prophylactically (e.g., to prevent or ameliorate the effects of a future infection), therapeutically (e.g., to treat or to empower the immune system of an infected subject) or both, in a manner compatible with the dosage formulation, and in such an amount and manner as will be prophylactically and/or therapeutically effective.

In an alternative embodiment, polynucleotides encoding a fusion protein according to the invention may be administered as a DNA composition which can be administered at dosages such as in the range of 0.05-3 μg/μl. Other factors that can form the basis of what dosage range to implement include but are not limited the size of the subject, the particular pathogen or disease being treated and the particular type of interferon or other biologically active molecule encoded.

A polynucleotide-based composition may be given in a single dose; two dose schedule, for example two to eight weeks apart; or a multiple dose schedule. A multiple dose schedule is one in which a primary course of administration may include 1 to 10 or more separate doses, followed by other doses administered at subsequent time intervals as required to maintain and/or reinforce the desired response on a subject's immune system.

"*Gaussia* luciferase" or "GLuc" describes luciferases produced by members of the genus *Gaussia*, amino acid sequence variants of native *Gaussia* luciferases, such as those having at least 70, 80, 90, 95, 99% sequence identity or homology to a native or previously engineered *Gaussia* luciferase or that contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acid deletions, substitutions or insertions to a native *Gaussia* luciferase amino acid sequence, and truncated native or variant *Gaussia* luciferases that retain luciferase activity. *Gaussia* luciferase or GLuc from *G. princeps* is commercially available (SEQ ID NO: 2). GLuc is a 185 amino acid naturally secreted luciferase isolated from *Gaussia princeps* and has a higher luminescence intensity than firefly or *Renilla* luciferases. It has been used to monitor tumor growth in vivo.

"Super-luminescent *Gaussia* luciferase" or "SGLuc" describes amino acid sequence variants of *Gaussia* luciferase containing an amino acid substitution at residues 89 and 90 of GLuc (SEQ ID NO:4) and which exhibit a higher stability than unmodified *G. princeps* luciferase in certain cell lysis buffers. This term encompasses other luciferase variants that are at least 70, 80, 90, 95, or 99% identical or similar to the GLuc or SGLuc of SEQ ID NO: 2 or 4, respectively, which exhibit substantially the same properties. The addition of 30 amino acid sequence comprising the FMDV 2A translational interrupter sequence, Δ1D2A, to the C-terminus of GLuc or the 8990 GLuc mutant (SGLuc) did not prevent either secretion or luminescence.

The luciferases described herein may be expressed in a form, or processed and expressed in a form that is capable of secretion from a host cell expressing a fusion polypeptide expressing them.

The term "interferon" includes native or previously-engineered mammalian Type I (IFN-α, IFN-β, IFN-ε, -κ, -δ, and -ζ, IFN-ω and IFN-ν), and non-mammalian interferons, such as those from birds, reptiles, amphibians, fish and other vertebrates. It also includes Type II interferon (IFN-γ) and Type III interferon (IFN-λ). Representative interferon polynucleotide or amino acids sequences are described by SEQ ID NOS: 23/24, 49/50, 53/54, 57/58, 61/62, 65/66, 71/72, 75/76, 79/80, 83/84, 87/88, or 91/92.

This term includes IFN α, β, and γ interferons, amino acid sequence variants of native interferons, such as those having at least 70, 80, 90, 95, 99% sequence identity or homology to a native or previously engineered interferon or that contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more deletions, substitutions or insertions to a native or previously engineered interferon amino acid sequence, and truncated native or variant interferons that retain at least one functional activity of the native or previously-engineered interferon.

An interferon may be obtained or derived from a human or other mammal, avian, or vertebrate, including but not limited to monkeys and other primates, mice, rats, rabbits, horses, domestic dogs and other *Canidae*, domestic cats and other *Felidae*, pigs and other *Suidae*, cows and other *Bovinae*, cattle, sheep, goats, water buffalos, yaks, reindeer, deer, elk, llamas, alpacas, bison, moose, camels, chamois, giraffes, hogs, warthogs, kudus, antelopes, gazelles, and wildebeests.

The term "interferon secretion sequence" includes, but is not limited to, native amino acid sequences that facilitate secretion of interferons, such as those described by the amino acid sequences of SEQ ID NOS: 26, 28, 30, 32, 34, 36, 38, 40, 42, 44 and 46. Other interferon secretion sequences include those that are at least 70, 80, 90, 95, 99% identical or similar to a native interferon secretion sequence which facilitate secretion of interferon or other biologically active proteins. Modified interferon secretion sequences also include those with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acid deletions, substitutions or insertions to a native sequence. Representative polynucleotides encoding these secretion sequences are described by SEQ ID NOS: 25, 27, 29, 31, 33, 35, 37, 39, 41, 43 and 45 as well as by degenerate versions of these sequences and by modified polynucleotide sequences that encode an interferon secretion sequence that is at least 70, 80, 90, 95, 99% identical or similar to a native interferon secretion sequence as described herein.

The term "biologically active" or "active" molecule includes members of the interferon family described herein, as well as other cytokines such as members of the IL-2 family (including IL-4, IL-7, IL-9, IL-15, IL-21, EPO, TPO and other molecules having a four alpha helix bundle), IL-10 family (including L-19, IL-20, IL-22, IL-24 and IL-26), IL-1 family (including IL-1 and IL-18), IL-17 family (including IL17A-IL17F) and cysteine-knot family (TNF-β1, TNF-β2, TNF-β3). It includes lymphokines, interleukins and chemokines as well as peptide hormones such as amyline, anti-mullerian hormone, adiponectin, adrenocorticotropic hormone, angiotensinogen, angiotensin, antidiuretic hormone, atrial-natriuretic peptide, brain natriuretic peptide, calcitonin, cholecystokinin, corticotropin-releasing hormone, cortistatin, enkephalin, endothelin, erythropoietin, follicle-stimulating hormone, galanin, gastric inhibitory polypeptide, gastrin, ghrelin, glucagon, glucagon-like peptide-1, gonadotropin-releasing hormone, growth hormone-releasing hormone, hepcidin, human chorionic gonadotropin, human placental lactogen, growth hormone, inhibin, insulin, insulin like growth factor, leptin, lipotropin, luteinizing hormone, melanocyte stimulating hormone, motilin, orexin, oxytocin, pancreatic polypeptide, parathyroid hormone, pituitary adenylate cyclase-activating peptide, prolactin, prolactin releasing hormone, relaxin, renin, secretin, somatostatin, thrombopoietin, thyroid-stimulating hormone, thyrotropin-releasing hormone, vasoactive intes-

tinal peptide, guanylin, and uroguanylin. Modified versions of these native molecules are included, such as those that are at least 70, 80, 90, 95, 99% identical or similar to a native biologically active molecule and which retain at least one activity thereof as well as those having 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acid deletions, substitutions or insertions to a native sequence.

A "translation interrupter" includes 2A, Δ1D2A, or other 2A-like translational interrupters. The 2A translation interrupter is well known in the art pertaining to Foot-and-mouth Disease Virus (FMDV). Other such translational interrupters from other viruses are known. Variants of such interrupters with 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 insertions, deletions or substitutions of an amino acid residues that retain the ability to interrupt translation also may be used to process fusion proteins described herein. Non-limiting examples of translation interrupter sequences or polynucleotides encoding them are described by SEQ ID NOS: 5-14.

A "pharmaceutically acceptable carrier", "adjuvant", or "excipient" is known in the art, including, but not limited to, physiological saline, mineral oil, vegetable oils, aqueous carboxymethyl cellulose or polyvinylpyrrolidone. The skilled practitioner will recognize that such carriers should be compatible with the fusion proteins or nucleic acid constructs. Phosphate buffered saline (PBS) is one example of an acceptable carrier. The concentration and amount of the proteins or nucleic acid constructs in the final composition may vary depending upon the desired use and type of response needed, and the host animal. The fusion proteins or nucleic acid constructs should be provided in an amount effective to induce the preferred response as determined by routine testing. Appropriate adjuvants as known in the art may also be included in the formulation. Without being limited thereto, suitable adjuvants include but are not limited to mineral oil, vegetable oils, alum, Freund's incomplete adjuvant, and microparticles or nanoparticles or beads of biocompatible matrix materials such as agar or polyacrylate. Other known immunogenic agents used in conventional vaccines for a subject may also be included in the formulation as well as other therapeutic agents, such as antibacterial or antiviral drugs.

Additional non-limiting aspects and embodiments of the disclosure are described in the following enumerated paragraphs. Some embodiments are directed to compositions containing polynucleotides, these include, without limitation, the following:

1. A polynucleotide that encodes at least one fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which, preferably, when expressed can be secreted, and at least one interferon, cytokine, enzyme, or other polypeptide of interest. Examples of polynucleotides encoding GLuc and SGLuc include those comprising the sequences of SEQ ID NO: 1 and SEQ ID NO: 3. Representative luciferase sequences are described by SEQ ID NO: 2 and SEQ ID NO: 4, respectively. The polynucleotides encoding the luciferase may be directly adjoined to those encoding the interferon or other polypeptide of interest or may be separated from the sequences encoding the interferon or other polypeptide of interest, for example, by an intervening translation interruption or interrupter sequence. A polynucleotide sequence encoding a luciferase may replace a polynucleotide sequence encoding the N-terminal portion of an interferon or other polypeptide of interest, for example, it may replace a native secretion sequence or sequence not essential for the biological activity (or immunogenicity) of an interferon or other polypeptide of interest.

The above-mentioned polynucleotide sequence may encode fusion proteins having their various components in any order. For example, it may encode a fusion protein comprising in order from the N-terminal: a luciferase amino acid sequence (such as GLuc or SGLuc), a translation interrupter amino acid sequence (such as 2A or Δ1D2A) and a biologically active molecule amino acid sequence (such as IFN α). In this embodiment the fusion polynucleotide, upon translation, can produce two separate proteins: the first comprising the luciferase-translation interrupter and the second comprising the biologically active amino acid sequence, e.g., (SGLuc-Δ1D2A and IFN α).

This embodiment may encode a fusion protein comprising in order from the N-terminal: a biologically active molecule amino acid sequence (such as IFN α), a translation interrupter amino acid sequence (such as 2A or Δ1D2A), and a luciferase amino acid sequence (such as GLuc or SGLuc). In this embodiment, upon translation, the fusion polynucleotide can produce two separate proteins: the first comprising the luciferase and the second comprising the translation interrupter sequence and the biologically active amino acid sequence which may be expressed without an N-terminal Met residue (e.g., IFNα-Δ1D2A and SGLuc Δ1M).

This embodiment it may encode a GLucON or SGLucON sequence comprising in order from the N-terminal a luciferase amino acid sequence (such as GLuc or SGLuc) fused to an active domain of a biologically active protein, such as IFN α with its native secretion domain replaced with GLuc or SGLuc secretion sequence. No translation interrupter sequence is required for this fusion protein construct which can be transported out of a host cell intact.

2. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises at least one promoter or other transcription regulatory element, at least one prokaryotic or eukaryotic translation initiation sequence or other translation regulatory element, at least one translational interrupter sequence, or at least one reporter gene operatively linked to, or embedded within the polynucleotide sequence encoding the at least one fusion protein.

3. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises at least one of a 2A, Δ1D2A, or other translational interrupter sequence.

4. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises at least one an Aphthovirus 2A, Δ1D2A, or other Aphthovirus translational interrupter sequence. Representative examples of polynucleotides encoding translation interrupter sequences include those comprising SEQ ID NOS: 5, 7, 9, 11, 13, 15, 17, 19, and 21. Representative encoded amino acid sequences are respectively described by SEQ ID NOS: 6, 8, 10, 12, 14, 16, 18, 20 and 22.

5. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises at least one of a foot and mouth disease virus (FMDV) 2A, FMDV Δ1D2A, or other FMDV translational interrupter sequence.

6. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises a Δ1D2A sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase.

7. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises a Δ1D2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase.

8. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises a translational

interrupter sequence engineered at the C-terminus of at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase.

9. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises a translational interrupter sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase.

10. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises an FMDV 2A sequence engineered at the C-terminus of at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase.

11. The polynucleotide of embodiment 1, wherein the at least one fusion protein further comprises an FMDV 2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase.

12. The polynucleotide of embodiment 1, wherein the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted does not have an N-terminal methionine residue.

13. The polynucleotide of embodiment 1 that encodes at least one fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase, and at least one interferon, cytokine, enzyme, or other polypeptide of interest. Representative, but not limited, polynucleotides may comprise one or more polynucleotide subsequences (e.g., encoding a luciferase, a secretion polypeptide, interferon or other biologically active molecule, translation terminator, translation interrupter sequence, etc.) described in the sequence listing or may comprise a fusion polynucleotide such as those described by SEQ ID NOS: 97-103 and 108-109. Modified polynucleotides, which retain the functional properties of those described herein are included, such as polynucleotides that are at least 70, 80, 90, 95, or 99% identical or similar to those of SEQ ID NOS: 97-109 and which encode functional luciferases, translational terminators, or interferons or fusions or secretable fusions thereof. The polynucleotides described herein may be incorporated into a vector, including transposons, or into a host chromosome.

Other embodiments of the invention are directed to vectors these include, without limitation, the following:

14. A vector comprising the polynucleotide of embodiment 1 which encodes at least one fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase, preferably, in a form which can be secreted, and at least one interferon, cytokine, enzyme, or other polypeptide of interest.

15. The vector of embodiment 14, wherein the polynucleotide encoding the at least one fusion protein further comprises at least one promoter or other transcription regulatory element, at least one prokaryotic or eukaryotic translation initiation sequence or other translation regulatory element, at least one translational interrupter sequence, or at least one reporter gene operatively linked to, or embedded within, the polynucleotide sequence encoding the at least one fusion protein.

16. The vector of embodiment 14, wherein the at least one fusion protein further comprises at least one of a 2A, Δ1D2A, or other translational interrupter sequence.

17. The vector of embodiment 14, wherein the at least one fusion protein further comprises at least one an Aphthovirus 2A, Δ1D2A, or other Aphthovirus translational interrupter sequence.

18. The vector of embodiment 14, wherein the at least one fusion protein further comprises at least one of a foot and mouth disease virus (FMDV) 2A, FMDV Δ1D2A, or other FMDV translational interrupter sequence.

19. The vector of embodiment 14, wherein the at least one fusion protein further comprises a Δ1D2A sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

20. The vector of embodiment 14, wherein the at least one fusion protein further comprises a Δ1D2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

21. The vector of embodiment 14, wherein the at least one fusion protein further comprises a translational interrupter sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

22. The vector of embodiment 14, wherein the at least one fusion protein further comprises a translational interrupter sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

23. The vector of embodiment 14, wherein the at least one fusion protein further comprises an FMDV 2A sequence engineered at the C-terminus of at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

24. The vector of embodiment 14, wherein the at least one fusion protein further comprises an FMDV 2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

25. The vector of embodiment 14, wherein the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted does not have an N-terminal methionine residue.

26. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a eukaryotic cell.

27. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a yeast cell.

28. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a fungus cell.

29. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in an insect cell.

30. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a vertebrate cell.

31. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a mammalian cell.

32. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a prokaryotic cell.

33. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a gram-positive prokaryote.

34. The vector of embodiment 14 that expresses the at least one engineered polypeptide of interest in a gram-negative prokaryote.

35. The vector of embodiment 14 that is a minicircle vector, a replication deficient adenovirus vector, a vaccinia virus vector, or other viral vector that expresses the at least

one fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest.

36. The vector of embodiment 14, further comprising a polynucleotide described by any of embodiments 1-13. A vector includes episomes, plasmids, phage sequences, viral sequences, transposons, and other polynucleotide constructs that can transform a host cell or be expressed by a host cell.

Other embodiments of the invention are directed to host cells, these include, without limitation, the following:

37. A host cell comprising a vector of embodiment 14, wherein the host cell expresses the at least one fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest.

38. The host cell of embodiment 37, wherein the vector comprises at least one promoter or other transcription regulatory element, at least one prokaryotic or eukaryotic translation initiation sequence or other translation regulatory element, at least one translational interrupter sequence, or at least one reporter gene operatively linked to, or embedded within, the polynucleotide sequence encoding the at least one fusion protein.

39. The host cell of embodiment 37, wherein the at least one fusion protein further comprises at least one of a 2A, Δ1D2A, or other translational interrupter sequence.

40. The host cell of embodiment 37, wherein the at least one fusion protein further comprises at least one of an Aphthovirus 2A, Δ1D2A, or other Aphthovirus translational interrupter sequence.

41. The host cell of embodiment 37 wherein the at least one fusion protein further comprises at least one of a foot and mouth disease virus (FMDV) 2A, FMDV Δ1D2A, or other FMDV translational interrupter sequence.

42. The host cell of embodiment 37, wherein the at least one fusion protein further comprises a Δ1D2A sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

43. The host cell of embodiment 37, wherein the at least one fusion protein further comprises a Δ1D2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

44. The host cell of embodiment 37, wherein the at least one fusion protein further comprises a translational interrupter sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

45. The host cell of embodiment 37, wherein the at least one fusion protein further comprises a translational interrupter sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

46. The host cell of embodiment 37, wherein the at least one fusion protein further comprises an FMDV 2A sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

47. The host cell of embodiment 37, wherein the at least one fusion protein further comprises an FMDV 2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

48. The host cell of embodiment 37, wherein the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted does not have an N-terminal methionine residue.

49. The host cell of embodiment 37 that is a eukaryotic cell.

50. The host cell of embodiment 37 that is a yeast cell.

51. The host cell of embodiment 37 that is a fungus cell.

52. The host cell of embodiment 37 that is an insect cell.

53. The host cell of embodiment 37 that is a vertebrate cell.

54. The host cell of embodiment 37 that is mammalian cell.

55. The host cell of embodiment 37 that is a prokaryotic cell.

56. The host cell of embodiment 37 that is a gram-positive prokaryote.

57. The host cell of embodiment 37 that is a gram-negative prokaryote.

58. The host cell of embodiment 37, wherein the vector is a minicircle vector, a replication deficient adenovirus vector, a vaccinia virus vector, or other viral vector that expresses the at least one fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest.

59. The host cell of embodiment 37, wherein the vector further comprises a polynucleotide selected from the group of polynucleotide sequences or vectors described by embodiments 1-36.

Other embodiments of the invention are directed to polypeptides or fusion proteins these include, without limitation, the following:

60. A fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase, preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest. The fusion protein may be expressed intact with the luciferase and polypeptide of interest fused together, or may be expressed, for example, via translation interruption, where the fusion protein is separated into at least two polypeptide components.

61. The fusion protein of embodiment 60, which is encoded by a polynucleotide or vector further comprising at least one promoter or other transcription regulatory element, at least one prokaryotic or eukaryotic translation initiation sequence or other translation regulatory element, at least one translational interrupter sequence, or at least one reporter gene operatively linked to, or embedded within, the polynucleotide sequence encoding the fusion protein.

62. The fusion protein of embodiment 60, further comprising at least one of a 2A, Δ1D2A, or other translational interrupter sequence.

63. The fusion protein of embodiment 60, further comprising at least one of an Aphthovirus 2A, Δ1D2A, or other Aphthovirus translational interrupter sequence.

64. The fusion protein of embodiment 60, further comprising at least one of a foot and mouth disease virus (FMDV) 2A, FMDV Δ1D2A, or other FMDV translational interrupter sequence.

65. The fusion protein of embodiment 60, further comprising a Δ1D2A sequence engineered at the C-terminus of

the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

66. The fusion protein of embodiment 60, further comprising a Δ1D2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

67. The fusion protein of embodiment 60, further comprising a translator interrupter sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

68. The fusion protein of embodiment 60, further comprising a translator interrupter sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

69. The fusion protein of embodiment 60, further comprising an FMDV 2A sequence engineered at the N-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

70. The fusion protein of embodiment 60, further comprising an FMDV 2A sequence engineered at the C-terminus of the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted.

71. The fusion protein of embodiment 60, wherein the at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase which can be secreted does not have an N-terminal methionine residue.

72. The fusion protein of embodiment 60 that encoded by any of the polynucleotide or vector embodiments 1-36 or which expressed by the host cells of any of embodiments 37-59.

Other embodiments of the invention are directed to vaccines, these include, without limitation, the following:

73. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 60 and a suitable carrier, excipient or adjuvant.

74. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 61 and a suitable carrier, excipient or adjuvant.

75. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 62 and a suitable carrier, excipient or adjuvant.

76. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 63 and a suitable carrier, excipient or adjuvant.

77. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 64 and a suitable carrier, excipient or adjuvant.

78. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 65 and a suitable carrier, excipient or adjuvant.

79. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 66 and a suitable carrier, excipient or adjuvant.

80. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 67 and a suitable carrier, excipient or adjuvant.

81. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 68 and a suitable carrier, excipient or adjuvant.

82. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 69 and a suitable carrier, excipient or adjuvant.

83. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 70 and a suitable carrier, excipient or adjuvant.

84. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 71 and a suitable carrier, excipient or adjuvant.

85. An antigen, immunogen, or vaccine comprising the fusion protein of embodiment 72 and a suitable carrier, excipient or adjuvant.

The antigen, immunogen or vaccine described above may comprise an intact fusion protein or may be in the form of one or more immunologically active fragments of such a fusion protein. Suitable carriers, excipients or adjuvants are known in the art and are described elsewhere herein.

Other embodiments of the invention include a method of making fusion protein and include, without limitation, the following:

86. A method for making, expressing and/or processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase, preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 37 in a suitable medium and recovering the fusion protein.

87. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase, preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 38 in a suitable medium and recovering the fusion protein.

88. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 39 in a suitable medium and recovering the fusion protein.

89. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 40 in a suitable medium and recovering the fusion protein.

90. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 41 in a suitable medium and recovering the fusion protein.

91. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell

according to embodiment 42 in a suitable medium and recovering the fusion protein.

92. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 43 in a suitable medium and recovering the fusion protein.

93. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 44 in a suitable medium and recovering the fusion protein.

94. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 45 in a suitable medium and recovering the fusion protein.

95. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 46 in a suitable medium and recovering the fusion protein.

96. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 47 in a suitable medium and recovering the fusion protein.

97. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to any of embodiments 48-57 in a suitable medium and recovering the fusion protein.

98. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 58 in a suitable medium and recovering the fusion protein.

99. A method for expressing and processing a fusion protein comprising at least one of *Gaussia* Luciferase (GLuc), super-luminescent *Gaussia* luciferase (SGLuc) or other luciferase preferably in a form which can be secreted, and at least one interferon, cytokine, enzyme or other polypeptide of interest, comprising culturing the host cell according to embodiment 59 in a suitable medium and recovering the fusion protein.

In preferred embodiments of the method described above, the luciferase will be one that can be expressed and exported from the cell. Prior to export or secretion from the cell, it may be processed, for example, by action of a translation interruption sequence, to separate it from other sequences encoded by a fusion polynucleotide. Alternatively, if may be exported or secreted as part of a fusion polypeptide.

Other embodiments of the invention include a method for quantifying an amount of interferon, cytokine, enzyme or other polypeptide of interest and include, without limitation, the following:

100. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:

providing the vector according to embodiment 14;

transforming the vector into a host cell;

culturing the cells in a medium;

harvesting the medium; and

quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

101. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:

providing the vector according to embodiment 15;

transforming the vector into a host cell;

culturing the cells in a medium;

harvesting the medium; and

quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

102. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:

providing the vector according to embodiment 16;

transforming the vector into a host cell;

culturing the cells in a medium;

harvesting the medium; and

quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

103. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:

providing the vector according to embodiment 17;

transforming the vector into a host cell;

culturing the cells in a medium;

harvesting the medium; and

quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

104. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:

providing the vector according to embodiment 18;

transforming the vector into a host cell;

culturing the cells in a medium;

harvesting the medium; and

quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

105. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 19;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

106. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 20;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

107. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 21;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

108. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 22;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output.

109. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 23;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

110. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 24;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

111. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 25;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

112. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 35;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

113. A method for quantifying an amount of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 36;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the amount of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

In the methods described above the intensity of the luminescent output in the harvested medium is usually measured. This luminescent output may be correlated to the amount of luciferase or fusion protein containing luciferase in the medium and used to quantify expression or activity of a biological molecule. However, in some embodiments, the luminescent intensity of cells separated from the harvested medium may be measured, or measurements may be taken for a combination of both cells and medium or for each separately. In other embodiments, the harvested medium or cells may be further processed, diluted, or purified prior to detection of luminescence. This method may be practiced in conjunction with conventional methods for determining the presence, activity or quantity of a biologically active molecule, such as antibody-based methods, as described herein. Luminescence may be detected or quantified by equipment or methods known in the art, for example, spectrophotometrically.

Other embodiments of the invention include a method for quantifying a concentration of interferon, cytokine, enzyme or other polypeptide of interest and include, without limitation, the following:

114. A method for quantifying a concentration of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 14;
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the concentration of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

115. A method for quantifying a concentration of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to embodiment 15,
transforming the vector into a host cell;

culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the concentration of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

116. A method for quantifying a concentration of an interferon, cytokine, enzyme produced in an expression system comprising:
providing the vector according to embodiment 16,
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output in the harvested medium, thus quantifying the concentration of the interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system.

117. A method for quantifying a concentration of an interferon, cytokine, enzyme or other polypeptide of interest produced in an expression system comprising:
providing the vector according to any one embodiments 17-36,
transforming the vector into a host cell;
culturing the cells in a medium;
harvesting the medium; and
quantifying the intensity of luminescent output.

In the methods described above the intensity of the luminescent output in the harvested medium is usually measured. This luminescent output may be correlated to the concentration of luciferase or fusion protein containing luciferase in the medium and used to quantify expression or activity of a biological molecule. However, in some embodiments, the luminescent intensity of cells separated from the harvested medium may be measured, or measurements may be taken for a combination of both cells and medium or for each separately. In other embodiments, the harvested medium or cells may be further processed, diluted, or purified prior to detection of luminescence. This method may be practiced in conjunction with conventional methods for determining the presence, activity or quantity of a biologically active molecule, such as antibody-based methods, as described herein. Luminescence may be detected or quantified by equipment or methods known in the art, for example, spectrophotometrically.

Other embodiments of the invention include a method for facilitating secretion of a fusion protein and include, without limitation, the following:

118. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 14;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

119. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 15;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

120. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 16;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

121. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 17;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

122. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 18;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

123. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 19;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

124. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 20;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

125. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 21;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

126. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 22;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

127. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 23;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

128. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 24;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

129. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to any one of embodiments 25-34;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

130. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 35;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

131. A method for facilitating secretion of a fusion protein from a host cell comprising:
providing the vector according to embodiment 36;
transforming the vector into a host cell;
culturing the cells in a medium; and
recovering the secretable fusion protein from the medium.

Recovery of a fusion protein includes concentration, purification, and/or isolation from other polypeptide com-

ponents or nonpolypeptide components of a medium, cells or cell lysate. Examples of recovery methods include chromatographic isolation or separation of a fusion protein, affinity purification using antibodies or ligands that bind to epitopes of tags in a target fusion protein, PAGE, isoelectric focusing, or dialysis and concentration. A recovered fusion protein may be purified to homogeneity or to represent 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 99% by mass of the protein content (or the solid, nonaqueous content) in a recovered fusion protein composition.

Other embodiments of the invention include a method for measuring an amount of a biotherapeutic peptide in a subject and include, without limitation, the following:

132. A method for measuring an amount of a biotherapeutic peptide (or biotherapeutic polypeptide) in a subject in need thereof comprising:

providing the vector according to embodiment 14;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

133. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 15;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

134. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 16;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

135. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 17;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

136. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 18;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

137. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 19;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

138. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 20;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

139. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 21;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

140. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 22;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

141. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 23;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

142. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 24;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

143. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to any of embodiments 25-34;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

144. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 35;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

145. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

providing the vector according to embodiment 36;

transforming the vector into the subject;

recovering from the subject a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a biotherapeutic peptide and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby determining an amount of a biotherapeutic peptide in the subject.

Recovery of a fusion protein comprising a biotherapeutic peptide or polypeptide includes concentration, dilution, purification, and/or isolation from other polypeptide components or nonpolypeptide components of a medium, cells or cell lysate. Examples of recovery methods include chromatographic isolation or separation of a fusion protein, affinity purification using antibodies or ligands that bind to epitopes of tags in a target fusion protein, PAGE, isoelectric focusing, or dialysis and concentration. In some embodiments luminescence may be determined directly from a biological sample or a diluted biological sample. A recovered biotherapeutic peptide or polypeptide may be purified to homogeneity or to represent 10, 20, 30, 40, 50, 60, 70, 80, 90, 95, 99% by mass of the protein content (or the solid, nonaqueous content) in a recovered fusion protein composition.

Other embodiments of the invention include a method for certifying expression of a polypeptide vaccine in a subject and include, without limitation, the following:

146. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 14;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

147. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 15;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

148. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 16;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

149. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 17;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

150. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 18;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

151. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 19;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

152. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 20;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

153. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 21;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

154. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 22;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

155. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 23;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

156. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 24;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

157. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 25-34;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

158. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 35;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

159. A method for certifying vaccine expression in vivo comprising:

providing the vector according to embodiment 36;

transforming the vector into a host organism;

recovering from the host organism a sample of biological material, such as blood, serum, plasma, CSF, or urine, containing a fusion protein comprising a vaccine peptide (or polypeptide) and a luciferase, or a luciferase expressed by the vector; and

detecting or quantifying the intensity of luminescent output in the sample thereby certifying expression of the vaccine peptide or polypeptide in the host organism.

Recovery of a fusion protein comprising a vaccine peptide or polypeptide includes concentration, dilution, purification, and/or isolation from other polypeptide components or non-polypeptide components of a medium, cells or cell lysate. Examples of recovery methods include chromatographic isolation or separation of a fusion protein, affinity purification using antibodies or ligands that bind to epitopes of tags in a target fusion protein, PAGE, isoelectric focusing, or dialysis and concentration. In some embodiments luminescence may be determined directly from a biological sample or a diluted biological sample. In the methods above, vaccine expression may be formally certified such as by a formal medical or scientific statement, attestation, logs or other records or less formally detected, determined, or recorded, for example in a laboratory notebook or workbook, photo, audio/visual recording, or other record.

Other embodiments of the invention include a pharmaceutical composition containing a fusion protein and include, without limitation, the following:

160. A pharmaceutical composition comprising the fusion protein of embodiment 60 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

161. A pharmaceutical composition comprising the fusion protein of embodiment 61 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

162. A pharmaceutical composition comprising the fusion protein of embodiment 62 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

163. A pharmaceutical composition comprising the fusion protein of embodiment 63 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

164. A pharmaceutical composition comprising the fusion protein of embodiment 64 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

165. A pharmaceutical composition comprising the fusion protein of embodiment 65 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

166. A pharmaceutical composition comprising the fusion protein of embodiment 66 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

167. A pharmaceutical composition comprising the fusion protein of embodiment 67 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

168. A pharmaceutical composition comprising the fusion protein of embodiment 68 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

169. A pharmaceutical composition comprising the fusion protein of embodiment 69 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

170. A pharmaceutical composition comprising the fusion protein of embodiment 70 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

171. A pharmaceutical composition comprising the fusion protein of embodiment 71 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

172. A pharmaceutical composition comprising the fusion protein of embodiment 72 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient

Other embodiments of the invention include a biotherapeutic comprising a fusion protein and include, without limitation, the following:

173. A biotherapeutic comprising the fusion protein of embodiment 60 and a suitable carrier, excipient or adjuvant.

174. A biotherapeutic comprising the fusion protein of embodiment 61 and a suitable carrier, excipient or adjuvant.

175. A biotherapeutic comprising the fusion protein of embodiment 62 and a suitable carrier, excipient or adjuvant.

176. A biotherapeutic comprising the fusion protein of embodiment 63 and a suitable carrier, excipient or adjuvant.

177. A biotherapeutic comprising the fusion protein of embodiment 64 and a suitable carrier, excipient or adjuvant.

178. A biotherapeutic comprising the fusion protein of embodiment 65 and a suitable carrier, excipient or adjuvant.

179. A biotherapeutic comprising the fusion protein of embodiment 66 and a suitable carrier, excipient or adjuvant.

180. A biotherapeutic comprising the fusion protein of embodiment 67 and a suitable carrier, excipient or adjuvant.

181. A biotherapeutic comprising the fusion protein of embodiment 68 and a suitable carrier, excipient or adjuvant.

182. A biotherapeutic comprising the fusion protein of embodiment 69 and a suitable carrier, excipient or adjuvant.

183. A biotherapeutic comprising the fusion protein of embodiment 70 and a suitable carrier, excipient or adjuvant.

184. A biotherapeutic comprising the fusion protein of embodiment 71 and a suitable carrier, excipient or adjuvant.

185. A biotherapeutic comprising the fusion protein of embodiment 72 and a suitable carrier, excipient or adjuvant.

In the biotherapeutics described above, the fusion protein preferably comprises a biologically active polypeptide, such as an interferon (e.g., interferon-alpha or interferon-beta or modified versions thereof) or an immunogenic polypeptide. These biotherapeutics may constitute a fusion protein according to the invention or a polynucleotide encoding such a fusion protein. The fusion protein may be intact or processed, for example, into separate fusion protein fragments by action of a translation interruption sequence. The fusion protein may be in a purified form isolated from other cellular components of a host cell expressing it, or may be contained within a host cell or transformed cell, such as a cell obtained from a subject being treated for a particular disease, disorder or condition. A biotherapeutic may comprise a living cell, such as a leukocyte, bone marrow, muscle, endothelial, or stem cell, that expresses interferon or other polypeptide of interest that produced by transformation of a subject's or patient's cells with a vector as described herein. It may be homologous to the subject or patient or obtained from a suitable donor.

Other embodiments of the invention include a method of treating a subject and include, without limitation, the following:

186. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 160 to a subject in need thereof.

187. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 161 to a subject in need thereof.

188. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 162 to a subject in need thereof.

189. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 163 to a subject in need thereof.

190. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 164 to a subject in need thereof.

191. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 165 to a subject in need thereof.

192. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 166 to a subject in need thereof.

193. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 167 to a subject in need thereof.

194. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 168 to a subject in need thereof.

195. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 169 to a subject in need thereof.

196. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 170 to a subject in need thereof.

197. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 171 to a subject in need thereof.

198. A method for treating Foot-and-Mouth Disease comprising administering the composition according to embodiment 172 to a subject in need thereof.

199. A method for treating malignant melanoma comprising administering the composition according to embodiment 160 to a subject in need thereof.

200. A method for treating malignant melanoma comprising administering the composition according to embodiment 161 to a subject in need thereof.

201. A method for treating malignant melanoma comprising administering the composition according to embodiment 162 to a subject in need thereof.

202. A method for treating malignant melanoma comprising administering the composition according to embodiment 163 to a subject in need thereof.

203. A method for treating malignant melanoma comprising administering the composition according to embodiment 164 to a subject in need thereof.

204. A method for treating malignant melanoma comprising administering the composition according to embodiment 165 to a subject in need thereof.

205. A method for treating malignant melanoma comprising administering the composition according to embodiment 166 to a subject in need thereof.

206. A method for treating malignant melanoma comprising administering the composition according to embodiment 167 to a subject in need thereof.

207. A method for treating malignant melanoma comprising administering the composition according to embodiment 168 to a subject in need thereof.

208. A method for treating malignant melanoma comprising administering the composition according to embodiment 169 to a subject in need thereof.

209. A method for treating malignant melanoma comprising administering the composition according to embodiment 170 to a subject in need thereof.

210. A method for treating malignant melanoma comprising administering the composition according to embodiment 171 to a subject in need thereof.

211. A method for treating malignant melanoma comprising administering the composition according to embodiment 172 to a subject in need thereof.

212. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 160 to a subject in need thereof.

213. A method for treating hepatitis B, hepatitis C or other viral infection comprising administering the composition according to embodiment 161 to a subject in need thereof.

214. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 162 to a subject in need thereof.

215. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 163 to a subject in need thereof.

216. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 164 to a subject in need thereof.

217. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 165 to a subject in need thereof.

218. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 166 to a subject in need thereof.

219. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 167 to a subject in need thereof.

220. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 168 to a subject in need thereof.

221. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 169 to a subject in need thereof.

222. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 170 to a subject in need thereof.

223. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 171 to a subject in need thereof.

224. A method for treating hepatitis B, hepatitis C, or other viral infection comprising administering the composition according to embodiment 172 to a subject in need thereof.

In the methods described above, the fusion protein preferably comprises a biologically active polypeptide that induces a protective effect against the particular pathological condition or pathogens mentioned, such as an interferon (e.g., interferon-alpha or interferon-beta or modified versions thereof) that enhances immune responses to FMDV, melanoma or other tumors or cancers, or hepatitis B or C infection, or such as an immunogen that induces cellular or humoral immunity against tumors or viral pathogens. This method may be performed by administering a fusion protein according to the invention or a polynucleotide encoding such a fusion protein, for example, by transformation of a cell with a vector encoding a fusion protein, and administration of the transformed cells to a subject or patient in need treatment for a particular disease, disorder or condition.

Other embodiments of the invention include a method of treating a subject and include, without limitation, the following:

225. A method for cytokine therapy comprising administering the composition according to embodiment 160 to a subject in need thereof.

226. A method for cytokine therapy comprising administering the composition according to embodiment 161 to a subject in need thereof.

227. A method for cytokine therapy comprising administering the composition according to embodiment 162 to a subject in need thereof.

228. A method for cytokine therapy comprising administering the composition according to embodiment 163 to a subject in need thereof.

229. A method for cytokine therapy comprising administering the composition according to embodiment 164 to a subject in need thereof.

230. A method for cytokine therapy comprising administering the composition according to embodiment 165 to a subject in need thereof.

231. A method for cytokine therapy comprising administering the composition according to embodiment 166 to a subject in need thereof.

232. A method for cytokine therapy comprising administering the composition according to embodiment 167 to a subject in need thereof.

233. A method for cytokine therapy comprising administering the composition according to embodiment 168 to a subject in need thereof.

234. A method for cytokine therapy comprising administering the composition according to embodiment 169 to a subject in need thereof.

235. A method for cytokine therapy comprising administering the composition according to embodiment 170 to a subject in need thereof.

236. A method for cytokine therapy comprising administering the composition according to embodiment 171 to a subject in need thereof.

237. A method for cytokine therapy comprising administering the composition according to embodiment 172 to a subject in need thereof.

In the method described above, the fusion protein preferably comprises a biologically active cytokine that modulates or enhances a subject's immune system. This method may be performed by administering a fusion protein according to the invention or a polynucleotide encoding such a fusion protein. It may be practiced with cells transformed to express a fusion protein or fusion protein fragments having cytokine activity, for example, by transformation of a cell

with a vector encoding a fusion protein, and administration of the transformed cells to a subject or patient in need of cytokine activity.

Other embodiments of the invention include a method of treating a subject and include, without limitation, the following:

238. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 160 to the animal in need thereof.

239. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 161 to the animal in need thereof.

240. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 162 to the animal in need thereof.

241. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 163 to the animal in need thereof.

242. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 164 to the animal in need thereof.

243. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 165 to the animal in need thereof.

244. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 166 to the animal in need thereof.

245. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 167 to the animal in need thereof.

246. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 168 to the animal in need thereof.

247. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 169 to the animal in need thereof.

248. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 170 to the animal in need thereof.

249. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 171 to the animal in need thereof.

250. A method for treating Feline Herpesvirus 1, Feline infectious peritonitis, Feline Immunodeficiency Virus, Feline Leukemia Virus, Canine papilloma virus or other viral infection in domestic or wild animals comprising administering the composition according to embodiment 172 to the animal in need thereof.

In the methods described above, the fusion protein preferably comprises a biologically active cytokine that modulates or enhances a subject's immune system response to the above-mentioned viruses or that comprises protective antigens or epitopes of said viruses. This method may be performed by administering a fusion protein according to the invention or a polynucleotide encoding such a fusion protein.

The methods described above for treating feline diseases or disorders may be practiced with *Felis catus* α, β and/or γ interferon(s) such as those encoded by Accession numbers: NM_001031830.1 or GI:73611927 (a interferon); NM_001009297.1 or GI:57163828 ((β interferon); or NM_001009873.1 or GI:57619124 (γ interferon); or analogs, derivatives or modified forms thereof as described herein. These accession numbers are incorporated by reference.

The methods described above for treating canine diseases or disorders may be practiced with *Canis lupus familiaris* α, β and/or γ interferon(s) such as those encoded by Accession numbers: M28624.1 or GI:163973 (α), GenBank: E11229.1 ((β) and EF095772.1 or GI: 118505119 (γ); or analogs, derivatives or modified forms thereof as described herein. These accession numbers are incorporated by reference.

Example 1

Δ1D2A Constructs Retain Luciferase and Interferon Secretion

Two constructs comprising interferon and luciferase sequences were made utilizing the translation interrupter Δ1D2A to separate SGLuc and IFN α, see FIG. **1**.

These constructs expressed two polypeptides which differed as to which polypeptide retained the Δ1D2A sequence, see FIG. **1**. The addition of the Δ1D2A sequence to either the N-terminus or C-terminus of SGLuc was found to not inhibit either secretion or luminescence of the SGLuc and as shown by FIG. **2**A top two bars (media luminescence) and FIG. **2**B (Western blot of harvested media). To confirm that the addition of an IFN α sequence to either the N-terminus, in the case of IFNα-Δ1D2A-SGLuc Δ1M, or to the C-terminus, in the case of SGLuc-Δ1D2A-IFNα, did not alter critical luminescence properties, media from HEK293-T cells transfected with constructs pTarget IFNα-Δ1D2A-SGLuc Δ1M and pTarget SGLuc-Δ1D2A-IFNα was evaluated for luciferase activity, see FIG. **2**A. HEK293-T cells transfected with constructs pTarget SGLuc-Δ1D2A and pTarget Δ1D2A-SGLuc Δ1M were used as controls, see FIG. **2**A.

Confirmation of the presence of GLuc in the media and of separation of the fusion protein by Δ1D2A was performed by western blotting using a polyclonal anti-GLuc antibody, see FIG. **2**B, which shows efficient separation of GLuc from fusion polypeptides. Only a small amount of unseparated fused peptide was present in the media, FIG. **2**B.

To confirm that the addition of an IFN α sequence to either the N-terminus, in the case of IFNα-Δ1D2A-SGLuc Δ1M, or to the C-terminus, in the case of SGLuc-Δ1D2A-IFNα, did not alter critical secretion properties the presence of IFNα and IFNα-Δ1D2A in cell culture media was determined using a commercially available ELISA assay. A standard curve of IFN α concentration was determined using nine different concentrations of an IFN α standard Four different dilutions of media from cells transfected with pTarget IFN α, pTarget IFNα-Δ1D2A-SGLuc Δ1M, pTarget SGLuc-Δ1D2A-IFNα, pTarget SGLuc-Δ1D2A, and pTarget Δ1D2A-SGLuc Δ1M were assayed using the same ELISA assay, see FIG. **7**. The ELISA results of media show in FIG. **7** demonstrate that IFNα is present in the media of cells transfected with plasmids pTarget IFN α, pTarget IFNα-Δ1D2A-SGLuc Δ1M, and pTarget SGLuc-Δ1D2A-IFNα but not in cells transfected with the control plasmids pTarget SGLuc-Δ1D2A, and pTarget Δ1D2A-SGLuc Δ1M. This confirms that the addition of the Δ1D2A peptide to either the N- or C-terminus of IFNα does not prevent secretion.

This example demonstrates that the Δ1D2A sequence can be successfully used to separate SGLuc and IFN α components of a fusion polypeptide and that both the SGLuc and IFN α components retain the ability to be secreted.

