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Materials and methods for prevention and treatment of RNA viral diseases

Shyam S. Mohapatra

Aruna K. Behera

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(54) **MATERIALS AND METHODS FOR
PREVENTION AND TREATMENT OF RNA
VIRAL DISEASES**

(71) Applicant: **University of South Florida**, Tampa, FL
(US)

(72) Inventors: **Shyam S. Mohapatra**, Lutz, FL (US);
Aruna K. Behera, Watertown, MA (US)

(73) Assignee: **University of South Florida**, Tampa, FL
(US)

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See application file for complete search history.

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Primary Examiner — Jane Zara

(74) *Attorney, Agent, or Firm* — Saliwanchik, Lloyd &
Eisenschenk

(57) **ABSTRACT**

The subject invention concerns a method of inhibiting an
RNA virus infection within a patient by increasing the
amount of 2-5 oligoadenylate synthetase (2-5 AS) activity
within the patient. Preferably, the preventative and therapeutic
methods of the present invention involve administering a
nucleotide encoding 2-5 AS, or at least one catalytically
active fragment thereof, such as the p40, p69, p100 subunits,
to a patient in need thereof. The present inventors have deter-
mined that overexpression of 2-5AS causes a reduction in
epithelial cell damage, reduction in infiltration of mono-
nuclear cells in the peribronchiolar and perivascular regions,
and reduction in thickening of the septa in the lungs. Levels of
chemokines, such as MIP1- α , are also reduced upon overex-
pression of 2-5AS. The subject invention also pertains to
pharmaceutical compositions containing a nucleotide
sequence encoding 2-5 AS and a pharmaceutically acceptable
carrier, as well as vectors for delivery of the 2-5 AS nucleotide
sequence.

8 Claims, 14 Drawing Sheets

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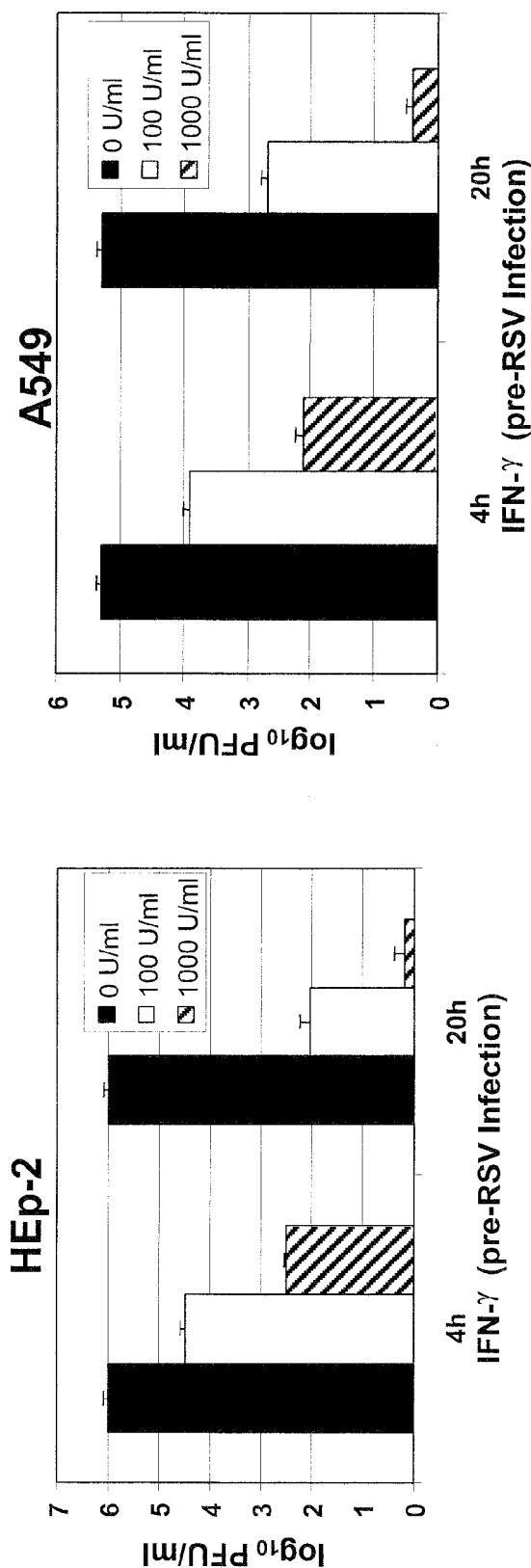


FIG. 1A

FIG. 1B

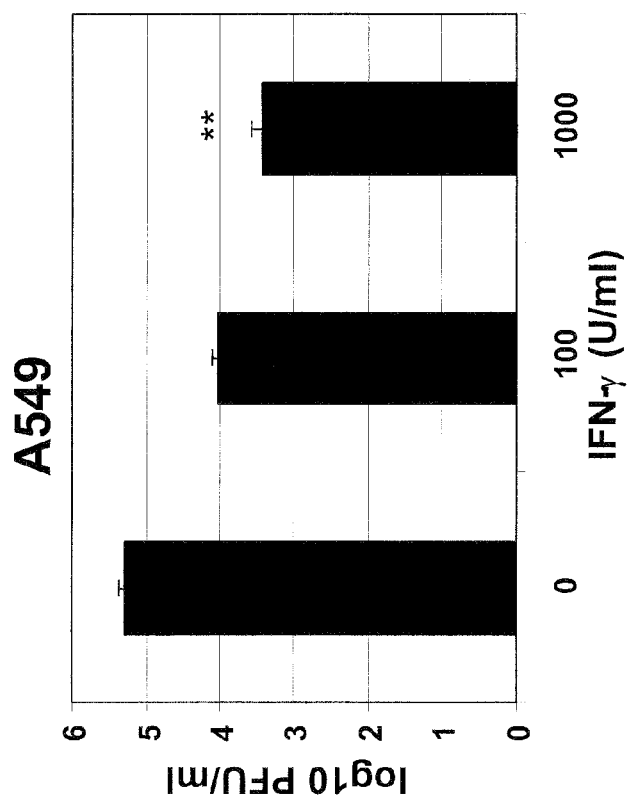


FIG. 1C

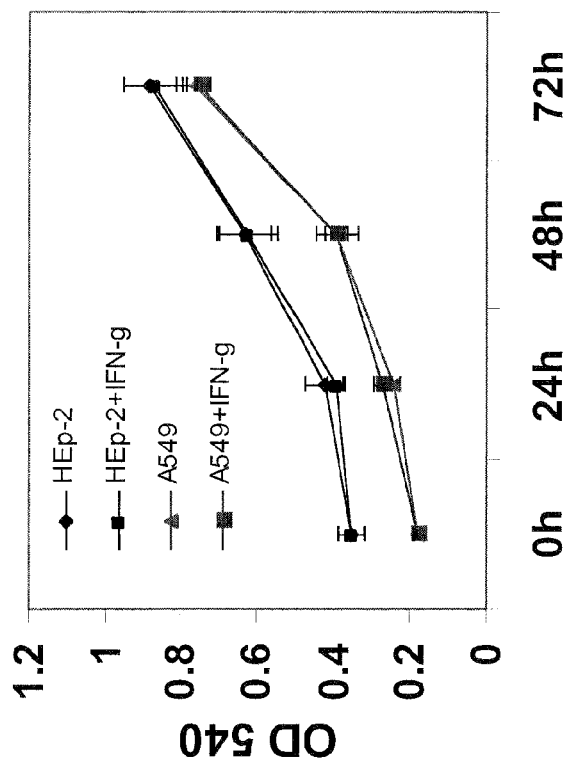


FIG. 1D

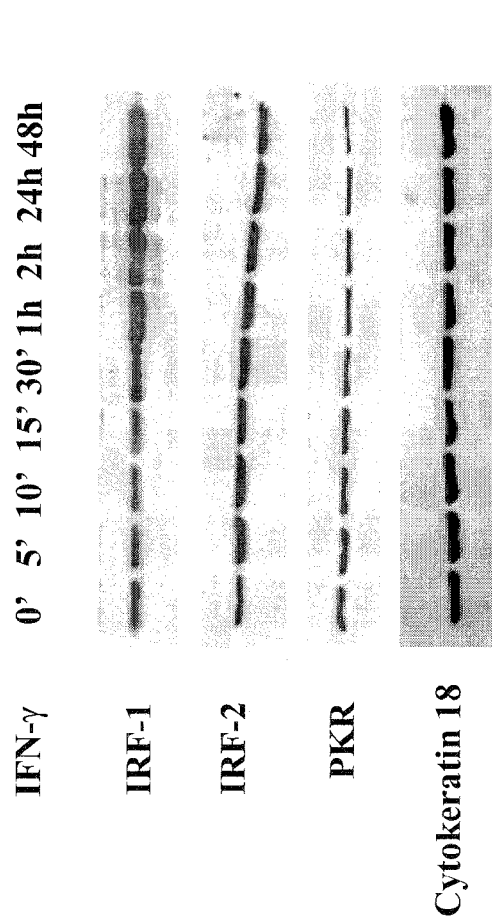


FIG. 2A

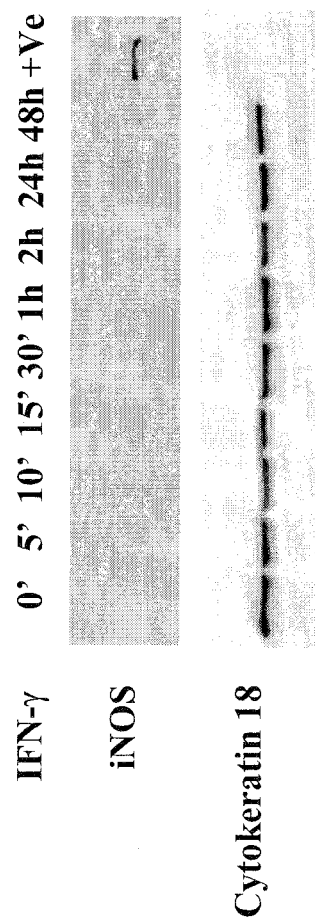
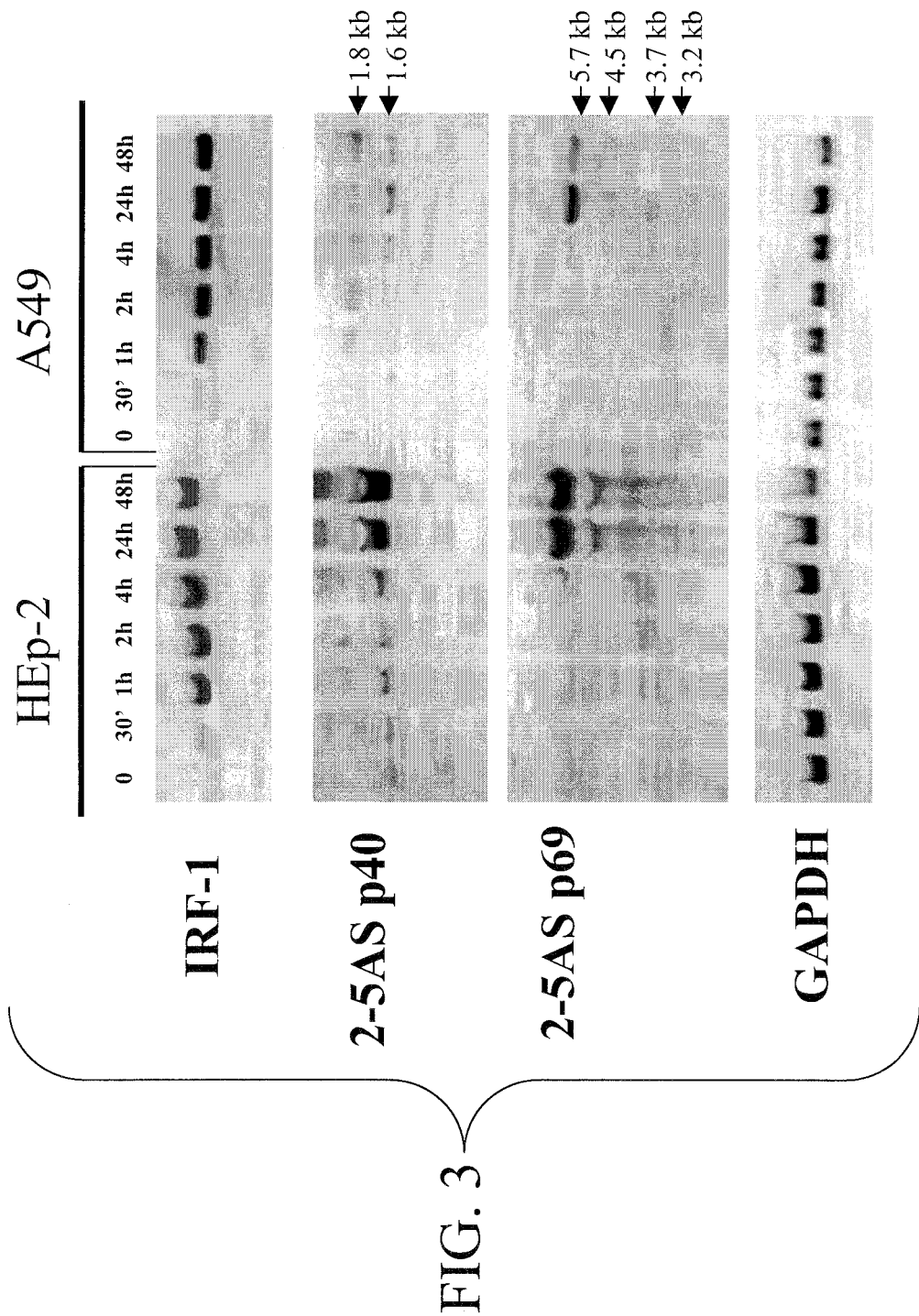


FIG. 2B



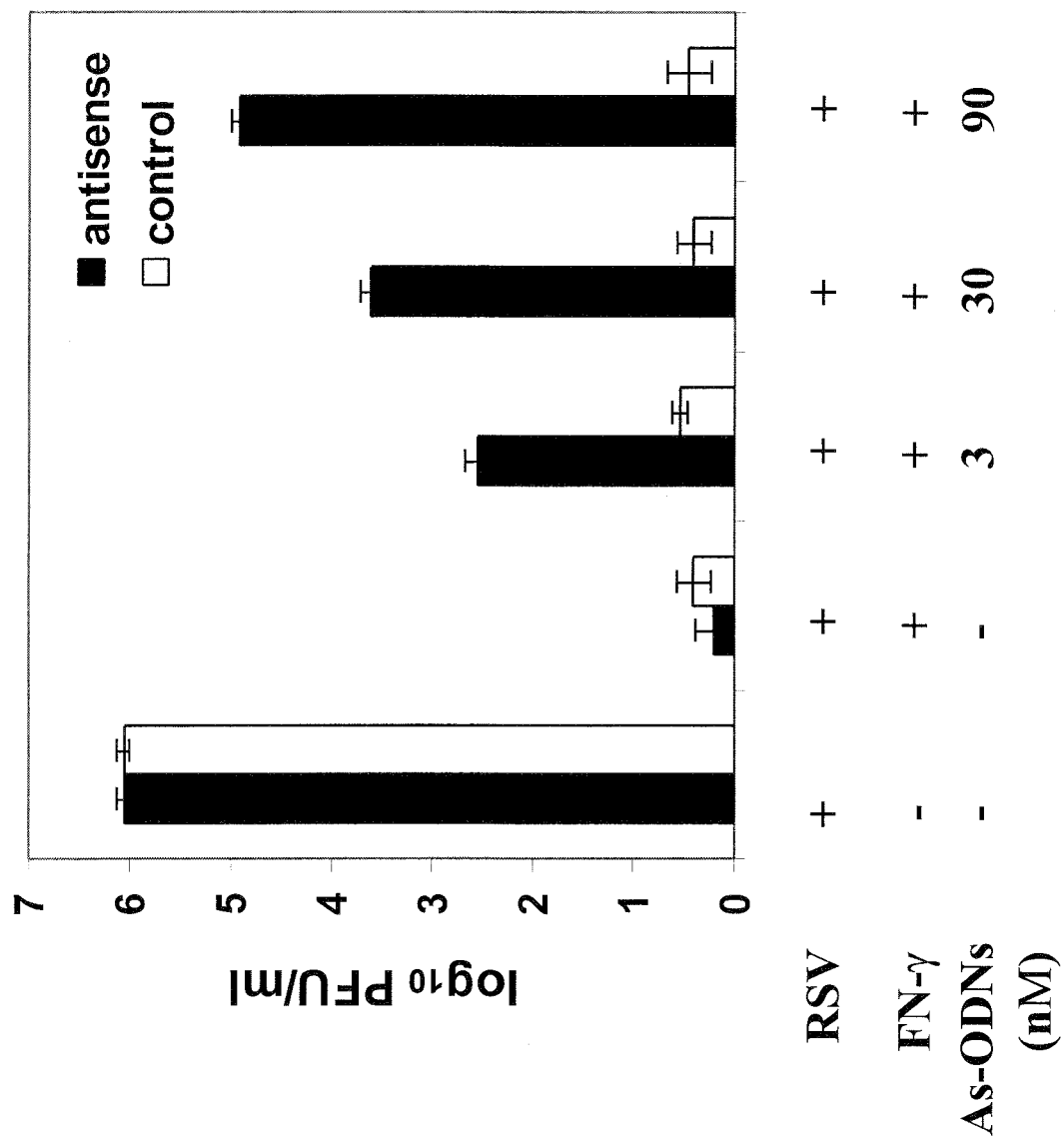
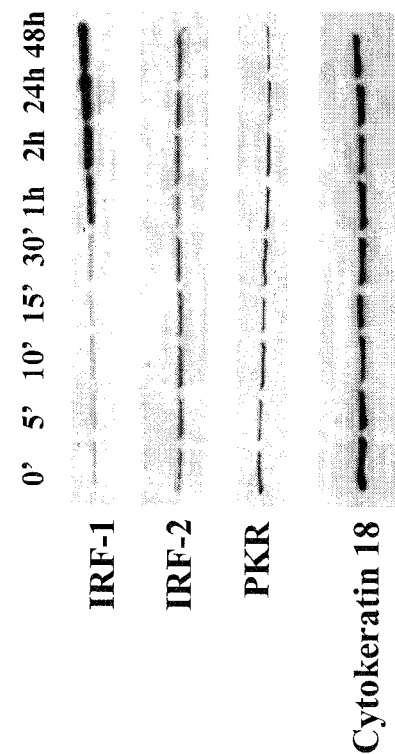
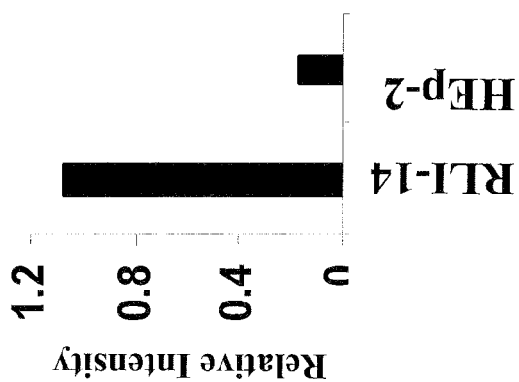
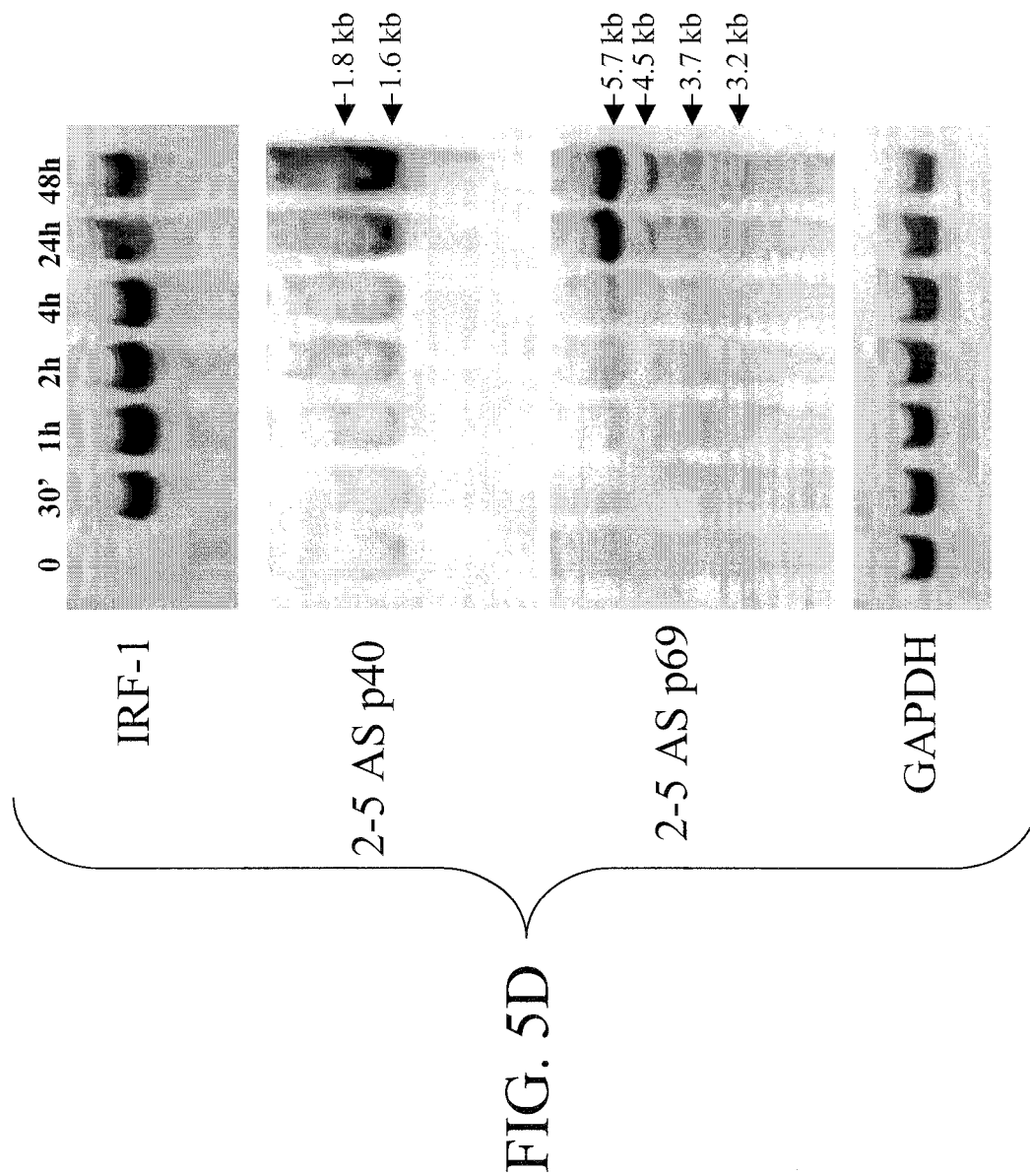