These results provide a new way to design a luciferase assay that can be used to quantify the amount of IFN produced in an expression system without the drawbacks of an antibody-based system. Such an assay provides a fast and reliable way to substantially determine the absolute concentration of a molecule in an expression system. The amount of GLuc or SGLuc moieties secreted into culture medium measured by luminescence, after these are released from a longer precursor fusion polypeptide by translational interruption, provides a proportionate way to substantially determine the absolute amount of interferon expressed. The amount of interferon expressed by the expression system will directly correlate with the amount of luminescence appearing in the culture medium. No interferon-binding antibodies are necessary.

This new method provides a more reliable way to standardize samples and avoid the unpredictability and problems associated with antibody-based systems like ELISA. As described above, many of these problems are attributable to the variation of antibody binding affinities for different interferon mutants, different kinds of interferons, or interferons in different kinds of samples.

While constructs using the Δ1D2A sequence can be conveniently used to monitor interferon expression, they do not directly quantify interferon concentrations. That is because they detect extracellular luminescence produced by the luciferase, not a direct and dependent property of interferon. Indirect methods using Δ1D2A may be biased by differential expression, degradation or trafficking of soluble GLuc moieties into the extracellular medium. For example, differential rates of GLuc or SGLuc moiety degradation for a mutant compared to a non-mutant IFN might bias results. To address these problems the inventors tested interferon-luciferase constructs that did not contain the Δ1D2A translation interruption sequence, see FIG. **4**. The luminescent moieties in such constructs are directly attached to interferon and thus luminescence detected extracellularly indicates the amount of interferon present.

Example 2

Comparison of Secretion of Interferon to GLucON Constructs

Native interferons contain an N-terminal secretion domain to facilitate their secretion into the extracellular medium. Examples of the secretion domains for interferons are described by SEQ ID NOS: 25-46. This secretion sequence is not necessary to elicit a desired immune stimulatory response. To this end the inventors constructed fusion peptides that contain the SGLuc luciferase and the non-secretion domain of four different interferons, α, β, γ, and λ, collectively identified as SGLucONs and depicted by FIG. **4**.

The secretion of two types of porcine interferons, α and β, and two types of bovine interferons, γ and λ, were compared to SGLucON constructs containing the same interferon types. The SGLucON constructs take advantage of the naturally secretable properties of SGLuc to facilitate the secretion of the fusion peptide.

All four interferons and all four SGLucON constructs were demonstrated to be secreted into the extracellular medium as shown in FIGS. **5**A and **5**B. This confirms that the creation of these fusion peptides does not prevent the secretion of the peptide from the cell. Since all SGLucONs (α, β, γ, λ) showed retention of secretion, FIG. **5**A, we tested media samples harvested from transfected HEK293-T cells for luciferase activity, FIG. **5**B. Media harvested from cells expressing Interferon (α, β, γ, λ) samples was also tested for luciferase activity to ensure that any luciferase activity observed was the result of the presence of the SGLuc component. All four SGLucON samples (α, β, γ, λ) and only the SGLucON samples showed luciferase activity, FIG. **5**B. This confirms that the addition of the interferon sequence to SGLuc does not prevent luminescence.

The SGLucON λ sample showed a more than two-fold higher luciferase readings than the other three other SGLucON samples, FIG. **5**B, but did not appear to have a proportionally greater concentration when examined by western blotting with the anti-GLuc antibody, FIG. **5**A. This result suggests that in the case of SGLucON λ the addition of the IFN λ sequence may either enhance luminescence or hinder luminescence less than the other IFN sequences, α, β, γ, when comparing amongst the SGLucON constructs.

Control constructs of IFN α, β, and γ were also shown to be secreted by usage of antibodies specific to each one. There was no reliable available antibody to bovine IFN γ limiting the ability to confirm its presence. Western blots using anti-GLuc, anti-IFN α, anti-IFN β, and anti-IFN λ show that the SGLucON chimeras retain both luciferase and interferon components fused together and are not post-translationally processed, FIG. **5**A. In the case of Interferon β there was a notable difference in post-translational modifications between IFN β and SGLucON β, FIG. **5**A. IFN β shows substantial post-translational modifications, possibly through glycosylation or differential processing, resulting in multiple bands being present in the anti-IFN β western blot FIG. **5**A. SGLucON β is predominantly in a single band as shown by FIG. **5**A, suggesting that SGLucON β is not subject to the same degree of post-translational modifications as IFN β.

These results demonstrate that direct fusion of SGLuc to an interferon can be successfully secreted by a cell and then

detected by luminescence. These constructs do not rely on separation of SGLuc from the interferon and thus are not subject to the same risks associated with the utilization of a Δ1D2A translation interruption sequence to produce two separate molecules.

Quantifying luciferase activity with SGLucON samples is a direct quantification of the concentration in the sample rather than an indirect quantification as is the case when utilizing the Δ1D2A sequence. This removes variables that may alter concentrations of either SGLuc or IFN after translation such as differential secretion rates and the potential for preferential protein degradation.

Example 3

Δ1D2A IFN Constructs Retain Biological Activity

An IFN α ELISA assay was performed to quantify the concentrations of IFN α in the cell culture media of HEK293-T cells transfected with plasmids pTarget IFN α, pTarget SGLuc-Δ1D2A-IFNα, pTarget IFNα-Δ1D2A-SGLuc Δ1M, and pTarget SGLuc-Δ1D2A. These concentrations were used to set up a dilution series to test for retention of antiviral activity against VSV and to compare this activity to an established commercially available porcine IFNα, FIG. **6** and FIG. **8**.

The results show that IFN α produced from constructs pTarget SGLuc-Δ1D2A-IFNα and pTarget IFNα-Δ1D2A-SGLuc Δ1M retains anti-viral activity, FIG. **6** and FIG. **8**. This was particularly novel as the IFN α produced from these constructs contains additional amino acids compared to a native IFN α sequence. The IFN α produced from the pTarget SGLuc-Δ1D2A-IFNα construct contains an addition N-terminal proline while the IFN α produced from the pTarget IFNα-Δ1D2A-SGLuc Δ1M construct contains an additional 40 amino acids, containing the Δ1D2A sequence, on the C-terminus, FIG. **1**. For the pTarget IFNα-Δ1D2A-SGLuc Δ1M construct the 40 additional amino acids represent a 20% increase in length for the resulting molecule. The substantial increase in the size of the molecule makes the result that it retained anti-viral activity all the more unexpected.

IFN α produced from the pTarget IFN α serves as a control to compare effectiveness to an unmodified protein produced in a similar manner. The IFN α samples only showed plaques at 0.625 ng/mL suggesting that a protective concentration was 1.25 ng/mL or less. Both the IFN α produced from the pTarget SGLuc-Δ1D2A-IFNα construct and that from the pTarget IFNα-Δ1D2A-SGLuc Δ1M construct provided complete protection at 2.5 ng/mL with plaques present at 1.25 ng/mL, FIG. **6**. Even at the lowest doses tested, 0.1265 ng/mL, the plaques present in samples were noticeably smaller than those present in the SGLuc-Δ1D2A negative control.

Example 4

GLucON a Construct Retains Biological Activity

An IFN α ELISA assay was performed to quantify the concentrations of both IFN α and SGLucON α in harvested media. Equivalent concentrations of each were determined and used in a plaque assay for interferon anti-viral activity against Vesicular Stomatitis Virus (VSV). The results are shown by FIG. **6** and FIG. **8**.

The results show that SGLucON α retained anti-viral activity against VSV. A concentration of less than or equal to 1.25 ng/mL but greater than 0.625 ng/mL of SGLucON α was sufficient to completely inhibit VSV and concentrations as low as 0.1265 ng/mL were shown to partially inhibit VSV when compared to the negative control SGLuc-Δ1D2A.

IFN α produced by the same means was also able to provide complete protection at a concentration of less than or equal to 1.25 ng/mL but greater than 0.3125 ng/mL. This suggests that SGLucON α has at least equivalent anti-viral activity than IFN α, FIG. **6** and FIG. **8**. Interestingly SGLucON α gives consistently lower PFUs than IFN α alone at equivalent concentrations FIG. **8**. While complete protection from VSV was obtained at the same concentration for both IFN α and SGLucON α consistently lower PFU numbers at susceptible dilutions suggest that SGLucON α offers better protection than IFN α, FIG. **8**.

Terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting of the invention. For example, as used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. It will be further understood that the terms "comprises" and/or "comprising," when used in this specification, specify the presence of stated features, steps, operations, elements, and/or components, but do not preclude the presence or addition of one or more other features, steps, operations, elements, components, and/or groups thereof. As used herein, the term "and/or" includes any and all combinations of one or more of the associated listed items and may be abbreviated as "/".

Spatially relative terms, such as "under", "below", "lower", "over", "upper" and the like, may be used herein for ease of description to describe one element or feature's relationship to another element(s) or feature(s) as illustrated in the figures. It will be understood that the spatially relative terms are intended to encompass different orientations of the device in use or operation in addition to the orientation depicted in the figures. For example, if a device in the figures is inverted, elements described as "under" or "beneath" other elements or features would then be oriented "over" the other elements or features. Thus, the exemplary term "under" can encompass both an orientation of over and under. The device may be otherwise oriented (rotated 90 degrees or at other orientations) and the spatially relative descriptors used herein interpreted accordingly. Similarly, the terms "upwardly", "downwardly", "vertical", "horizontal" and the like are used herein for the purpose of explanation only unless specifically indicated otherwise.

Although the terms "first" and "second" may be used herein to describe various features/elements (including steps), these features/elements should not be limited by these terms, unless the context indicates otherwise. These terms may be used to distinguish one feature/element from another feature/element. Thus, a first feature/element discussed below could be termed a second feature/element, and similarly, a second feature/element discussed below could be termed a first feature/element without departing from the teachings of the present invention.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising" means various components can be co-jointly employed in the methods and articles (e.g., compositions and apparatuses including device and methods). For example, the term "comprising" will be understood to imply the inclusion of any stated elements or steps but not the exclusion of any other elements or steps.

As used herein in the specification and claims, including as used in the examples and unless otherwise expressly specified, all numbers may be read as if prefaced by the word "substantially", "about" or "approximately," even if the term does not expressly appear. The terms "substantially", "substantially no", "substantially free", "about" or "approximately" may be used when describing magnitude and/or position to indicate that the value and/or position described is within a reasonable expected range of values and/or positions. For example, a numeric value may have a value that is +/−0.1% of the stated value (or range of values), +/−1% of the stated value (or range of values), +/−2% of the stated value (or range of values), +/−5% of the stated value (or range of values), +/−10% of the stated value (or range of values), etc. Any numerical range recited herein is intended to include all sub-ranges subsumed therein.

When a feature or element is herein referred to as being "on" another feature or element, it can be directly on the other feature or element or intervening features and/or elements may also be present. In contrast, when a feature or element is referred to as being "directly on" another feature or element, there are no intervening features or elements present. It will also be understood that, when a feature or element is referred to as being "connected", "attached" or "coupled" to another feature or element, it can be directly connected, attached or coupled to the other feature or element or intervening features or elements may be present. In contrast, when a feature or element is referred to as being "directly connected", "directly attached" or "directly coupled" to another feature or element, there are no intervening features or elements present. Although described or shown with respect to one embodiment, the features and elements so described or shown can apply to other embodiments. It will also be appreciated by those of skill in the art that references to a structure or feature that is disposed "adjacent" another feature may have portions that overlap or underlie the adjacent feature.

Although various illustrative embodiments are described above, any of a number of changes may be made to various embodiments without departing from the scope of the invention as described by the claims. For example, the order in which various described method steps are performed may often be changed in alternative embodiments, and in other alternative embodiments one or more method steps may be skipped altogether. Optional features of various device and system embodiments may be included in some embodiments and not in others. Therefore, the foregoing description is provided primarily for exemplary purposes and should not be interpreted to limit the scope of the invention as it is set forth in the claims.

The examples and illustrations included herein show, by way of illustration and not of limitation, specific embodiments in which the subject matter may be practiced. As mentioned, other embodiments may be utilized and derived there from, such that structural and logical substitutions and changes may be made without departing from the scope of this disclosure. Such embodiments of the inventive subject matter may be referred to herein individually or collectively by the term "invention" merely for convenience and without intending to voluntarily limit the scope of this application to any single invention or inventive concept, if more than one is, in fact, disclosed. Thus, although specific embodiments have been illustrated and described herein, any arrangement calculated to achieve the same purpose may be substituted for the specific embodiments shown. This disclosure is intended to cover any and all adaptations or variations of various embodiments. Combinations of the above embodiments, and other embodiments not specifically described herein, will be apparent to those of skill in the art upon reviewing the above description.

All publications and patent applications mentioned in this specification are herein incorporated by reference in their entirety to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference, especially referenced is disclosure appearing in the same sentence, paragraph, page or section of the specification in which the incorporation by reference appears.

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<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(7)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(13)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (24)..(24)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (36)..(36)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (51)..(51)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(60)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (66)..(66)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (87)..(87)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (90)..(90)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 5

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nrn mrn nhn vmn nyn ryn rvn syn ghn arr car vyn ykn ary tty gay       48
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Phe Asp
1               5                   10                  15

ytn ytn aar ytn gcn ggn gay gtn gar tcn aay ccn ggn ccn               90
Leu Leu Lys Leu Ala Gly Asp Val Glu Xaa Asn Pro Gly Pro
            20                  25                  30
```

<210> SEQ ID NO 6
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: The 'Xaa' at location 1 stands for Arg, Ser, Lys, Asn, Gly, Glu, Asp, Gln, His, Trp, Cys, or Tyr.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: The 'Xaa' at location 2 stands for Arg, Ser, Lys, Asn, Gln, or His.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: The 'Xaa' at location 3 stands for Lys, Asn, Thr, Ile, Met, Glu, Asp, Ala, Val, Gln, His, Pro, Leu, Tyr, Ser, or Phe.
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys, Asn, Thr, Glu, Asp, Ala, Gln, His, or Pro.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: The 'Xaa' at location 5 stands for Thr, Ile, Met, Ala, Val, Pro, Leu, Ser, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: The 'Xaa' at location 6 stands for Ala, Val, Thr, Ile, or Met.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: The 'Xaa' at location 7 stands for Glu, Asp, Gly, Ala, Lys, Asn, Arg, Ser, or Thr.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: The 'Xaa' at location 8 stands for Ala, Val, Pro, or Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: The 'Xaa' at location 9 stands for Glu, Asp, Ala, or Val.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: The 'Xaa' at location 10 stands for Arg, or Lys.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: The 'Xaa' at location 12 stands for Thr, Ile, Met, Ala, Val, Pro, or Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: The 'Xaa' at location 13 stands for Arg, Leu, Trp, Cys, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: The 'Xaa' at location 14 stands for Ser, or Asn.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: The 'Xaa' at location 26 stands for Ser.
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 6

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Phe Asp
1 5 10 15

Leu Leu Lys Leu Ala Gly Asp Val Glu Xaa Asn Pro Gly Pro
20 25 30

<210> SEQ ID NO 7
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Translation interrupter motif 2
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(57)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (24)..(24)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (33)..(33)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (51)..(51)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(57)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 7

```
ryn hbn ary wwn kmn ctn ctn mwn cdn gcn ggn gay rtn gar wsn aay       48
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Gly Asp Xaa Glu Ser Asn
1               5                   10                  15

ccn ggn ccn                                                           57
Pro Gly Pro
```

<210> SEQ ID NO 8
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: The 'Xaa' at location 1 stands for Ala, Val, Thr, Ile, or Met.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: The 'Xaa' at location 2 stands for Arg, Ser,

Thr, Ile, Met, Pro, Leu, Trp, Cys, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: The 'Xaa' at location 3 stands for Ser, or Asn.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys, Asn, Ile, Met, Tyr, Leu, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: The 'Xaa' at location 5 stands for Glu, Asp, Ala, Tyr, or Ser.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: The 'Xaa' at location 6 stands for Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: The 'Xaa' at location 7 stands for Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: The 'Xaa' at location 8 stands for Lys, Asn, Ile, Met, Gln, His, or Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: The 'Xaa' at location 9 stands for Gln, His, Arg, or Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: The 'Xaa' at location 13 stands for Val, Ile, or Met.
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 8

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Gly Asp Xaa Glu Ser Asn
1 5 10 15

Pro Gly Pro

<210> SEQ ID NO 9
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Translation interruptor motif 3
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(30)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (24)..(24)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 9

gcn ggn gay rtn gar wsn aay ccn ggn ccn 30
Ala Gly Asp Xaa Glu Ser Asn Pro Gly Pro
1 5 10

<210> SEQ ID NO 10
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: The 'Xaa' at location 4 stands for Val, Ile, or Met.
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 10

Ala Gly Asp Xaa Glu Ser Asn Pro Gly Pro
1 5 10

<210> SEQ ID NO 11
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Translation interruptor 4
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(42)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(12)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (22)..(24)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(30)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(36)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (42)..(42)
<223> OTHER INFORMATION: n is a, c, g, or t

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<400> SEQUENCE: 11

ctn ctn nnn nnn gcn ggn gay nnn gar nnn aay ccn ggn ccn 42
Xaa Xaa Xaa Xaa Ala Gly Asp Xaa Glu Xaa Asn Pro Gly Pro
1 5 10

<210> SEQ ID NO 12
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: The 'Xaa' at location 1 stands for Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: The 'Xaa' at location 2 stands for Leu.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: The 'Xaa' at location 3 stands for Lys, Asn,
Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro,
Leu, Tyr, Trp, Cys, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys, Asn,
Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro,
Leu, Tyr, Trp, Cys, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: The 'Xaa' at location 8 stands for Lys, Asn,
Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro,
Leu, Tyr, Trp, Cys, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: The 'Xaa' at location 10 stands for Lys, Asn,
Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro,
Leu, Tyr, Trp, Cys, or Phe.
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 12

Xaa Xaa Xaa Xaa Ala Gly Asp Xaa Glu Xaa Asn Pro Gly Pro
1 5 10

<210> SEQ ID NO 13
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Translation interruptor sequence 5
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(24)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (24)..(24)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 13

gay nnn gar nnn aay ccn ggn ccn 24
Asp Xaa Glu Xaa Asn Pro Gly Pro
1 5

<210> SEQ ID NO 14
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: The 'Xaa' at location 2 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 14

Asp Xaa Glu Xaa Asn Pro Gly Pro
1 5

<210> SEQ ID NO 15
<211> LENGTH: 90
<212> TYPE: DNA
<213> ORGANISM: Foot-and-mouth disease virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(90)
<223> OTHER INFORMATION: Delta-2A

<400> SEQUENCE: 15

cac aag caa aag atc att gca cca gca aag cag ctt ctg aat ttt gac 48
His Lys Gln Lys Ile Ile Ala Pro Ala Lys Gln Leu Leu Asn Phe Asp
1 5 10 15

ctg ctc aag ttg gcc gga gac gtt gag tcc aac cct gga ccc 90
Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25 30

<210> SEQ ID NO 16
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Foot-and-mouth disease virus

<400> SEQUENCE: 16

His Lys Gln Lys Ile Ile Ala Pro Ala Lys Gln Leu Leu Asn Phe Asp
1 5 10 15

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25 30

<210> SEQ ID NO 17
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Foot-and-mouth disease virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(60)
<223> OTHER INFORMATION: FMDV 2A polynucleotide

<400> SEQUENCE: 17

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cag ctt ctg aat ttt gac ctg ctc aag ttg gcc gga gac gtt gag tcc       48
Gln Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1               5                   10                  15

aac cct ggg ccc                                                     60
Asn Pro Gly Pro
            20


<210> SEQ ID NO 18
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Foot-and-mouth disease virus

<400> SEQUENCE: 18

Gln Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1               5                   10                  15

Asn Pro Gly Pro
            20


<210> SEQ ID NO 19
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Bovine rhinitis virus A
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(63)
<223> OTHER INFORMATION: Bovine rhinitis A 2A

<400> SEQUENCE: 19

tct ggt ata agc aac aag gac ctg cta ttg cag gcc ggt gat gtt gag       48
Ser Gly Ile Ser Asn Lys Asp Leu Leu Leu Gln Ala Gly Asp Val Glu
1               5                   10                  15

aca aac cct ggt ccc                                                 63
Thr Asn Pro Gly Pro
            20


<210> SEQ ID NO 20
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Bovine rhinitis virus A

<400> SEQUENCE: 20

Ser Gly Ile Ser Asn Lys Asp Leu Leu Leu Gln Ala Gly Asp Val Glu
1               5                   10                  15

Thr Asn Pro Gly Pro
            20


<210> SEQ ID NO 21
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Equine rhinitis B
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(51)
<223> OTHER INFORMATION: Equine rhinitis B 2A

<400> SEQUENCE: 21

aac ttt gac ctg ctc aaa ctg gca ggc gat gtg gaa tca aac cca ggc       48
Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
1               5                   10                  15

ccc                                                                 51
Pro


<210> SEQ ID NO 22
<211> LENGTH: 17
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<212> TYPE: PRT
<213> ORGANISM: Equine rhinitis B

<400> SEQUENCE: 22

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
1 5 10 15

Pro

<210> SEQ ID NO 23
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(570)
<223> OTHER INFORMATION: Porcine Interferon Alpha

<400> SEQUENCE: 23

atg gcc cca acc tca gcc ttc ctc acg gcc ctg gtg cta ctc agc tgc 48
Met Ala Pro Thr Ser Ala Phe Leu Thr Ala Leu Val Leu Leu Ser Cys
1 5 10 15

aat gcc atc tgc tct ctg ggc tgt gac ctg cct cag acc cac agc ctg 96
Asn Ala Ile Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30

gct cac acc aga gcc ctg agg ctc ctg gca caa atg agg aga atc tct 144
Ala His Thr Arg Ala Leu Arg Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45

ccc ttc tcc tgc ctg gac cac aga agg gac ttt ggt tcc cct cat gag 192
Pro Phe Ser Cys Leu Asp His Arg Arg Asp Phe Gly Ser Pro His Glu
50 55 60

gct ttt ggg ggc aac cag gtc cag aag gct caa gcc atg gct ctg gtg 240
Ala Phe Gly Gly Asn Gln Val Gln Lys Ala Gln Ala Met Ala Leu Val
65 70 75 80

cat gag atg ctc cag cag acc ttc cag ctc ttc agc aca gag ggc tcg 288
His Glu Met Leu Gln Gln Thr Phe Gln Leu Phe Ser Thr Glu Gly Ser
85 90 95

gct gct gcc tgg aat gag agc ctc ctg cac cag ttc tgc act gga ctg 336
Ala Ala Ala Trp Asn Glu Ser Leu Leu His Gln Phe Cys Thr Gly Leu
100 105 110

gat cag cag ctc agg gac ctg gaa gcc tgt gtc atg cag gag gcg ggg 384
Asp Gln Gln Leu Arg Asp Leu Glu Ala Cys Val Met Gln Glu Ala Gly
115 120 125

ctg gaa ggg acc ccc ctg ctg gag gag gac tcc atc ctg gct gtg agg 432
Leu Glu Gly Thr Pro Leu Leu Glu Glu Asp Ser Ile Leu Ala Val Arg
130 135 140

aaa tac ttc cac aga ctc acc ctc tat ctg caa gag aag agc tac agc 480
Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln Glu Lys Ser Tyr Ser
145 150 155 160

ccc tgt gcc tgg gag atc gtc agg gca gaa gtc atg aga tcc ttc tct 528
Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Val Met Arg Ser Phe Ser
165 170 175

tcc tcc aga aac ctg caa gac aga ctc agg aag aag gag tga 570
Ser Ser Arg Asn Leu Gln Asp Arg Leu Arg Lys Lys Glu
180 185

<210> SEQ ID NO 24
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 24

Met Ala Pro Thr Ser Ala Phe Leu Thr Ala Leu Val Leu Leu Ser Cys

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1               5                   10                  15

Asn Ala Ile Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
            20                  25                  30

Ala His Thr Arg Ala Leu Arg Leu Leu Ala Gln Met Arg Arg Ile Ser
        35                  40                  45

Pro Phe Ser Cys Leu Asp His Arg Arg Asp Phe Gly Ser Pro His Glu
    50                  55                  60

Ala Phe Gly Gly Asn Gln Val Gln Lys Ala Gln Ala Met Ala Leu Val
65                  70                  75                  80

His Glu Met Leu Gln Gln Thr Phe Gln Leu Phe Ser Thr Glu Gly Ser
                85                  90                  95

Ala Ala Ala Trp Asn Glu Ser Leu Leu His Gln Phe Cys Thr Gly Leu
            100                 105                 110

Asp Gln Gln Leu Arg Asp Leu Glu Ala Cys Val Met Gln Glu Ala Gly
        115                 120                 125

Leu Glu Gly Thr Pro Leu Leu Glu Glu Asp Ser Ile Leu Ala Val Arg
    130                 135                 140

Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln Glu Lys Ser Tyr Ser
145                 150                 155                 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Val Met Arg Ser Phe Ser
                165                 170                 175

Ser Ser Arg Asn Leu Gln Asp Arg Leu Arg Lys Lys Glu
            180                 185


<210> SEQ ID NO 25
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(66)
<223> OTHER INFORMATION: Porcine Interferon Alpha Secretion Peptide

<400> SEQUENCE: 25

atg gcc cca acc tca gcc ttc ctc acg gcc ctg gtg cta ctc agc tgc       48
Met Ala Pro Thr Ser Ala Phe Leu Thr Ala Leu Val Leu Leu Ser Cys
1               5                   10                  15

aat gcc atc tgc tct ctg                                              66
Asn Ala Ile Cys Ser Leu
            20


<210> SEQ ID NO 26
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 26

Met Ala Pro Thr Ser Ala Phe Leu Thr Ala Leu Val Leu Leu Ser Cys
1               5                   10                  15

Asn Ala Ile Cys Ser Leu
            20


<210> SEQ ID NO 27
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(69)
<223> OTHER INFORMATION: Human Interferon Alpha Secretion peptide
```

-continued

<400> SEQUENCE: 27

atg gcc tcg ccc ttt gct tta ctg atg gtc ctg gtg gtg ctc agc tgc 48
Met Ala Ser Pro Phe Ala Leu Leu Met Val Leu Val Val Leu Ser Cys
1 5 10 15

aag tca agc tgc tct ccg ggc 69
Lys Ser Ser Cys Ser Pro Gly
20

<210> SEQ ID NO 28
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

Met Ala Ser Pro Phe Ala Leu Leu Met Val Leu Val Val Leu Ser Cys
1 5 10 15

Lys Ser Ser Cys Ser Pro Gly
20

<210> SEQ ID NO 29
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(63)
<223> OTHER INFORMATION: Bovine Interferon Beta Secretion Peptide

<400> SEQUENCE: 29

atg acc tac cgg tgc ctc ctc cag atg gtt ctc ctg ctg tgt ttc tcc 48
Met Thr Tyr Arg Cys Leu Leu Gln Met Val Leu Leu Leu Cys Phe Ser
1 5 10 15

acc aca gct ctt tcc 63
Thr Thr Ala Leu Ser
20

<210> SEQ ID NO 30
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 30

Met Thr Tyr Arg Cys Leu Leu Gln Met Val Leu Leu Leu Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser
20

<210> SEQ ID NO 31
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(63)
<223> OTHER INFORMATION: Porcine Interferon Beta Secretion Peptide

<400> SEQUENCE: 31

atg gct aac aag tgc atc ctc caa atc gct ctc ctg atg tgt ttc tcc 48
Met Ala Asn Lys Cys Ile Leu Gln Ile Ala Leu Leu Met Cys Phe Ser
1 5 10 15

acc aca gct ctt tcc 63
Thr Thr Ala Leu Ser
20

-continued

<210> SEQ ID NO 32
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 32

Met Ala Asn Lys Cys Ile Leu Gln Ile Ala Leu Leu Met Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser
20

<210> SEQ ID NO 33
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(63)
<223> OTHER INFORMATION: Human Interferon Beta Secretion peptide

<400> SEQUENCE: 33

atg acc aac aag tgt ctc ctc caa att gct ctc ctg ttg tgc ttc tcc 48
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1 5 10 15

acg aca gct ctt tcc 63
Thr Thr Ala Leu Ser
20

<210> SEQ ID NO 34
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser
20

<210> SEQ ID NO 35
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(69)
<223> OTHER INFORMATION: Bovine Interferon Gamma Secretion peptide

<400> SEQUENCE: 35

atg aaa tat aca agc tat ttc tta gct tta ctg ctc tgt ggg ctt ttg 48
Met Lys Tyr Thr Ser Tyr Phe Leu Ala Leu Leu Leu Cys Gly Leu Leu
1 5 10 15

ggt ttt tct ggt tct tat ggc 69
Gly Phe Ser Gly Ser Tyr Gly
20

<210> SEQ ID NO 36
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 36

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

Gly Phe Ser Gly Ser Tyr Gly

```
            20


<210> SEQ ID NO 37
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(69)
<223> OTHER INFORMATION: Porcine Interferon Gamma Secretion peptide

<400> SEQUENCE: 37

atg agt tat aca act tat ttc tta gct ttt cag ctt tgc gtg act ttg       48
Met Ser Tyr Thr Thr Tyr Phe Leu Ala Phe Gln Leu Cys Val Thr Leu
1               5                   10                  15

tgt ttt tct ggc tct tac tgc                                         69
Cys Phe Ser Gly Ser Tyr Cys
            20


<210> SEQ ID NO 38
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 38

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

Cys Phe Ser Gly Ser Tyr Cys
            20


<210> SEQ ID NO 39
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(69)
<223> OTHER INFORMATION: Human Interferon Gamma Secretion peptide

<400> SEQUENCE: 39

atg aaa tat aca agt tat atc ttg gct ttt cag ctc tgc atc gtt ttg       48
Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1               5                   10                  15

ggt tct ctt ggc tgt tac tgc                                         69
Gly Ser Leu Gly Cys Tyr Cys
            20


<210> SEQ ID NO 40
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

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

Gly Ser Leu Gly Cys Tyr Cys
            20


<210> SEQ ID NO 41
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(57)
<223> OTHER INFORMATION: Bovine Interferon Lambda Secretion peptide
```

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<400> SEQUENCE: 41

atg gcc ccg ggc tgc acg ctg gtg ctg gtg ctg atg ctg acg acc gtg 48
Met Ala Pro Gly Cys Thr Leu Val Leu Val Leu Met Leu Thr Thr Val
1 5 10 15

gcg ctg agc 57
Ala Leu Ser

<210> SEQ ID NO 42
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 42

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

Ala Leu Ser

<210> SEQ ID NO 43
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(48)
<223> OTHER INFORMATION: Porcine Interferon Lambda Secretion peptide

<400> SEQUENCE: 43

atg gct aca gct tgg atc gtg gtg ctg gcg act gtg atg ctg gac ttg 48
Met Ala Thr Ala Trp Ile Val Val Leu Ala Thr Val Met Leu Asp Leu
1 5 10 15

<210> SEQ ID NO 44
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 44

Met Ala Thr Ala Trp Ile Val Val Leu Ala Thr Val Met Leu Asp Leu
1 5 10 15

<210> SEQ ID NO 45
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(45)
<223> OTHER INFORMATION: Human Interferon Lambda Secretion peptide

<400> SEQUENCE: 45

atg gct gca gct tgg acc gtg gtg ctg gtg act ttg gtg cta ggc 45
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly
1 5 10 15

<210> SEQ ID NO 46
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly
1 5 10 15

<210> SEQ ID NO 47

-continued

<211> LENGTH: 1065
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1065)
<223> OTHER INFORMATION: Porcine SGLucON Alpha

<400> SEQUENCE: 47

```
atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttt gcg acc acg gat ctc gat gct gac cga ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag tgg ctc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gat att cct gag att cct ggg ttc aag gac ttg gag cca atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc ggg tgt gac ctg cct      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gly Cys Asp Leu Pro
            180                 185                 190

cag acc cac agc ctg gct cac acc aga gcc ctg agg ctc ctg gca caa      624
Gln Thr His Ser Leu Ala His Thr Arg Ala Leu Arg Leu Leu Ala Gln
        195                 200                 205

atg agg aga atc tct ccc ttc tcc tgc ctg gac cac aga agg gac ttt      672
Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Asp His Arg Arg Asp Phe
    210                 215                 220

ggt tcc cct cat gag gct ttt ggg ggc aac cag gtc cag aag gct caa      720
Gly Ser Pro His Glu Ala Phe Gly Gly Asn Gln Val Gln Lys Ala Gln
225                 230                 235                 240

gcc atg gct ctg gtg cat gag atg ctc cag cag acc ttc cag ctc ttc      768
Ala Met Ala Leu Val His Glu Met Leu Gln Gln Thr Phe Gln Leu Phe
                245                 250                 255

agc aca gag ggc tcg gct gct gcc tgg aat gag agc ctc ctg cac cag      816
Ser Thr Glu Gly Ser Ala Ala Ala Trp Asn Glu Ser Leu Leu His Gln
            260                 265                 270

ttc tgc act gga ctg gat cag cag ctc agg gac ctg gaa gcc tgt gtc      864
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Phe Cys Thr Gly Leu Asp Gln Gln Leu Arg Asp Leu Glu Ala Cys Val
        275                 280                 285

atg cag gag gcg ggg ctg gaa ggg acc ccc ctg ctg gag gag gac tcc      912
Met Gln Glu Ala Gly Leu Glu Gly Thr Pro Leu Leu Glu Glu Asp Ser
    290                 295                 300

atc ctg gct gtg agg aaa tac ttc cac aga ctc acc ctc tat ctg caa      960
Ile Leu Ala Val Arg Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln
305                 310                 315                 320

gag aag agc tac agc ccc tgt gcc tgg gag atc gtc agg gca gaa gtc     1008
Glu Lys Ser Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Val
                325                 330                 335

atg aga tcc ttc tct tcc tcc aga aac ctg caa gac aga ctc agg aag     1056
Met Arg Ser Phe Ser Ser Ser Arg Asn Leu Gln Asp Arg Leu Arg Lys
            340                 345                 350

aag gag tga                                                        1065
Lys Glu


<210> SEQ ID NO 48
<211> LENGTH: 354
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 48

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gly Cys Asp Leu Pro
            180                 185                 190

Gln Thr His Ser Leu Ala His Thr Arg Ala Leu Arg Leu Leu Ala Gln
        195                 200                 205

Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Asp His Arg Arg Asp Phe
    210                 215                 220

Gly Ser Pro His Glu Ala Phe Gly Gly Asn Gln Val Gln Lys Ala Gln
225                 230                 235                 240

Ala Met Ala Leu Val His Glu Met Leu Gln Gln Thr Phe Gln Leu Phe
                245                 250                 255

Ser Thr Glu Gly Ser Ala Ala Ala Trp Asn Glu Ser Leu Leu His Gln
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            260                 265                 270

Phe Cys Thr Gly Leu Asp Gln Gln Leu Arg Asp Leu Glu Ala Cys Val
        275                 280                 285

Met Gln Glu Ala Gly Leu Glu Gly Thr Pro Leu Leu Glu Glu Asp Ser
    290                 295                 300

Ile Leu Ala Val Arg Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln
305                 310                 315                 320

Glu Lys Ser Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Val
                325                 330                 335

Met Arg Ser Phe Ser Ser Ser Arg Asn Leu Gln Asp Arg Leu Arg Lys
            340                 345                 350

Lys Glu


<210> SEQ ID NO 49
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(570)
<223> OTHER INFORMATION: Human Interferon Alpha

<400> SEQUENCE: 49

atg gcc tcg ccc ttt gct tta ctg atg gtc ctg gtg gtg ctc agc tgc       48
Met Ala Ser Pro Phe Ala Leu Leu Met Val Leu Val Val Leu Ser Cys
1               5                   10                  15

aag tca agc tgc tct ccg ggc tgt gat ctc cct gag acc cac agc ctg       96
Lys Ser Ser Cys Ser Pro Gly Cys Asp Leu Pro Glu Thr His Ser Leu
            20                  25                  30

gat aac agg agg acc ttg atg ctc ctg gca caa atg agc aga atc tct      144
Asp Asn Arg Arg Thr Leu Met Leu Leu Ala Gln Met Ser Arg Ile Ser
        35                  40                  45

cct tcc tcc tgt ctg atg gac aga cat gac ttt gga ttt ccc cag gag      192
Pro Ser Ser Cys Leu Met Asp Arg His Asp Phe Gly Phe Pro Gln Glu
    50                  55                  60

gag ttt gat ggc aac cag ttc cag aag gct cca gcc atc tct gtc ctc      240
Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Pro Ala Ile Ser Val Leu
65                  70                  75                  80

caa gag ctg atc cag cag atc ttc aac ctc ttt acc aca aaa gat tca      288
Gln Glu Leu Ile Gln Gln Ile Phe Asn Leu Phe Thr Thr Lys Asp Ser
                85                  90                  95

tct gct gct tgg gat gag gac ctc cta gac aaa ttc tgc acc gaa ctc      336
Ser Ala Ala Trp Asp Glu Asp Leu Leu Asp Lys Phe Cys Thr Glu Leu
            100                 105                 110

tac cag cag ctg aat gac ttg gaa gcc tgt gtg atg cag gag gag agg      384
Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Met Gln Glu Glu Arg
        115                 120                 125

gtg gga gaa act ccc ctg atg aat gcg gac tcc atc ttg gct gtg aag      432
Val Gly Glu Thr Pro Leu Met Asn Ala Asp Ser Ile Leu Ala Val Lys
    130                 135                 140

aaa tac ttc cga aga atc act ctc tat ctg acg gag aag aaa tac agc      480
Lys Tyr Phe Arg Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
145                 150                 155                 160

cct tgt gcc tgg gag gtt gtc aga gca gaa atc gtg aga tcc ctc tct      528
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Val Arg Ser Leu Ser
                165                 170                 175

tta tca aca aac ttg caa gaa aga tta agg agg aag gaa taa              570
Leu Ser Thr Asn Leu Gln Glu Arg Leu Arg Arg Lys Glu
            180                 185
```

<210> SEQ ID NO 50
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

Met Ala Ser Pro Phe Ala Leu Leu Met Val Leu Val Val Leu Ser Cys
1 5 10 15

Lys Ser Ser Cys Ser Pro Gly Cys Asp Leu Pro Glu Thr His Ser Leu
20 25 30

Asp Asn Arg Arg Thr Leu Met Leu Leu Ala Gln Met Ser Arg Ile Ser
35 40 45

Pro Ser Ser Cys Leu Met Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60

Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Pro Ala Ile Ser Val Leu
65 70 75 80

Gln Glu Leu Ile Gln Gln Ile Phe Asn Leu Phe Thr Thr Lys Asp Ser
85 90 95

Ser Ala Ala Trp Asp Glu Asp Leu Leu Asp Lys Phe Cys Thr Glu Leu
100 105 110

Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Met Gln Glu Glu Arg
115 120 125

Val Gly Glu Thr Pro Leu Met Asn Ala Asp Ser Ile Leu Ala Val Lys
130 135 140

Lys Tyr Phe Arg Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
145 150 155 160

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Val Arg Ser Leu Ser
165 170 175

Leu Ser Thr Asn Leu Gln Glu Arg Leu Arg Arg Lys Glu
180 185

<210> SEQ ID NO 51
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1056)
<223> OTHER INFORMATION: Human GlucON Alpha

<400> SEQUENCE: 51

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag 48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1 5 10 15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc 96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
20 25 30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc 144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
35 40 45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc 192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
50 55 60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc 240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65 70 75 80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc 288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
85 90 95

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tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac tgt gat ctc cct gag acc cac      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Cys Asp Leu Pro Glu Thr His
            180                 185                 190

agc ctg gat aac agg agg acc ttg atg ctc ctg gca caa atg agc aga      624
Ser Leu Asp Asn Arg Arg Thr Leu Met Leu Leu Ala Gln Met Ser Arg
        195                 200                 205

atc tct cct tcc tcc tgt ctg atg gac aga cat gac ttt gga ttt ccc      672
Ile Ser Pro Ser Ser Cys Leu Met Asp Arg His Asp Phe Gly Phe Pro
    210                 215                 220

cag gag gag ttt gat ggc aac cag ttc cag aag gct cca gcc atc tct      720
Gln Glu Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Pro Ala Ile Ser
225                 230                 235                 240

gtc ctc caa gag ctg atc cag cag atc ttc aac ctc ttt acc aca aaa      768
Val Leu Gln Glu Leu Ile Gln Gln Ile Phe Asn Leu Phe Thr Thr Lys
                245                 250                 255

gat tca tct gct gct tgg gat gag gac ctc cta gac aaa ttc tgc acc      816
Asp Ser Ser Ala Ala Trp Asp Glu Asp Leu Leu Asp Lys Phe Cys Thr
            260                 265                 270

gaa ctc tac cag cag ctg aat gac ttg gaa gcc tgt gtg atg cag gag      864
Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Met Gln Glu
        275                 280                 285

gag agg gtg gga gaa act ccc ctg atg aat gcg gac tcc atc ttg gct      912
Glu Arg Val Gly Glu Thr Pro Leu Met Asn Ala Asp Ser Ile Leu Ala
    290                 295                 300

gtg aag aaa tac ttc cga aga atc act ctc tat ctg acg gag aag aaa      960
Val Lys Lys Tyr Phe Arg Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys
305                 310                 315                 320

tac agc cct tgt gcc tgg gag gtt gtc aga gca gaa atc gtg aga tcc     1008
Tyr Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Val Arg Ser
                325                 330                 335

ctc tct tta tca aca aac ttg caa gaa aga tta agg agg aag gaa taa     1056
Leu Ser Leu Ser Thr Asn Leu Gln Glu Arg Leu Arg Arg Lys Glu
            340                 345                 350
```

<210> SEQ ID NO 52
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30
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Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Cys Asp Leu Pro Glu Thr His
            180                 185                 190

Ser Leu Asp Asn Arg Arg Thr Leu Met Leu Leu Ala Gln Met Ser Arg
        195                 200                 205

Ile Ser Pro Ser Ser Cys Leu Met Asp Arg His Asp Phe Gly Phe Pro
    210                 215                 220

Gln Glu Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Pro Ala Ile Ser
225                 230                 235                 240

Val Leu Gln Glu Leu Ile Gln Gln Ile Phe Asn Leu Phe Thr Thr Lys
                245                 250                 255

Asp Ser Ser Ala Ala Trp Asp Glu Asp Leu Leu Asp Lys Phe Cys Thr
            260                 265                 270

Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Met Gln Glu
        275                 280                 285

Glu Arg Val Gly Glu Thr Pro Leu Met Asn Ala Asp Ser Ile Leu Ala
    290                 295                 300

Val Lys Lys Tyr Phe Arg Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys
305                 310                 315                 320

Tyr Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Val Arg Ser
                325                 330                 335

Leu Ser Leu Ser Thr Asn Leu Gln Glu Arg Leu Arg Arg Lys Glu
            340                 345                 350


<210> SEQ ID NO 53
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(570)
<223> OTHER INFORMATION: Bovine Interferon Alpha

<400> SEQUENCE: 53

atg gcc cca gcc tgg tcc ttc ctg cta tcc ctg ttg ctg ctc agc tgc       48
Met Ala Pro Ala Trp Ser Phe Leu Leu Ser Leu Leu Leu Leu Ser Cys
1               5                   10                  15

aac gcc atc tgc tct ctg ggt tgc cac ctg cct cac acc cac agc ctg       96
Asn Ala Ile Cys Ser Leu Gly Cys His Leu Pro His Thr His Ser Leu
            20                  25                  30
```