FIG. 4



FIG. 5B





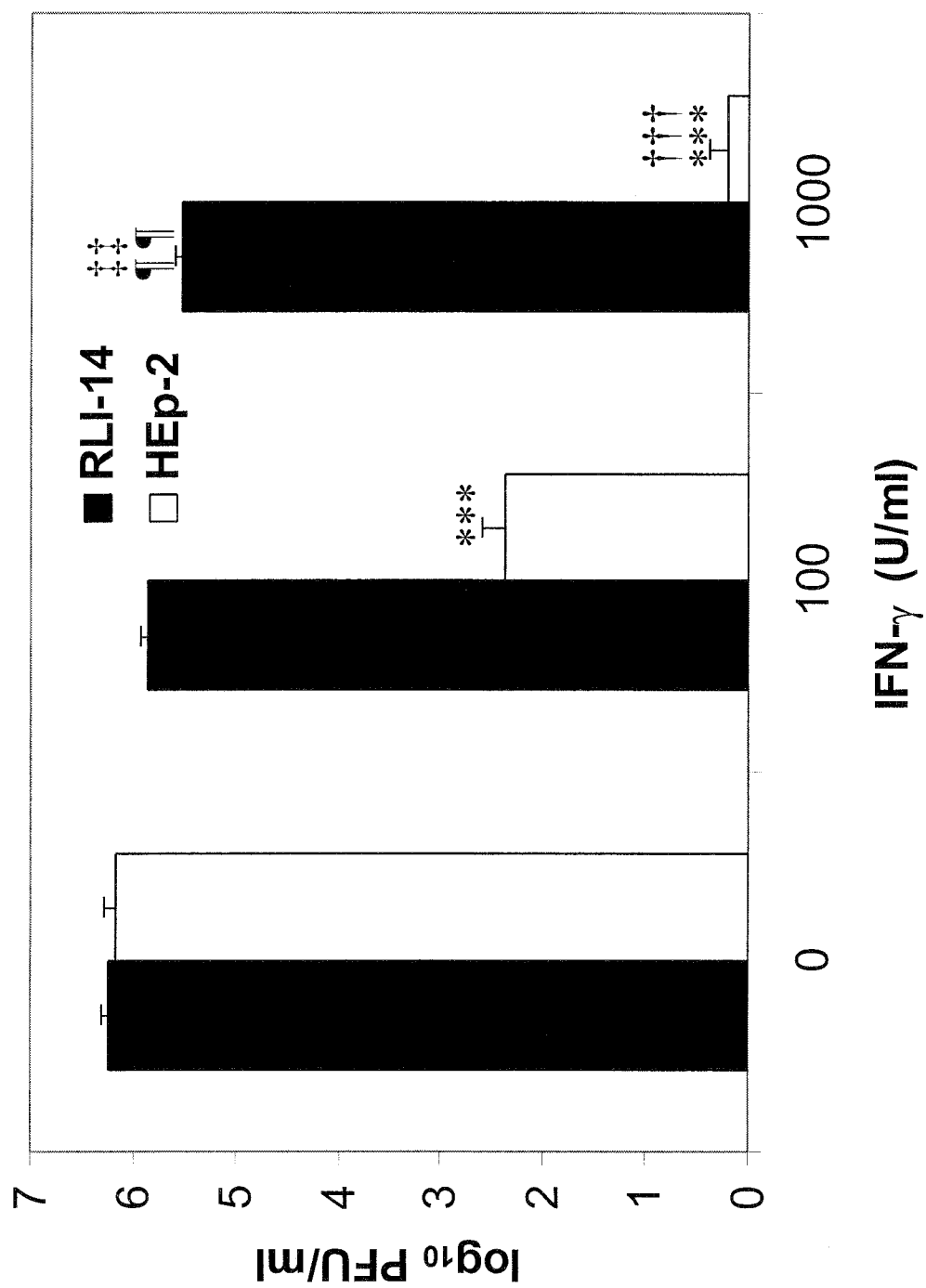


FIG. 6

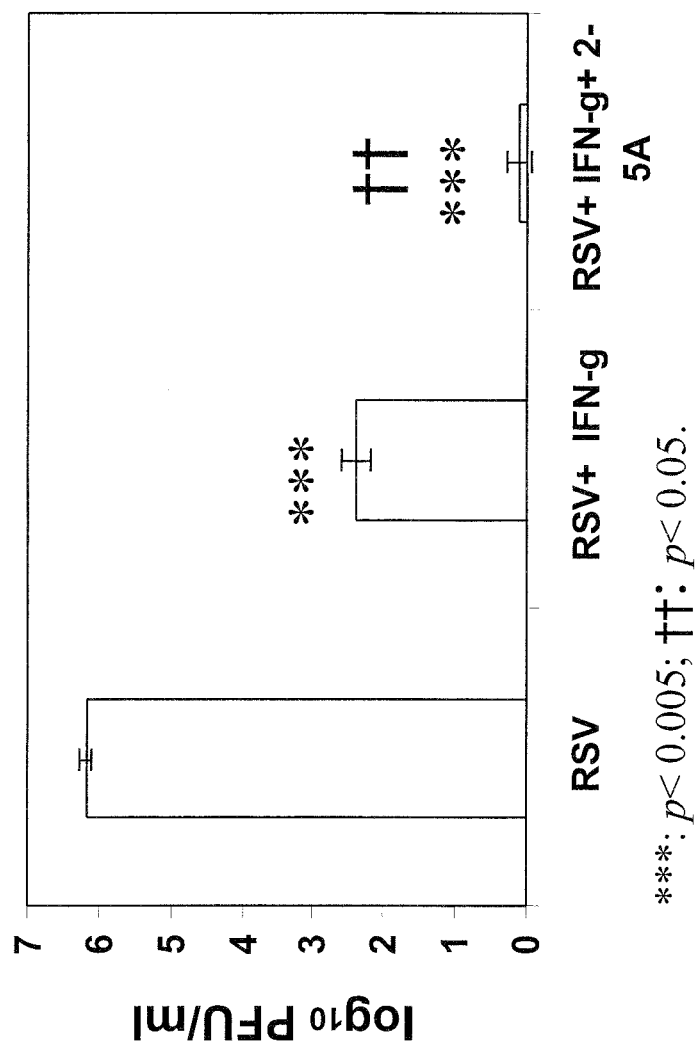
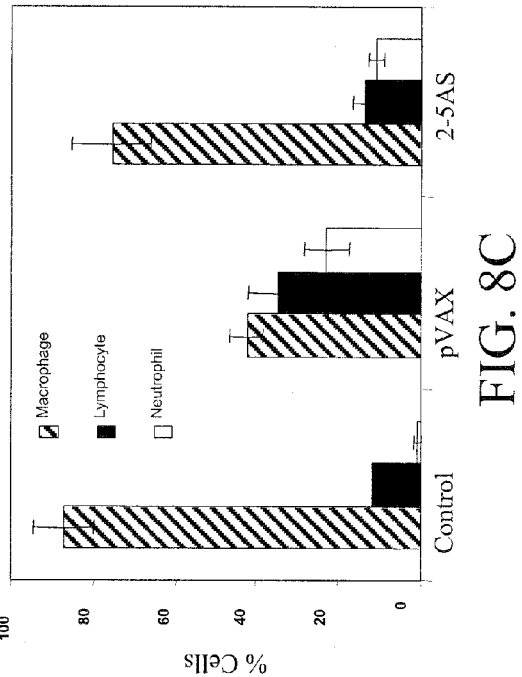
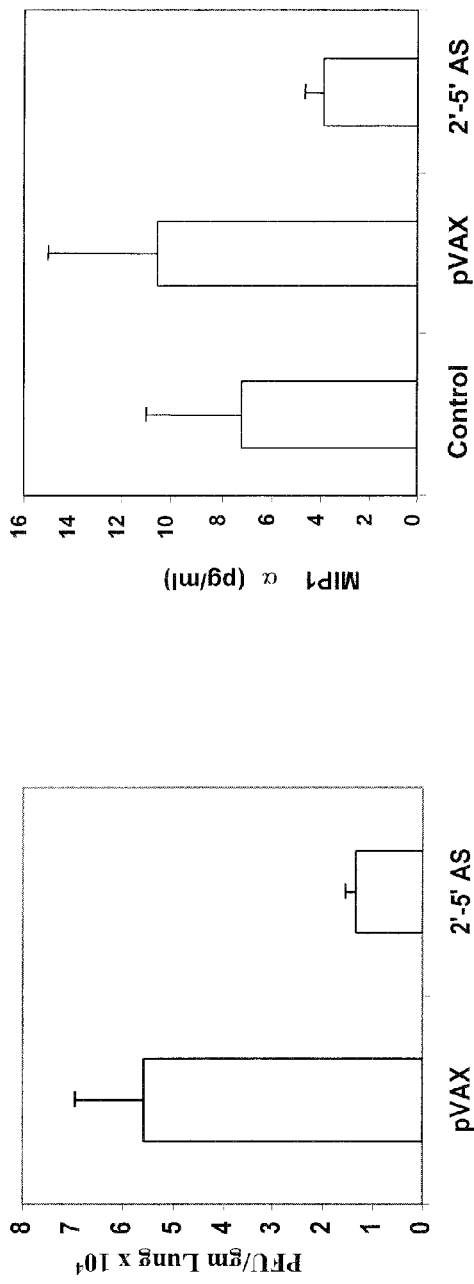


FIG. 7



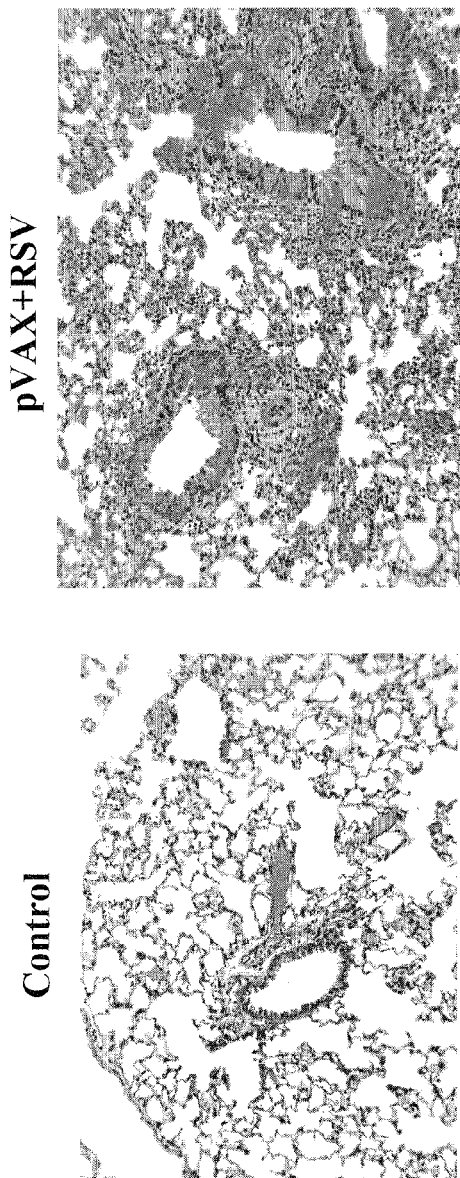


FIG. 9A

FIG. 9B

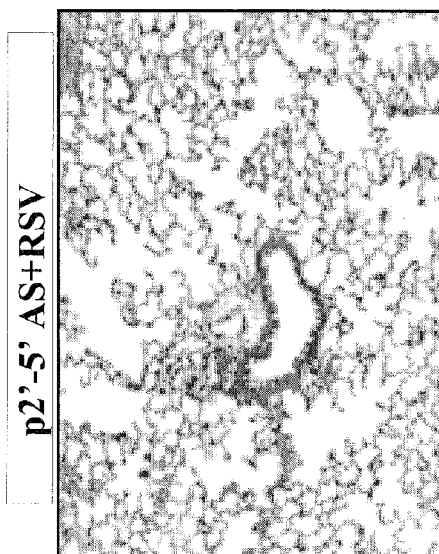


FIG. 9C

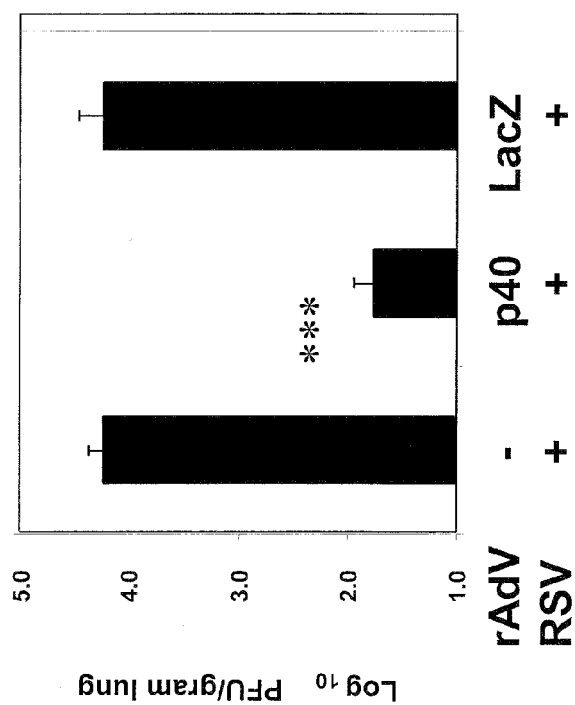


FIG. 10

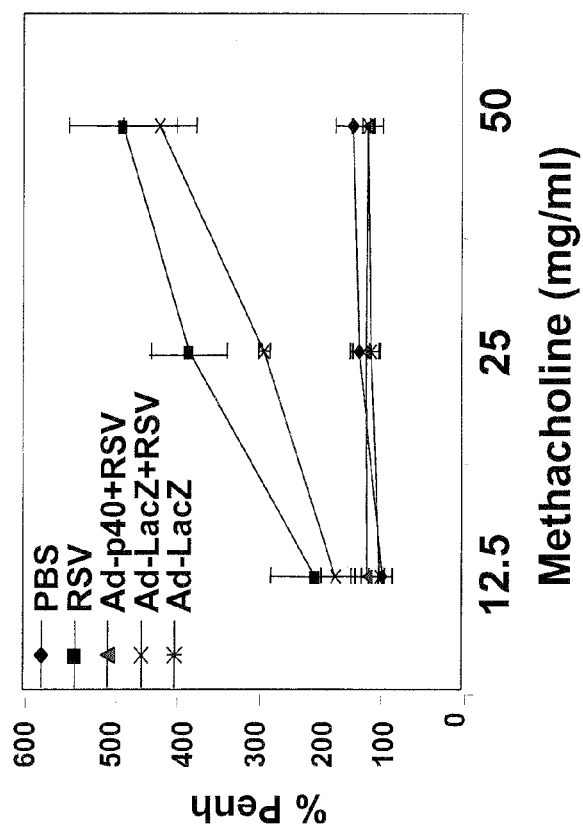


FIG. 11

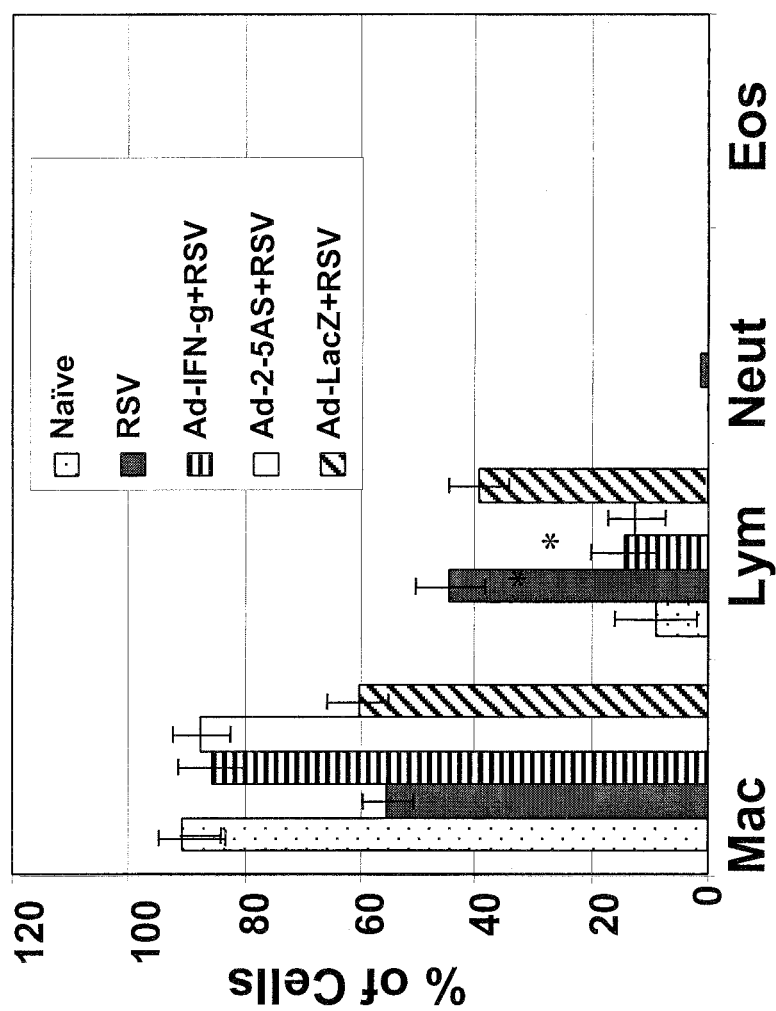


FIG. 12

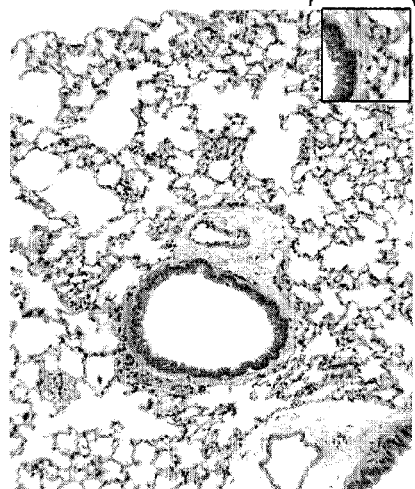


FIG. 13B

FIG. 13A

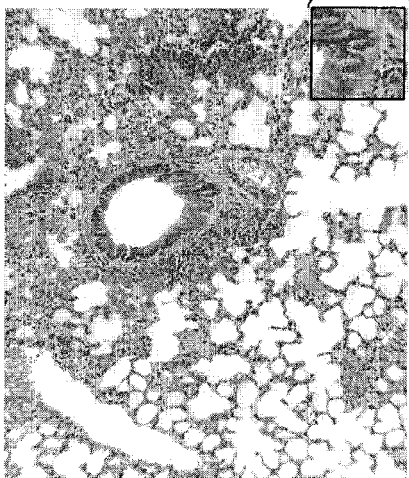


FIG. 13D

FIG. 13C

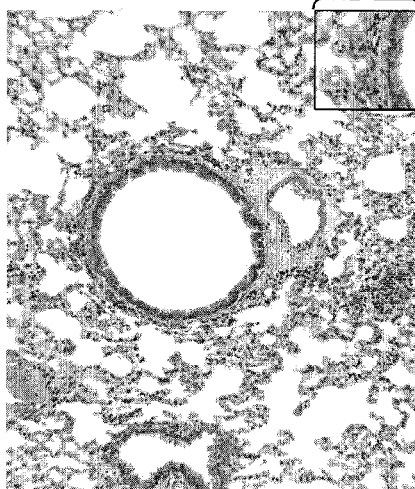


FIG. 13F

FIG. 13E

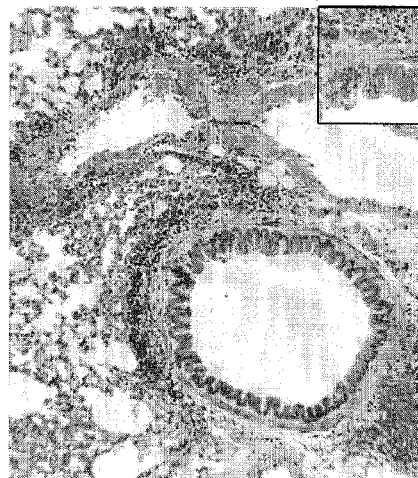


FIG. 13H

FIG. 13G

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MATERIALS AND METHODS FOR PREVENTION AND TREATMENT OF RNA VIRAL DISEASES

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application is a continuation of U.S. application Ser. No. 12/638,800, filed Dec. 15, 2009, which is a continuation of U.S. application Ser. No. 12/016,041, filed Jan. 17, 2008, which is a divisional of U.S. application Ser. No. 10/426,436, filed Apr. 30, 2003, now U.S. Pat. No. 7,354,908, which claims the benefit of provisional patent application Ser. No. 60/319,313, filed Jun. 12, 2002, and provisional patent application Ser. No. 60/319,216, filed Apr. 30, 2002, all of which are hereby incorporated by reference in their entirety, including all nucleic acid sequences, amino acid sequences, figures, tables, and drawings.

BACKGROUND OF INVENTION

Respiratory syncytial virus (RSV) is a major respiratory pathogen in infants, young children, and the elderly, causing severe bronchiolitis, pneumonia, and exacerbation of asthma. In the United States alone, RSV causes approximately 4 million cases of respiratory tract infection annually, which results in 149,000 hospitalizations and 11,000 deaths. It has been established that interferon-gamma (IFN- γ) gene therapy is effective against RSV infection in BALB/c mice (Kumar et al., Vaccine 18, 558-567, 1999).

Intranasal administration of a plasmid expressing IFN- γ cDNA proved to be an effective prophylaxis in mice. Furthermore, IFN- γ expressed by a recombinant respiratory syncytial virus attenuates virus replication in mice without compromising immunogenicity. IFN- γ , a type II interferon, is a pleiotropic cytokine which plays an important role in modulating nearly all phases of immune and inflammatory responses. IFNs bind to specific receptors on cells and activate the JAK-STAT signaling cascade, which culminates in the transcriptional induction of IFN-stimulated genes (ISGs). The Jak1 and Jak2 phosphorylate STAT-1 following the binding of IFN- γ to its receptor. Once phosphorylated, STAT molecules dimerize and translocate to the nucleus and bind to gamma activated sequence (GAS) elements present in the regulatory regions of various ISGs. The antiviral mechanism of IFN- γ may involve one or more of a number of ISG-encoded products, including interferon regulatory factor-1 (IRF-1) double stranded RNA-dependent protein kinase (PKR), the Mx family of proteins, a family of 2'-5'-oligoadenylate synthetases (2-5 AS), and RNase L.

RNase L is constitutively expressed in most mammalian cells and is found in an inactive form bound to RNase L inhibitor (RLI), a 68 kDa protein not regulated by IFN- γ . The 2-5 AS produces a series of 5' phosphorylated, 2', and 5'-linked oligoadenylates (2-5 A) from ATP, when activated by double-stranded ribonucleic acid (dsRNA). Upon binding of 2-5 AS with RNase L, RLI is released and consequently, RNase L is dimerized and activated, mediating the cleavage of single-stranded RNA. However, the mechanism of the induction and activation of each of these genes is different in different cells and for the types of viruses. The mechanism of the IFN- γ -mediated anti-viral activity remains to be elucidated for many clinically important viruses.

BRIEF SUMMARY OF THE INVENTION

The present invention provides materials and methods useful for inhibiting viral infections caused by ribonucleic acid

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(RNA) viruses that transiently produce double-stranded RNA during replication. The subject invention concerns therapeutic methods for preventing or decreasing the severity of symptoms associated with an RNA viral infection by increasing endogenous levels of 2'-5' oligoadenylate synthetase (2-5 AS) activity within the patient. Preferably, the endogenous levels of the 2-5 AS p40 subunit (e.g., the 40 kDa, 42 kDa, 46 kDa, or other splice variants), p69 subunit, (e.g., the 69 kDa, 71 kDa, or other splice variants), p100 subunit, or combinations thereof, are increased within the patient.

The materials and methods of present invention are effective for treating or preventing human or animal infections from RNA viruses such as, members of the family paramyxoviridae, respiratory syncytial virus (RSV), Rhinovirus, Vaccinia, Reovirus, human immunodeficiency virus (HIV), encephalomyocarditis virus (EMCV), Hepatitis B, Hepatitis C, as well as bovine respiratory syncytial virus (BRSV), which infect cattle, sheep, and goats; Measles virus; Sendai virus; Parainfluenza 1, 2, and 3; Mumps virus, Simian virus; and Newcastle virus.

In one aspect, the method of the present invention involves the administration of a nucleotide sequence encoding 2-5 AS, or at least one catalytically active fragment of 2-5 AS, such as the p40, p69, or p100 subunits of 2-5 AS, to a patient in need thereof. The nucleotide sequence encoding 2-5 AS or at least one catalytically active fragment thereof can be administered to the patient, for example, in a viral vector or non-viral vector, such as plasmid deoxyribonucleic acid (DNA). In cases wherein the RNA virus is one which infects the patient's respiratory system, the nucleotide sequence encoding 2-5 AS, or at least one catalytically active fragment thereof, is preferably administered orally or intranasally to the epithelial mucosa of the respiratory system.

The present invention also pertains to pharmaceutical compositions comprising a nucleotide sequence encoding 2-5 AS, or at least one catalytically active fragment thereof, such as the p40, p69, or p100 subunits of 2-5 AS, and a pharmaceutically acceptable carrier. The pharmaceutical compositions of the present invention are useful for preventing or decreasing the severity of symptoms associated with RNA viral infections. In another embodiment, the pharmaceutical compositions of the present invention comprise the 2-5 AS polypeptide, or at least one catalytically active fragment of the 2-5 AS polypeptide, and a pharmaceutically acceptable carrier. The pharmaceutical compositions of the present invention can include various agents that protect the nucleic acid or amino acid contents from protein degradation.

In another aspect, the present invention concerns vectors containing a nucleotide sequence encoding 2-5 AS, or at least one catalytically active fragment thereof, such as the p40, p69, or p100 subunits of 2-5 AS. Optionally, the vector can further include a promoter sequence operatively linked to the nucleotide encoding 2-5 AS or at least one catalytically active fragment thereof, permitting expression of the nucleotide sequence within a host cell. In another aspect, the present invention includes host cells that have been genetically modified with a nucleotide sequence encoding 2-5 AS, or at least one catalytically active fragment thereof, such as the p40, p69, or p100 subunits of 2-5 AS.

BRIEF DESCRIPTION OF DRAWINGS

FIGS. 1A-D show the results of pre-incubation of HEP-2 cells for 4-20 hours with different concentrations of IFN- γ and subsequent infection with RSV.

FIGS. 2A and 2B show results of a western blot analysis using specific antibodies to IRF-1, IRF-2, cytokeratin-18,

double stranded RNA protein kinase (PKR), and inducible nitric oxide synthase (iNOS). Proteins were analyzed from cells at various time points post treatment with IFN- γ (1000 U/ml). Cytokeratin-18 was used as an internal control.

FIG. 3 show results of northern analysis performed using gene specific probes for IRF-1 and the p40 and p69 isoforms of 2-5 AS.

FIG. 4 shows results of exposure of HEp-2 cells to IFN- γ (1000 U/ml at 20 hours pre-infection) and treatment with equimolar mixtures of antisense oligonucleotides (ODNs) to both p40 and p69 isoforms of 2-5 AS. Scrambled mismatch of the antisense ODN sequence to p40 and p69 at the same concentration were used as control.

FIGS. 5A-D show the results of northern analyses of (i) RNAs from RNase L inhibitor (RLI) and HEp-2 using a gene specific probe for RLI and (ii) the level of mRNA expression of IRF-1, p40, and p69 isoforms of 2-5 AS.

FIG. 6 show the results of treatment of both HEp-2 cells and RLI-14 cells with IFN- γ (at 100-1000 U/ml at 20 hours pre-infection) and subsequent infection with RSV.

FIG. 7 shows the results of treatment of HEp-2 cells with IFN- γ (at 100-1000 U/ml at 20 hours pre-infection) and subsequent infection with RSV. 2-5 A was transfected at 3 hours prior to RSV infection. Cells were harvested at 72 hours post infection and the clear cell homogenate was used for the RSV plaque assay (***: $p < 0.005$; ††: $p < 0.05$).

FIGS. 8A-8C show lung titers of RSV in infected mice following 2-5 AS cDNA vaccination. BALB/c mice ($n=4$) were intranasally administered with p2'-5' AS (25 mg of DNA each time complexed with lipofectamine) or an equal amount of empty pVAX (CLONTECH, Palo Alto, Calif., USA) vector DNA (as a transfection control) 3 times in 2 day intervals. As shown in FIG. 8A, 2-5 AS cDNA vaccination significantly attenuated lung titers of RSV. FIG. 8B shows that vaccination with 2-5 AS cDNA decreases production of the chemokine macrophage inflammatory protein-1 alpha (MIP-1 α). The results of bronchoalveolar lavage (BAL) cell differential (FIG. 8C) show that 2-5 AS does not significantly alter the cellular composition of the lung, although the percent of neutrophils is increased in the lungs of mice treated with 2-5 AS cDNA.

FIGS. 9A-9C show representative photomicrographs of lungs stained with hematoxylin and eosin (H & E). FIG. 9A is an untreated control. FIGS. 9B and 9C show histological sections of RSV infected lungs following treatment with the empty pVAX vector and p2'-5' AS, respectively.

FIG. 10 shows results of treatment with adenoviral vector (Ad)-2-5 AS (p40) results in attenuation of RSV replication. BALB/c mice were intranasally administered with Ad-p40 and then infected with RSV. Lungs were harvested five days post RSV infection and RSV replication was assayed by RT-PCR analysis of RSV-N gene. GAPDH was used as internal control.

FIG. 11 shows that Ad-p40 attenuates RSV lung titers. Mice were intranasally given Ad-p40 and then infected with RSV. Lungs were harvested five days post RSV infection and lung homogenate was used for RSV plaque assay. Ad-LacZ was used as control.

FIG. 12 shows that Ad-p40 inhibits RSV induced airway reactivity. BALB/c mice were intranasally administered with Ad-p40 and subsequently infected with RSV. AHR was measured on day 4 post-RSV infection. Ad-p40 treatment significantly decreased pulmonary inflammation.

FIGS. 13A-13H show that Ad-p40 overexpression normalizes macrophage and lymphocyte numbers in the lung in RSV infected mice. BAL cell differential was performed and percentages of macrophage, lymphocytes and neutrophils was

determined. Both Ad-IFN γ and Ad-p40 treatment reduced the lymphocyte population to normal, compared to RSV-infected mice. Histological sections from lungs were stained with hematoxylin and eosin and representative photomicrographs are shown. Sections shown are as follows: Naive mice (FIG. 13A; with magnified inset FIG. 13B); RSV infected mice (FIG. 13C; with magnified inset, FIG. 13D); Ad-p40 treated mice (FIG. 13E; with magnified inset, FIG. 13F); and Ad-lacZ treated mice (FIG. 13G; with magnified inset, FIG. 13H).

BRIEF DESCRIPTION OF SEQUENCES

SEQ ID NO: 1 is a nucleotide coding sequence (CDS) for the human 40 kDa splice variant of the 40/46 kDa subunit ("p40 subunit") of 2'-5' oligoadenylate synthetase (National Center for Biotechnology Information (NCBI) Accession Number NM_016816).

SEQ ID NO: 2 is an amino acid sequence of the human 40 kDa splice variant of the 40/46 kDa subunit ("p40 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number NM_016816).

SEQ ID NO: 3 is a nucleotide coding sequence (CDS) for the human 46 kDa splice variant of the 40/46 kDa subunit ("p40 subunit") of 2'-5' oligoadenylate synthetase (National Center for Biotechnology Information (NCBI) Accession Number NM_016816).

SEQ ID NO: 4 is an amino acid sequence of the human 46 kDa splice variant of the 40/46 kDa subunit ("p40 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number NM_016816).

SEQ ID NO: 5 is a nucleotide coding sequence (CDS) for the human 69 kDa splice variant of the 69/71 kDa subunit ("p69 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number NM_002535).

SEQ ID NO: 6 is an amino acid sequence of the human 69 kDa splice variant of the 69/71 kDa subunit ("p69 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number NM_002535).

SEQ ID NO: 7 is a nucleotide coding sequence (CDS) for the human 71 kDa splice variant of the 69/71 kDa subunit ("p69 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number NM_002535).

SEQ ID NO: 8 is an amino acid sequence of the human 71 kDa splice variant of the 69/71 kDa subunit ("p69 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number NM_002535).

SEQ ID NO: 9 is a nucleotide coding sequence (CDS) for the human 100 kDa subunit ("p100 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number AF063613).

SEQ ID NO: 10 is an amino acid sequence of the human 100 kDa subunit ("p100 subunit") of 2'-5' oligoadenylate synthetase (NCBI Accession Number AF063613).

SEQ ID NO: 11 is a nucleotide coding sequence (CDS) for the mouse homolog of the 2'-5' oligoadenylate synthetase 40 kDa splice variant (p40 subunit) (NCBI Accession Number M33863).

SEQ ID NO: 12 is the amino acid sequence for the mouse homolog of the 2'-5' oligoadenylate synthetase 40 kDa splice variant (p40 subunit) (NCBI Accession Number M33863).

SEQ ID NO: 13 is the human 2'-5' oligoadenylate synthetase 40/46 kDa (p40 subunit) gene (NCBI Accession Number NM_016816).

SEQ ID NO: 14 is the human 2'-5' oligoadenylate synthetase 69/71 kDa (p69 subunit) gene (NCBI Accession Number NM_002535).

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SEQ ID NO: 15 is the human 2'-5' oligoadenylate synthetase 100 kDa (p100 subunit) gene (NCBI Accession Number AF063613).

SEQ ID NO: 16 is the mouse homolog of the 2'-5' oligoadenylate synthetase 40 kDa (p40 subunit) gene (NCBI Accession Number M33863).

SEQ ID NO: 17 is a phosphorothioate antisense oligonucleotide (ODN) designed against the p40 subunit of 2'-5' oligoadenylate synthetase.

SEQ ID NO: 18 is an ODN designed against the p69 subunit of 2'-5' oligoadenylate synthetase.

SEQ ID NO: 19 is a scramble of the antisense sequence to p40, i.e., identical in base composition.

SEQ ID NO: 20 is a scramble of the antisense sequence to p69.

DETAILED DISCLOSURE OF THE INVENTION

The subject invention concerns a method of inhibiting an RNA virus infection within a patient by increasing the endogenous levels of 2-5 oligoadenylate synthetase (2-5 AS) activity within the patient. Preferably, the endogenous levels of the 2-5 AS p40 subunit (e.g., 40 kDa, 42 kDa, 46 kDa, or other splice variant), p69 subunit (e.g., 69 kDa, 71 kDa, or other splice variant), p100 subunit, or combinations thereof, are increased within the patient.

The present inventors have determined that overexpression of the 2-5 AS, or catalytically active fragments thereof, causes a reduction in epithelial cell damage, reduction in infiltration of mononuclear cells in the peribronchiolar and perivascular regions, and reduction in the thickening of the septa in the lungs of patients suffering from respiratory RNA viruses, such as respiratory syncytial virus (RSV). Levels of chemokines, such as MIP1- α , are also reduced upon overexpression of 2-5 AS.

Infections from members of the family paramyxoviridae that produce double-stranded RNA as a requirement of replication can be prevented or treated using the present invention. Thus, infections by members of the genera paramyxovirus, morbillivirus, rubulavirus, pneumovirus, and others can be inhibited in humans and animals. Examples of RNA viruses that produce double-stranded RNA during intermediate replication and which infect humans include, but are not limited to, respiratory syncytial virus (RSV), Rhinovirus, Vaccinia, Reovirus, HIV, EMCV, Hepatitis B, and Hepatitis C. Examples of RNA viruses that infect animals and produce double-stranded RNA during intermediate replication include, but are not limited to, bovine respiratory syncytial virus (BRSV), which infect cattle, sheep, and goats; Measles virus; Sendai virus; Parainfluenza 1, 2, and 3; Mumps virus, Simian virus; and Newcastle virus. Infections caused by coronavirus (such as that responsible for severe acute respiratory syndrome (SARS)), rotavirus, parainfluenza virus, West Nile virus, as well as other viruses in which interferon actively inhibits viral replication can be inhibited using the methods and compositions of the present invention.

In one aspect, the subject invention concerns a method of treating or preventing an RNA virus infection within a patient by increasing the in vivo concentration of 2-5 AS or a catalytically active fragment thereof within the patient, thereby inhibiting the RNA virus infection. Preferably, the methods of the present invention do not involve administration of interferon or a polynucleotide encoding interferon, such as interferon-alpha (IFN- α), interferon-beta (IFN- β), or interferon-gamma (IFN- γ), or the administration of such IFN polypeptides. Thus, the methods and compositions of the present invention are directed to increasing the in vivo con-

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centration of 2-5 AS or a catalytically active fragment thereof, which is an IFN- γ -induced downstream molecule. Advantageously, the methods and compositions of the present invention exhibit an antiviral effect without the adverse effects associated with IFN- γ .

The in vivo concentration of the 2-5 AS, or a catalytically active fragment thereof, can be increased, for example, by exogenous administration of the 2-5 AS polypeptide, or a catalytically active fragment of the polypeptide. Preferably, the in vivo concentration of the 2-5 AS polypeptide or catalytically active fragment is increased by increasing or up-regulating the functional expression of the nucleotide sequence encoding 2-5 AS or at least one catalytically active fragment thereof, such as the p40, p69, or p100 subunits, as gene therapy. More preferably, a nucleotide sequence encoding 2-5 AS or at least one catalytically active fragment thereof can be administered to a patient and expressed in order to increase the endogenous level of 2-5 AS enzymatic activity within the patient. For example, at least one nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 14, 15, 16, and 17, or a catalytically active fragment thereof, can be administered to the patient. The nucleotide sequence can be administered to a patient's cells in vivo or in vitro (including ex vivo, genetically modifying the patient's own cells ex vivo and subsequently administering the modified cells back into the patient).

In another aspect of the invention, 2-5 AS polypeptide, or at least one catalytically active fragment thereof, is administered to a patient in order to increase the antiviral function of 2-5 AS within the patient. Preferably, the polypeptides utilized are those disclosed herein. The polypeptides can comprise catalytically active fragments of the full-length 2-5 AS amino acid sequence, such as the p40, p69, or p100 subunits, including splice variants of these subunits, or mammalian homologs of these subunits (e.g., the p46 isoform of OAS-1; accession number NP_058132.1), such as murine homologs. For example, the polypeptides can comprise one or more amino acid sequences set forth herein as SEQ ID NOs: 2, 4, 6, 8, 10, 12, 13, 14, 15 or 16, or catalytically active fragments of these amino acid sequences.

Various means for delivering polypeptides to a cell can be utilized to carry out the methods of the subject invention. For example, protein transduction domains (PTDs) can be fused to the polypeptide, producing a fusion polypeptide, in which the PTDs are capable of transducing the polypeptide cargo across the plasma membrane (Wadia, J. S., and Dowdy, S. F., *Curr. Opin. Biotechnol.*, 2002, 13 (1)52-56). Examples of PTDs include the *Drosophila* homeotic transcription protein antennapedia (Antp), the herpes simplex virus structural protein VP22, and the human immuno-deficiency virus 1 (HIV-1) transcriptional activator Tat protein.

According to the method of RNA virus inhibition of the subject invention, recombinant cells can be administered to a patient, wherein the recombinant cells have been genetically modified to express the gene encoding 2-5 AS or at least one catalytically active fragment thereof, such as the p40, p69, or p100 subunits of 2-5 AS. If the cells to be genetically modified already express a gene encoding 2-5 AS, the genetic modification can serve to enhance or increase expression of the gene encoding 2-5 AS or a catalytically active fragment of 2-5 AS beyond the normal or constitutive amount (e.g., "overexpression").

The method of RNA virus inhibition of the subject invention can be used to treat a patient suffering from an RNA virus infection, or as a preventative of RNA virus infection (i.e., prophylactic treatment). According to the methods of the subject invention, various other compounds, such as antiviral

compounds, can be administered in conjunction with (before, during, or after) increasing the in vivo concentrations of 2-5 AS or at least one catalytically active fragment within the patient. Various compositions and methods for preventing or treating RNA virus infection can be used in conjunction with the compositions and methods of the subject invention, such as those described in U.S. Pat. No. 6,489,306, filed Feb. 23, 1999, and U.S. published patent application Serial No. 2003/00068333, filed Feb. 12, 2002, which are incorporated herein by reference in their entirety. For example, nucleotide sequences encoding 2-5 AS or at least one catalytically active fragment thereof can be conjugated with chitosan, a biodegradable, human-friendly cationic polymer that increases mucosal absorption of the gene expression vaccine without any adverse effects, as described in U.S. published patent application Serial No. 2003/00068333.

The nucleotide sequence can be formulated in the form of nanospheres with chitosan. Chitosan allows increased bioavailability of the DNA because of protection from degradation by serum nucleases in the matrix and thus has great potential as a mucosal gene delivery system, for example. Chitosan exhibits various beneficial effects, such as anticoagulant activity, wound-healing properties, and immunostimulatory activity, and is capable of modulating immunity of the mucosa and bronchus-associated lymphoid tissue.

Nucleotide, polynucleotide, or nucleic acid sequences(s) are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA, products of transcription of the said DNAs (e.g., RNA molecules), or corresponding RNA molecules that are not products of transcription. It should also be understood that the present invention does not relate to the genomic nucleotide sequences encoding 2-5 AS or catalytically active fragments thereof in their natural/native environment or natural/native state. The nucleic acid, polynucleotide, or nucleotide sequences of the invention have been isolated, purified (or partially purified), by separation methods including, but not limited to, ion-exchange chromatography, molecular size exclusion chromatography, affinity chromatography, or by genetic engineering methods such as amplification, cloning or subcloning.

Optionally, the polynucleotide sequence encoding 2-5 AS or catalytically active fragment thereof can also contain one or more polynucleotides encoding heterologous polypeptide sequences (e.g., tags that facilitate purification of the polypeptides of the invention (see, for example, U.S. Pat. No. 6,342,362, hereby incorporated by reference in its entirety; Altendorf et al. [1999-WWW, 2000] "Structure and Function of the F_o Complex of the ATP Synthase from *Escherichia Coli*," *J. of Experimental Biology* 203:19-28, The Co. of Biologists, Ltd., G. B.; Baneyx [1999] "Recombinant Protein Expression in *Escherichia coli*," *Biotechnology* 10:411-21, Elsevier Science Ltd.; Eihauer et al. [2001] "The FLAG Peptide, a Versatile Fusion Tag for the Purification of Recombinant Proteins," *J. Biochem Biophys Methods* 49:455-65; Jones et al. [1995] *J. Chromatography* 707:3-22; Jones et al. [1995] "Current Trends in Molecular Recognition and Bio-separation," *J. of Chromatography A* 707:3-22, Elsevier Science B. V.; Margolin [2000] "Green Fluorescent Protein as a Reporter for Macromolecular Localization in Bacterial Cells," *Methods* 20:62-72, Academic Press; Puig et al. [2001] "The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification," *Methods* 24:218-29, Academic Press; Sassanfeld [1990] "Engineering Proteins for Purification," *TibTech* 8:88-93; Sheibani [1999] "Prokaryotic Gene Fusion Expression Systems and Their Use in Structural and Functional Studies of Proteins," *Prep. Biochem. & Biotechnol.* 29(1):77-90, Marcel Dekker, Inc.;

Skerra et al. [1999] "Applications of a Peptide Ligand for Streptavidin: the Strep-tag", *Biomolecular Engineering* 16:79-86, Elsevier Science, B. V.; Smith [1998] "Cookbook for Eukaryotic Protein Expression: Yeast, Insect, and Plant Expression Systems," *The Scientist* 12 (22):20; Smyth et al. [2000] "Eukaryotic Expression and Purification of Recombinant Extracellular Matrix Proteins Carrying the Strep II Tag", *Methods in Molecular Biology*, 139:49-57; Unger [1997] "Show Me the Money: Prokaryotic Expression Vectors and Purification Systems," *The Scientist* 11 (17):20, each of which is hereby incorporated by reference in their entirety), or commercially available tags from vendors such as STRATAGENE (La Jolla, Calif.), NOVAGEN (Madison, Wis.), QIAGEN, Inc., (Valencia, Calif.), or INVITROGEN (San Diego, Calif.).

Other aspects of the invention provide vectors containing one or more of the polynucleotides of the invention, such as vectors containing nucleotides encoding 2-5 AS or catalytically active fragments of 2-5 AS, such as the p40 and/or p69 subunits. The vectors can be vaccine, replication, or amplification vectors. In some embodiments of this aspect of the invention, the polynucleotides are operably associated with regulatory elements capable of causing the expression of the polynucleotide sequences. Such vectors include, among others, chromosomal, episomal and virus-derived vectors, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, lentiviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations of the aforementioned vector sources, such as those derived from plasmid and bacteriophage genetic elements (e.g., cosmids and phagemids). Preferably, the vector is an adenoaviral vector or adeno-associated virus vector.

As indicated above, vectors of this invention can also comprise elements necessary to provide for the expression and/or the secretion of 2-5 AS, or a catalytically active fragment thereof, encoded by the nucleotide sequences of the invention in a given host cell. The vector can contain one or more elements selected from the group consisting of a promoter sequence, signals for initiation of translation, signals for termination of translation, and appropriate regions for regulation of transcription. In certain embodiments, the vectors can be stably maintained in the host cell and can, optionally, contain signal sequences directing the secretion of translated protein. Other embodiments provide vectors that are not stable in transformed host cells. Vectors can integrate into the host genome or be autonomously-replicating vectors.