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```
gcc aac agg agg gtc ctg atg ctc ctg caa caa ctg aga agg gtc tcc      144
Ala Asn Arg Arg Val Leu Met Leu Leu Gln Gln Leu Arg Arg Val Ser
        35                  40                  45

cct tcc tcc tgc ctg cag gac aga aat gac ttc gaa ttc ctc cag gag      192
Pro Ser Ser Cys Leu Gln Asp Arg Asn Asp Phe Glu Phe Leu Gln Glu
    50                  55                  60

gct ctg ggt ggc agc cag ttg cag aag gct caa gcc atc tct gtg ctc      240
Ala Leu Gly Gly Ser Gln Leu Gln Lys Ala Gln Ala Ile Ser Val Leu
65                  70                  75                  80

cac gag gtg acc cag cac acc ttc cag ctc ttc agc aca gag ggc tcg      288
His Glu Val Thr Gln His Thr Phe Gln Leu Phe Ser Thr Glu Gly Ser
                85                  90                  95

ccc gcc acg tgg gac aag agc ctc ctg gac aag cta cgc gct gcg ctg      336
Pro Ala Thr Trp Asp Lys Ser Leu Leu Asp Lys Leu Arg Ala Ala Leu
            100                 105                 110

gat cag cag ctc act gac ctg caa gcc tgt ctg acg cag gag gag ggg      384
Asp Gln Gln Leu Thr Asp Leu Gln Ala Cys Leu Thr Gln Glu Glu Gly
        115                 120                 125

ctg cga ggg gct ccc ctg ctc aag gag gac tcc agc ctg gct gtg agg      432
Leu Arg Gly Ala Pro Leu Leu Lys Glu Asp Ser Ser Leu Ala Val Arg
    130                 135                 140

aaa tac ttc cac aga ctc act ctc tat ctg caa gag aag aga cac agc      480
Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln Glu Lys Arg His Ser
145                 150                 155                 160

cct tgt gcc tgg gag gtt gtc aga gca gaa gtc atg aga gcc ttc tct      528
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Met Arg Ala Phe Ser
                165                 170                 175

tcc tca aca aac ttg cag gag agt ttc agg aga aag gac tga              570
Ser Ser Thr Asn Leu Gln Glu Ser Phe Arg Arg Lys Asp
            180                 185


<210> SEQ ID NO 54
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 54

Met Ala Pro Ala Trp Ser Phe Leu Leu Ser Leu Leu Leu Leu Ser Cys
1               5                   10                  15

Asn Ala Ile Cys Ser Leu Gly Cys His Leu Pro His Thr His Ser Leu
            20                  25                  30

Ala Asn Arg Arg Val Leu Met Leu Leu Gln Gln Leu Arg Arg Val Ser
        35                  40                  45

Pro Ser Ser Cys Leu Gln Asp Arg Asn Asp Phe Glu Phe Leu Gln Glu
    50                  55                  60

Ala Leu Gly Gly Ser Gln Leu Gln Lys Ala Gln Ala Ile Ser Val Leu
65                  70                  75                  80

His Glu Val Thr Gln His Thr Phe Gln Leu Phe Ser Thr Glu Gly Ser
                85                  90                  95

Pro Ala Thr Trp Asp Lys Ser Leu Leu Asp Lys Leu Arg Ala Ala Leu
            100                 105                 110

Asp Gln Gln Leu Thr Asp Leu Gln Ala Cys Leu Thr Gln Glu Glu Gly
        115                 120                 125

Leu Arg Gly Ala Pro Leu Leu Lys Glu Asp Ser Ser Leu Ala Val Arg
    130                 135                 140

Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln Glu Lys Arg His Ser
145                 150                 155                 160
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Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Met Arg Ala Phe Ser
                165                 170                 175

Ser Ser Thr Asn Leu Gln Glu Ser Phe Arg Arg Lys Asp
            180                 185


<210> SEQ ID NO 55
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1056)
<223> OTHER INFORMATION: Bovine GlucON Alpha

<400> SEQUENCE: 55

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac tgc cac ctg cct cac acc cac      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Cys His Leu Pro His Thr His
            180                 185                 190

agc ctg gcc aac agg agg gtc ctg atg ctc ctg caa caa ctg aga agg      624
Ser Leu Ala Asn Arg Arg Val Leu Met Leu Leu Gln Gln Leu Arg Arg
        195                 200                 205

gtc tcc cct tcc tcc tgc ctg cag gac aga aat gac ttc gaa ttc ctc      672
Val Ser Pro Ser Ser Cys Leu Gln Asp Arg Asn Asp Phe Glu Phe Leu
    210                 215                 220

cag gag gct ctg ggt ggc agc cag ttg cag aag gct caa gcc atc tct      720
Gln Glu Ala Leu Gly Gly Ser Gln Leu Gln Lys Ala Gln Ala Ile Ser
225                 230                 235                 240

gtg ctc cac gag gtg acc cag cac acc ttc cag ctc ttc agc aca gag      768
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```
Val Leu His Glu Val Thr Gln His Thr Phe Gln Leu Phe Ser Thr Glu
                245                 250                 255

ggc tcg ccc gcc acg tgg gac aag agc ctc ctg gac aag cta cgc gct      816
Gly Ser Pro Ala Thr Trp Asp Lys Ser Leu Leu Asp Lys Leu Arg Ala
            260                 265                 270

gcg ctg gat cag cag ctc act gac ctg caa gcc tgt ctg acg cag gag      864
Ala Leu Asp Gln Gln Leu Thr Asp Leu Gln Ala Cys Leu Thr Gln Glu
        275                 280                 285

gag ggg ctg cga ggg gct ccc ctg ctc aag gag gac tcc agc ctg gct      912
Glu Gly Leu Arg Gly Ala Pro Leu Leu Lys Glu Asp Ser Ser Leu Ala
    290                 295                 300

gtg agg aaa tac ttc cac aga ctc act ctc tat ctg caa gag aag aga      960
Val Arg Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln Glu Lys Arg
305                 310                 315                 320

cac agc cct tgt gcc tgg gag gtt gtc aga gca gaa gtc atg aga gcc     1008
His Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Met Arg Ala
                325                 330                 335

ttc tct tcc tca aca aac ttg cag gag agt ttc agg aga aag gac tga     1056
Phe Ser Ser Ser Thr Asn Leu Gln Glu Ser Phe Arg Arg Lys Asp
            340                 345                 350


<210> SEQ ID NO 56
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 56

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Cys His Leu Pro His Thr His
            180                 185                 190

Ser Leu Ala Asn Arg Arg Val Leu Met Leu Leu Gln Gln Leu Arg Arg
        195                 200                 205

Val Ser Pro Ser Ser Cys Leu Gln Asp Arg Asn Asp Phe Glu Phe Leu
    210                 215                 220

Gln Glu Ala Leu Gly Gly Ser Gln Leu Gln Lys Ala Gln Ala Ile Ser
225                 230                 235                 240
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Val Leu His Glu Val Thr Gln His Thr Phe Gln Leu Phe Ser Thr Glu
                245                 250                 255

Gly Ser Pro Ala Thr Trp Asp Lys Ser Leu Leu Asp Lys Leu Arg Ala
            260                 265                 270

Ala Leu Asp Gln Gln Leu Thr Asp Leu Gln Ala Cys Leu Thr Gln Glu
        275                 280                 285

Glu Gly Leu Arg Gly Ala Pro Leu Leu Lys Glu Asp Ser Ser Leu Ala
    290                 295                 300

Val Arg Lys Tyr Phe His Arg Leu Thr Leu Tyr Leu Gln Glu Lys Arg
305                 310                 315                 320

His Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Met Arg Ala
                325                 330                 335

Phe Ser Ser Ser Thr Asn Leu Gln Glu Ser Phe Arg Arg Lys Asp
            340                 345                 350


<210> SEQ ID NO 57
<211> LENGTH: 564
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(564)
<223> OTHER INFORMATION: Human Interferon Beta

<400> SEQUENCE: 57

atg acc aac aag tgt ctc ctc caa att gct ctc ctg ttg tgc ttc tcc       48
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1               5                   10                  15

acg aca gct ctt tcc atg agc tac aac ttg ctt gga ttc cta caa aga       96
Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
            20                  25                  30

agc agc aat tgt cag tgt cag aag ctc ctg tgg caa ttg aat ggg agg      144
Ser Ser Asn Cys Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
        35                  40                  45

ctt gaa tac tgc ctc aag gac agg agg aac ttt gac atc cct gag gag      192
Leu Glu Tyr Cys Leu Lys Asp Arg Arg Asn Phe Asp Ile Pro Glu Glu
    50                  55                  60

att aag cag ctg cag cag ttc cag aag gag gac gcc gca gtg acc atc      240
Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Val Thr Ile
65                  70                  75                  80

tat gag atg ctc cag aac atc ttt gct att ttc aga caa gat tca tcg      288
Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
                85                  90                  95

agc act ggc tgg aat gag act att gtt gag aac ctc ctg gct aat gtc      336
Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

tat cat cag aga aac cat ctg aag aca gtc ctg gaa gaa aaa ctg gag      384
Tyr His Gln Arg Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

aaa gaa gat ttc acc agg gga aaa cgc atg agc agt ctg cac ctg aaa      432
Lys Glu Asp Phe Thr Arg Gly Lys Arg Met Ser Ser Leu His Leu Lys
    130                 135                 140

aga tat tat ggg agg att ctg cat tac ctg aag gcc aag gag gac agt      480
Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Asp Ser
145                 150                 155                 160

cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg aac ttt tac      528
His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

gtc att aac aga ctt aca ggt tac ctc cga aac tga                      564
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Val Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
            180                 185


<210> SEQ ID NO 58
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1               5                   10                  15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
            20                  25                  30

Ser Ser Asn Cys Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
        35                  40                  45

Leu Glu Tyr Cys Leu Lys Asp Arg Arg Asn Phe Asp Ile Pro Glu Glu
    50                  55                  60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Val Thr Ile
65                  70                  75                  80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
                85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

Tyr His Gln Arg Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

Lys Glu Asp Phe Thr Arg Gly Lys Arg Met Ser Ser Leu His Leu Lys
    130                 135                 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Asp Ser
145                 150                 155                 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

Val Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
            180                 185


<210> SEQ ID NO 59
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1056)
<223> OTHER INFORMATION: Human GlucON Beta

<400> SEQUENCE: 59

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80
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aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac atg agc tac aac ttg ctt gga      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Met Ser Tyr Asn Leu Leu Gly
            180                 185                 190

ttc cta caa aga agc agc aat tgt cag tgt cag aag ctc ctg tgg caa      624
Phe Leu Gln Arg Ser Ser Asn Cys Gln Cys Gln Lys Leu Leu Trp Gln
        195                 200                 205

ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg agg aac ttt gac      672
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Arg Asn Phe Asp
    210                 215                 220

atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc      720
Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
225                 230                 235                 240

gca gtg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga      768
Ala Val Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
                245                 250                 255

caa gat tca tcg agc act ggc tgg aat gag act att gtt gag aac ctc      816
Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
            260                 265                 270

ctg gct aat gtc tat cat cag aga aac cat ctg aag aca gtc ctg gaa      864
Leu Ala Asn Val Tyr His Gln Arg Asn His Leu Lys Thr Val Leu Glu
        275                 280                 285

gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa cgc atg agc agt      912
Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Arg Met Ser Ser
    290                 295                 300

ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc      960
Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
305                 310                 315                 320

aag gag gac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta     1008
Lys Glu Asp Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
                325                 330                 335

agg aac ttt tac gtc att aac aga ctt aca ggt tac ctc cga aac tga     1056
Arg Asn Phe Tyr Val Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
            340                 345                 350


<210> SEQ ID NO 60
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15
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Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Met Ser Tyr Asn Leu Leu Gly
            180                 185                 190

Phe Leu Gln Arg Ser Ser Asn Cys Gln Cys Gln Lys Leu Leu Trp Gln
        195                 200                 205

Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Arg Asn Phe Asp
    210                 215                 220

Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
225                 230                 235                 240

Ala Val Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
                245                 250                 255

Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
            260                 265                 270

Leu Ala Asn Val Tyr His Gln Arg Asn His Leu Lys Thr Val Leu Glu
        275                 280                 285

Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Arg Met Ser Ser
    290                 295                 300

Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
305                 310                 315                 320

Lys Glu Asp Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
                325                 330                 335

Arg Asn Phe Tyr Val Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
            340                 345                 350


<210> SEQ ID NO 61
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(561)
<223> OTHER INFORMATION: Bovine Interferon Beta

<400> SEQUENCE: 61

atg acc tac cgg tgc ctc ctc cag atg gtt ctc ctg ctg tgt ttc tcc       48
Met Thr Tyr Arg Cys Leu Leu Gln Met Val Leu Leu Leu Cys Phe Ser
1               5                   10                  15
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acc aca gct ctt tcc agg agc tac agc ttg ctt cga ttc caa caa cgt       96
Thr Thr Ala Leu Ser Arg Ser Tyr Ser Leu Leu Arg Phe Gln Gln Arg
            20                  25                  30

cag agc ctt aaa gag tgt cag aaa ctc ctg ggg cag tta cct tca act      144
Gln Ser Leu Lys Glu Cys Gln Lys Leu Leu Gly Gln Leu Pro Ser Thr
        35                  40                  45

cct caa cat tgc ctc gag gcc agg atg gac ttc cag atg cct gag gag      192
Pro Gln His Cys Leu Glu Ala Arg Met Asp Phe Gln Met Pro Glu Glu
    50                  55                  60

atg aag caa gaa cag cag ttc cag aag gaa gat gcc ata ttg gtc atg      240
Met Lys Gln Glu Gln Gln Phe Gln Lys Glu Asp Ala Ile Leu Val Met
65                  70                  75                  80

tat gag gtg ctc cag cac atc ttc ggc att ctc acc aga gac ttc tcc      288
Tyr Glu Val Leu Gln His Ile Phe Gly Ile Leu Thr Arg Asp Phe Ser
                85                  90                  95

agc act ggc tgg tct gag acc atc atc gag gac ctc ctt gag gaa ctc      336
Ser Thr Gly Trp Ser Glu Thr Ile Ile Glu Asp Leu Leu Glu Glu Leu
            100                 105                 110

tat ggg cag atg aat cgt ctg cag cca atc cag aag gaa ata atg cag      384
Tyr Gly Gln Met Asn Arg Leu Gln Pro Ile Gln Lys Glu Ile Met Gln
        115                 120                 125

aag caa aac acc aca gcg gga gac acg atc gtt ccc cac cta ggg aaa      432
Lys Gln Asn Thr Thr Ala Gly Asp Thr Ile Val Pro His Leu Gly Lys
    130                 135                 140

tat tac ttc aac ctc atg cag tac ctg gag tcc aag gag tac gac agg      480
Tyr Tyr Phe Asn Leu Met Gln Tyr Leu Glu Ser Lys Glu Tyr Asp Arg
145                 150                 155                 160

tgt gcc tgg aca gtc gtg caa gtg caa ata ctc acg aac gtt tct ttc      528
Cys Ala Trp Thr Val Val Gln Val Gln Ile Leu Thr Asn Val Ser Phe
                165                 170                 175

ctg atg aga cta aca ggt tac gtc cgt gac tga                          561
Leu Met Arg Leu Thr Gly Tyr Val Arg Asp
            180                 185


<210> SEQ ID NO 62
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 62

Met Thr Tyr Arg Cys Leu Leu Gln Met Val Leu Leu Leu Cys Phe Ser
1               5                   10                  15

Thr Thr Ala Leu Ser Arg Ser Tyr Ser Leu Leu Arg Phe Gln Gln Arg
            20                  25                  30

Gln Ser Leu Lys Glu Cys Gln Lys Leu Leu Gly Gln Leu Pro Ser Thr
        35                  40                  45

Pro Gln His Cys Leu Glu Ala Arg Met Asp Phe Gln Met Pro Glu Glu
    50                  55                  60

Met Lys Gln Glu Gln Gln Phe Gln Lys Glu Asp Ala Ile Leu Val Met
65                  70                  75                  80

Tyr Glu Val Leu Gln His Ile Phe Gly Ile Leu Thr Arg Asp Phe Ser
                85                  90                  95

Ser Thr Gly Trp Ser Glu Thr Ile Ile Glu Asp Leu Leu Glu Glu Leu
            100                 105                 110

Tyr Gly Gln Met Asn Arg Leu Gln Pro Ile Gln Lys Glu Ile Met Gln
        115                 120                 125

Lys Gln Asn Thr Thr Ala Gly Asp Thr Ile Val Pro His Leu Gly Lys
    130                 135                 140
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Tyr Tyr Phe Asn Leu Met Gln Tyr Leu Glu Ser Lys Glu Tyr Asp Arg
145                 150                 155                 160

Cys Ala Trp Thr Val Val Gln Val Gln Ile Leu Thr Asn Val Ser Phe
                165                 170                 175

Leu Met Arg Leu Thr Gly Tyr Val Arg Asp
            180                 185


<210> SEQ ID NO 63
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1053)
<223> OTHER INFORMATION: GlucON Beta Bovine

<400> SEQUENCE: 63

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac agg agc tac agc ttg ctt cga      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Arg Ser Tyr Ser Leu Leu Arg
            180                 185                 190

ttc caa caa cgt cag agc ctt aaa gag tgt cag aaa ctc ctg ggg cag      624
Phe Gln Gln Arg Gln Ser Leu Lys Glu Cys Gln Lys Leu Leu Gly Gln
        195                 200                 205

tta cct tca act cct caa cat tgc ctc gag gcc agg atg gac ttc cag      672
Leu Pro Ser Thr Pro Gln His Cys Leu Glu Ala Arg Met Asp Phe Gln
    210                 215                 220

atg cct gag gag atg aag caa gaa cag cag ttc cag aag gaa gat gcc      720
Met Pro Glu Glu Met Lys Gln Glu Gln Gln Phe Gln Lys Glu Asp Ala
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225                 230                 235                 240

ata ttg gtc atg tat gag gtg ctc cag cac atc ttc ggc att ctc acc      768
Ile Leu Val Met Tyr Glu Val Leu Gln His Ile Phe Gly Ile Leu Thr
                245                 250                 255

aga gac ttc tcc agc act ggc tgg tct gag acc atc atc gag gac ctc      816
Arg Asp Phe Ser Ser Thr Gly Trp Ser Glu Thr Ile Ile Glu Asp Leu
            260                 265                 270

ctt gag gaa ctc tat ggg cag atg aat cgt ctg cag cca atc cag aag      864
Leu Glu Glu Leu Tyr Gly Gln Met Asn Arg Leu Gln Pro Ile Gln Lys
        275                 280                 285

gaa ata atg cag aag caa aac acc aca gcg gga gac acg atc gtt ccc      912
Glu Ile Met Gln Lys Gln Asn Thr Thr Ala Gly Asp Thr Ile Val Pro
    290                 295                 300

cac cta ggg aaa tat tac ttc aac ctc atg cag tac ctg gag tcc aag      960
His Leu Gly Lys Tyr Tyr Phe Asn Leu Met Gln Tyr Leu Glu Ser Lys
305                 310                 315                 320

gag tac gac agg tgt gcc tgg aca gtc gtg caa gtg caa ata ctc acg     1008
Glu Tyr Asp Arg Cys Ala Trp Thr Val Val Gln Val Gln Ile Leu Thr
                325                 330                 335

aac gtt tct ttc ctg atg aga cta aca ggt tac gtc cgt gac tga         1053
Asn Val Ser Phe Leu Met Arg Leu Thr Gly Tyr Val Arg Asp
            340                 345                 350


<210> SEQ ID NO 64
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 64

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Arg Ser Tyr Ser Leu Leu Arg
            180                 185                 190

Phe Gln Gln Arg Gln Ser Leu Lys Glu Cys Gln Lys Leu Leu Gly Gln
        195                 200                 205

Leu Pro Ser Thr Pro Gln His Cys Leu Glu Ala Arg Met Asp Phe Gln
    210                 215                 220
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Met Pro Glu Glu Met Lys Gln Glu Gln Gln Phe Gln Lys Glu Asp Ala
225                 230                 235                 240

Ile Leu Val Met Tyr Glu Val Leu Gln His Ile Phe Gly Ile Leu Thr
                245                 250                 255

Arg Asp Phe Ser Ser Thr Gly Trp Ser Glu Thr Ile Ile Glu Asp Leu
            260                 265                 270

Leu Glu Glu Leu Tyr Gly Gln Met Asn Arg Leu Gln Pro Ile Gln Lys
        275                 280                 285

Glu Ile Met Gln Lys Gln Asn Thr Thr Ala Gly Asp Thr Ile Val Pro
    290                 295                 300

His Leu Gly Lys Tyr Tyr Phe Asn Leu Met Gln Tyr Leu Glu Ser Lys
305                 310                 315                 320

Glu Tyr Asp Arg Cys Ala Trp Thr Val Val Gln Val Gln Ile Leu Thr
                325                 330                 335

Asn Val Ser Phe Leu Met Arg Leu Thr Gly Tyr Val Arg Asp
            340                 345                 350


<210> SEQ ID NO 65
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(561)
<223> OTHER INFORMATION: Porcine Interferon Beta