In a specific embodiment, a vector comprises a promoter operably linked to a 2-5 AS-encoding nucleic acid sequence (or a catalytically active fragment thereof), one or more origins of replication, and, optionally, one or more selectable markers (e.g., an antibiotic resistance gene). Non-limiting exemplary vectors for the expression of the polypeptides of the invention include pBr-type vectors, pET-type plasmid vectors (PROMEGA), pBAD plasmid vectors (INVITROGEN), and pVAX plasmid vectors (INVITROGEN), or others provided in the examples below. Furthermore, vectors according to the invention are useful for transforming host cells for the cloning or expression of the nucleotide sequences of the invention.

Promoters which may be used to control expression include, but are not limited to, the CMV promoter, the SV40 early promoter region (Berndt and Chambon [1981] *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al. [1980] *Cell*

22:787-797), the herpes thymidine kinase promoter (Wagner et al. [1981] *Proc. Natl. Acad. Sci. USA* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al. [1982] *Nature* 296:39-42); prokaryotic vectors containing promoters such as the β -lactamase promoter (Villa-Komaroff, et al. [1978] *Proc. Natl. Acad. Sci. USA* 75:3727-3731), or the tac promoter (DeBoer, et al. [1983] *Proc. Natl. Acad. Sci. USA* 80:21-25); the lung specific promoters such as surfactant protein B promoter (Venkatesh et al., *Am. J. Physiol.* 268 (*Lung Cell Mol. Physiol.* 12):L674-L682, 1995); see also, "Useful Proteins from Recombinant Bacteria" in *Scientific American*, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella et al. [1983] *Nature* 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, et al. [1981] *Nucl. Acids Res.* 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al. [1984] *Nature* 310:115-120); promoter elements from yeast or fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, and/or the alkaline phosphatase promoter.

The subject invention also provides for "homologous" or "modified" nucleotide sequences. Modified nucleic acid sequences will be understood to mean any nucleotide sequence obtained by mutagenesis according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the normal sequences. For example, mutations in the regulatory and/or promoter sequences for the expression of a polypeptide that result in a modification of the level of expression of a polypeptide according to the invention provide for a "modified nucleotide sequence". Likewise, substitutions, deletions, or additions of nucleic acid to the polynucleotides of the invention provide for "homologous" or "modified" nucleotide sequences. In various embodiments, "homologous" or "modified" nucleic acid sequences have substantially the same biological activity as the native (naturally occurring) 2-5 AS or subunit thereof. A "homologous" or "modified" nucleotide sequence will also be understood to mean a subunit or a splice variant of the polynucleotides of the instant invention or any nucleotide sequence encoding a "modified polypeptide" as defined below.

A homologous nucleotide sequence, for the purposes of the present invention, encompasses a nucleotide sequence having a percentage identity with the bases of the nucleotide sequences of between at least (or at least about) 20.00% to 99.99% (inclusive), and which encodes a catalytically active polypeptide. The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 20.00% and 99.99%. These percentages are purely statistical and differences between two nucleic acid sequences can be distributed randomly and over the entire sequence length.

In various embodiments, homologous sequences exhibiting a percentage identity with the bases of the nucleotide sequences of the present invention can have 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent identity with the polynucleotide sequences of the instant invention.

Both protein and nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to,

TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman [1988] *Proc. Natl. Acad. Sci. USA* 85 (8):2444-2448; Altschul et al. [1990] *J. Mol. Biol.* 215 (3): 403-410; Thompson et al. [1994] *Nucleic Acids Res.* 22 (2): 4673-4680; Higgins et al. [1996] *Methods Enzymol.* 266:383-402; Altschul et al. [1990] *J. Mol. Biol.* 215 (3):403-410; Altschul et al. [1993] *Nature Genetics* 3:266-272).

Nucleotide sequences encoding polypeptides with enhanced 2-5 AS catalytic activity can be obtained by "gene shuffling" (also referred to as "directed evolution", and "directed mutagenesis"), and used in the compositions and methods of the present invention. Gene shuffling is a process of randomly recombining different sequences of functional genes (recombining favorable mutations in a random fashion) (U.S. Pat. Nos. 5,605,793; 5,811,238; 5,830,721; and 5,837,458). Thus, protein engineering can be accomplished by gene shuffling, random complex permutation sampling, or by rational design based on three-dimensional structure and classical protein chemistry (Cramer et al., *Nature*, 391:288-291, 1998; and Wulff et al., *The Plant Cell*, 13:255-272, 2001).

The subject invention also provides nucleotide sequences complementary to any of the polynucleotide sequences disclosed herein. Thus, the invention is understood to include any DNA whose nucleotides are complementary to those of 2-5 AS polynucleotide sequence of the invention, or catalytically active fragments thereof, and whose orientation is reversed (e.g., an antisense sequence).

The present invention further provides catalytically active fragments of the 2-5 AS polynucleotide sequences, including catalytically active fragments of the 2-5 AS subunit nucleotide sequences, provided herein. Representative fragments of the polynucleotide sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 or 9 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. The upper limit for such fragments is the total number of polynucleotides found in the full-length sequence (or, in certain embodiments, of the full length open reading frame (ORF) identified herein). It is understood that, optionally, such fragments refer only to portions of the disclosed polynucleotide sequences that are not listed in a publicly available database or prior art references. However, it should be understood that with respect to the method for inhibiting RSV of the subject invention, disclosed nucleotides (and polypeptides encoded by such nucleotides) that are listed in a publicly available database or prior art reference can also be utilized. For example, nucleotide sequences that are 2-5 AS p40 or p69 subunit homologs, or fragments thereof, which have been previously identified, can be utilized to carry out the method for inhibiting RNA virus infection of the subject invention.

In other embodiments, fragments contain from one nucleotide less than the full length 2-5 AS enzyme, or from one nucleotide less than a catalytically active subunit thereof, such as p40 or p69 subunit polynucleotide CDS sequences (e.g., 1,203 and 1,207 nucleotides for the 40 kDa splice variant and 46 kDa splice variant, respectively; and 2063 and 2,168 nucleotides for the 69 kDa splice variant and 71 kDa splice variant, respectively) to fragments containing the smallest number of nucleotides encoding a polypeptide that retains at least some 2-5 AS enzymatic activity.

Among these representative fragments, those capable of hybridizing under stringent conditions with a nucleotide sequence encoding 2-5 AS or subunits thereof are preferred. Conditions of high or intermediate stringency are provided

infra and are chosen to allow for hybridization between two complementary DNA fragments. Hybridization conditions for a polynucleotide of about 1,000 to 3,000 bases in size will be adapted by persons skilled in the art for larger- or smaller-sized oligonucleotides, according to methods well known in the art (see, for example, Sambrook et al. [1989] *Molecular Cloning, A Laboratory Manual, Second Edition*, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57).

The subject invention also provides detection probes (e.g., fragments of the disclosed polynucleotide sequences) for hybridization with a target sequence or an amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 9, 12, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides. Alternatively, detection probes can comprise 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127 and up to, for example, 1,203 consecutive nucleotides, 1,207 consecutive nucleotides, 2,064 consecutive nucleotides, 2,186 consecutive nucleotides, 3,264 consecutive nucleotides, and 1,104 consecutive nucleotides of those disclosed herein, which correspond, respectively, to the human 40 kDa splice variant of the 2-5 AS p40 subunit (SEQ ID NO:1), human 46 kDa splice variant 2-5 AS p40 subunit (SEQ ID NO:3), human 69 kDa splice variant of the 2-5 AS p69 subunit (SEQ ID NO:5), human 71 kDa splice variant of the 2-5 AS p69 subunit (SEQ ID NO:7), human p100 subunit (SEQ ID NO:9), and the mouse homolog of the 2-5 AS p40 subunit (SEQ ID NO: 11). The detection probes can also be used as labeled probe or primer in the subject invention. Labeled probes or primers are labeled with a radioactive compound or with another type of label. Alternatively, non-labeled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labeled with a radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or with a molecule such as biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, or fluorescein to provide probes that can be used in numerous applications.

The nucleotide sequences according to the invention may also be used in analytical systems, such as DNA chips. DNA chips and their uses are well known in the art and (see for example, U.S. Pat. Nos. 5,561,071; 5,753,439; 6,214,545; Schena et al. [1996] *BioEssays* 18:427-431; Bianchi et al. [1997] *Clin. Diagn. Virol.* 8:199-208; each of which is hereby incorporated by reference in their entirety) and/or are provided by commercial vendors such as AFFYMETRIX, Inc. (Santa Clara, Calif.).

Various degrees of stringency of hybridization can be employed. The more severe the conditions, the greater the complementarity that is required for duplex formation. Severity of conditions can be controlled by temperature, probe concentration, probe length, ionic strength, time, and the like. Preferably, hybridization is conducted under moderate to high stringency conditions by techniques well known in the art, as described, for example, in Keller, G. H., M. M. Manak [1987] *DNA Probes*, Stockton Press, New York, N.Y., pp. 169-170.

By way of example, hybridization of immobilized DNA on Southern blots with ^{32}P -labeled gene-specific probes can be performed by standard methods (Maniatis et al. [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York). In general, hybridization and

subsequent washes can be carried out under moderate to high stringency conditions that allow for detection of target sequences with homology to the exemplified polynucleotide sequence. For double-stranded DNA gene probes, hybridization can be carried out overnight at 20-25° C. below the melting temperature (T_m) of the DNA hybrid in 6×SSPE, 5×Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature is described by the following formula (Beltz et al. [1983] *Methods of Enzymology*, R. Wu, L. Grossman and K. Moldave [eds.] Academic Press, New York 100:266-285).

$$T_m = 81.5^\circ \text{C} + 16.6 \log [\text{Na}^+] + 0.41(\% \text{G+C}) - 0.61(\% \text{formamide}) - 600/\text{length of duplex in base pairs}.$$

Washes are typically carried out as follows:

- (1) twice at room temperature for 15 minutes in 1×SSPE, 0.1% SDS (low stringency wash);
- (2) once at T_m -20°C for 15 minutes in 0.2×SSPE, 0.1% SDS (moderate stringency wash).

For oligonucleotide probes, hybridization can be carried out overnight at 10-20° C. below the melting temperature (T_m) of the hybrid in 6×SSPE, 5×Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. T_m for oligonucleotide probes can be determined by the following formula:

$$T_m (^\circ \text{C.}) = 2(\text{number T/A base pairs}) + 4(\text{number G/C base pairs}) \text{ (Suggs et al. [1981] } ICN-UCLA \text{ Symp. Dev. Biol. Using Purified Genes, D. D. Brown [ed.], Academic Press, New York, 23:683-693).}$$

Washes can be carried out as follows:

- (1) twice at room temperature for 15 minutes 1×SSPE, 0.1% SDS (low stringency wash);
- (2) once at the hybridization temperature for 15 minutes in 1×SSPE, 0.1% SDS (moderate stringency wash).

In general, salt and/or temperature can be altered to change stringency. With a labeled DNA fragment >70 or so bases in length, the following conditions can be used:

Low: 1 or 2×SSPE, room temperature

Low: 1 or 2×SSPE, 42° C.

Moderate: 0.2× or 1×SSPE, 65° C.

High: 0.1×SSPE, 65° C.

By way of another non-limiting example, procedures using conditions of high stringency can also be performed as follows: Pre-hybridization of filters containing DNA is carried out for 8 h to overnight at 65° C. in buffer composed of 6×SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65° C., the preferred hybridization temperature, in pre-hybridization mixture containing 100 g/ml denatured salmon sperm DNA and 5-20×10⁶ cpm of ^{32}P -labeled probe. Alternatively, the hybridization step can be performed at 65° C. in the presence of SSC buffer, 1×SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37° C. for 1 h in a solution containing 2×SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1×SSC at 50° C. for 45 min. Alternatively, filter washes can be performed in a solution containing 2×SSC and 0.1% SDS, or 0.5×SSC and 0.1% SDS, or 0.1×SSC and 0.1% SDS at 68° C. for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art (see, for example, Sambrook et al. [1989] *Molecular Cloning, A Laboratory Manual, Second Edition*, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al. [1989] *Current Pro-*

ocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y., each incorporated herein in its entirety).

A further non-limiting example of procedures using conditions of intermediate stringency are as follows: Filters containing DNA are pre-hybridized, and then hybridized at a temperature of 60° C. in the presence of a 5×SSC buffer and labeled probe. Subsequently, filter washes are performed in a solution containing 2×SSC at 50° C. and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art (see, for example, Sambrook et al. [1989] *Molecular Cloning, A Laboratory Manual, Second Edition*, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al. [1989] *Current Protocols in Molecular Biology*, Green Publishing Associates and Wiley Interscience, N.Y., each of which is incorporated herein in its entirety).

Duplex formation and stability depend on substantial complementarity between the two strands of a hybrid and, as noted above, a certain degree of mismatch can be tolerated. Therefore, the probe sequences of the subject invention include mutations (both single and multiple), deletions, insertions of the described sequences, and combinations thereof, wherein said mutations, insertions and deletions permit formation of stable hybrids with the target polynucleotide of interest. Mutations, insertions and deletions can be produced in a given polynucleotide sequence in many ways, and these methods are known to an ordinarily skilled artisan. Other methods may become known in the future.

It is also well known in the art that restriction enzymes can be used to obtain functional fragments of the subject DNA sequences. For example, Bal31 exonuclease can be conveniently used for time-controlled limited digestion of DNA (commonly referred to as "erase-a-base" procedures). See, for example, Maniatis et al. [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York; Wei et al. [1983] *J. Biol. Chem.* 258:13006-13512. The nucleic acid sequences of the subject invention can also be used as molecular weight markers in nucleic acid analysis procedures.

The invention also provides host cells transformed by a polynucleotide according to the invention and the production of 2-5 AS or a catalytically active fragment thereof, by the transformed host cells. In some embodiments, transformed cells comprise an expression vector containing 2-5 AS nucleotide sequences or a catalytically active fragment thereof. Other embodiments provide for host cells transformed with nucleic acids. Yet other embodiments provide transformed cells comprising an expression vector containing fragments of 2-5 AS p40 and/or p69 subunit nucleotide sequences. Transformed host cells according to the invention are cultured under conditions allowing the replication and/or the expression of the 2-5 AS nucleotide sequence or a catalytically active fragment thereof, such as the p40 and/or p69 subunits. Expressed polypeptides are recovered from culture media and purified, for further use, according to methods known in the art.

The host cell may be chosen from eukaryotic or prokaryotic systems, for example bacterial cells (Gram negative or Gram positive), yeast cells, animal cells, human cells, plant cells, and/or insect cells using baculovirus vectors. In some embodiments, the host cell for expression of the polypeptides include, and are not limited to, those taught in U.S. Pat. Nos. 6,319,691; 6,277,375; 5,643,570; 5,565,335; Unger [1997] *The Scientist* 11 (17):20; or Smith [1998] *The Scientist* 12(22):20, each of which is incorporated by reference in its entirety, including all references cited within each respective

patent or reference. Other exemplary, and non-limiting, host cells include *Staphylococcus* spp., *Enterococcus* spp., *E. coli*, and *Bacillus subtilis*; fungal cells, such as *Streptomyces* spp., *Aspergillus* spp., *S. cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Hansela polymorpha*, *Kluveromyces lactis*, and *Yarrowia lipolytica*; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells. A great variety of expression systems can be used to produce the 2-5 AS polypeptides or catalytically active fragments thereof and encoding polynucleotides can be modified according to methods known in the art to provide optimal codon usage for expression in a particular expression system.

Furthermore, a host cell strain may be chosen that modulates the expression of the inserted sequences, modifies the gene product, and/or processes the gene product in the specific fashion. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product whereas expression in yeast will produce a glycosylated product. Expression in mammalian cells can be used to provide "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

Nucleic acids and/or vectors encoding 2-5 AS, or catalytically active fragments thereof, such as the p40 and/or p69 subunits, can be introduced into host cells by well-known methods, such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection (see, for example, Sambrook et al. [1989] *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

The subject invention also provides for the expression of the 2-5 AS p40 or p69 subunit, derivative, or an analogue (e.g., a splice variant) encoded by a polynucleotide sequence disclosed herein. Alternatively, the invention provides for the expression of a polynucleotide encoding a fragment of a 2-5 AS p40 or p69 subunit. In either embodiment, the disclosed sequences can be regulated by a second nucleic acid sequence so that the polypeptide or fragment is expressed in a host transformed with a recombinant DNA molecule according to the subject invention. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art.

In the context of the instant invention, the terms polypeptide, peptide and protein are used interchangeably. Likewise, the terms analogue and homologous are also used interchangeably. It should be understood that the invention does not relate to the polypeptides in natural form or native environment. Peptides and polypeptides according to the invention have been isolated or obtained by purification from natural sources (or their native environment), chemically synthesized, or obtained from host cells prepared by genetic manipulation (e.g., the polypeptides, or fragments thereof, are recombinantly produced by host cells). Polypeptides according to the instant invention may also contain non-natural amino acids, as will be described below.

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"Analogues" or "homologous" polypeptides will be understood to designate the polypeptides containing, in relation to the native polypeptide, modifications such as deletion, addition, or substitution of at least one amino acid, truncation, extension, or the addition of chimeric heterologous polypeptides. Optionally, "analogues" or "homologous" polypeptides can contain a mutation or post-translational modifications. Among the "analogues" or "homologous" polypeptides, those whose amino acid sequence exhibits 20.00% to 99.99% (inclusive) identity to the native polypeptide sequence are preferred. The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 50.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two polypeptide sequences can be distributed randomly and over the entire sequence length.

"Analogues" or "homologous" polypeptide sequences exhibiting a percentage identity with the human 2-5 AS polypeptides, or subunits thereof, can alternatively have 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent identity with the polypeptide sequences of the instant invention. The expression equivalent amino acid is intended here to designate any amino acid capable of being substituted for one of the amino acids in the basic structure without, however, essentially modifying the biological activities of the corresponding peptides and as provided below.

By way of example, amino acid substitutions can be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; for example, the replacement of leucine with valine or isoleucine; aspartic acid with glutamic acid; glutamine with asparagine; arginine with lysine; and the reverse substitutions can be performed without substantial modification of the biological activity of the polypeptides.

The subject invention also provides catalytically active fragments of the 2-5 AS polypeptide, and catalytically active fragments of the 2-5 AS subunits, according to the invention, which are capable of eliciting an immune response against RSV. The immune response can provide components (either antibodies or components of the cellular immune response (e.g., B-cells, helper, cytotoxic, and/or suppressor T-cells) reactive with the catalytically active fragment of the polypeptide, the intact, full length, unmodified polypeptide, or both the catalytically active fragment of the polypeptide and the intact, full length, unmodified polypeptides.

Catalytically active fragments according to the invention can comprise from five (5) amino acids to one amino acid less than the full length of any polypeptide sequence provided herein. For example, fragments comprising 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, and up to one amino acid less than the full length amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, and SEQ ID NO:12, are provided herein.

Fragments, as described herein, can be obtained by cleaving the polypeptides of the invention with a proteolytic enzyme (such as trypsin, chymotrypsin, or collagenase) or with a chemical reagent, such as cyanogen bromide (CNBr). Alternatively, polypeptide fragments can be generated in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by

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chemical synthesis or using hosts transformed with an expression vector containing nucleic acids encoding polypeptide fragments according to the invention. The transformed host cells contain a nucleic acid and are cultured according to well-known methods; thus, the invention allows for the expression of these fragments, under the control of appropriate elements for regulation and/or expression of the polypeptide fragments.

Modified polypeptides according to the invention are understood to designate a polypeptide obtained by variation in the splicing of transcriptional products of the 2-5 AS gene, genetic recombination, or by chemical synthesis as described below. Modified polypeptides contain at least one modification in relation to the normal polypeptide sequence. These modifications can include the addition, substitution, or deletion of amino acids contained within the polypeptides of the invention.

Conservative substitutions whereby an amino acid of one class is replaced with another amino acid of the same type fall within the scope of the subject invention so long as the substitution does not materially alter the biological activity of the polypeptide. For example, the class of nonpolar amino acids include Ala, Val, Leu, Ile, Pro, Met, Phe, and Trp; the class of uncharged polar amino acids includes Gly, Ser, Thr, Cys, Tyr, Asn, and Gln; the class of acidic amino acids includes Asp and Glu; and the class of basic amino acids includes Lys, Arg, and His. In some instances, non-conservative substitutions can be made where these substitutions do not significantly detract from the biological activity of the polypeptide.

In order to extend the life of the polypeptides of the invention, it may be advantageous to use non-natural amino acids, for example in the D form, or alternatively amino acid analogs, such as sulfur-containing forms of amino acids. Alternative means for increasing the life of polypeptides can also be used in the practice of the instant invention. For example, polypeptides of the invention, and fragments thereof, can be recombinantly modified to include elements that increase the plasma, or serum half-life of the polypeptides of the invention. These elements include, and are not limited to, antibody constant regions (see for example, U.S. Pat. No. 5,565,335, hereby incorporated by reference in its entirety, including all references cited therein), or other elements such as those disclosed in U.S. Pat. No. 6,319,691; 6,277,375; or 5,643,570, each of which is incorporated by reference in its entirety, including all references cited within each respective patent. Alternatively, the 2-5 AS polynucleotides, or catalytically active fragments thereof, used in the instant invention can be recombinantly fused to elements that are useful in the preparation of immunogenic constructs for the purposes of vaccine formulation or elements useful for the isolation of the polypeptides of the invention.

The polypeptides, fragments, and immunogenic fragments of the invention may further contain linkers that facilitate the attachment of the fragments to a carrier molecule for delivery or diagnostic purposes. The linkers can also be used to attach fragments according to the invention to solid support matrices for use in affinity purification protocols. In this aspect of the invention, the linkers specifically exclude, and are not to be considered anticipated, where the fragment is a subsequence of another peptide, polypeptide, or protein as identified in a search of protein sequence databases as indicated in the preceding paragraph. In other words, the non-identical portions of the other peptide, polypeptide, or protein is not considered to be a "linker" in this aspect of the invention. Non-limiting examples of "linkers" suitable for the practice of the invention include chemical linkers (such as those sold by Pierce, Rockford, Ill.), peptides that allow for the connection of the immu-

nogenic fragment to a carrier molecule (see, for example, linkers disclosed in U.S. Pat. Nos. 6,121,424; 5,843,464; 5,750,352; and 5,990,275, hereby incorporated by reference in their entirety). In various embodiments, the linkers can be up to 50 amino acids in length, up to 40 amino acids in length, up to 30 amino acids in length, up to 20 amino acids in length, up to 10 amino acids in length, or up to 5 amino acids in length.