<400> SEQUENCE: 65

atg gct aac aag tgc atc ctc caa atc gct ctc ctg atg tgt ttc tcc       48
Met Ala Asn Lys Cys Ile Leu Gln Ile Ala Leu Leu Met Cys Phe Ser
1               5                   10                  15

acc aca gct ctt tcc atg agc tat gat gtg ctt cga tac caa caa agg       96
Thr Thr Ala Leu Ser Met Ser Tyr Asp Val Leu Arg Tyr Gln Gln Arg
            20                  25                  30

agc agc aat ttg gca tgt cag aag ctc ctg gga cag ttg cct ggg act      144
Ser Ser Asn Leu Ala Cys Gln Lys Leu Leu Gly Gln Leu Pro Gly Thr
        35                  40                  45

cct caa tat tgc ctc gaa gat agg atg aac ttt gag gtc cct gag gag      192
Pro Gln Tyr Cys Leu Glu Asp Arg Met Asn Phe Glu Val Pro Glu Glu
    50                  55                  60

att atg caa cca cca caa ttc cag aag gaa gat gca gta ttg att atc      240
Ile Met Gln Pro Pro Gln Phe Gln Lys Glu Asp Ala Val Leu Ile Ile
65                  70                  75                  80

cac gag atg ctc cag cag atc ttc ggc att ctc aga aga aat ttc tct      288
His Glu Met Leu Gln Gln Ile Phe Gly Ile Leu Arg Arg Asn Phe Ser
                85                  90                  95

agc act ggc tgg aat gaa acc gtc att aag act atc ctt gtg gaa ctt      336
Ser Thr Gly Trp Asn Glu Thr Val Ile Lys Thr Ile Leu Val Glu Leu
            100                 105                 110

gat ggg cag atg gat gac ctg gag aca atc ctg gag gaa atc atg gag      384
Asp Gly Gln Met Asp Asp Leu Glu Thr Ile Leu Glu Glu Ile Met Glu
        115                 120                 125

gag gaa aat ttc ccc agg gga gac atg acc att ctt cac ctg aag aaa      432
Glu Glu Asn Phe Pro Arg Gly Asp Met Thr Ile Leu His Leu Lys Lys
    130                 135                 140

tat tac ttg agc att ctg cag tac ctg aag tcc aag gag tac aga agc      480
Tyr Tyr Leu Ser Ile Leu Gln Tyr Leu Lys Ser Lys Glu Tyr Arg Ser
145                 150                 155                 160

tgt gcc tgg aca gtc gtc caa gtg gaa atc ctc agg aac ttt tct ttc      528
Cys Ala Trp Thr Val Val Gln Val Glu Ile Leu Arg Asn Phe Ser Phe
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                165                 170                 175

ctt aac aga ctt aca gat tac ctc cgg aac tga                          561
Leu Asn Arg Leu Thr Asp Tyr Leu Arg Asn
            180                 185


<210> SEQ ID NO 66
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 66

Met Ala Asn Lys Cys Ile Leu Gln Ile Ala Leu Leu Met Cys Phe Ser
1               5                   10                  15

Thr Thr Ala Leu Ser Met Ser Tyr Asp Val Leu Arg Tyr Gln Gln Arg
            20                  25                  30

Ser Ser Asn Leu Ala Cys Gln Lys Leu Leu Gly Gln Leu Pro Gly Thr
        35                  40                  45

Pro Gln Tyr Cys Leu Glu Asp Arg Met Asn Phe Glu Val Pro Glu Glu
    50                  55                  60

Ile Met Gln Pro Pro Gln Phe Gln Lys Glu Asp Ala Val Leu Ile Ile
65                  70                  75                  80

His Glu Met Leu Gln Gln Ile Phe Gly Ile Leu Arg Arg Asn Phe Ser
                85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Val Ile Lys Thr Ile Leu Val Glu Leu
            100                 105                 110

Asp Gly Gln Met Asp Asp Leu Glu Thr Ile Leu Glu Glu Ile Met Glu
        115                 120                 125

Glu Glu Asn Phe Pro Arg Gly Asp Met Thr Ile Leu His Leu Lys Lys
    130                 135                 140

Tyr Tyr Leu Ser Ile Leu Gln Tyr Leu Lys Ser Lys Glu Tyr Arg Ser
145                 150                 155                 160

Cys Ala Trp Thr Val Val Gln Val Glu Ile Leu Arg Asn Phe Ser Phe
                165                 170                 175

Leu Asn Arg Leu Thr Asp Tyr Leu Arg Asn
            180                 185


<210> SEQ ID NO 67
<211> LENGTH: 1059
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1059)
<223> OTHER INFORMATION: GLucON Beta porcine

<400> SEQUENCE: 67

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
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Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc atg agc tat gat gtg      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Met Ser Tyr Asp Val
            180                 185                 190

ctt cga tac caa caa agg agc agc aat ttg gca tgt cag aag ctc ctg      624
Leu Arg Tyr Gln Gln Arg Ser Ser Asn Leu Ala Cys Gln Lys Leu Leu
        195                 200                 205

gga cag ttg cct ggg act cct caa tat tgc ctc gaa gat agg atg aac      672
Gly Gln Leu Pro Gly Thr Pro Gln Tyr Cys Leu Glu Asp Arg Met Asn
    210                 215                 220

ttt gag gtc cct gag gag att atg caa cca cca caa ttc cag aag gaa      720
Phe Glu Val Pro Glu Glu Ile Met Gln Pro Pro Gln Phe Gln Lys Glu
225                 230                 235                 240

gat gca gta ttg att atc cac gag atg ctc cag cag atc ttc ggc att      768
Asp Ala Val Leu Ile Ile His Glu Met Leu Gln Gln Ile Phe Gly Ile
                245                 250                 255

ctc aga aga aat ttc tct agc act ggc tgg aat gaa acc gtc att aag      816
Leu Arg Arg Asn Phe Ser Ser Thr Gly Trp Asn Glu Thr Val Ile Lys
            260                 265                 270

act atc ctt gtg gaa ctt gat ggg cag atg gat gac ctg gag aca atc      864
Thr Ile Leu Val Glu Leu Asp Gly Gln Met Asp Asp Leu Glu Thr Ile
        275                 280                 285

ctg gag gaa atc atg gag gag gaa aat ttc ccc agg gga gac atg acc      912
Leu Glu Glu Ile Met Glu Glu Glu Asn Phe Pro Arg Gly Asp Met Thr
    290                 295                 300

att ctt cac ctg aag aaa tat tac ttg agc att ctg cag tac ctg aag      960
Ile Leu His Leu Lys Lys Tyr Tyr Leu Ser Ile Leu Gln Tyr Leu Lys
305                 310                 315                 320

tcc aag gag tac aga agc tgt gcc tgg aca gtc gtc caa gtg gaa atc     1008
Ser Lys Glu Tyr Arg Ser Cys Ala Trp Thr Val Val Gln Val Glu Ile
                325                 330                 335

ctc agg aac ttt tct ttc ctt aac aga ctt aca gat tac ctc cgg aac     1056
Leu Arg Asn Phe Ser Phe Leu Asn Arg Leu Thr Asp Tyr Leu Arg Asn
            340                 345                 350

tga                                                                1059


<210> SEQ ID NO 68
<211> LENGTH: 352
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa
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<400> SEQUENCE: 68

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
20 25 30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
35 40 45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
50 55 60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65 70 75 80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
85 90 95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
100 105 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
115 120 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
130 135 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145 150 155 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
165 170 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Met Ser Tyr Asp Val
180 185 190

Leu Arg Tyr Gln Gln Arg Ser Ser Asn Leu Ala Cys Gln Lys Leu Leu
195 200 205

Gly Gln Leu Pro Gly Thr Pro Gln Tyr Cys Leu Glu Asp Arg Met Asn
210 215 220

Phe Glu Val Pro Glu Glu Ile Met Gln Pro Pro Gln Phe Gln Lys Glu
225 230 235 240

Asp Ala Val Leu Ile Ile His Glu Met Leu Gln Gln Ile Phe Gly Ile
245 250 255

Leu Arg Arg Asn Phe Ser Ser Thr Gly Trp Asn Glu Thr Val Ile Lys
260 265 270

Thr Ile Leu Val Glu Leu Asp Gly Gln Met Asp Asp Leu Glu Thr Ile
275 280 285

Leu Glu Glu Ile Met Glu Glu Glu Asn Phe Pro Arg Gly Asp Met Thr
290 295 300

Ile Leu His Leu Lys Lys Tyr Tyr Leu Ser Ile Leu Gln Tyr Leu Lys
305 310 315 320

Ser Lys Glu Tyr Arg Ser Cys Ala Trp Thr Val Val Gln Val Glu Ile
325 330 335

Leu Arg Asn Phe Ser Phe Leu Asn Arg Leu Thr Asp Tyr Leu Arg Asn
340 345 350

<210> SEQ ID NO 69
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1062)
<223> OTHER INFORMATION: SGLucON Beta porcine

<400> SEQUENCE: 69

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atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttt gcg acc acg gat ctc gat gct gac cga ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag tgg ctc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gat att cct gag att cct ggg ttc aag gac ttg gag cca atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc ggg atg agc tat gat      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gly Met Ser Tyr Asp
            180                 185                 190

gtg ctt cga tac caa caa agg agc agc aat ttg gca tgt cag aag ctc      624
Val Leu Arg Tyr Gln Gln Arg Ser Ser Asn Leu Ala Cys Gln Lys Leu
        195                 200                 205

ctg gga cag ttg cct ggg act cct caa tat tgc ctc gaa gat agg atg      672
Leu Gly Gln Leu Pro Gly Thr Pro Gln Tyr Cys Leu Glu Asp Arg Met
    210                 215                 220

aac ttt gag gtc cct gag gag att atg caa cca cca caa ttc cag aag      720
Asn Phe Glu Val Pro Glu Glu Ile Met Gln Pro Pro Gln Phe Gln Lys
225                 230                 235                 240

gaa gat gca gta ttg att atc cac gag atg ctc cag cag atc ttc ggc      768
Glu Asp Ala Val Leu Ile Ile His Glu Met Leu Gln Gln Ile Phe Gly
                245                 250                 255

att ctc aga aga aat ttc tct agc act ggc tgg aat gaa acc gtc att      816
Ile Leu Arg Arg Asn Phe Ser Ser Thr Gly Trp Asn Glu Thr Val Ile
            260                 265                 270

aag act atc ctt gtg gaa ctt gat ggg cag atg gat gac ctg gag aca      864
Lys Thr Ile Leu Val Glu Leu Asp Gly Gln Met Asp Asp Leu Glu Thr
        275                 280                 285

atc ctg gag gaa atc atg gag gag gaa aat ttc ccc agg gga gac atg      912
Ile Leu Glu Glu Ile Met Glu Glu Glu Asn Phe Pro Arg Gly Asp Met
    290                 295                 300

acc att ctt cac ctg aag aaa tat tac ttg agc att ctg cag tac ctg      960
Thr Ile Leu His Leu Lys Lys Tyr Tyr Leu Ser Ile Leu Gln Tyr Leu
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305                 310                 315                 320

aag tcc aag gag tac aga agc tgt gcc tgg aca gtc gtc caa gtg gaa     1008
Lys Ser Lys Glu Tyr Arg Ser Cys Ala Trp Thr Val Val Gln Val Glu
                325                 330                 335

atc ctc agg aac ttt tct ttc ctt aac aga ctt aca gat tac ctc cgg     1056
Ile Leu Arg Asn Phe Ser Phe Leu Asn Arg Leu Thr Asp Tyr Leu Arg
            340                 345                 350

aac tga                                                             1062
Asn


<210> SEQ ID NO 70
<211> LENGTH: 353
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 70

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gly Met Ser Tyr Asp
            180                 185                 190

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

Leu Gly Gln Leu Pro Gly Thr Pro Gln Tyr Cys Leu Glu Asp Arg Met
    210                 215                 220

Asn Phe Glu Val Pro Glu Glu Ile Met Gln Pro Pro Gln Phe Gln Lys
225                 230                 235                 240

Glu Asp Ala Val Leu Ile Ile His Glu Met Leu Gln Gln Ile Phe Gly
                245                 250                 255

Ile Leu Arg Arg Asn Phe Ser Ser Thr Gly Trp Asn Glu Thr Val Ile
            260                 265                 270

Lys Thr Ile Leu Val Glu Leu Asp Gly Gln Met Asp Asp Leu Glu Thr
        275                 280                 285

Ile Leu Glu Glu Ile Met Glu Glu Glu Asn Phe Pro Arg Gly Asp Met
    290                 295                 300

Thr Ile Leu His Leu Lys Lys Tyr Tyr Leu Ser Ile Leu Gln Tyr Leu
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305                 310                 315                 320

Lys Ser Lys Glu Tyr Arg Ser Cys Ala Trp Thr Val Val Gln Val Glu
                325                 330                 335

Ile Leu Arg Asn Phe Ser Phe Leu Asn Arg Leu Thr Asp Tyr Leu Arg
            340                 345                 350

Asn


<210> SEQ ID NO 71
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(501)
<223> OTHER INFORMATION: Human Interferon Gamma

<400> SEQUENCE: 71

atg aaa tat aca agt tat atc ttg gct ttt cag ctc tgc atc gtt ttg       48
Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1               5                   10                  15

ggt tct ctt ggc tgt tac tgc cag gac cca tat gta aaa gaa gca gaa       96
Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
            20                  25                  30

aac ctt aag aaa tat ttt aat gca ggt cat tca gat gta gcg gat aat      144
Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
        35                  40                  45

gga act ctt ttc tta ggc att ttg aag aat tgg aaa gag gag agt gac      192
Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
    50                  55                  60

aga aaa ata atg cag agc caa att gtc tcc ttt tac ttc aaa ctt ttt      240
Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65                  70                  75                  80

aaa aac ttt aaa gat gac cag agc atc caa aag agt gtg gag acc atc      288
Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
                85                  90                  95

aag gaa gac atg aat gtc aag ttt ttc aat agc aac aaa aag aaa cga      336
Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
            100                 105                 110

gat gac ttc gaa aag ctg act aat tat tcg gta act gac ttg aat gtc      384
Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
        115                 120                 125

caa cgc aaa gca ata cat gaa ctc atc caa gtg atg gct gaa ctg tcg      432
Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
    130                 135                 140

cca gca gct aaa aca ggg aag cga aaa agg agt cag atg ctg ttt cga      480
Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145                 150                 155                 160

ggt cga aga gca tcc cag taa                                         501
Gly Arg Arg Ala Ser Gln
                165


<210> SEQ ID NO 72
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

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

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
            20                  25                  30
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Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
        35                  40                  45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
    50                  55                  60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65                  70                  75                  80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
                85                  90                  95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
            100                 105                 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
        115                 120                 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
    130                 135                 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145                 150                 155                 160

Gly Arg Arg Ala Ser Gln
                165


<210> SEQ ID NO 73
<211> LENGTH: 987
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(987)
<223> OTHER INFORMATION: Human GlucON Gamma

<400> SEQUENCE: 73

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160
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ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac cag gac cca tat gta aaa gaa      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gln Asp Pro Tyr Val Lys Glu
            180                 185                 190

gca gaa aac ctt aag aaa tat ttt aat gca ggt cat tca gat gta gcg      624
Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala
        195                 200                 205

gat aat gga act ctt ttc tta ggc att ttg aag aat tgg aaa gag gag      672
Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu
    210                 215                 220

agt gac aga aaa ata atg cag agc caa att gtc tcc ttt tac ttc aaa      720
Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys
225                 230                 235                 240

ctt ttt aaa aac ttt aaa gat gac cag agc atc caa aag agt gtg gag      768
Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu
                245                 250                 255

acc atc aag gaa gac atg aat gtc aag ttt ttc aat agc aac aaa aag      816
Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys
            260                 265                 270

aaa cga gat gac ttc gaa aag ctg act aat tat tcg gta act gac ttg      864
Lys Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu
        275                 280                 285

aat gtc caa cgc aaa gca ata cat gaa ctc atc caa gtg atg gct gaa      912
Asn Val Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu
    290                 295                 300

ctg tcg cca gca gct aaa aca ggg aag cga aaa agg agt cag atg ctg      960
Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu
305                 310                 315                 320

ttt cga ggt cga aga gca tcc cag taa                                 987
Phe Arg Gly Arg Arg Ala Ser Gln
                325


<210> SEQ ID NO 74
<211> LENGTH: 328
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140
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Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gln Asp Pro Tyr Val Lys Glu
            180                 185                 190

Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala
        195                 200                 205

Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu
    210                 215                 220

Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys
225                 230                 235                 240

Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu
                245                 250                 255

Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys
            260                 265                 270

Lys Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu
        275                 280                 285

Asn Val Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu
    290                 295                 300

Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu
305                 310                 315                 320

Phe Arg Gly Arg Arg Ala Ser Gln
                325


<210> SEQ ID NO 75
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(501)
<223> OTHER INFORMATION: 75)Bovine Interferon Gamma

<400> SEQUENCE: 75

atg aaa tat aca agc tat ttc tta gct tta ctg ctc tgt ggg ctt ttg       48
Met Lys Tyr Thr Ser Tyr Phe Leu Ala Leu Leu Leu Cys Gly Leu Leu
1               5                   10                  15

ggt ttt tct ggt tct tat ggc cag ggc caa ttt ttt aga gaa ata gaa       96
Gly Phe Ser Gly Ser Tyr Gly Gln Gly Gln Phe Phe Arg Glu Ile Glu
            20                  25                  30

aac tta aag gag tat ttt aat gca agt agc cca gat gta gct aag ggt      144
Asn Leu Lys Glu Tyr Phe Asn Ala Ser Ser Pro Asp Val Ala Lys Gly
        35                  40                  45

ggg cct ctc ttc tca gaa att ttg aag aat tgg aaa gat gaa agt gac      192
Gly Pro Leu Phe Ser Glu Ile Leu Lys Asn Trp Lys Asp Glu Ser Asp
    50                  55                  60

aaa aaa att att cag agc caa att gtc tcc ttc tac ttc aaa ctc ttt      240
Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65                  70                  75                  80

gaa aac ctc aaa gat aac cag gtc att caa agg agc atg gat atc atc      288
Glu Asn Leu Lys Asp Asn Gln Val Ile Gln Arg Ser Met Asp Ile Ile
                85                  90                  95

aag caa gac atg ttt cag aag ttc ttg aat ggc agc tct gag aaa ctg      336
Lys Gln Asp Met Phe Gln Lys Phe Leu Asn Gly Ser Ser Glu Lys Leu
            100                 105                 110

gag gac ttc aaa aag ctg att caa att ccg gtg gat gat ctg cag atc      384
Glu Asp Phe Lys Lys Leu Ile Gln Ile Pro Val Asp Asp Leu Gln Ile
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```
        115                 120                 125

cag cgc aaa gcc ata aat gaa ctc atc aaa gtg atg aat gac ctg tca      432
Gln Arg Lys Ala Ile Asn Glu Leu Ile Lys Val Met Asn Asp Leu Ser
    130                 135                 140

cca aaa tct aac ctc aga aag cgg aag aga agt cag aat ctc ttt cga      480
Pro Lys Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln Asn Leu Phe Arg
145                 150                 155                 160

ggc cgg aga gca tca acg taa                                         501
Gly Arg Arg Ala Ser Thr
                165


<210> SEQ ID NO 76
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 76

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

Gly Phe Ser Gly Ser Tyr Gly Gln Gly Gln Phe Phe Arg Glu Ile Glu
            20                  25                  30

Asn Leu Lys Glu Tyr Phe Asn Ala Ser Ser Pro Asp Val Ala Lys Gly
        35                  40                  45

Gly Pro Leu Phe Ser Glu Ile Leu Lys Asn Trp Lys Asp Glu Ser Asp
    50                  55                  60

Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65                  70                  75                  80

Glu Asn Leu Lys Asp Asn Gln Val Ile Gln Arg Ser Met Asp Ile Ile
                85                  90                  95

Lys Gln Asp Met Phe Gln Lys Phe Leu Asn Gly Ser Ser Glu Lys Leu
            100                 105                 110

Glu Asp Phe Lys Lys Leu Ile Gln Ile Pro Val Asp Asp Leu Gln Ile
        115                 120                 125

Gln Arg Lys Ala Ile Asn Glu Leu Ile Lys Val Met Asn Asp Leu Ser
    130                 135                 140

Pro Lys Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln Asn Leu Phe Arg
145                 150                 155                 160

Gly Arg Arg Ala Ser Thr
                165


<210> SEQ ID NO 77
<211> LENGTH: 993
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(993)
<223> OTHER INFORMATION: Bovine GlucON Gamma