In other specific embodiments, the 2-5 AS polypeptide or 2-5 AS subunit polypeptide, peptides, derivatives, or analogs thereof may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (e.g., a different protein)). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art (see, for example, U.S. Pat. No. 6,342,362, hereby incorporated by reference in its entirety; Altendorf et al. [1999-WWW, 2000] "Structure and Function of the F₀ Complex of the ATP Synthase from *Escherichia Coli*," *J. of Experimental Biology* 203:19-28, The Co. of Biologists, Ltd., G. B.; Baneyx [1999] "Recombinant Protein Expression in *Escherichia coli*," *Biotechnology* 10:411-21, Elsevier Science Ltd.; Eihauer et al. [2001] "The FLAG Peptide, a Versatile Fusion Tag for the Purification of Recombinant Proteins," *J. Biochem Biophys Methods* 49:455-65; Jones et al. [1995] *J. Chromatography* 707:3-22; Jones et al. [1995] "Current Trends in Molecular Recognition and Bio-separation," *J. Chromatography A* 707:3-22, Elsevier Science B. V.; Margolin [2000] "Green Fluorescent Protein as a Reporter for Macromolecular Localization in Bacterial Cells," *Methods* 20:62-72, Academic Press; Puig et al. [2001] "The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification," *Methods* 24:218-29, Academic Press; Sassenfeld [1990] "Engineering Proteins for Purification," *TibTech* 8:88-93; Sheibani [1999] "Prokaryotic Gene Fusion Expression Systems and Their Use in Structural and Functional Studies of Proteins," *Prep. Biochem. & Biotechnol.* 29 (1):77-90, Marcel Dekker, Inc.; Skerra et al. [1999] "Applications of a Peptide Ligand for Streptavidin: The Strep-tag", *Biomolecular Engineering* 16:79-86, Elsevier Science, B. V.; Smith [1998] "Cookbook for Eukaryotic Protein Expression Yeast, Insect, and Plant Expression Systems," *The Scientist* 12(22):20; Smyth et al. [2000] "Eukaryotic Expression and Purification of Recombinant Extracellular Matrix Proteins Carrying the Strep II Tag", *Methods in Molecular Biology*, 139:49-57; Unger [1997] "Show Me the Money: Prokaryotic Expression Vectors and Purification Systems," *The Scientist* 11 (17):20, each of which is hereby incorporated by reference in their entireties). Alternatively, such a chimeric product may be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Fusion peptides can comprise polypeptides of the subject invention and one or more protein transduction domains, as described above. Such fusion peptides are particularly useful for delivering the cargo polypeptide through the cell membrane.

Increasing the amount of 2-5 AS enzymatic activity (e.g., p40, p69, and/or p100 subunit activity) within a tissue is useful in preventing an RNA virus infection, or in treating an existing RNA virus infection. Thus, according to the methods of the subject invention, the amount of 2-5 AS activity can be increased within a tissue by directly administering the 2-5 AS polypeptide or a catalytically active fragment thereof to a patient suffering from or susceptible to an RNA virus infec-

tion (such as exogenous delivery of the 2-5 AS p40, p69, and/or p100 subunit polypeptide) or by indirect or genetic means (such as delivery of a nucleotide sequence encoding the 2-5 AS polypeptide or a catalytically active fragment thereof, or upregulating the endogenous 2-5 AS polypeptide activity).

As used herein, the term "administration" or "administering" refers to the process of delivering an agent to a patient, wherein the agent directly or indirectly increases 2-5 AS enzymatic function within the patient and, preferably, at the target site. The process of administration can be varied, depending on the agent, or agents, and the desired effect. Thus, wherein the agent is genetic material, such as DNA, the process of administration involves administering a DNA encoding 2-5 AS, or a catalytically active fragment thereof, to a patient in need of such treatment. Administration can be accomplished by any means appropriate for the therapeutic agent, for example, by parenteral, mucosal, pulmonary, topical, catheter-based, or oral means of delivery. Parenteral delivery can include for example, subcutaneous intravenous, intramuscular, intra-arterial, and injection into the tissue of an organ, particularly tumor tissue. Mucosal delivery can include, for example, intranasal delivery. According to the method of the present invention, a nucleotide sequence encoding the 2-5 AS or catalytically active fragment is preferably administered into the airways of a patient, i.e., nose, sinus, throat, lung, for example, as nose drops, by nebulization, vaporization, or other methods known in the art. Oral or intranasal delivery can include the administration of a propellant. Pulmonary delivery can include inhalation of the agent. Catheter-based delivery can include delivery by ion-tropheric catheter-based delivery. Oral delivery can include delivery of a coated pill, or administration of a liquid by mouth. Administration can generally also include delivery with a pharmaceutically acceptable carrier, such as, for example, a buffer, a polypeptide, a peptide, a polysaccharide conjugate, a liposome, and/or a lipid. Gene therapy protocol is also considered an administration in which the therapeutic agent is a polynucleotide capable of accomplishing a therapeutic goal when expressed as a transcript or a polypeptide into the patient. Further information concerning applicable gene therapy protocols is provided in the examples disclosed herein.

The pharmaceutical compositions of the subject invention can be formulated according to known methods for preparing pharmaceutically useful compositions. Formulations are described in a number of sources which are well known and readily available to those skilled in the art. For example, *Remington's Pharmaceutical Science* (Martin E W [1995] Easton Pennsylvania, Mack Publishing Company, 19th ed.) describes formulations which can be used in connection with the subject invention. Formulations suitable for parenteral administration include, for example, aqueous sterile injection solutions, which may contain antioxidants, buffers, bacteriostats, and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example sealed ampoules and vials, and may be stored in a freeze dried (lyophilized) condition requiring only the condition of the sterile liquid carrier, for example, water for injections, prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powder, granules, tablets, etc. It should be understood that in addition to the ingredients particularly mentioned above, the formulations of the subject

invention can include other agents conventional in the art having regard to the type of formulation in question.

Therapeutically effective and optimal dosage ranges for 2-5 AS or catalytically active fragments thereof can be determined using methods known in the art. Guidance as to appropriate dosages to achieve an anti-viral effect is provided from the exemplified assays disclosed herein.

As used herein, the term "catalytic activity" with respect to fragments, analogues, and homologs of the 2-5 AS polypeptide, or to fragments, analogues, and homologs of nucleotide sequences encoding the 2-5 AS polypeptide, refers to 2'-5' oligoadenylate synthetase activity. As used herein, "2'-5' oligoadenylate synthetase activity" refers to polymerization of ATP to produce 2'-5' linked oligoadenylates, which in turn, activate a latent ribonuclease, RNase L, that degrades RNAs (see, for example, Katze et al., *Nat. Rev. Immunol.*, September 2002, 2 (9):675-687; Justesen et al., *Cell Mol. Life. Sci.*, 57:1593-1612, 2000; Hartmann et al., *J. Bio. Chem.*, 273(6): 3236-3246, 1998; U.S. Pat. No. 5,766,864). Preferably, the catalytic activity is an amount effective to inhibit RNA virus infection (pre-infection or post-infection). 2'-5' oligoadenylate synthetase activity can be determined directly or indirectly in vivo, or in vitro, using methods known in the art. Thus, cell-based assays can be utilized to determine whether an agent, such as a nucleotide sequence or polypeptide, exhibits the relevant catalytic activity, and can be utilized to carry out the method of RNA virus inhibition of the subject invention.

RNA virus infections that can be inhibited using the present invention include those that must produce double-stranded RNA as an intermediate step in viral replication and those viruses for which interferon can actively inhibit viral replication. These RNA viruses can include single-stranded or double-stranded RNA viruses, and have genomes of positive (+) or negative (-) strand polarity.

The present invention further provides methods of making the host cells, pharmaceutical compositions, and vectors described herein by combining the various components using methods known in the art.

The term "patient", as used herein, refers to any vertebrate species. Preferably, the patient is of a mammalian species. Mammalian species which benefit from the disclosed methods of treatment include, and are not limited to, apes, chimpanzees, orangutans, humans, monkeys; domesticated animals (e.g., pets) such as dogs, cats, guinea pigs, hamsters, Vietnamese pot-bellied pigs, rabbits, and ferrets; domesticated farm animals such as cows, buffalo, bison, horses, donkey, swine, sheep, and goats; exotic animals typically found in zoos, such as bear, lions, tigers, panthers, elephants, hippopotamus, rhinoceros, giraffes, antelopes, sloth, gazelles, zebras, wildebeests, prairie dogs, koala bears, kangaroo, opossums, raccoons, pandas, hyena, seals, sea lions, elephant seals, otters, porpoises, dolphins, and whales. Human or non-human animal patients can range in age from neonates to elderly. The nucleotide sequences and polypeptides can be administered to patients of the same species or from different species. For example, mammalian, homologs can be administered to human patients.

The terms "2-5 AS p40 subunit" and "2-5 AS p40 subunit polypeptide" are used herein interchangeably to refer to the 2'-5' oligoadenylate synthetase p40 subunit gene or its coding sequence (CDS), its polypeptide product, or a catalytically active fragment or analogue of the polypeptide product, and includes 2-5 AS p40 subunit peptide homologs (such as mammalian orthologs (e.g., SEQ ID NOs: 11 and 12); NCBI Accession Number M33863) and isoforms, unless otherwise noted. Thus, the term includes all splice variants of the p40

subunit, such as the 40 kDa (SEQ ID NOs: 1 and 2), 42 kDa, and 46 kDa (SEQ ID NOs:3 and 4) splice variants of the 2-5 AS p40 subunit (NCBI Accession Number NM_016816).

The terms "2-5 AS p69 subunit" and "2-5 AS p69 subunit polypeptide" are used herein interchangeably to refer to the 2'-5' oligoadenylate synthetase p69 subunit gene or its coding sequence (CDS), its polypeptide product, or a catalytically active fragment or analogue of the polypeptide product, and includes 2-5 AS p69 subunit peptide homologs (such as mammalian orthologs) and isoforms, unless otherwise noted. Thus, the term includes all splice variants of the p69 subunit, such as the 69 kDa (SEQ ID NOs:5 and 6) and 71 kDa (SEQ ID NOs:7 and 8) splice variants of the 2-5 AS p69 subunit (NCBI Accession Number NM_002535).

The terms "2-5 AS p100 subunit" and "2-5 AS p100 subunit polypeptide" are used herein interchangeably to refer to the 2'-5' oligoadenylate synthetase p100 subunit gene or its coding sequence (CDS) (SEQ ID NO:9), its polypeptide product (SEQ ID NO:10), or a catalytically active fragment or analogue of the polypeptide product, and includes 2-5 AS p100 subunit peptide homologs (such as mammalian orthologs) and isoforms, unless otherwise noted. Thus, the term includes all splice variants of the p100 subunit (NCBI Accession Number AF063613).

The terms "comprising", "consisting of", and "consisting essentially of" are defined according to their standard meaning and may be substituted for one another throughout the instant application in order to attach the specific meaning associated with each term.

Materials and Methods

Epithelial Cell Culture, Virus Infection and Plaque Assay. The Hep-2 (ATCC CCL-23) cell line was obtained from the American Type Culture Collection (Manassas, Va.) and was maintained in Minimum Essential medium with Hank's salts (MEM) supplemented with 5% fetal bovine serum (FBS) (ATLANTA BIOLOGICALS, Norcross, Ga.) at 37° C. with 5% CO₂. Respiratory syncytial virus (RSV) A2 strain was obtained from ATCC (VR-1302) and was propagated in Hep-2 cells grown in MEM with 2% FBS on a monolayer culture. Viral stocks were prepared from infected Hep-2 cells 5 days post infection (p.i.), stored at -70° C. in aliquots and used as the viral inoculum. RSV titers were quantified by plaque assay as described earlier (21).

MTT Cytotoxicity Assay. The effect of IFN- γ on the viability of cells was determined using a MTT [3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide] (SIGMA, St. Louis, Mo.) cytotoxicity assay. Triplicate sets of cell monolayers were used for each IFN- γ dose tested and for each time point. In this system, the mitochondrial dehydrogenase enzymes of living cells cleave the tetrazolium ring of the yellow MTT to form purple formazan crystals, which are insoluble in aqueous solutions. The crystals were dissolved in acidified isopropanol, and the absorbance of the resulting purple solution was spectrophotometrically measured at 540 nm. An increase or decrease in the viable cell number results in a concomitant change in the amount of formazan formed, indicating the degree of cytotoxicity caused by the indicated dose of IFN- γ .

Immunoblot Analysis. IFN- γ treated cells were washed in cold PBS, pH 7.4 and scraped into PBS at various time points. The cells were collected by centrifugation at 6000 rpm for 3 min at 4° C. and the cell pellet was suspended in a 2-pack volume of cell lysis buffer (50 mM Tris-HCl, pH7.4; 1% NP-40; 150 mM NaCl; 1 mM EGTA; 1 mM PMSF; 1 mg/ml aprotinin, leupeptin, pepstatin) and vortexed thoroughly. The

cell lysate was spun at 13,000 rpm for 15' at 4° C. to remove cellular debris. The supernatant was collected and the protein content estimated using the BCA (bicinchoninic acid) assay (PIERCE, Rockford, Ill.). 30 mg of total protein was mixed with an equal volume of 2×SDS sample buffer (22) and loaded onto a 10% SDS-PAGE and run at a 30 mA constant current for 2 to 2.5 hours. For the detection of iNOS, the lysate of the IFN- γ and LPS-stimulated murine macrophage (RAW 264.7) was loaded onto the gel as a positive control. The proteins were transferred to a nitrocellulose membrane overnight at a 12 mA constant current in transfer buffer (39 mM glycine, 48 mM Tris-HCl, 20% methanol) at 4° C.

Following protein transfer to the nitrocellulose membrane, the blots were immediately placed into blocking buffer (5% non-fat dry milk, 10 mM Tris-HCl, pH 7.5, 100 mM NaCl, 0.1% Tween 20) and incubated for 30' at room temperature. The blots were then individually incubated overnight with mAbs to IRF-1, IRF-2, PKR, cytokeratin-18 (SANTA CRUZ BIOTECHNOLOGY Inc, Santa Cruz, Calif.), iNOS (TRANSDUCTION LABORATORIES, Lexington, Ky.) and phospho-eIF-2 α (CELL SIGNALING, Beverly, Mass.) at 4° C. Blots were washed three times in washing buffer (10 mM Tris-HCl, pH 7.5, 100 mM NaCl, 0.1% Tween 20) and were subsequently incubated with anti-mouse IgG HRP conjugate (BOEHRINGER MANNHEIM, Indianapolis, Ind.) (1:5000) for 30' at room temperature. The blots were again washed in washing buffer and developed by the addition of ECL chemiluminescent detection reagents (0.125 ml/cm²) according to the manufacturer's instructions (AMERSHAM LIFE SCIENCES, Arlington Heights, Ill.). The blots were wrapped in saran wrap and exposed to Kodak X-OMAT AR films (EASTMAN KODAK, Rochester, N.Y.).

Nitrite Assay. Nitrite, a stable breakdown product of NO in physiological systems, was assayed using the Griess reaction (23). Cell culture supernatants (100 μ L) were added in triplicates to 100 μ L of Griess reagent (sulfanilamide 1%, naphthylethylenediamine dihydrochloride 0.1%, phosphoric acid 2.5%) using 96-well plates (SIGMA, St. Louis, Mo.). After incubation at room temperature for 10 min, absorbance at 550 nm was measured. A doubling dilution of a 50 M sodium nitrite solution was used to generate a standard curve. The lower limit of the standard curve was 0.25 μ M.

Northern Analysis. Northern blot analysis was performed to examine the mRNA expression profile of IFN- γ -induced genes. Total cellular RNA was isolated from cells using TRIzol reagent (Life Technologies, Gaithersburg, Md.) following the manufacturer's instructions. Probes for northern hybridization were prepared by RT-PCR using gene specific primers for IRF-1 (nucleotides 7-359), 2-5 AS p40 (nucleotides 2-492), 2-5 AS p69 (nucleotides 21-503), RSV G (nucleotides 4688-5584), RSV F (nucleotides 5661-7385) and glyceraldehyde 3 phosphate dehydrogenase (GAPDH) (nucleotides 1-360). The PCR products were confirmed by sequencing. The probes were labeled using BrightStar Psoralen-Biotin labeling kit (AMBION, Austin, Tex.) following manufacturer's protocol. 10 mg of total RNA was size fractionated on 1% formaldehyde agarose gel, and transferred to nylon membranes (HYBOND N+, AMERSHAM, Piscataway, N.J.) using standard protocol (24) and cross-linked by UV irradiation (UV STRATALINKER 1800, STRATAGENE, San Diego, Calif.). Hybridization was carried out at 42° C. overnight with 2-4 μ M labeled probe and UltraHyb hybridization solution (AMBION, Austin, Tex.).

The blots were washed twice with 2×SSC, 0.1% SDS for 5 minutes each and two more washes with 0.1×SSC, 0.1% SDS for 15 minutes each at 42° C. The blots were processed for detection using the BRIGHTSTAR BIODETECT Kit (AM-

BION, Austin, Tex.) following manufacturer's protocol. The blots were exposed to KODAK X-OMAT AR films (EASTMAN KODAK, Rochester, N.Y.) for 1-15 minutes. The bands were quantified by using Advanced Quantifier software (BIOIMAGE, Ann Arbor, Mich.) and the signals were normalized with the respective GAPDH signal.

Antisense Blocking of 2'-5' Oligoadenylate Synthetase. Phosphorothioate antisense oligonucleotides (ODNs) were designed against p40 and p69 subunits of 2'-5' oligoadenylate synthetase. The sequences of antisense ODNs are as follows: p40 subunit, 5'-TTT CTG AGA TCC ATC ATT GA-3' (SEQ ID NO: 17) and p69 subunit, 5'-TCC CCA TTT CCC ATT GC-3' (SEQ ID NO: 18). The control ODN sequences 5'-GTC TAT GAA TAC TTT CCT AG-3' (SEQ ID NO: 19) and 5'-CAC CTC TAT CTC TCT CG-3' (SEQ ID NO: 20) are a scramble of the antisense sequence to p40 and p69 isomers, respectively, i.e., identical in base composition. HEp-2 cells were treated with 1000 U/ml of IFN- γ protein for 20 hours. At the same time equimolar mixture of antisense ODNs to both the isoforms of 2-5 AS or their scrambled mismatch ODNs were added at concentrations 0, 3, 30 and 90 nM. Cells were infected with RSV at 20 h post-IFN- γ -treatment, as described earlier. After 1 h of virus adsorption, cultures were supplemented with complete medium, which contained 1000 U/ml of IFN- γ and respective concentrations of ODNs, and incubated for 72 hrs. ODNs were supplemented every 8 hours. At 72 h pi, cells were washed three times with cold PBS, pH 7.4, harvested and the clear cell homogenate was used for plaque assay.

2-5 AS Assay. A 2-5 Assay was done following the method described previously (Ghosh et al., *J. Biol. Chem.* 272:15452-15458, 1997). Briefly, 20 μ L of reaction mixture containing the cell homogenate, 20 mM Tris-HCl, pH 7.5, 20 mM magnesium acetate, 2.5 mM dithiothreitol, 5 mM ATP, 5 μ Ci of [a-32P] ATP, and 50 μ g/ml poly(I).poly(C) was incubated for 3 h at 30° C. The reaction was stopped by boiling for 3 min and centrifuged, and was incubated for 3 h at 37° C. with 3 μ L of 1 unit/ μ L calf intestine alkaline phosphatase to convert the unreacted [a-32P]ATP to inorganic phosphate. Two μ L of the sample were then spotted on a polyethylenimine-cellulose thin layer chromatography plate and resolved in 750 mM KH₂PO₄, pH 3.5. The 2-5 A formed was then quantified by using Advanced Quantifier software (BIOIMAGE, Ann Arbor, Mich.) and expressed as arbitrary units.

Generation of Stable Cell Line Overexpressing RNase L Inhibitor. Human RLI cDNA was amplified as KpnI-BamHI cassette and cloned in pcDNA3.1 (INVITROGEN, Carlsbad, Calif.) by the standard procedure (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, and ed., Cold Spring Harbor Laboratory, NY, 1989). HEp-2 cells were transfected with 5 mg of pcDNA3.1-RLI using lipofectine (LIFE TECHNOLOGIES, Gaithersburg, Md.). The empty pcDNA3.1 vector was used as a control. Stable transfectants were selected by culturing the cells in the presence of G418 (LIFE TECHNOLOGIES, Gaithersburg, Md.). Individual clones were isolated and analyzed for the expression of RLI mRNA. The clone that expressed RLI at the highest level and had a normal morphology and growth pattern was selected and named RLI-14.

RNase L Assay. An RNase L assay was done by ribosomal RNA cleavage assay (Player et al., *Methods*, 15:243-253, 1998). Briefly, cells were harvested in NP-40 lysis buffer (10 mM HEPES, pH 7.5, 90 mM KCl, 1 mM magnesium acetate, 0.5% (v/v) NP-40, 2 mM 2-mercaptoethanol, 100 mg/ml leupeptin) and S10 lysate was prepared and protein content was estimated using the BCA (bicinchoninic acid) assay (Pierce, Rockford, Ill.). Ribosomal RNA cleavage by RNase L was assayed in a 20 ml reaction containing 200 mg protein,

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2 ml of 10× cleavage buffer (100 mM HEPES, pH 7.5, 1 mM KCl, 50 mM magnesium acetate, 10 mM ATP, 0.14 M 2-mercaptoethanol), 100 nM 2'-5'A and incubated at 30° C. for 2 h. RNA was isolated from the reaction using TRIZOL reagent (LIFE TECHNOLOGIES, Gaithersburg, Md.) following the manufacturer's instructions. 2 mg of RNA was separated on agarose gel electrophoresis and the rRNA cleavage products were compared.

Animals. Female 6-8 weeks old wild type and STAT4^{-/-} BALB/c mice from Jackson Laboratory (Bar Harbor, Me.) were maintained in pathogen free conditions at the animal center at USF College of Medicine. All procedures were reviewed and approved by the committee on animal research at the University of South Florida College of Medicine.

Cloning and recombination of adenoviral vectors. Murine 25 AS (p40) cDNA was cloned into adenoviral transfer vector pShuttle-CMV (STRATAGENE, CA) at KpnI and XhoI sites. The left and right arms of pShuttle-CMV vector contains Ad5 nucleotides 34,931-35,935 and 3,534-5,790, which mediate homologous recombination with pAdEasy-1 vector in *E. coli*, plus inverted terminal repeat (ITR) and packaging signal sequences (nucleotides 1-480 of Ad5) required for viral production in mammalian cells. pAdEasy-1 adenoviral plasmid (STRATAGENE, CA) contains all Ad5 sequences except nucleotides 1-3,533 (encompassing the E1 gene) and nucleotides 28,130-30,820 (encompassing E3).