<400> SEQUENCE: 77

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45
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```
ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtt gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc cag ggc caa ttt ttt      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gln Gly Gln Phe Phe
            180                 185                 190

aga gaa ata gaa aac tta aag gag tat ttt aat gca agt agc cca gat      624
Arg Glu Ile Glu Asn Leu Lys Glu Tyr Phe Asn Ala Ser Ser Pro Asp
        195                 200                 205

gta gct aag ggt ggg cct ctc ttc tca gaa att ttg aag aat tgg aaa      672
Val Ala Lys Gly Gly Pro Leu Phe Ser Glu Ile Leu Lys Asn Trp Lys
    210                 215                 220

gat gaa agt gac aaa aaa att att cag agc caa att gtc tcc ttc tac      720
Asp Glu Ser Asp Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr
225                 230                 235                 240

ttc aaa ctc ttt gaa aac ctc aaa gat aac cag gtc att caa agg agc      768
Phe Lys Leu Phe Glu Asn Leu Lys Asp Asn Gln Val Ile Gln Arg Ser
                245                 250                 255

atg gat ata atc aag caa gac atg ttt cag aag ttc ttg aat ggc agc      816
Met Asp Ile Ile Lys Gln Asp Met Phe Gln Lys Phe Leu Asn Gly Ser
            260                 265                 270

tct gag aaa ctg gag gac ttc aaa aag ctg att caa att ccg gtg gat      864
Ser Glu Lys Leu Glu Asp Phe Lys Lys Leu Ile Gln Ile Pro Val Asp
        275                 280                 285

gat ctc cag atc cag cgc aaa gcc ata aat gaa ctc atc aaa gtg atg      912
Asp Leu Gln Ile Gln Arg Lys Ala Ile Asn Glu Leu Ile Lys Val Met
    290                 295                 300

aat gac ctg tca cca aaa tct aac ctc aga aag cgg aag aga agt cag      960
Asn Asp Leu Ser Pro Lys Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln
305                 310                 315                 320

aat ctc ttt cga ggc cgg aga gca tca acg taa                         993
Asn Leu Phe Arg Gly Arg Arg Ala Ser Thr
                325                 330
```

<210> SEQ ID NO 78
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 78

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gln Gly Gln Phe Phe
            180                 185                 190

Arg Glu Ile Glu Asn Leu Lys Glu Tyr Phe Asn Ala Ser Ser Pro Asp
        195                 200                 205

Val Ala Lys Gly Gly Pro Leu Phe Ser Glu Ile Leu Lys Asn Trp Lys
    210                 215                 220

Asp Glu Ser Asp Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr
225                 230                 235                 240

Phe Lys Leu Phe Glu Asn Leu Lys Asp Asn Gln Val Ile Gln Arg Ser
                245                 250                 255

Met Asp Ile Ile Lys Gln Asp Met Phe Gln Lys Phe Leu Asn Gly Ser
            260                 265                 270

Ser Glu Lys Leu Glu Asp Phe Lys Lys Leu Ile Gln Ile Pro Val Asp
        275                 280                 285

Asp Leu Gln Ile Gln Arg Lys Ala Ile Asn Glu Leu Ile Lys Val Met
    290                 295                 300

Asn Asp Leu Ser Pro Lys Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln
305                 310                 315                 320

Asn Leu Phe Arg Gly Arg Arg Ala Ser Thr
                325                 330


<210> SEQ ID NO 79
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(501)
<223> OTHER INFORMATION: Porcine Interferon Gamma

<400> SEQUENCE: 79

atg agt tat aca act tat ttc tta gct ttt cag ctt tgc gtg act ttg       48
Met Ser Tyr Thr Thr Tyr Phe Leu Ala Phe Gln Leu Cys Val Thr Leu
1               5                  10                  15
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```
tgt ttt tct ggc tct tac tgc cag gcg ccc ttt ttt aaa gaa ata acg       96
Cys Phe Ser Gly Ser Tyr Cys Gln Ala Pro Phe Phe Lys Glu Ile Thr
            20                  25                  30

atc cta aag gac tat ttt aat gca agt acc tca gat gta cct aat ggt      144
Ile Leu Lys Asp Tyr Phe Asn Ala Ser Thr Ser Asp Val Pro Asn Gly
        35                  40                  45

gga cct ctt ttc tta gaa att ttg aag aat tgg aaa gag gag agt gac      192
Gly Pro Leu Phe Leu Glu Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
    50                  55                  60

aaa aaa ata att cag agc caa att gtc tcc ttc tac ttc aaa ttc ttt      240
Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Phe Phe
65                  70                  75                  80

gaa atc ttc aaa gat aac cag gcc att caa agg agc atg gat gtg atc      288
Glu Ile Phe Lys Asp Asn Gln Ala Ile Gln Arg Ser Met Asp Val Ile
                85                  90                  95

aag caa gac atg ttt cag agg ttc cta aat ggt agc tct ggg aaa ctg      336
Lys Gln Asp Met Phe Gln Arg Phe Leu Asn Gly Ser Ser Gly Lys Leu
            100                 105                 110

aat gac ttc gaa aag ctg att aaa att ccg gta gat aat ctg cag atc      384
Asn Asp Phe Glu Lys Leu Ile Lys Ile Pro Val Asp Asn Leu Gln Ile
        115                 120                 125

cag cgc aaa gcc atc agt gaa ctc atc aaa gtg atg aat gat ctg tca      432
Gln Arg Lys Ala Ile Ser Glu Leu Ile Lys Val Met Asn Asp Leu Ser
    130                 135                 140

cca aga tct aac cta aga aag cgg aag aga agt cag act atg ttc caa      480
Pro Arg Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln Thr Met Phe Gln
145                 150                 155                 160

ggc cag aga gca tca aaa taa                                         501
Gly Gln Arg Ala Ser Lys
                165


<210> SEQ ID NO 80
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 80

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

Cys Phe Ser Gly Ser Tyr Cys Gln Ala Pro Phe Phe Lys Glu Ile Thr
            20                  25                  30

Ile Leu Lys Asp Tyr Phe Asn Ala Ser Thr Ser Asp Val Pro Asn Gly
        35                  40                  45

Gly Pro Leu Phe Leu Glu Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
    50                  55                  60

Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Phe Phe
65                  70                  75                  80

Glu Ile Phe Lys Asp Asn Gln Ala Ile Gln Arg Ser Met Asp Val Ile
                85                  90                  95

Lys Gln Asp Met Phe Gln Arg Phe Leu Asn Gly Ser Ser Gly Lys Leu
            100                 105                 110

Asn Asp Phe Glu Lys Leu Ile Lys Ile Pro Val Asp Asn Leu Gln Ile
        115                 120                 125

Gln Arg Lys Ala Ile Ser Glu Leu Ile Lys Val Met Asn Asp Leu Ser
    130                 135                 140

Pro Arg Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln Thr Met Phe Gln
145                 150                 155                 160
```

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```
Gly Gln Arg Ala Ser Lys
                165


<210> SEQ ID NO 81
<211> LENGTH: 987
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(987)
<223> OTHER INFORMATION: Porcine GLucON Gamma

<400> SEQUENCE: 81

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                  10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac cag gcg ccc ttt ttt aaa gaa      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gln Ala Pro Phe Phe Lys Glu
            180                 185                 190

ata acg atc cta aag gac tat ttt aat gca agt acc tca gat gta cct      624
Ile Thr Ile Leu Lys Asp Tyr Phe Asn Ala Ser Thr Ser Asp Val Pro
        195                 200                 205

aat ggt gga cct ctt ttc tta gaa att ttg aag aat tgg aaa gag gag      672
Asn Gly Gly Pro Leu Phe Leu Glu Ile Leu Lys Asn Trp Lys Glu Glu
    210                 215                 220

agt gac aaa aaa ata att cag agc caa att gtc tcc ttc tac ttc aaa      720
Ser Asp Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys
225                 230                 235                 240

ttc ttt gaa atc ttc aaa gat aac cag gcc att caa agg agc atg gat      768
Phe Phe Glu Ile Phe Lys Asp Asn Gln Ala Ile Gln Arg Ser Met Asp
                245                 250                 255
```

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```
gtg atc aag caa gac atg ttt cag agg ttc cta aat ggt agc tct ggg      816
Val Ile Lys Gln Asp Met Phe Gln Arg Phe Leu Asn Gly Ser Ser Gly
            260                 265                 270

aaa ctg aat gac ttc gaa aag ctg att aaa att ccg gta gat aat ctg      864
Lys Leu Asn Asp Phe Glu Lys Leu Ile Lys Ile Pro Val Asp Asn Leu
        275                 280                 285

cag atc cag cgc aaa gcc atc agt gaa ctc atc aaa gtg atg aat gat      912
Gln Ile Gln Arg Lys Ala Ile Ser Glu Leu Ile Lys Val Met Asn Asp
    290                 295                 300

ctg tca cca aga tct aac cta aga aag cgg aag aga agt cag act atg      960
Leu Ser Pro Arg Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln Thr Met
305                 310                 315                 320

ttc caa ggc cag aga gca tca aaa taa                                 987
Phe Gln Gly Gln Arg Ala Ser Lys
                325


<210> SEQ ID NO 82
<211> LENGTH: 328
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 82

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gln Ala Pro Phe Phe Lys Glu
            180                 185                 190

Ile Thr Ile Leu Lys Asp Tyr Phe Asn Ala Ser Thr Ser Asp Val Pro
        195                 200                 205

Asn Gly Gly Pro Leu Phe Leu Glu Ile Leu Lys Asn Trp Lys Glu Glu
    210                 215                 220

Ser Asp Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys
225                 230                 235                 240

Phe Phe Glu Ile Phe Lys Asp Asn Gln Ala Ile Gln Arg Ser Met Asp
                245                 250                 255

Val Ile Lys Gln Asp Met Phe Gln Arg Phe Leu Asn Gly Ser Ser Gly
            260                 265                 270
```

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```
Lys Leu Asn Asp Phe Glu Lys Leu Ile Lys Ile Pro Val Asp Asn Leu
        275                 280                 285

Gln Ile Gln Arg Lys Ala Ile Ser Glu Leu Ile Lys Val Met Asn Asp
    290                 295                 300

Leu Ser Pro Arg Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln Thr Met
305                 310                 315                 320

Phe Gln Gly Gln Arg Ala Ser Lys
                325
```

<210> SEQ ID NO 83
<211> LENGTH: 588
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(588)
<223> OTHER INFORMATION: Bovine Interferon Lambda IL29

<400> SEQUENCE: 83

```
atg gcc ccg ggc tgc acg ctg gtg ctg gtg ctg atg ctg acg acc gtg       48
Met Ala Pro Gly Cys Thr Leu Val Leu Val Leu Met Leu Thr Thr Val
1               5                   10                  15

gcg ctg agc agg aca gga gca gtt cct gtg ccc tct gcc ccc agg gcc       96
Ala Leu Ser Arg Thr Gly Ala Val Pro Val Pro Ser Ala Pro Arg Ala
            20                  25                  30

ctc cca cct gcc agg ggc tgc cac gtg gcc cag ttc aag tct ctg tcc      144
Leu Pro Pro Ala Arg Gly Cys His Val Ala Gln Phe Lys Ser Leu Ser
        35                  40                  45

cct caa gag ctg cag gcc ttc aag acg gcc agg gat gcc ttt gaa gac      192
Pro Gln Glu Leu Gln Ala Phe Lys Thr Ala Arg Asp Ala Phe Glu Asp
    50                  55                  60

tcg ttc ttg cca aag gac tgg gac tgc agc acc cac ctt ttc ccc agg      240
Ser Phe Leu Pro Lys Asp Trp Asp Cys Ser Thr His Leu Phe Pro Arg
65                  70                  75                  80

acc cgg gac ctg aag cac ctg cag gtg tgg gag cgc cct gtg gct ctg      288
Thr Arg Asp Leu Lys His Leu Gln Val Trp Glu Arg Pro Val Ala Leu
                85                  90                  95

gag gca gag ctg gcc ctg aca ctg acg gtc ctg gag gcc atg gct aac      336
Glu Ala Glu Leu Ala Leu Thr Leu Thr Val Leu Glu Ala Met Ala Asn
            100                 105                 110

tca tcc ctg ggc cac agc ctg gag cag ccc ctt ctc acg ctg cag aac      384
Ser Ser Leu Gly His Ser Leu Glu Gln Pro Leu Leu Thr Leu Gln Asn
        115                 120                 125

atc cac tcc aag ctc cag gcc tgt gtc cca gct cag ccc aca gca agc      432
Ile His Ser Lys Leu Gln Ala Cys Val Pro Ala Gln Pro Thr Ala Ser
    130                 135                 140

tcc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgc ctc cag gag      480
Ser Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu
145                 150                 155                 160

gcc cgg aag gag tcc cag gac tgc ctc gaa gcc tct gtg atg ttc aac      528
Ala Arg Lys Glu Ser Gln Asp Cys Leu Glu Ala Ser Val Met Phe Asn
                165                 170                 175

ctc ctc cgc ctc ctc acc cgg gac ctg aaa tgt gtt gcc agc gga gac      576
Leu Leu Arg Leu Leu Thr Arg Asp Leu Lys Cys Val Ala Ser Gly Asp
            180                 185                 190

cag tgt gtc tga                                                      588
Gln Cys Val
        195
```

<210> SEQ ID NO 84
<211> LENGTH: 195

-continued

<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 84

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

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

Leu Pro Pro Ala Arg Gly Cys His Val Ala Gln Phe Lys Ser Leu Ser
35 40 45

Pro Gln Glu Leu Gln Ala Phe Lys Thr Ala Arg Asp Ala Phe Glu Asp
50 55 60

Ser Phe Leu Pro Lys Asp Trp Asp Cys Ser Thr His Leu Phe Pro Arg
65 70 75 80

Thr Arg Asp Leu Lys His Leu Gln Val Trp Glu Arg Pro Val Ala Leu
85 90 95

Glu Ala Glu Leu Ala Leu Thr Leu Thr Val Leu Glu Ala Met Ala Asn
100 105 110

Ser Ser Leu Gly His Ser Leu Glu Gln Pro Leu Leu Thr Leu Gln Asn
115 120 125

Ile His Ser Lys Leu Gln Ala Cys Val Pro Ala Gln Pro Thr Ala Ser
130 135 140

Ser Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu
145 150 155 160

Ala Arg Lys Glu Ser Gln Asp Cys Leu Glu Ala Ser Val Met Phe Asn
165 170 175

Leu Leu Arg Leu Leu Thr Arg Asp Leu Lys Cys Val Ala Ser Gly Asp
180 185 190

Gln Cys Val
195

<210> SEQ ID NO 85
<211> LENGTH: 1092
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1092)
<223> OTHER INFORMATION: Bovine GLucON Lambda

<400> SEQUENCE: 85

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag 48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1 5 10 15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc 96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
20 25 30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc 144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
35 40 45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc 192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
50 55 60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc 240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65 70 75 80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc 288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
85 90 95

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```
tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtt gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc agg aca gga gca gtt      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Arg Thr Gly Ala Val
            180                 185                 190

cct gtg ccc tct gcc ccc agg gca ctc cca cct gcc agg ggc tgc cac      624
Pro Val Pro Ser Ala Pro Arg Ala Leu Pro Pro Ala Arg Gly Cys His
        195                 200                 205

gtg gcc cag ttc aag tct ctg tcc cct caa gag ctg caa gcc ttc aag      672
Val Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys
    210                 215                 220

acg gcc agg gat gcc ttt gaa gac tcg ttc ttg ccg aag gac tgg gac      720
Thr Ala Arg Asp Ala Phe Glu Asp Ser Phe Leu Pro Lys Asp Trp Asp
225                 230                 235                 240

tgt agc acc cac ctt ttc ccc agg aca cga gac ctg aag cac ctg caa      768
Cys Ser Thr His Leu Phe Pro Arg Thr Arg Asp Leu Lys His Leu Gln
                245                 250                 255

gtg tgg gag cgc cct gtg gct ctg gag gca gag ctg gcc ctg aca ctg      816
Val Trp Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
            260                 265                 270

acg gtc ctg gag gca atg gct aac tca tcc ctg ggc cac agc ctg gag      864
Thr Val Leu Glu Ala Met Ala Asn Ser Ser Leu Gly His Ser Leu Glu
        275                 280                 285

cag ccc ctt ctc acg ctg caa aac atc cac tcc aag ctc cag gcc tgt      912
Gln Pro Leu Leu Thr Leu Gln Asn Ile His Ser Lys Leu Gln Ala Cys
    290                 295                 300

gtc cca gct cag ccc aca gca agc tcc aga ccc cga ggc cgc ctc cac      960
Val Pro Ala Gln Pro Thr Ala Ser Ser Arg Pro Arg Gly Arg Leu His
305                 310                 315                 320

cac tgg ctg cac cgc ctc caa gag gcc cgg aag gag tcc cag gac tgc     1008
His Trp Leu His Arg Leu Gln Glu Ala Arg Lys Glu Ser Gln Asp Cys
                325                 330                 335

ctc gaa gcc tct gtg atg ttc aac ctc ctc cgc ctc ctc acc cga gac     1056
Leu Glu Ala Ser Val Met Phe Asn Leu Leu Arg Leu Leu Thr Arg Asp
            340                 345                 350

ctg aaa tgt gtt gcc agc gga gac cag tgt gtc tga                     1092
Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
        355                 360
```

<210> SEQ ID NO 86
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 86

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

-continued

```
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Arg Thr Gly Ala Val
            180                 185                 190

Pro Val Pro Ser Ala Pro Arg Ala Leu Pro Pro Ala Arg Gly Cys His
        195                 200                 205

Val Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys
    210                 215                 220

Thr Ala Arg Asp Ala Phe Glu Asp Ser Phe Leu Pro Lys Asp Trp Asp
225                 230                 235                 240

Cys Ser Thr His Leu Phe Pro Arg Thr Arg Asp Leu Lys His Leu Gln
                245                 250                 255

Val Trp Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
            260                 265                 270

Thr Val Leu Glu Ala Met Ala Asn Ser Ser Leu Gly His Ser Leu Glu
        275                 280                 285

Gln Pro Leu Leu Thr Leu Gln Asn Ile His Ser Lys Leu Gln Ala Cys
    290                 295                 300

Val Pro Ala Gln Pro Thr Ala Ser Ser Arg Pro Arg Gly Arg Leu His
305                 310                 315                 320

His Trp Leu His Arg Leu Gln Glu Ala Arg Lys Glu Ser Gln Asp Cys
                325                 330                 335

Leu Glu Ala Ser Val Met Phe Asn Leu Leu Arg Leu Leu Thr Arg Asp
            340                 345                 350

Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
        355                 360


<210> SEQ ID NO 87
<211> LENGTH: 603
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(603)
<223> OTHER INFORMATION: Human Interferon Lambda 1 (IL29)

<400> SEQUENCE: 87
```

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```
atg gct gca gct tgg acc gtg gtg ctg gtg act ttg gtg cta ggc ttg       48
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
1               5                   10                  15

gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag       96
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
            20                  25                  30

ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg      144
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
        35                  40                  45

agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa      192
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
    50                  55                  60

aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg      240
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
65                  70                  75                  80

ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc      288
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
                85                  90                  95

ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac      336
Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
            100                 105                 110

gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc      384
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
        115                 120                 125

cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc      432
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
    130                 135                 140

cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag      480
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
145                 150                 155                 160

tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc      528
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
                165                 170                 175

ctc acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga      576
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg
            180                 185                 190

acg tca acc cac cct gag tcc acc tga                                  603
Thr Ser Thr His Pro Glu Ser Thr
        195                 200


<210> SEQ ID NO 88
<211> LENGTH: 200
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 88

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
1               5                   10                  15

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

Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
        35                  40                  45

Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
    50                  55                  60

Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
65                  70                  75                  80

Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
                85                  90                  95

Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
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            100                 105                 110

Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
        115                 120                 125

Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
    130                 135                 140

Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
145                 150                 155                 160

Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
                165                 170                 175

Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg
            180                 185                 190

Thr Ser Thr His Pro Glu Ser Thr
        195                 200


<210> SEQ ID NO 89
<211> LENGTH: 1113
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1113)
<223> OTHER INFORMATION: Human GlucON Lambda

<400> SEQUENCE: 89

atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                   10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ttg gcc gtg gca ggc cct gtc      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Leu Ala Val Ala Gly Pro Val
            180                 185                 190
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ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg      624
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
        195                 200                 205

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg      672
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
    210                 215                 220

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct      720
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
225                 230                 235                 240

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag      768
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
                245                 250                 255

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg      816
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
            260                 265                 270

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt      864
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
        275                 280                 285

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct      912
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
    290                 295                 300

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg      960
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
305                 310                 315                 320

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag     1008
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
                325                 330                 335

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa     1056
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
            340                 345                 350

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag     1104
Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
        355                 360                 365

tcc acc tga                                                        1113
Ser Thr
    370
```

<210> SEQ ID NO 90
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 90

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
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        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Leu Ala Val Ala Gly Pro Val
            180                 185                 190

Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
        195                 200                 205

Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
    210                 215                 220

Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
225                 230                 235                 240

Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
                245                 250                 255

Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
            260                 265                 270

Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
        275                 280                 285

His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
    290                 295                 300

Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
305                 310                 315                 320

His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
                325                 330                 335

Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
            340                 345                 350

Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
        355                 360                 365

Ser Thr
    370
```

<210> SEQ ID NO 91
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(576)
<223> OTHER INFORMATION: Porcine Interferon Lambda 1 (IL29

<400> SEQUENCE: 91

```
atg gct aca gct tgg atc gtg gtg ctg gcg act gtg atg ctg gac ttg       48
Met Ala Thr Ala Trp Ile Val Val Leu Ala Thr Val Met Leu Asp Leu
1               5                   10                  15

gcc aga gct ggc cct gtc ccc act ttc aag ccc acc aca acc agg aag       96
Ala Arg Ala Gly Pro Val Pro Thr Phe Lys Pro Thr Thr Thr Arg Lys
            20                  25                  30

ggc tgc cac atg ggc cag ttc caa tct ctg tca cca cag gag ctg aag      144
Gly Cys His Met Gly Gln Phe Gln Ser Leu Ser Pro Gln Glu Leu Lys
        35                  40                  45

ggc ttc aag aaa gcc aag gat gct ttg gaa gag tca ctc tca ctg aag      192
Gly Phe Lys Lys Ala Lys Asp Ala Leu Glu Glu Ser Leu Ser Leu Lys
    50                  55                  60

aac tgg agc tgc agc tct ccc ctc ttc ccc agg acc cgg gac ctg agg      240
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```
Asn Trp Ser Cys Ser Ser Pro Leu Phe Pro Arg Thr Arg Asp Leu Arg
65                  70                  75                  80

cag ctg cag gtg tgg gag cgc ctc gtg gcc tta gag gct gag cta gac      288
Gln Leu Gln Val Trp Glu Arg Leu Val Ala Leu Glu Ala Glu Leu Asp
                85                  90                  95

ttg act ctg aag gtc cta agg gcc gcg gct gac tca tcc ctg ggg gtc      336
Leu Thr Leu Lys Val Leu Arg Ala Ala Ala Asp Ser Ser Leu Gly Val
            100                 105                 110

acc ctg gac cag cca ctt cgc acg ctg cat cac atc cac gtc gaa ctt      384
Thr Leu Asp Gln Pro Leu Arg Thr Leu His His Ile His Val Glu Leu
        115                 120                 125

cag gct tgc atc agg gct cag ccc acg gca gga tcc cgg ctc cag ggc      432
Gln Ala Cys Ile Arg Ala Gln Pro Thr Ala Gly Ser Arg Leu Gln Gly
    130                 135                 140

cgc ctc aac cac tgg ctg cac cgg ctc caa gaa gcc aca aag aaa gag      480
Arg Leu Asn His Trp Leu His Arg Leu Gln Glu Ala Thr Lys Lys Glu
145                 150                 155                 160

tcc caa ggc tgc ctt gag gcc tct gtg aca ttc aac ctc ttc cac ctc      528
Ser Gln Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe His Leu
                165                 170                 175

ctc gta agg gac ctg aga agt gtt acc agt gga gac ttg cac atc tga      576
Leu Val Arg Asp Leu Arg Ser Val Thr Ser Gly Asp Leu His Ile
            180                 185                 190


<210> SEQ ID NO 92
<211> LENGTH: 191
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 92

Met Ala Thr Ala Trp Ile Val Val Leu Ala Thr Val Met Leu Asp Leu
1               5                   10                  15

Ala Arg Ala Gly Pro Val Pro Thr Phe Lys Pro Thr Thr Thr Arg Lys
            20                  25                  30

Gly Cys His Met Gly Gln Phe Gln Ser Leu Ser Pro Gln Glu Leu Lys
        35                  40                  45

Gly Phe Lys Lys Ala Lys Asp Ala Leu Glu Glu Ser Leu Ser Leu Lys
    50                  55                  60

Asn Trp Ser Cys Ser Ser Pro Leu Phe Pro Arg Thr Arg Asp Leu Arg
65                  70                  75                  80

Gln Leu Gln Val Trp Glu Arg Leu Val Ala Leu Glu Ala Glu Leu Asp
                85                  90                  95

Leu Thr Leu Lys Val Leu Arg Ala Ala Ala Asp Ser Ser Leu Gly Val
            100                 105                 110

Thr Leu Asp Gln Pro Leu Arg Thr Leu His His Ile His Val Glu Leu
        115                 120                 125

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

Arg Leu Asn His Trp Leu His Arg Leu Gln Glu Ala Thr Lys Lys Glu
145                 150                 155                 160

Ser Gln Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe His Leu
                165                 170                 175

Leu Val Arg Asp Leu Arg Ser Val Thr Ser Gly Asp Leu His Ile
            180                 185                 190


<210> SEQ ID NO 93
<211> LENGTH: 1083
<212> TYPE: DNA
```