For generation of recombinant adenovirus plasmid, pShuttle-CMV-p40/LacZ plasmids were linearized with PmeI and co-transformed with pAdEasy-1 plasmid into recombination proficient BJ5183 cells. The recombination was confirmed by PacI digestion. The recombined clones were re-transformed into DH5α cells for large-scale plasmid purification.

Generation and purification of recombinant adenovirus. HEK293 cells, which produce the deleted E1 genes in trans, were transfected with 4 μg of PacI digested recombinant adenovirus plasmid DNA with lipofectin (LIFE TECHNOLOGIES, MD). Cells were harvested 7-10 days post-transfection, resuspended in PBS and recombinant virus was collected by 3-4 freeze-thaw cycles. The recombinant virus expressing murine p40 and LacZ were termed Ad-p40 and Ad-LacZ, respectively. The viruses were amplified by infecting fresh HEK-293 cells. Viruses were further purified by CsCl banding (Becker et al., *Methods Cell Biol.*, 43 Pt. A:161-189, 1994). The viral band was extracted and CsCl was removed by passing through Centricon-100 columns (MILLIPORE, MA).

Quantitation of RSV titers in lung. To quantify RSV titers in the mouse lung whole lungs were first weighed and placed immediately in EMEM media supplemented with 10% FBS. Lungs were homogenized, centrifuged at 10,000 RPM for 10 minutes at 4° C., the clear supernatants were used for plaque assays by shell vial technique (Kumar et al., 2002).

Pulmonary Function. To evaluate the pulmonary function in vaccinated and control groups, mice were administered IGT, as described earlier. Three days later, airway responsiveness was assessed non-invasively in conscious, unrestrained mice with a whole body plethysmograph (BUXCO ELECTRONICS, Troy, N.Y.), as previously described (Matsuse et al., *J. Immunol.* 164:6583-6592, 2000). With this system, the volume changes that occur during a normal respiratory cycle are recorded as the pressure difference between an animal-containing chamber and a reference chamber. The resulting signal is used to calculate respiratory frequency, minute volume, tidal volume, and enhanced pause (Penh). Penh was used as the measure of bronchoconstriction and was calculated from the formula: Penh=pause×(peak expiratory pres-

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sure/peak inspiratory pressure), where pause is the ratio of time required to exhale the last 30% of tidal volume relative to the total time of expiration. Mice were placed in the plethysmograph and the chamber was equilibrated for 10 min. They were exposed to aerosolized PBS (to establish baseline) followed by incremental doses (6, 12.5, 25, and 50 mg/ml) of methacholine (SIGMA CHEMICALS, St. Louis, Mo.). Each dose of methacholine was aerosolized for 5 min, and respiratory measurements were recorded for 5 min afterward. During the recording period, an average of each variable was derived from every 30 breaths (or 30 s, whichever occurred first). The maximum Penh value after each dose as used to measure the extent of bronchoconstriction.

Bronchoalveolar lavage (BAL) and histology of the lung. Bronchoalveolar lavage were performed on Ad-p40 administered and control mice, as described before (Kumar et al., 1999). Histological staining and a semiquantitative analysis of airway inflammation from the lungs of p40 treated and control groups of mice were performed, as described earlier (Kumar et al., 1999). Lung inflammation was assessed after staining the sections with hematoxylin and eosin (HE). The entire lung section was reviewed, and pathological changes were evaluated for epithelial damage, peribronchovascular cell infiltrate, and interstitial-alveolar cell infiltrate for the mononuclear cells and polymorphonuclear cells.

Statistical Analysis. Experiments were repeated 2 to 4 times for each experiment as indicated. Statistical significance was analyzed using paired two-tailed student's t-test. Differences were considered statistically significant when the p-value was less than 0.05.

Example 1

IFN-γ Attenuates RSV Infection in Human Epithelial Cells

To examine the effect of IFN-γ on RSV infection, HEP-2 cells were pre-incubated for 4-20 h with different concentrations of IFN-γ and subsequently infected with RSV. Respective concentrations of IFN-γ were added back to the cells in complete medium after the removal of viral inoculum. Cells were harvested at 72 h p.i., and viral titer was determined by plaque assay. RSV replication was inhibited significantly with the addition of various concentrations of IFN-γ to both cell lines prior to RSV infection (FIGS. 1A and B). A 97% inhibition of replication was observed in HEP-2 and A549 cells, at 1000 U/ml of IFN-γ added at 20 h pre-infection. Cells treated with IFN-γ 4 h pre-infection also showed significant reduction (p<0.01) in RSV titer (50% reduction). A significant decrease (p<0.01) in RSV titer (39% reduction) was observed in A549 cells, which were not treated with IFN-γ before infection, but were only treated at 1 h post infection (FIG. 1C). To rule out the possibility that the reduction in RSV titers could be due to cytotoxicity of IFN-γ, a MTT cytotoxicity assay was performed. The results indicate that the cells were metabolically as viable as the untreated control cells when treated with the highest concentrations of IFN-γ (1,000 U/ml; FIG. 1D). Thus, IFN-γ did not exhibit any cytotoxic or growth inhibitory effect on these cells. These results suggest that the treatment of cells with soluble IFN-γ results in a significant decrease in RSV infection in epithelial cells.

Example 2

IFN-γ Induces IRF-1 Protein Expression

ISGs implicated in the antiviral activity of IFNs include IRFs, double stranded RNA activated protein kinase (PKR)

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and inducible nitric oxide synthase (iNOS). To identify the ISGs in these cells potentially involved in protection against RSV infection, proteins were analyzed from cells at various time points post treatment with IFN- γ (1000 U/ml). A western blot analysis was performed using specific antibodies to IRF-1, IRF-2 and PKR (FIG. 2A). There was increased expression of IRF-1 but no change in the expression of IRF-2 following IFN- γ addition. Expression of IRF-1 increased after 30' of IFN- γ addition. The expression of PKR decreased gradually over time (FIG. 2B) and no change in the expression of phospho-eIF-2a was observed following IFN- γ addition. Cytokeratin-18 was used as an internal control, the expression of which did not change with the addition of IFN- γ . To examine if IFN- γ induced iNOS plays a role in antiviral action, iNOS expression was examined by western blotting (FIG. 2B). The expression of iNOS protein could not be detected before and after IFN- γ addition. Murine macrophage cell lysate containing iNOS was used as a positive control, which did not bind to the cytokeratin-18 antibody used as internal control. To rule out completely the involvement of iNOS in the antiviral effect of IFN- γ , the level of nitric oxide (NO) was examined in the culture supernatant of both Hep-2 and A549 cells before and after the addition of IFN- γ at various time points. No detectable level of NO (lowest concentration of standard was 0.25 mM) was observed in both cell lines at any time point, i.e., before or after IFN- γ addition in both cell lines. A similar expression pattern was observed for IRF1, IRF2, PKR and iNOS in A549 cells. These results indicate that IFN- γ up-regulates IRF-1 in these cells and neither PKR nor iNOS play any role in the antiviral activity of IFN- γ against RSV infection in human epithelial cell lines.

Example 3

Exogenous IFN- γ Upregulates mRNA Synthesis of IRF-1 and 2-5 AS

IRF-1 has been reported to play a role in antiviral activity via the induction and activation of 2-5 AS (Reis et al., *EMBO J.* 11:185-193, 1992). Northern analysis was performed using gene specific probes for IRF-1 and the p40 and p69 isoforms of 2-5 AS (FIG. 3). The IRF-1 mRNA was induced at 30 min after addition of IFN- γ and continued to increase gradually thereafter until 48 h post exposure. The induction of the p40 and p69 isoforms of 2-5 AS was observed starting at 4 h and peaked at 24 h post exposure. The p40 probe hybridized to two transcripts of 1.8 and 1.6 kbp. Similarly, the p69 probe hybridized to four expected transcripts of 5.7, 4.5, 3.7 and 3.2 kbp of which 5.7 kbp was the major transcript. These results suggest that IFN- γ induces IRF-1, which in turn, up regulates 2-5 AS, suggesting that the latter may be involved in the anti-RSV mechanism of IFN- γ .

Example 4

2-5 as Antisense Oligonucleotides Abrogate the Antiviral Effect of IFN- γ in HEp-2 Cells

To investigate whether IFN- γ induced anti-RSV activity is mediated by 2-5 AS, IFN- γ exposed (1000 U/ml at 20 h pre-infection) HEp-2 cells were treated with equimolar mixture of antisense oligonucleotides (ODNs) to both p40 and p69 isoforms of 2-5 AS. Scrambled mismatch of the antisense ODN sequence to p40 and p69 at the same concentration were used as control. RSV infection was barely detectable in cells either treated with IFN- γ alone or with cells treated with IFN- γ and control ODNs but not in those treated with IFN- γ

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and antisense ODNs, as shown in FIG. 4. Addition of antisense ODN significantly reverted ($p < 0.01$) the antiviral effect of IFN- γ against RSV infection and this reversal was dose-dependent and increased with increasing concentrations of antisense ODNs. As shown in FIG. 4, 2-5 AS activity was reduced in a dose dependent manner in the cells treated with antisense ODN to 2-5 AS but not control ODN. These results indicate that the addition of antisense ODNs to 2-5 AS to IFN- γ -treated cells reduced 2-5 AS activity in these cells and in turn the antiviral effect of IFN- γ .

Example 5

Overexpression of RNase L Inhibitor (RLI) does not Alter the IFN- γ Responses in HEp-2 Cells

In addition to RNase L, RNase L inhibitor (RLI) has been implicated in the antiviral effect of IFN- γ . To determine the role of 2-5 A/RNase L-mediated antiviral mechanism, a stable cell line expressing RLI, RLI-14, was established. A northern analysis of RNAs from RLI-14 and HEp-2 using gene specific probe for RLI showed a major 3.5 kb transcript and a minor 2.8 Kb transcript (FIGS. 5A and 5B). A seven-fold increase in the major RLI transcript expression was observed in RLI-14 cells when compared to HEp-2 cells. The analysis of IFN- γ induced proteins in RLI-14 cell line by western blotting showed that IFN- γ induced expression of IRF-1, but not IRF-2, at 30 min post induction and IRF-1 expression continued to increase thereafter until 48 h (FIG. 5C) as in HEp-2 cells (FIG. 2A). Also, a time-specific decrease in PKR protein concentration was observed after IFN- γ addition in the RLI-14 cell line. The expression of cytokeratin-18, used as an internal control, remained unchanged with IFN- γ addition. The level of mRNA expression of IRF-1, p40 and p69 isoforms of 2-5 AS was observed by northern analysis, and the expression level showed a gradual increase over time following IFN- γ stimulation (FIG. 5D) as in HEp-2 cells (FIG. 3). These results suggest that overexpression of RLI does not change the expression pattern of the IFN- γ -induced genes involved in antiviral activity of these cells.

Example 6

RNase L Inhibitor (RLI) Overexpression Decreases the Antiviral Activity of IFN- γ

To examine the effect of the overexpression of the RNase L inhibitor, both HEp-2 and RLI-14 cells were treated with IFN- γ at 100-1000 U/ml at 20 h pre-infection and subsequently infected with RSV. IFN- γ was added back to the cells at respective concentrations following RSV infection. HEp-2 cells treated with 100 and 1000 U/ml of IFN- γ showed significant inhibition ($p < 0.001$) of RSV infection (72% and 97% reduction, respectively) when compared to untreated cells. In marked contrast, RLI-14 cells showed significantly lower inhibition of infection (only 12% and 22% reduction, respectively) compared to HEp-2 cells at respective concentrations of IFN- γ , as showed in FIG. 6. In absence of IFN- γ treatment, both cell lines exhibited identical RSV titers upon infection. However, the viral titer significantly decreased ($p < 0.01$) when the concentration of IFN- γ was increased from 100 U/ml to 1000 U/ml in RLI-14 cells. This demonstrates that increase in IFN- γ led to higher expression of 2-5 AS and in turn production of 2-5 A, which subsequently bound to RNase L and increased the level of active RNase L by releasing RNase L from its inactive complex. Reduction in virus repli-

cation was inhibited in RLI-14 cells (%) when compared to HEP-2 cells (%), as shown in FIG. 6. In order to examine whether the reduction in inhibition of RSV infection in RLI-14 cells was due to reduced RNase L activity in these cells, RNase L assay was done using ribosomal RNA cleavage assay. This reaction uses cell lysate as a source of both substrate and enzyme, thus giving a comparison of the ribonuclease activity of RNase L in different cell types. The results confirm that ribonuclease activity of RNase L is indeed reduced in RLI-14 cells when compared to HEP-2 cells as evident from the rRNA cleavage products, as shown in FIG. 6. Together, these results confirm the involvement of 2-5 A/RNase L in the antiviral effect of IFN- γ against RSV infection.

The finding that treatment of HEP-2 and A549 cells at 20 h pre-infection with as low as 100 U/ml of IFN- γ proteins inhibits RSV infection and replication when compared to untreated cells, has significant therapeutic implications. HEP-2 and A549 cells treated with 1000 U/ml of IFN- γ at 20 h pre-infection exhibited a 97% (30-31 fold in log 10 PFU/ml) reduction in RSV titer. The RSV titer also decreased by 39% (1.7 fold reduction in log 10 PFU/ml) in these cells, which were not treated with IFN- γ prior to infection but were only treated immediately after RSV infection. RSV is resistant to the antiviral effects of type-I interferons and human MxA. It has been reported that overexpression of IFN- γ by gene transfer and by recombinant RSV attenuates RSV replication in a mouse model of RSV infection. However, the mechanism of antiviral action of IFN- γ against RSV is not known.

The elucidation of the mechanism underlying IFN- γ -mediated resistance to RSV infection in human epithelial cells has been the main focus of this invention. The mechanism of antiviral action of IFN- γ is complex and may be unique for individual cell lines and viruses. A profile of ISGs, relevant to antiviral activity in these epithelial cells, establish that IFN- γ exposure results in induction of both the mRNA and protein for IRF-1 but not IRF2. In non-induced cells the IRF-2 protein functions as a repressor of ISGs. IFN- γ induction temporarily removes this repression and activates ISGs including IRF-1. IRF-1 and IRF-2 compete for the same cis acting recognition sequences but with opposite effects. Findings in these epithelial cells are consistent with those found for human macrophages, where IFN- γ treatment does not enhance IRF-2 gene expression, despite strong upregulation of IRF-1 mRNA expression. Two additional ISGs, PKR and iNOS proteins were examined for their role in IFN- γ induced antiviral activity. IFN- γ activates PKR, which in turn phosphorylates and inactivates eukaryotic initiation factor-2a (eIF-2a) and leads to restriction of cellular as well as viral protein synthesis. The iNOS is also known to mediate antiviral property of IFN- γ . However, a time specific decrease in PKR expression and no change in phosphorylation of eIF-2a and the lack of detectable levels of iNOS protein or NO in IFN- γ -stimulated HEP-2 and A549 cells indicate that neither PKR and phospho-eIF-2a nor iNOS play any role in IFN- γ mediated inhibition of RSV infection in these cells.

To further dissect the mechanism of IFN- γ mediated anti-RSV activity in HEP-2 and A549 cells, IRF-1 induced expression of 2-5 AS was examined. Of the four isoforms (p40, p46, p69, and p100) of 2-5 AS detected in human cells to date, the expression pattern of the p40 and p69 isoforms following IFN- γ stimulation was examined in this study because of the following. The p40 and p46 isoforms of 2-5 AS, which are dependent on dsRNA for activation, are derived from the same gene by differential splicing between the fifth and an additional sixth exon of this gene and are thus identical for the first 346 residues, except for their C-terminal ends. Of the two

high molecular weight isoforms, p69, but not p100, requires dsRNA for activation. The expression of 2-5 AS p40 and p69 are induced by IFN- γ in these cells at 4 h and peaks at 24 h post IFN- γ addition. Therefore, the antiviral effect of IFN- γ in these cells is observed when the cells are treated with IFN- γ at 4 h pre-infection and is highest when treated at 20 h pre-infection as the level of 2-5 AS is at peak at that time. These data suggest that the antiviral mechanism of IFN- γ against RSV infection is mediated by the activation of IRF-1, which in turn activates the 2-5 AS system. A dose-dependent abrogation of 2'-5' AS activity and in turn the anti-RSV effect of IFN- γ by the addition of an equimolar mixture of antisense ODNs to p40 and p69, but not by the scrambled mismatch ODNs, provide evidence supporting the role of 2-5 AS in the antiviral mechanism of IFN- γ against RSV infection.

2-5 AS induces 2-5 A, which binds to and activate RNase L, which cleaves double stranded RNA 3' of UpN residues. The levels of RNase L are increased in growth-arrested cells and following IFN- γ treatment; however, its biological activity is thought to be controlled at the level of enzymatic activation rather than through regulation of its transcription and translation. Increasing endogenous levels of 2-5 A leads to enhanced RNase L activity, which suggests that intracellular levels of 2-5 A are rate limiting in the activation of RNase L, whereas cellular levels of RNase L are sufficient for maximal biological activity. Furthermore, RNase L remains in an inactive form in the cells being bound to an inhibitor, RLI, which codes for a 68 kDa protein whose mRNA is not regulated by IFN- γ . RLI induces neither 2-5 A degradation nor reversible modification of RNase L when expressed in a reticulocyte lysate, but antagonizes the binding of 2-5 A to RNase L, thus, its nuclease activity, since 2-5 A binding is a prerequisite to RNase L dimerization and activation.

RLI-14, a stable cell line overexpressing RLI, was established from HEP-2 cells and characterized to determine precisely the involvement of RNase L in the antiviral mechanism of RSV infected epithelial cells. The finding that RLI-14 was almost identical to the parent HEP-2 cells in its response to IFN- γ shows that RLI overexpression does not alter the induction of ISGs in these cells (FIGS. 5A-D). Nonetheless, reduced RNase L activity and antiviral activity of IFN- γ in RLI-14 cells (FIG. 6), confirmed that the RNase L activity is indeed critical to the antiviral effect of IFN- γ and is only partly controlled by the elevated levels of 2-5 AS in these cells following IFN- γ treatment. The reduction in antiviral effect of IFN- γ in these cells was dependent on the dose of IFN- γ , indicating that the level of 2-5 A, which is regulated by IFN- γ and the level of RLI are crucial in determining which pathway cells will follow. The importance of the level of 2-5 A was confirmed by preliminary findings which showed significant reduction in RSV infection when HEP-2 cells were treated with 100 U/ml of IFN- γ 20 h pre-infection and transfected with 1 mM 2-5 A 2 h pre-infection, when compared to the cells treated with 100 U/ml of IFN- γ alone. Similarly the importance of the level of RLI in the antiviral activity was reported for HIV, where RLI is induced during HIV1 infection and down regulates the 2-5 A/RNase L pathway in human T cells.

In summary, these results demonstrate that IFN- γ inhibits RSV infection of human epithelial cells. Specifically, in HEP-2 and A549 epithelial cells, IFN- γ upregulates IRF-1, which in turn, induces 2-5 AS. Further, the 2-5 AS generates 2-5 A that activates RNase L, which is normally found in the cytoplasm in inactive state bound to RLI. Thus, RNase L-mediated cleavage of viral RNA is governed by the ying-yang mechanism involving 2-5 A and RLI. In a 2-5 A-dominant state cells are protected from RSV infection due to the acti-

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vation of RNase L. In contrast, an RLI-dominant condition attenuates the antiviral effect by inactivation of RNase L. Since, 2-5 A and RLI are respectively, governed by IFN- γ -dependent and independent mechanisms, treatment with IFN- γ or overexpression of 2-5 AS should provide an efficient means to redirect the 2-5 A:RLI ratio toward a shift in favor of 2-5 A and achieve a profound antiviral effect.

Example 7

2-5 AS Plasmid DNA Vaccination Attenuates RSV Infection and Pathogenesis

As shown in FIG. 8A, 2-5 AS pDNA vaccine decreases lung RSV titers. BALB/c mice (n=4) were intranasally administered with p2'-5' AS (25 mg of DNA each time complexed with lipofectamine) or an equal amount of empty pVAX vector DNA 3 times in 2-day intervals. Mice were infected with RSV seven days after last DNA administration and were sacrificed on day 5 post-infection. BAL was performed and lungs were collected. RSV titer was determined by plaque assay from the lung homogenate. The results show that 2-5 AS cDNA vaccination can significantly attenuate lung titers of RSV in infected mice.

FIG. 8B shows that reduction of viral titers is associated with reduction in MIP-1 α . Expression level of MIP-1 α was determined from lung homogenate by ELISA. The results show that vaccination with 2-5 AS cDNA decreases production of chemokine MIP-1 α which is known to be proinflammatory in action.

In FIG. 8C, 2-5 AS overexpression increased the macrophage population significantly compared to RSV infected mice. BAL cell differential was performed and percentages of macrophage, lymphocytes, and neutrophils were determined. The results show that 2-5 AS does not alter the cellular composition of the lung. No significant changes are seen in lymphocytes and macrophages, however the percent of neutrophils is increased in the lungs of mice treated with 2-5 AS cDNA. FIGS. 9A-9C show that 2-5 AS vaccination significantly decreased pulmonary inflammation. Histological sections from lungs were stained with hematoxylin and eosin and representative photomicrographs are shown.

Example 8

AD-2-5 AS (P40) Decreases Lung RSV Titers

A reduction in virus titer is the gold standard by which the effectiveness of an antiviral therapy is measured. Mice were intranasally administered with 10^8 PFU/ml rAD-p40 and then infected with RSV 4 h later. Analysis of lung virus titers following acute, live RSV infection at day 5 post infection show a significant (100-fold, $P<0.01$) reduction in RSV titers in Ad-p40 treated mice compared to controls (FIG. 10). These results indicate that the rAD-p40 treatment constitutes an effective prophylaxis against RSV infection.

Example 9

AD-2-5 AS (P40) Decreases AHR in Mice

The safety of an antiviral therapy especially can be measured by a decrease in RSV-induced AHR. To test whether Ad-p40 administration reduces RSV-induced airway hyperactivity, the % baseline enhanced pause (Penh) was measured in a group of mice treated with rAD-p40 prior to RSV infection and their AHR was compared with untreated RSV

30

infected group. Mice receiving Ad-p40 exhibited a similar response to methacholine challenge when compared to uninfected PBS control group (FIG. 10). These results suggest that the Ad-p40 induced decrease in RSV infection decreases AHR.

Example 10

AD-2-5 AS (P40) Normalizes Cellular Infiltration to the Lung

The inflammation in the lung due to RSV infection is due to infiltration into the lung of a large number of macrophages and lymphocytes. To determine whether treatment with rAD-p40 affects migration of these cells to the lung, mice administered with rAD-p40 and RSV infected were compared to RSV infected mice without treatment and naïve mice as control and to rAd-lacZ as control. Mice with p40 gene transfer and RSV infection show a BAL cell differential similar to that of normal uninfected animals, lack of AHR compared to RSV-infected animals without p40 gene transfer and lack of the peribronchiolar and perivascular inflammation suggesting that intranasal p40 can potentially be an effective antiviral approach in vivo for RSV infection.

Example 11

AD-2-5 AS(P40) Decreases RSV Infection-Induced Pulmonary Inflammation

Lung inflammation was examined in different groups of mice. Mice treated with Ad-p40 and Ad-lacZ upon acute RSV infection exhibit relatively less disruption of the epithelium and cellular infiltration. Representative pathological features reveal that groups of mice receiving Ad-p40 exhibit less epithelial damage, and reduced mononuclear cell (MNC) and polymorphonuclear cell (PMNC) infiltrates in the interstitial and peribronchovascular region, as compared to Ad-lacZ controls (FIGS. 12A-12H). These results suggest that the Ad-p40 protects mice from RSV infection-induced pulmonary inflammation. These results suggest that Ad-p40 protects mice from RSV infection-induced pulmonary inflammation.

The finding that transient gene expression therapy can substantially reduce lung RSV titers by 2 logs (100-fold), inhibit RSV-infection induced AHR and make the lung resistant to inflammation by acute RSV infection is very significant. These results suggest tremendous therapeutic potential of this approach. The other members of this family include the measles virus, the sendai virus, parainfluenza 1, 2, and 3, the mumps virus, the simian virus, and the newcastle virus. This finding is also important for other Paramyxoviruses, such as rotavirus that causes juvenile diarrhea in millions of children worldwide. Furthermore, beyond this family of viruses, the 2-5 AS/RNase L cascade has been implicated in the anti-viral activity of picorna viruses, (Hassel, B A et al. *Embo J*, 1993, 12 (8):3297-304; Benavente, J et al. *J. Virol.* 1984, 51 (3): 866-71; Goswami, B B and Sharma, O K. *J Biol Chem*, 1984, 259 (3):1371-4; Nilsen, T W et al. *Mol Cell Biol*, 1983, 3 (1):64-9), vaccinia virus (Maitra, R K and Silverman, R H. *J Virol*, 1998, 72 (2):1146-52; Banerjee, R et al. *Virology*, 1990, 179 (1):410-5), reovirus (Kumar, R et al. *J Virol*, 1988, 62 (9):3175-81), HIV (Saito, H et al. *Keio J Med*, 1996, 45 (3):161-7; 45), EMCV (Glezen, W P et al. *Am J Dis Child*, 1986, 140 (6):543-6), Hepatitis B and C virus (Groothuis, J R et al. *Pediatrics*, 1988, 82 (2):199-203; Nelson W E, Behrman R E, Kliegman R. *Nelson Textbook of Pediatrics*. 15 ed. Philadelphia).

Moreover, besides human disease, this finding may have implications, for RSV of cattle (BRVS), sheep, and goats. If 2-5 AS mediated approach is successful, the mortality and morbidity due to RSV infection can be reduced. Also, RSV has been linked with the development of asthma, and hence, prevention or successful treatment of RSV is expected to decrease the incidence of asthma and fatal exacerbation of asthma due to RSV. Adults infected with RSV miss work for an average of 7-9 days as opposed those with flu who miss an average of 6-7 days. Therapeutic treatment can reduce the number of absences from the work, which exceeds the flu infection. Also, prophylaxis prior to and during viral season and treatment immediately after infection can lead to a substantial decrease in hospitalization and emergency visits due to RSV infection.

RSV is one of the important viral respiratory pathogens that produce an annual epidemic of respiratory illness. In children, common diseases associated with RSV infection primarily include interstitial lung diseases, such as bronchiolitis, and asthma. RSV is estimated to cause 85% of the cases of acute bronchiolitis that affects infants and young children (Shay, D K et al. *Jama*, 1999, 282 (15):1440-6). Some children may become infected during three or four successive RSV seasons. Each year, RSV is responsible for up to an estimated 125,000 pediatric hospitalizations, with a mortality rate of approximately 2% (Heilman, C A. *J Infect Dis* 1990, 161 (3):402-6; Shay, D K et al. *J Infect Dis*, 2001, 183 (1): 16-22; Altman, C A et al. *Pediatr Cardiol*, 2000, 21 (5):433-8; Simoes, E A. *Lancet*, 1999, 354 (9181):847-52; Falsey, A R. et al. *J Infect Dis*, 1995, 172 (2):389-94). Among hospitalized infants with chronic lung and heart disease, the RSV mortality rate may be as high as 5%. Up to half of all pediatric admissions for bronchiolitis and one-quarter of admissions for pneumonia are due to RSV (La Via et al., *Clin. Pediatr. (Phila)*, 32 (8):450-454, 1993). RSV is a major risk factor for a number of other health conditions, such as immunodeficiency, cardiac arrhythmia, congenital heart disease, and unusual atrial tachycardia (Donnerstein et al., *J. Pediatr.* 125 (1):23-28, 1994).

Emerging evidence also suggests that RSV is an important pathogen in profusely healthy adults as well (Hall et al., *Clin. Infect. Dis.* 33(6):792-796, 2001). In a study of 15 adults who were challenged by RSV after a natural infection, 50% were reinfectd after two months; by 26 months 73% were reinfectd (Fixler, D E. et al. *Pediatr Cardiol*, 1996, 17 (3):163-8). RSV infection is also clinically important in previously healthy working adults (Hogg, J C. et al. *American Journal of Respiratory & Critical Care Medicine*, 1999, 160 (5):S26-S28). In this study, of a total of 2960 18-60 year-old adults studied during 1975 to 1995, 211 (7%) acquired RSV infection; 84% of infections were symptomatic—74% upper respiratory tract infection, 26% lower respiratory tract infection and 40% were febrile. RSV is a major risk factor for the development and/or exacerbation of asthma and chronic obstructive pulmonary disorder (COPD), and about 30 million of Americans suffers from asthma and COPD.

The prevalence of bronchiolitis in infants as well as asthma and COPD has increased throughout the world, including in the United States, over the past two decades. The rates of death from asthma have increased from 0.8 per 100,000 in 1977-78 to 2.0 per 100,000 in 1991, and these rates have increased in almost all age groups in the United States (Sly, R M. *Ann Allergy*. 1994, 73 (3):259-68). Asthma is the most common cause of the admission of children to the hospital, and it is the most common chronic illness causing absence from school and work in North America (Nelson, R P, Jr., et al. *J Allergy Clin Immunol*, 1996, 98 (2):258-63). The total costs

of illnesses related to asthma in 1990 were 6.2 billion, a 53% increase in direct medical expenditures and a 23% increase in indirect costs since 1985 (Weiss, K B et al. *N Engl J Med*, 1992, 326 (13):862-6). The total estimated cost in 1995 for the treatment of allergic diseases, asthma, chronic sinusitis, otitis media, and nasal polyps, was about \$10 billion (Baraniuk, J N. *J Resp Dis*, 1996, 17 (S11)). Together, these diseases lead to a significant reduction in the quality of life and a tremendous economic loss.

Finally, although studies with 2-5 AS (p40) in the adenovirus system provides the "proof of concept" for the anti-RSV activity, other virus vectors, including adeno-associated vectors (Zhao, N et al. *Mol Biotechnol*, 2001, 19 (3):229-37; Monahan, P E et al. *Mol Med Today*, 2000, 6 (11):433-40; Senior, K. *Lancet*, 2002, 359 (9313):1216) can be used to express this p-40 or other 2-5 AS gene(s) for the antiviral activity.

Example 12

Gene Therapy

In the therapeutic and prophylactic methods of the present invention, the nucleotide sequence encoding 2-5 AS, or a catalytically active fragment thereof, can be administered to a patient in various ways. It should be noted that the vaccine can be administered as the compound or as pharmaceutically acceptable salt and can be administered alone or as an active ingredient in combination with pharmaceutically acceptable carriers, diluents, adjuvants and vehicles. In those cases in which the RNA virus is a virus that infects the patient's respiratory system, the compounds can be administered intranasally, bronchially, via inhalation pathways, for example. The patient being treated is a warm-blooded animal and, in particular, mammals including man. The pharmaceutically acceptable carriers, diluents, adjuvants and vehicles as well as implant carriers generally refer to inert, non-toxic solid or liquid fillers, diluents or encapsulating material not reacting with the active ingredients of the present invention.

It is noted that humans are treated generally longer than the mice exemplified herein, which treatment has a length proportional to the length of the disease process and drug effectiveness. The doses may be single doses or multiple doses over a period of several days, but single doses are preferred.

The carrier for gene therapy can be a solvent or dispersing medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils.

Proper fluidity, when desired, can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Nonaqueous vehicles such a cottonseed oil, sesame oil, olive oil, soybean oil, corn oil, sunflower oil, or peanut oil and esters, such as isopropyl myristate, may also be used as solvent systems for compound compositions. Additionally, various additives that enhance the stability, sterility, and isotonicity of the compositions, including antimicrobial preservatives, antioxidants, chelating agents, and buffers, can be added. Prevention of the action of microorganisms can be ensured by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, and the like. In many cases, it will be desirable to include isotonic agents, for example, sugars, sodium chloride, and the like. Prolonged absorption of the injectable pharmaceutical form can be brought about by the use of agents delaying absorption, for example, aluminum

monostearate and gelatin. According to the present invention, however, any vehicle, diluent, or additive used would have to be compatible with the compounds.

Examples of delivery systems useful in the present invention include, but are not limited to: U.S. Pat. Nos. 5,225,182; 5,169,383; 5,167,616; 4,959,217; 4,925,678; 4,487,603; 4,486,194; 4,447,233; 4,447,224; 4,439,196; and 4,475,196. Many other delivery systems and modules are well known to those skilled in the art.

A pharmacological formulation of the nucleotide sequence utilized in the present invention can be administered orally to the patient. Conventional methods such as administering the compounds in tablets, suspensions, solutions, emulsions, capsules, powders, syrups and the like are usable. Known techniques which deliver the vaccine orally or intravenously and retain the biological activity are preferred.

In one embodiment, the nucleotide sequence can be administered initially by nasal infection to increase the local levels of 2-5 AS enzymatic activity. The patient's 2-5 AS activity levels are then maintained by an oral dosage form, although other forms of administration, dependent upon the patient's condition and as indicated above, can be used. The quantity of vaccine to be administered will vary for the patient being treated and will vary from about 100 ng/kg of body weight to 100 mg/kg of body weight per day and preferably will be from 10 mg/kg to 10 mg/kg per day.

As indicated above, standard molecular biology techniques known in the art and not specifically described can be generally followed as in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York (1989), and in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Md. (1989) and in Perbal, *A Practical Guide to Molecular Cloning*, John Wiley & Sons, New York (1988), and in Watson et al., *Recombinant DNA*, Scientific American Books, New York and in Birren et al. (eds) *Genome Analysis: A Laboratory Manual Series*, Vols. 1-4 Cold Spring Harbor Laboratory Press, New York (1998) and methodology as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659; and 5,272,057, the contents of which are incorporated herein by reference in their entirety. Polymerase chain reaction (PCR) can be carried out generally as in PCR Protocols: A Guide To Methods And Applications, Academic Press, San Diego, Calif. (1990). In-situ (In-cell) PCR in combination with Flow Cytometry can be used for detection of cells containing specific DNA and mRNA sequences (Testoni et al., 1996, *Blood* 87:3822).

As used herein, the term "gene therapy" refers to the transfer of genetic material (e.g., DNA or RNA) of interest into a host to treat or prevent a genetic or acquired disease or condition phenotype. The genetic material of interest encodes a product (e.g., a protein, polypeptide, peptide or functional RNA) whose production in vivo is desired. For example, in addition to the nucleotide encoding 2-5 AS, or a catalytically active fragment thereof, the genetic material of interest can encode a hormone, receptor, or other enzyme, polypeptide or peptide of therapeutic value. For a review see, in general, the text "Gene Therapy" (*Advances in Pharmacology* 40, Academic Press, 1997).

Two basic approaches to gene therapy have evolved: (1) ex vivo and (2) in vivo gene therapy. In ex vivo gene therapy, cells are removed from a patient, and while being cultured are treated in vitro. Generally, a functional replacement gene is introduced into the cell via an appropriate gene delivery vehicle/method (transfection, transduction, homologous recombination, etc.) and an expression system as needed and then the genetically modified cells are expanded in culture

and returned to the host/patient. These genetically reimplanted cells produce the transfected gene product in situ. Alternatively, a xenogenic or allogeneic donor's cells can be genetically modified with the nucleotide sequence in vitro and subsequently administered to the patient.

In in vivo gene therapy, target cells are not removed from the patient; rather, the gene to be transferred is introduced into the cells of the recipient organism in situ, that is within the recipient. Alternatively, if the host gene is defective, the gene is repaired in situ. These genetically modified cells produce the transfected gene product in situ.

The gene expression vehicle is capable of delivery/transfer of heterologous nucleic acids into a host cell. As indicated previously, the expression vehicle may include elements to control targeting, expression and transcription of the nucleotide sequence in a cell selective or tissue-specific manner, as is known in the art. It should be noted that often the 5'UTR and/or 3'UTR of the gene may be replaced by the 5'UTR and/or 3'UTR of the expression vehicle. Therefore as used herein the expression vehicle may, as needed, not include the 5'UTR and/or 3'UTR and only include the specific amino acid coding region.

The expression vehicle can include a promoter for controlling transcription of the heterologous material and can be either a constitutive or inducible promoter to allow selective transcription. Enhancers that may be required to obtain necessary transcription levels can optionally be included. Enhancers are generally any non-translated DNA sequence which works contiguously with the coding sequence (in cis) to change the basal transcription level dictated by the promoter. The expression vehicle can also include a selection gene as described herein below.

Vectors can be introduced into cells or tissues by any one of a variety of known methods within the art. Such methods can be found generally described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Harbor Laboratory, New York (1989, 1992); in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Md. (1989); Chang et al., *Somatic Gene Therapy*, CRC Press, Ann Arbor, Mich. (1995); Vega et al., *Gene Targeting*, CRC Press, Ann Arbor, Mich. (1995); *Vectors: A Survey of Molecular Cloning Vectors and Their Uses*, Butterworths, Boston Mass. (1988); and Gilboa et al. (1986) and include, for example, stable or transient transfection, lipofection, electroporation and infection with recombinant viral vectors. In addition, see U.S. Pat. No. 4,866,042 for vectors involving the central nervous system and also U.S. Pat. Nos. 5,464,764 and 5,487,992 for positive-negative selection methods.

Introduction of nucleic acids by infection offers several advantages over the other listed methods. Higher efficiency can be obtained due to their infectious nature. Moreover, viruses are very specialized and typically infect and propagate in specific cell types. Thus, their natural specificity can be used to target the vectors to specific cell types in vivo or within a tissue or mixed culture of cells. Viral vectors can also be modified with specific receptors or ligands to alter target specificity through receptor mediated events.

A specific example of a DNA viral vector for introducing and expressing recombinant nucleotide sequences is the adenovirus derived vector Adenop53TK. This vector expresses a herpes virus thymidine kinase (TK) gene for either positive or negative selection and an expression cassette for desired recombinant sequences. This vector can be used to infect cells that have an adenovirus receptor which includes most cancers of epithelial origin as well as others. This vector as well as others that exhibit similar desired

functions can be used to treat a mixed population of cells and can include, for example, an in vitro or ex vivo culture of cells, a tissue or a human subject.

Additional features can be added to the vector to ensure its safety and/or enhance its therapeutic efficacy. Such features include, for example, markers that can be used to negatively select against cells infected with the recombinant virus. An example of such a negative selection marker is the TK gene described above that confers sensitivity to the antibiotic ganciclovir. Negative selection is therefore a means by which infection can be controlled because it provides inducible suicide through the addition of antibiotic. Such protection ensures that if, for example, mutations arise that produce altered forms of the viral vector or recombinant sequence, cellular transformation will not occur. Features that limit expression to particular cell types or tissue types can also be included. Such features include, for example, promoter and regulatory elements that are specific for the desired cell type or tissue type.

In addition, recombinant viral vectors are useful for in vivo expression of a desired nucleic acid because they offer advantages such as lateral infection and targeting specificity. Lateral infection is inherent in the life cycle of, for example, retrovirus and is the process by which a single infected cell produces many progeny virions that bud off and infect neighboring cells. The result is that a large area becomes rapidly infected, most of which was not initially infected by the original viral particles. This is in contrast to vertical-type of infection in which the infectious agent spreads only through daughter progeny. Viral vectors can also be produced that are unable to spread laterally. This characteristic can be useful if the desired purpose is to introduce a specified gene into only a localized number of targeted cells.

As described above, viruses are very specialized infectious agents that have evolved, in many cases, to elude host defense mechanisms. Typically, viruses infect and propagate in specific cell types. The targeting specificity of viral vectors utilizes its natural specificity to specifically target predetermined cell types and thereby introduce a recombinant gene into the infected cell. The vector to be used in the methods of the present invention will depend on desired the cell type or cell types to be targeted and will be known to those skilled in the art. For example, if RSV infection is to be inhibited (i.e., treated or prevented), then a vector specific for such respiratory mucosal epithelial cells would preferably be used.

Retroviral vectors can be constructed to function either as infectious particles or to undergo only a single initial round of infection. In the former case, the genome of the virus is modified so that it maintains all the necessary genes, regulatory sequences and packaging signals to synthesize new viral proteins and RNA. Once these molecules are synthesized, the host cell packages the RNA into new viral particles that are capable of undergoing further rounds of infection. The vector's genome is also engineered to encode and express the desired recombinant nucleotide sequence. In the case of non-infectious viral vectors, the vector genome is usually mutated to destroy the viral packaging signal that is required to encapsulate the RNA into viral particles. Without such a signal, any particles that are formed will not contain a genome and therefore cannot proceed through subsequent rounds of infection. The specific type of vector will depend upon the intended application. The actual vectors are also known and readily available within the art or can be constructed by one skilled in the art using well-known methodology.

The recombinant vector can be administered in several ways. If viral vectors are used, for example, the procedure can take advantage of their target specificity and consequently, do

not have to be administered locally at the diseased site. However, local administration can provide a quicker and more effective treatment, administration can also be performed by, for example, intravenous or subcutaneous injection into the subject. Injection of the viral vectors into a spinal fluid can also be used as a mode of administration, especially in the case of RNA virus infections of the central nervous system. Following injection, the viral vectors will circulate until they recognize host cells with the appropriate target specificity for infection.

An alternate mode of administration can be by direct inoculation locally at the site of the disease or pathological condition or by inoculation into the vascular system supplying the site with nutrients or into the spinal fluid. Local administration is advantageous because there is no dilution effect and, therefore, a smaller dose is required to achieve expression in a majority of the targeted cells. Additionally, local inoculation can alleviate the targeting requirement required with other forms of administration since a vector can be used that infects all cells in the inoculated area. If expression is desired in only a specific subset of cells within the inoculated area, then promoter and regulatory elements that are specific for the desired subset can be used to accomplish this goal. Such non-targeting vectors can be, for example, viral vectors, viral genome, plasmids, phagemids and the like. Transfection vehicles such as liposomes and colloidal polymeric particles can also be used to introduce the non-viral vectors described above into recipient cells within the inoculated area. Such transfection vehicles are known to those skilled within the art.

Direct DNA inoculations can be administered as a method of vaccination. Plasmid DNAs encoding influenza virus hemagglutinin glycoproteins have been tested for the ability to provide protection against lethal influenza challenges. In immunization trials using inoculations of purified DNA in saline, 67-95% of test mice and 25-63% of test chickens were protected against the lethal challenge. Good protection was achieved by intramuscular, intravenous and intradermal injections. In mice, 95% protection was achieved by gene gun delivery of 250-2500 times less DNA than the saline inoculations. Successful DNA vaccination by multiple routes of inoculation and the high efficiency of gene-gun delivery highlight the potential of this promising new approach to immunization. Plasmid DNAs expressing influenza virus hemagglutinin glycoproteins have been tested for their ability to raise protective immunity against lethal influenza challenges of the same subtype. In trials using two inoculations of from 50 to 300 micrograms of purified DNA in saline, 67-95% of test mice and 25-63% of test chickens have been protected against a lethal influenza challenge. Parenteral routes of inoculation that achieved good protection included intramuscular and intravenous injections. Successful mucosal routes of vaccination included DNA drops administered to the nares or trachea. By far, the most efficient DNA immunizations were achieved by using a gene gun to deliver DNA-coated gold beads to the epidermis. In mice, 95% protection was achieved by two immunizations with beads loaded with as little as 0.4 micrograms of DNA. The breadth of routes supporting successful DNA immunizations, coupled with the very small amounts of DNA required for gene-gun immunizations, highlight the potential of this remarkably simple technique for the development of subunit vaccines. In contrast to the DNA based antigen vaccines, the present invention provides the development of an intranasal gene transfer method using 2-5 AS, or a catalytically active fragment thereof, which can be used as a prophylaxis against multiple respiratory infections. In a preferred embodiment, the preventative and therapeutic method is used against respiratory RNA viral infection, most preferably against RSV.

All patents, patent applications, provisional applications, and publications referred to or cited herein are incorporated by reference in their entirety, including all figures and tables, to the extent they are not inconsistent with the explicit teachings of this specification.

It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application.