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<213> ORGANISM: Sus scrofa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1083)
<223> OTHER INFORMATION: Porcine GLucON Lambda

<400> SEQUENCE: 93

```
atg gga gtc aaa gtt ctg ttt gcc ctg atc tgc atc gct gtg gcc gag       48
Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1               5                  10                  15

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttc gcg acc acg gat ctc gat gct gac cgc ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag ttc atc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gac att cct gag att cct ggg ttc aag gac ttg gag ccc atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac gcc aga gct ggc cct gtc ccc      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Ala Arg Ala Gly Pro Val Pro
            180                 185                 190

act ttc aag ccc acc aca acc agg aag ggc tgc cac atg ggc cag ttc      624
Thr Phe Lys Pro Thr Thr Thr Arg Lys Gly Cys His Met Gly Gln Phe
        195                 200                 205

caa tct ctg tca cca cag gag ctg aag ggc ttc aag aaa gcc aag gat      672
Gln Ser Leu Ser Pro Gln Glu Leu Lys Gly Phe Lys Lys Ala Lys Asp
    210                 215                 220

gct ttg gaa gag tca ctc tca ctg aag aac tgg agc tgc agc tct ccc      720
Ala Leu Glu Glu Ser Leu Ser Leu Lys Asn Trp Ser Cys Ser Ser Pro
225                 230                 235                 240

ctc ttc ccc agg acc cgg gac ctg agg cag ctg cag gtg tgg gag cgc      768
Leu Phe Pro Arg Thr Arg Asp Leu Arg Gln Leu Gln Val Trp Glu Arg
                245                 250                 255

ctc gtg gcc tta gag gct gag cta gac ttg act ctg aag gtc cta agg      816
Leu Val Ala Leu Glu Ala Glu Leu Asp Leu Thr Leu Lys Val Leu Arg
            260                 265                 270

gcc gcg gct gac tca tcc ctg ggg gtc acc ctg gac cag cca ctt cgc      864
Ala Ala Ala Asp Ser Ser Leu Gly Val Thr Leu Asp Gln Pro Leu Arg
        275                 280                 285
```

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```
acg ctg cat cac atc cac gtc gaa ctt cag gct tgc atc agg gct cag      912
Thr Leu His His Ile His Val Glu Leu Gln Ala Cys Ile Arg Ala Gln
    290                 295                 300

ccc acg gca gga tcc cgg ctc cag ggc cgc ctc aac cac tgg ctg cac      960
Pro Thr Ala Gly Ser Arg Leu Gln Gly Arg Leu Asn His Trp Leu His
305                 310                 315                 320

cgg ctc caa gaa gcc aca aag aaa gag tcc caa ggc tgc ctt gag gcc     1008
Arg Leu Gln Glu Ala Thr Lys Lys Glu Ser Gln Gly Cys Leu Glu Ala
                325                 330                 335

tct gtg aca ttc aac ctc ttc cac ctc ctc gta agg gac ctg aga agt     1056
Ser Val Thr Phe Asn Leu Phe His Leu Leu Val Arg Asp Leu Arg Ser
            340                 345                 350

gtt acc agt gga gac ttg cac atc tga                                1083
Val Thr Ser Gly Asp Leu His Ile
        355                 360


<210> SEQ ID NO 94
<211> LENGTH: 360
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa

<400> SEQUENCE: 94

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Ala Arg Ala Gly Pro Val Pro
            180                 185                 190

Thr Phe Lys Pro Thr Thr Thr Arg Lys Gly Cys His Met Gly Gln Phe
        195                 200                 205

Gln Ser Leu Ser Pro Gln Glu Leu Lys Gly Phe Lys Lys Ala Lys Asp
    210                 215                 220

Ala Leu Glu Glu Ser Leu Ser Leu Lys Asn Trp Ser Cys Ser Ser Pro
225                 230                 235                 240

Leu Phe Pro Arg Thr Arg Asp Leu Arg Gln Leu Gln Val Trp Glu Arg
                245                 250                 255

Leu Val Ala Leu Glu Ala Glu Leu Asp Leu Thr Leu Lys Val Leu Arg
            260                 265                 270
```

Ala Ala Ala Asp Ser Ser Leu Gly Val Thr Leu Asp Gln Pro Leu Arg
275 280 285

Thr Leu His His Ile His Val Glu Leu Gln Ala Cys Ile Arg Ala Gln
290 295 300

Pro Thr Ala Gly Ser Arg Leu Gln Gly Arg Leu Asn His Trp Leu His
305 310 315 320

Arg Leu Gln Glu Ala Thr Lys Lys Glu Ser Gln Gly Cys Leu Glu Ala
325 330 335

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

Val Thr Ser Gly Asp Leu His Ile
355 360

<210> SEQ ID NO 95
<211> LENGTH: 13
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Kozak Sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: R is A or G

<400> SEQUENCE: 95

gccgccrcca tgg 13

<210> SEQ ID NO 96
<211> LENGTH: 5670
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pTarget Empty Vector

<400> SEQUENCE: 96

tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120

aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactg 660

cgatcgcccg ccccgttgac gcaaatgggc ggtaggcgtg tacggtggga ggtctatata 720

agcagagctc gtttagtgaa ccgtcagatc actagaagct ttattgcggt agtttatcac 780

agttaaattg ctaacgcagt cagtgcttct gacacaacag tctcgaactt aagctgcagt 840

gactctctta aggtagcctt gcagaagttg gtcgtgaggc actgggcagg taagtatcaa 900

ggttacaaga caggtttaag gagaccaata gaaactgggc ttgtcgagac agagaagact 960

cttgcgtttc tgataggcac ctattggtct tactgacatc cactttgcct ttctctccac 1020

-continued

aggtgtccac tcccagttca attacagctc ttaaaaattg gatctccatt cgccattcag 1080

gctgcgcaac tgctgggaag gacgatcaga gcgggcctct tcgctattac gccagctggc 1140

gaaagggacg tggcaagcaa ggcgattaag ttgagttacg ccaggatttt cccagtcacg 1200

acgttgtaaa acgacggcca gagaattata atacgactca ctatagggcg aattcggatc 1260

cttgctagcc tcgagacgcg tgatatcttt cccgggggta ccgtcgactg cggccgcgaa 1320

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<223> OTHER INFORMATION: pTarget SGLuc-d1D2A

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<213> ORGANISM: Bos taurus
<220> FEATURE:
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<222> LOCATION: (1)..(993)
<223> OTHER INFORMATION: SGlucON Bovine gamma

<400> SEQUENCE: 110

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gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttt gcg acc acg gat ctc gat gct gac cga ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag tgg ctc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gat att cct gag att cct ggg ttc aag gac ttg gag cca atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc cag ggc caa ttt ttt      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gln Gly Gln Phe Phe
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Arg Glu Ile Glu Asn Leu Lys Glu Tyr Phe Asn Ala Ser Ser Pro Asp
        195                 200                 205

gta gct aag ggt ggg cct ctc ttc tca gaa att ttg aag aat tgg aaa      672
Val Ala Lys Gly Gly Pro Leu Phe Ser Glu Ile Leu Lys Asn Trp Lys
    210                 215                 220

gat gaa agt gac aaa aaa att att cag agc caa att gtc tcc ttc tac      720
Asp Glu Ser Asp Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr
225                 230                 235                 240

ttc aaa ctc ttt gaa aac ctc aaa gat aac cag gtc att caa agg agc      768
Phe Lys Leu Phe Glu Asn Leu Lys Asp Asn Gln Val Ile Gln Arg Ser
                245                 250                 255

atg gat atc atc aag caa gac atg ttt cag aag ttc ttg aat ggc agc      816
Met Asp Ile Ile Lys Gln Asp Met Phe Gln Lys Phe Leu Asn Gly Ser
            260                 265                 270

tct gag aaa ctg gag gac ttc aaa aag ctg att caa att ccg gtg gat      864
Ser Glu Lys Leu Glu Asp Phe Lys Lys Leu Ile Gln Ile Pro Val Asp
        275                 280                 285

gat ctg cag atc cag cgc aaa gcc ata aat gaa ctc atc aaa gtg atg      912
Asp Leu Gln Ile Gln Arg Lys Ala Ile Asn Glu Leu Ile Lys Val Met
    290                 295                 300

aat gac ctg tca cca aaa tct aac ctc aga aag cgg aag aga agt cag      960
Asn Asp Leu Ser Pro Lys Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln
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aat ctc ttt cga ggc cgg aga gca tca acg taa                          993
Asn Leu Phe Arg Gly Arg Arg Ala Ser Thr
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<210> SEQ ID NO 111
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 111

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Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Gln Gly Gln Phe Phe
            180                 185                 190
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Arg Glu Ile Glu Asn Leu Lys Glu Tyr Phe Asn Ala Ser Ser Pro Asp
        195                 200                 205

Val Ala Lys Gly Gly Pro Leu Phe Ser Glu Ile Leu Lys Asn Trp Lys
    210                 215                 220

Asp Glu Ser Asp Lys Lys Ile Ile Gln Ser Gln Ile Val Ser Phe Tyr
225                 230                 235                 240

Phe Lys Leu Phe Glu Asn Leu Lys Asp Asn Gln Val Ile Gln Arg Ser
                245                 250                 255

Met Asp Ile Ile Lys Gln Asp Met Phe Gln Lys Phe Leu Asn Gly Ser
            260                 265                 270

Ser Glu Lys Leu Glu Asp Phe Lys Lys Leu Ile Gln Ile Pro Val Asp
        275                 280                 285

Asp Leu Gln Ile Gln Arg Lys Ala Ile Asn Glu Leu Ile Lys Val Met
    290                 295                 300

Asn Asp Leu Ser Pro Lys Ser Asn Leu Arg Lys Arg Lys Arg Ser Gln
305                 310                 315                 320

Asn Leu Phe Arg Gly Arg Arg Ala Ser Thr
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<210> SEQ ID NO 112
<211> LENGTH: 1092
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1092)
<223> OTHER INFORMATION: SGlucON Lambda bovine

<400> SEQUENCE: 112

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

gcc aag ccc acc gag aac aac gaa gac ttc aac atc gtg gcc gtg gcc       96
Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

agc aac ttt gcg acc acg gat ctc gat gct gac cga ggg aag ttg ccc      144
Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

ggc aag aag ctg ccg ctg gag gtg ctc aaa gag atg gaa gcc aat gcc      192
Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

cgg aaa gct ggc tgc acc agg ggc tgt ctg atc tgc ctg tcc cac atc      240
Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

aag tgc acg ccc aag atg aag aag tgg ctc cca gga cgc tgc cac acc      288
Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95

tac gaa ggc gac aaa gag tcc gca cag ggc ggc ata ggc gag gcg atc      336
Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

gtc gat att cct gag att cct ggg ttc aag gac ttg gag cca atg gag      384
Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

cag ttc atc gca cag gtc gat ctg tgt gtg gac tgc aca act ggc tgc      432
Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

ctc aaa ggg ctt gcc aac gtg cag tgt tct gac ctg ctc aag aag tgg      480
Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160
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ctg ccg caa cgc tgt gcg acc ttt gcc agc aag atc cag ggc cag gtg      528
Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

gac aag atc aag ggg gcc ggt ggt gac ggg ccc agg aca gga gca gtt      576
Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Arg Thr Gly Ala Val
            180                 185                 190

cct gtg ccc tct gcc ccc agg gcc ctc cca cct gcc agg ggc tgc cac      624
Pro Val Pro Ser Ala Pro Arg Ala Leu Pro Pro Ala Arg Gly Cys His
        195                 200                 205

gtg gcc cag ttc aag tct ctg tcc cct caa gag ctg cag gcc ttc aag      672
Val Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys
    210                 215                 220

acg gcc agg gat gcc ttt gaa gac tcg ttc ttg cca aag gac tgg gac      720
Thr Ala Arg Asp Ala Phe Glu Asp Ser Phe Leu Pro Lys Asp Trp Asp
225                 230                 235                 240

tgc agc acc cac ctt ttc ccc agg acc cgg gac ctg aag cac ctg cag      768
Cys Ser Thr His Leu Phe Pro Arg Thr Arg Asp Leu Lys His Leu Gln
                245                 250                 255

gtg tgg gag cgc cct gtg gct ctg gag gca gag ctg gcc ctg aca ctg      816
Val Trp Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
            260                 265                 270

acg gtc ctg gag gcc atg gct aac tca tcc ctg ggc cac agc ctg gag      864
Thr Val Leu Glu Ala Met Ala Asn Ser Ser Leu Gly His Ser Leu Glu
        275                 280                 285

cag ccc ctt ctc acg ctg cag aac atc cac tcc aag ctc cag gcc tgt      912
Gln Pro Leu Leu Thr Leu Gln Asn Ile His Ser Lys Leu Gln Ala Cys
    290                 295                 300

gtc cca gct cag ccc aca gca agc tcc agg ccc cgg ggc cgc ctc cac      960
Val Pro Ala Gln Pro Thr Ala Ser Ser Arg Pro Arg Gly Arg Leu His
305                 310                 315                 320

cac tgg ctg cac cgc ctc cag gag gcc cgg aag gag tcc cag gac tgc     1008
His Trp Leu His Arg Leu Gln Glu Ala Arg Lys Glu Ser Gln Asp Cys
                325                 330                 335

ctc gaa gcc tct gtg atg ttc aac ctc ctc cgc ctc ctc acc cgg gac     1056
Leu Glu Ala Ser Val Met Phe Asn Leu Leu Arg Leu Leu Thr Arg Asp
            340                 345                 350

ctg aaa tgt gtt gcc agc gga gac cag tgt gtc tga                     1092
Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
        355                 360


<210> SEQ ID NO 113
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 113

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

Ala Lys Pro Thr Glu Asn Asn Glu Asp Phe Asn Ile Val Ala Val Ala
            20                  25                  30

Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
        35                  40                  45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
    50                  55                  60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65                  70                  75                  80

Lys Cys Thr Pro Lys Met Lys Lys Trp Leu Pro Gly Arg Cys His Thr
                85                  90                  95
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Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
            100                 105                 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
        115                 120                 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
    130                 135                 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
145                 150                 155                 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
                165                 170                 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp Gly Pro Arg Thr Gly Ala Val
            180                 185                 190

Pro Val Pro Ser Ala Pro Arg Ala Leu Pro Pro Ala Arg Gly Cys His
        195                 200                 205

Val Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys
    210                 215                 220

Thr Ala Arg Asp Ala Phe Glu Asp Ser Phe Leu Pro Lys Asp Trp Asp
225                 230                 235                 240

Cys Ser Thr His Leu Phe Pro Arg Thr Arg Asp Leu Lys His Leu Gln
                245                 250                 255

Val Trp Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
            260                 265                 270

Thr Val Leu Glu Ala Met Ala Asn Ser Ser Leu Gly His Ser Leu Glu
        275                 280                 285

Gln Pro Leu Leu Thr Leu Gln Asn Ile His Ser Lys Leu Gln Ala Cys
    290                 295                 300

Val Pro Ala Gln Pro Thr Ala Ser Ser Arg Pro Arg Gly Arg Leu His
305                 310                 315                 320

His Trp Leu His Arg Leu Gln Glu Ala Arg Lys Glu Ser Gln Asp Cys
                325                 330                 335

Leu Glu Ala Ser Val Met Phe Asn Leu Leu Arg Leu Leu Thr Arg Asp
            340                 345                 350

Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
        355                 360
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The invention claimed is:

1. A polynucleotide that encodes a fusion protein comprising a luciferase, and at least one interferon, wherein the polynucleotide encodes the fusion protein described by SEQ ID NOS: 48, 52, 56, 60, 64, 68, 70, 74, 78, 82, 86, 90, 94, 111, or 113.

2. The polynucleotide of claim **1** that further comprises a polynucleotide encoding at least one translational interrupter sequence.

3. The polynucleotide of claim **1** that further comprises a polynucleotide encoding at least one Aphthovirus translational interrupter sequence.

4. The polynucleotide of claim **1** that further comprises a polynucleotide encoding at least one foot-and-mouth disease virus (FMDV) translational interrupter sequence.

5. The polynucleotide of claim **1** that further comprises a polynucleotide encoding a FMDV 2A or Δ1D2A sequence.

6. The polynucleotide of claim **1** that comprises a polynucleotide sequence described by SEQ ID NOS: 47, 51, 55, 59, 63, 67, 69, 73, 77, 81, 85, 89, 93, 110 or 112.

7. A vector comprising the polynucleotide of claim **1**.

8. The vector of claim **7** that further comprises a polynucleotide encoding at least one promoter or other transcription regulatory element, at least one prokaryotic or eukaryotic translation initiation sequence or other translation regulatory element, at least one translational interrupter sequence, or at least one reporter polynucleotide sequence operatively linked to, or embedded within, the polynucleotide sequence encoding the fusion protein.

9. The vector of claim **7** that further comprises a polynucleotide encoding at least one FMDV translational interrupter sequence.

10. The vector of claim **7** that further comprises a polynucleotide encoding a FMDV 2A or Δ1D2A sequence.

11. The vector of claim **7** that is a mRNA, DNA plasmid, minicircle vector, a replication deficient adenovirus vector, a vaccinia virus vector, or other viral vector that expresses the fusion protein.

12. The vector of claim **7** that comprises a polynucleotide sequence described by SEQ ID NOS: 47, 51, 55, 59, 63, 67, 69, 73, 77, 81, 85, 89, 93, 110 or 112.

13. A host cell comprising the vector of claim **7**, wherein the host cell expresses the fusion protein.

14. The host cell of claim **13** that is an insect cell.

15. The host cell of claim **13** that is mammalian cell.

16. The host cell of claim 13 that is a prokaryotic cell.

17. A fusion protein, that is encoded by the polynucleotide of claim 1.

18. The fusion protein of claim 17, wherein the polynucleotide further comprises a polynucleotide encoding at least one translational interrupter sequence.

19. The fusion protein of claim 17, wherein the polynucleotide further comprises a polynucleotide encoding at least one Aphthovirus translational interrupter sequence.

20. The fusion protein of claim 17, wherein the polynucleotide further comprises a polynucleotide encoding at least one FMDV translational interrupter sequence.

21. The fusion protein of claim 17, wherein the polynucleotide further comprises a polynucleotide encoding a FMDV 2A or Δ1D2A sequence.

22. A composition comprising the fusion protein of claim 17 and at least one pharmaceutically acceptable carrier, excipient or adjuvant.

23. A method for producing the fusion protein of claim 17 comprising culturing a host cell that expresses the fusion protein in a suitable medium and recovering the fusion protein.

24. A method for quantifying an amount or concentration of an interferon produced in an expression system comprising:

a. providing the vector according to claim 7;
b. transforming the vector into a host cell;
c. culturing the cells in a medium;
d. harvesting the medium; and
e. quantifying the intensity of luminescent output.

25. A method for quantifying an amount or concentration of an interferon produced in an expression system comprising:

a. providing the vector according to claim 9;
b. transforming the vector into a host cell;
c. culturing the cells in a medium;
d. harvesting the medium; and
e. quantifying the intensity of luminescent output.

26. A method for quantifying an amount or concentration of an interferon produced in an expression system comprising:

a. providing the vector according to claim 10;
b. transforming the vector into a host cell;
c. culturing the cells in a medium;
d. harvesting the medium; and
e. quantifying the intensity of luminescent output, thus quantifying an amount or concentration of an interferon in the expression system.

27. A method for quantifying an amount or concentration of an interferon produced in an expression system comprising:

a. providing the vector according to claim 11;
b. transforming the vector into a host cell;
c. culturing the cells in a medium;
d. harvesting the medium; and
e. quantifying the intensity of luminescent output, thus quantifying an amount or concentration of an interferon in the expression system.

28. A method for quantifying an amount or concentration of an interferon in an expression system comprising:

a. providing the vector according to claim 12;
b. transforming the vector into a host cell;
c. culturing the cells in a medium;
d. harvesting the medium; and
e. quantifying the intensity of luminescent output, thus quantifying an amount or concentration of an interferon in the expression system.

29. A method for facilitating secretion of a fusion protein from a host cell comprising:

a. providing the vector according to claim 7;
b. transforming the vector into a host cell;
c. culturing the cells in a medium; and
d. recovering the secretable fusion protein from the medium.

30. A method for facilitating secretion of a fusion protein from a host cell comprising:

a. providing the vector according to claim 12;
b. transforming the vector into a host cell;
c. culturing the cells in a medium; and
d. Recovering the secretable fusion protein from the medium.

31. A method for measuring an amount of a biotherapeutic peptide in a subject in need thereof comprising:

a. providing the vector according to claim 12;
b. transforming the vector in the subject;
c. recovering biological material from the subject;
d. wherein the biological material comprises blood, serum, plasma, or urine.

32. A method for certifying vaccine expression in vivo comprising:

a. providing the vector according to claim 12;
b. transforming the vector into a host organism;
c. recovering biological material from the host organism;
d. wherein the biological material comprises blood, serum, plasma, or urine.

33. A pharmaceutical composition comprising the fusion protein of claim 17 and at least one pharmaceutically acceptable carrier, adjuvant, or excipient.

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