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<301> AUTHORS: Aissouni, Y., et al.
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<301> AUTHORS: Behera, A.K., et al.
<302> TITLE: 2'-5' Oligoadenylate synthesis plays a critical role in
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<303> JOURNAL: J. Biol. Chem.
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<302> TITLE: Identification of the substrate-binding sites of
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<301> AUTHORS: Hovnanian, A., et al.
<302> TITLE: The human 2',5'-oligoadenylate synthetase locus is composed
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<303> JOURNAL: Genomics
<304> VOLUME: 52
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<302> TITLE: Cloning and chromosomal location of human genes inducible
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<303> JOURNAL: EMBO J.
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<303> JOURNAL: Eur. J. Biochem.
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<301> AUTHORS: Benech, P., et al.
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<303> JOURNAL: FEBS Lett.
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<301> AUTHORS: Benech, P., et al.
<302> TITLE: Structure of two forms of the interferon-induced (2'-5')
        oligo A synthetase of human cells
<303> JOURNAL: EMBO J.
<304> VOLUME: 4
<305> ISSUE: 9
<306> PAGES: 2249-2256
<307> DATE: 1985
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Saunders, M.E., et al.
<302> TITLE: Human 2-5A synthetase: characterization of a novel cDNA
        and corresponding gene structure
<303> JOURNAL: EMBO J.
<304> VOLUME: 4
<305> ISSUE: 7
<306> PAGES: 1761-1768
<307> DATE: 1985
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
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<300> PUBLICATION INFORMATION:
<301> AUTHORS: Merlin, G., et al.
<302> TITLE: Molecular cloning and sequence of partial cDNA for
        interferon-induced (2'-5')oligo(A) synthetase mRNA from human
        cells
<303> JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
<304> VOLUME: 80
<305> ISSUE: 16
<306> PAGES: 4904-4908
<307> DATE: 1983
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06

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gaa gac tat ctc ttg cca gac acg tgt ttc cgc atg caa atc gac cat      96
Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asp His
20         25         30

gcc att gac atc atc tgt ggg ttc ctg aag gaa agg tgc ttc cga ggt     144
Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
35         40         45

agc tcc tac cct gtg tgt gtg tcc aag gtg gta aag ggt ggc tcc tca     192
Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
50         55         60

ggc aag ggc acc acc ctc aga ggc cga tct gac gct gac ctg gtt gtc     240
Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65         70         75         80

ttc ctc agt cct ctc acc act ttt cag gat cag tta aat cgc cgg gga     288
Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
85         90         95

gag ttc atc cag gaa att agg aga cag ctg gaa gcc tgt caa aga gag     336
Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
100        105        110

aga gca ctt tcc gtg aag ttt gag gtc cag gct cca cgc tgg ggc aac     384
Arg Ala Leu Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
115        120        125

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ccc cgt gcg ctc agc ttc gta ctg agt tgc ctc cag ctc ggg gag ggg      432
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gtg gag ttc gat gtg ctg cct gcc ttt gat gcc ctg ggt cag ttg act      480
Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
   145                               150                               155                               160

ggc agc tat aaa cct aac ccc caa atc tat gtc aag ctc atc gag gag      528
Gly Ser Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
                               165                               170                               175

tgc acc gac ctg cag aaa gag ggc gag ttc tcc acc tgc ttc aca gaa      576
Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr Glu
                               180                               185                               190

cta cag aga gac ttc ctg aag cag cgc ccc acc aag ctc aag agc ctc      624
Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
   195                               200                               205

atc cgc cta gtc aag cac tgg tac caa aat tgt aag aag aag ctt ggg      672
Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
   210                               215                               220

aag ctg cca cct cag tat gcc ctg gag ctc ctg acg gtc tat gct tgg      720
Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
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gag cga ggg agc atg aaa aca cat ttc aac aca gcc caa gga ttt cgg      768
Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
                               245                               250                               255

acg gtc ttg gaa tta gtc ata aac tac cag caa ctc tgc atc tac tgg      816
Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
   260                               265                               270

aca aag tat tat gac ttt aaa aac ccc att att gaa aag tac ctg aga      864
Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
   275                               280                               285

agg cag ctc acg aaa ccc agg cct gtg atc ctg gac ccg gcg gac cct      912
Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
   290                               295                               300

aca gga aac ttg ggt ggt gga gac cca aag ggt tgg agg cag ctg gca      960
Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
   305                               310                               315                               320

caa gag gct gag gcc tgg ctg aat tac cca tgc ttt aag aat tgg gat      1008
Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
   325                               330                               335

ggg tcc cca gtg agc tcc tgg att ctg ctg gct gaa agc aac agt aca      1056
Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Ala Glu Ser Asn Ser Thr
   340                               345                               350

gac gat gag acc gac gat ccc agg acg tat cag aaa tat ggt tac att      1104
Asp Asp Glu Thr Asp Asp Pro Arg Thr Tyr Gln Lys Tyr Gly Tyr Ile
   355                               360                               365

gga aca cat gag tac cct cat ttc tct cat aga ccc agc acg ctc cag      1152
Gly Thr His Glu Tyr Pro His Phe Ser His Arg Pro Ser Thr Leu Gln
   370                               375                               380

gca gca tcc acc cca cag gca gaa gag gac tgg acc tgc acc atc ctc      1200
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<210> SEQ ID NO 2

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<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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Glu	Asp	Tyr	Leu 20	Leu	Pro	Asp	Thr	Cys 25	Phe	Arg	Met	Gln 30	Ile	Asp	His
Ala	Ile	Asp 35	Ile	Ile	Cys	Gly	Phe 40	Leu	Lys	Glu	Arg 45	Cys	Phe	Arg	Gly
Ser	Ser 50	Tyr	Pro	Val	Cys	Val 55	Ser	Lys	Val	Val	Lys 60	Gly	Gly	Ser	Ser
Gly 65	Lys	Gly	Thr	Thr	Leu 70	Arg	Gly	Arg	Ser	Asp 75	Ala	Asp	Leu	Val	Val 80
Phe	Leu	Ser	Pro	Leu 85	Thr	Thr	Phe	Gln 90	Asp	Gln	Leu	Asn	Arg	Arg 95	Gly
Glu	Phe	Ile	Gln 100	Glu	Ile	Arg	Arg	Gln 105	Leu	Glu	Ala	Cys 110	Gln	Arg	Glu
Arg	Ala	Leu 115	Ser	Val	Lys	Phe	Glu 120	Val	Gln	Ala	Pro	Arg 125	Trp	Gly	Asn
Pro	Arg 130	Ala	Leu	Ser	Phe	Val 135	Leu	Ser	Ser	Leu	Gln 140	Leu	Gly	Glu	Gly
Val 145	Glu	Phe	Asp	Val	Leu 150	Pro	Ala	Phe	Asp	Ala 155	Leu	Gly	Gln	Leu	Thr 160
Gly	Ser	Tyr	Lys 165	Pro	Asn	Pro	Gln	Ile	Tyr 170	Val	Lys	Leu	Ile	Glu 175	Glu
Cys	Thr	Asp	Leu 180	Gln	Lys	Glu	Gly	Glu 185	Phe	Ser	Thr	Cys 190	Phe	Thr	Glu
Leu	Gln	Arg 195	Asp	Phe	Leu	Lys	Gln 200	Arg	Pro	Thr	Lys	Leu 205	Lys	Ser	Leu
Ile	Arg 210	Leu	Val	Lys	His	Trp 215	Tyr	Gln	Asn	Cys 220	Lys	Lys	Lys	Leu	Gly
Lys 225	Leu	Pro	Pro	Gln	Tyr 230	Ala	Leu	Glu	Leu	Leu 235	Thr	Val	Tyr	Ala	Trp 240
Glu	Arg	Gly	Ser	Met 245	Lys	Thr	His	Phe	Asn 250	Thr	Ala	Gln	Gly	Phe	Arg 255
Thr	Val	Leu	Glu 260	Leu	Val	Ile	Asn	Tyr 265	Gln	Gln	Leu	Cys 270	Ile	Tyr	Trp
Thr	Lys	Tyr 275	Tyr	Asp	Phe	Lys	Asn 280	Pro	Ile	Ile	Glu	Lys 285	Tyr	Leu	Arg
Arg	Gln 290	Leu	Thr	Lys	Pro	Arg 295	Pro	Val	Ile	Leu	Asp 300	Pro	Ala	Asp	Pro
Thr 305	Gly	Asn	Leu	Gly	Gly 310	Gly	Asp	Pro	Lys	Gly 315	Trp	Arg	Gln	Leu	Ala 320
Gln	Glu	Ala	Glu 325	Ala	Trp	Leu	Asn	Tyr 330	Pro	Cys	Phe	Lys	Asn	Trp	Asp 335
Gly	Ser	Pro	Val 340	Ser	Ser	Trp	Ile	Leu 345	Leu	Ala	Glu	Ser	Asn 350	Ser	Thr
Asp	Asp 355	Glu	Thr	Asp	Asp	Pro	Arg 360	Thr	Tyr	Gln	Lys	Tyr 365	Gly	Tyr	Ile
Gly	Thr 370	His	Glu	Tyr	Pro	His 375	Phe	Ser	His	Arg 380	Pro	Ser	Thr	Leu	Gln
Ala 385	Ala	Ser	Thr	Pro	Gln 390	Ala	Glu	Glu	Asp 395	Trp	Thr	Cys	Thr	Ile	Leu 400

<210> SEQ ID NO 3
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<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1206)
<223> OTHER INFORMATION:
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Benech et al.
<302> TITLE: Structure of two forms of the interferon-induced (2'-5')
        oligo A synthetase human cells based on cDNAs and gene sequences
<303> JOURNAL: EMBO J.
<304> VOLUME: 4
<305> ISSUE: 9
<306> PAGES: 2249-2256
<307> DATE: 1985
<308> DATABASE ACCESSION NUMBER: NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06

<400> SEQUENCE: 3

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1          5          10          15

gaa gac tat ctc ttg cca gac acg tgt ttc cgc atg caa atc gac cat      96
Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asp His
          20          25          30

gcc att gac atc atc tgt ggg ttc ctg aag gaa agg tgc ttc cga ggt     144
Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
          35          40          45

agc tcc tac cct gtg tgt gtg tcc aag gtg gta aag ggt ggc tcc tca     192
Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
          50          55          60

ggc aag ggc acc acc ctc aga ggc cga tct gac gct gac ctg gtt gtc     240
Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
          65          70          75          80

ttc ctc agt cct ctc acc act ttt cag gat cag tta aat cgc cgg gga     288
Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
          85          90          95

gag ttc atc cag gaa att agg aga cag ctg gaa gcc tgt caa aga gag     336
Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
          100          105          110

aga gca ctt tcc gtg aag ttt gag gtc cag gct cca cgc tgg ggc aac     384
Arg Ala Leu Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
          115          120          125

ccc cgt gcg ctc agc ttc gta ctg agt tcg ctc cag ctc ggg gag ggg     432
Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
          130          135          140

gtg gag ttc gat gtg ctg cct gcc ttt gat gcc ctg ggt cag ttg act     480
Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
          145          150          155          160

ggc agc tat aaa cct aac ccc caa atc tat gtc aag ctc atc gag gag     528
Gly Ser Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
          165          170          175

tgc acc gac ctg cag aaa gag ggc gag ttc tcc acc tgc ttc aca gaa     576
Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr Glu
          180          185          190

cta cag aga gac ttc ctg aag cag cgc ccc acc aag ctc aag agc ctc     624
Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
          195          200          205

atc cgc cta gtc aag cac tgg tac caa aat tgt aag aag aag ctt ggg     672
Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
          210          215          220

aag ctg cca cct cag tat gcc ctg gag ctc ctg acg gtc tat gct tgg     720
Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Thr Val Tyr Ala Trp
          225          230          235          240

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gag cga ggg agc atg aaa aca cat ttc aac aca gcc caa gga ttt cgg	768
Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg	
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acg gtc ttg gaa tta gtc ata aac tac cag caa ctc tgc atc tac tgg	816
Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp	
260 265 270	
aca aag tat tat gac ttt aaa aac ccc att att gaa aag tac ctg aga	864
Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg	
275 280 285	
agg cag ctc acg aaa ccc agg cct gtg atc ctg gac ccg gcg gac cct	912
Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro	
290 295 300	
aca gga aac ttg ggt ggt gga gac cca aag ggt tgg agg cag ctg gca	960
Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala	
305 310 315 320	
caa gag gct gag gcc tgg ctg aat tac cca tgc ttt aag aat tgg gat	1008
Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp	
325 330 335	
ggg tcc cca gtg agc tcc tgg att ctg ctg gct gaa agc aac agt aca	1056
Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Ala Glu Ser Asn Ser Thr	
340 345 350	
gac gat gag acc gac gat ccc agg acg tat cag aaa tat ggt tac att	1104
Asp Asp Glu Thr Asp Asp Pro Arg Thr Tyr Gln Lys Tyr Gly Tyr Ile	
355 360 365	
gga aca cat gag tac cct cat ttc tct cat aga ccc agc acg ctc cag	1152
Gly Thr His Glu Tyr Pro His Phe Ser His Arg Pro Ser Thr Leu Gln	
370 375 380	
gca gca tcc acc cca cag gca gaa gag gac tgg acc tgc acc atc ctc	1200
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tga atg c	1207
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<210> SEQ ID NO 4

<211> LENGTH: 400

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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20 25 30

Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
35 40 45

Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
50 55 60

Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
65 70 75 80

Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
85 90 95

Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
100 105 110

Arg Ala Leu Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
115 120 125

Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
130 135 140

Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr

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145	150	155	160
Gly Ser Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu	165	170	175
Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr Glu	180	185	190
Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu	195	200	205
Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly	210	215	220
Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp	225	230	235
Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg	245	250	255
Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp	260	265	270
Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg	275	280	285
Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro	290	295	300
Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala	305	310	315
Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp	325	330	335
Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Ala Glu Ser Asn Ser Thr	340	345	350
Asp Asp Glu Thr Asp Asp Pro Arg Thr Tyr Gln Lys Tyr Gly Tyr Ile	355	360	365
Gly Thr His Glu Tyr Pro His Phe Ser His Arg Pro Ser Thr Leu Gln	370	375	380
Ala Ala Ser Thr Pro Gln Ala Glu Glu Asp Trp Thr Cys Thr Ile Leu	385	390	395
			400

<210> SEQ ID NO 5
 <211> LENGTH: 2064
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(2064)
 <223> OTHER INFORMATION:
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Hovnanian, A., et al.
 <302> TITLE: The human 2', 5'-oligoadenylate synthetase locus is composed of three distinct genes
 <303> JOURNAL: Genomics
 <304> VOLUME: 52
 <305> ISSUE: 3
 <306> PAGES: 267-277
 <307> DATE: 1998
 <308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
 <309> DATABASE ENTRY DATE: 2003-04-03
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Marie, I. and Hovanessian, A.G.
 <302> TITLE: The 69-kDa 2-5A synthetase is composed of two homologous and adjacent functional domains
 <303> JOURNAL: J. Biol. Chem.
 <304> VOLUME: 267
 <305> ISSUE: 14
 <306> PAGES: 9933-9939
 <307> DATE: 1992
 <308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
 <309> DATABASE ENTRY DATE: 2003-04-03
 <300> PUBLICATION INFORMATION:

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<301> AUTHORS: Marie, I., et al.
<302> TITLE: Differential expression and distinct structure of 69- and
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<303> JOURNAL: J. Biol. Chem.
<304> VOLUME: 265
<305> ISSUE: 30
<306> PAGES: 18601-18607
<307> DATE: 1990
<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
<309> DATABASE ENTRY DATE: 2003-04-03
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Marie, I., et al.
<302> TITLE: Preparation and characterization of polyclonal antibodies
specific for the 69 and 100 k-dalton forms of human 2-5A
synthetase
<303> JOURNAL: Biochem. Biophys. Res. Commun.
<304> VOLUME: 160
<305> ISSUE: 2
<306> PAGES: 580-587
<307> DATE: 1989
<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
<309> DATABASE ENTRY DATE: 2003-04-03
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Hovanessian, A.G., et al.
<302> TITLE: Characterization of 69- and 100-kDa forms of
2-5A-synthetase from interferon-treated human cells
<303> JOURNAL: J. Biol. Chem.
<304> VOLUME: 263
<305> ISSUE: 10
<306> PAGES: 4959
<307> DATE: 1988
<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
<309> DATABASE ENTRY DATE: 2003-04-03
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Hovanessian, A.G., et al.
<302> TITLE: Identification of 69-kd and 100-kd forms of 2-5A synthetase
<303> JOURNAL: EMBO J.
<304> VOLUME: 6
<305> ISSUE: 5
<306> PAGES: 1273-1280
<307> DATE: 1987
<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
<309> DATABASE ENTRY DATE: 2003-04-03

<400> SEQUENCE: 5

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1          5          10          15

ggg tgg ttt atc cag gaa tac ctg aag ccc tac gaa gaa tgt cag aca      96
Gly Trp Phe Ile Gln Glu Tyr Leu Lys Pro Tyr Glu Glu Cys Gln Thr
          20          25          30

ctg atc gac gag atg gtg aac acc atc tgt gac gtc tgc agg aac ccc      144
Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Cys Arg Asn Pro
          35          40          45

gaa cag ttc ccc ctg gtg cag gga gtg gcc ata ggt ggc tcc tat gga      192
Glu Gln Phe Pro Leu Val Gln Gly Val Ala Ile Gly Gly Ser Tyr Gly
          50          55          60

cgg aaa aca gtc tta aga ggc aac tcc gat ggt acc ctt gtc ctt ttc      240
Arg Lys Thr Val Leu Arg Gly Asn Ser Asp Gly Thr Leu Val Leu Phe
          65          70          75          80

ttc agt gac tta aaa caa ttc cag gat cag aag aga agc caa cgt gac      288
Phe Ser Asp Leu Lys Gln Phe Gln Asp Gln Lys Arg Ser Gln Arg Asp
          85          90          95

atc ctc gat aaa act ggg gat aag ctg aag ttc tgt ctg ttc acg aag      336
Ile Leu Asp Lys Thr Gly Asp Lys Leu Lys Phe Cys Leu Phe Thr Lys
          100          105          110

tgg ttg aaa aac aat ttc gag atc cag aag tcc ctt gat ggg tcc acc      384
Trp Leu Lys Asn Asn Phe Glu Ile Gln Lys Ser Leu Asp Gly Ser Thr
          115          120          125

atc cag gtg ttc aca aaa aat cag aga atc tct ttc gag gtg ctg gcc      432

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Ala	Phe	Asn	Ala	Leu	Ser	Leu	Asn	Asp	Asn	Pro	Ser	Pro	Trp	Ile	Tyr	
145					150					155					160	
cga	gag	ctc	aaa	aga	tcc	ttg	gat	aag	aca	aat	gcc	agt	cct	ggt	gag	528
Arg	Glu	Leu	Lys	Arg	Ser	Leu	Asp	Lys	Thr	Asn	Ala	Ser	Pro	Gly	Glu	
				165					170					175		
ttt	gca	gtc	tgc	ttc	act	gaa	ctc	cag	cag	aag	ttt	ttt	gac	aac	cgt	576
Phe	Ala	Val	Cys	Phe	Thr	Glu	Leu	Gln	Gln	Lys	Phe	Phe	Asp	Asn	Arg	
			180					185					190			
cct	gga	aaa	cta	aag	gat	ttg	atc	ctc	ttg	ata	aag	cac	tgg	cat	caa	624
Pro	Gly	Lys	Leu	Lys	Asp	Leu	Ile	Leu	Leu	Ile	Lys	His	Trp	His	Gln	
		195				200						205				
cag	tgc	cag	aaa	aaa	atc	aag	gat	tta	ccc	tgc	ctg	tct	ccg	tat	gcc	672
Gln	Cys	Gln	Lys	Lys	Ile	Lys	Asp	Leu	Pro	Ser	Leu	Ser	Pro	Tyr	Ala	
210					215						220					
ctg	gag	ctg	ctt	acg	gtg	tat	gcc	tgg	gaa	cag	ggg	tgc	aga	aaa	gac	720
Leu	Glu	Leu	Leu	Thr	Val	Tyr	Ala	Trp	Glu	Gln	Gly	Cys	Arg	Lys	Asp	
225				230					235					240		
aac	ttt	gac	att	gct	gaa	ggc	gtc	aga	acg	gtt	ctg	gag	ctg	atc	aaa	768
Asn	Phe	Asp	Ile	Ala	Glu	Gly	Val	Arg	Thr	Val	Leu	Glu	Leu	Ile	Lys	
				245				250						255		
tgc	cag	gag	aag	ctg	tgt	atc	tat	tgg	atg	gtc	aac	tac	aac	ttt	gaa	816
Cys	Gln	Glu	Lys	Leu	Cys	Ile	Tyr	Trp	Met	Val	Asn	Tyr	Asn	Phe	Glu	
			260					265					270			
gat	gag	acc	atc	agg	aac	atc	ctg	ctg	cac	cag	ctc	caa	tca	gcg	agg	864
Asp	Glu	Thr	Ile	Arg	Asn	Ile	Leu	Leu	His	Gln	Leu	Gln	Ser	Ala	Arg	
		275				280						285				
cca	gta	atc	ttg	gat	cca	gtt	gac	cca	acc	aat	aat	gtg	agt	gga	gat	912
Pro	Val	Ile	Leu	Asp	Pro	Val	Asp	Pro	Thr	Asn	Asn	Val	Ser	Gly	Asp	
		290				295						300				
aaa	ata	tgc	tgg	caa	tgg	ctg	aaa	aaa	gaa	gct	caa	acc	tgg	ttg	act	960
Lys	Ile	Cys	Trp	Gln	Trp	Leu	Lys	Lys	Glu	Ala	Gln	Thr	Trp	Leu	Thr	
305				310					315					320		
tct	ccc	aac	ctg	gat	aat	gag	tta	cct	gca	cca	tct	tgg	aat	gtc	ctg	1008
Ser	Pro	Asn	Leu	Asp	Asn	Glu	Leu	Pro	Ala	Pro	Ser	Trp	Asn	Val	Leu	
			325					330					335			
cct	gca	cca	ctc	ttc	acg	acc	cca	ggc	cac	ctt	ctg	gat	aag	ttc	atc	1056
Pro	Ala	Pro	Leu	Phe	Thr	Thr	Pro	Gly	His	Leu	Leu	Asp	Lys	Phe	Ile	
			340					345					350			
aag	gag	ttt	ctc	cag	ccc	aac	aaa	tgc	ttc	cta	gag	cag	att	gac	agt	1104
Lys	Glu	Phe	Leu	Gln	Pro	Asn	Lys	Cys	Phe	Leu	Glu	Gln	Ile	Asp	Ser	
		355				360						365				
gct	gtt	aac	atc	atc	cgt	aca	ttc	ctt	aaa	gaa	aac	tgc	ttc	cga	caa	1152
Ala	Val	Asn	Ile	Ile	Arg	Thr	Phe	Leu	Lys	Glu	Asn	Cys	Phe	Arg	Gln	
		370				375					380					
tca	aca	gcc	aag	atc	cag	att	gtc	cgg	gga	gga	tca	acc	gcc	aaa	ggc	1200
Ser	Thr	Ala	Lys	Ile	Gln	Ile	Val	Arg	Gly	Gly	Ser	Thr	Ala	Lys	Gly	
				390					395					400		
aca	gct	ctg	aag	act	ggc	tct	gat	gcc	gat	ctc	gtc	gtg	ttc	cat	aac	1248
Thr	Ala	Leu	Lys	Thr	Gly	Ser	Asp	Ala	Asp	Leu	Val	Val	Phe	His	Asn	
				405				410						415		
tca	ctt	aaa	agc	tac	acc	tcc	caa	aaa	aac	gag	cgg	cac	aaa	atc	gtc	1296
Ser	Leu	Lys	Ser	Tyr	Thr	Ser	Gln	Lys	Asn	Glu	Arg	His	Lys	Ile	Val	
			420					425					430			
aag	gaa	atc	cat	gaa	cag	ctg	aaa	gcc	ttt	tgg	agg	gag	aag	gag	gag	1344
Lys	Glu	Ile	His	Glu	Gln	Leu	Lys	Ala	Phe	Trp	Arg	Glu	Lys	Glu	Glu	
		435				440						445				

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gag ctt gaa gtc agc ttt gag cct ccc aag tgg aag gct ccc agg gtg Glu Leu Glu Val Ser Phe Glu Pro Pro Lys Trp Lys Ala Pro Arg Val 450 455 460	1392
ctg agc ttc tct ctg aaa tcc aaa gtc ctc aac gaa agt gtc agc ttt Leu Ser Phe Ser Leu Lys Ser Lys Val Leu Asn Glu Ser Val Ser Phe 465 470 475 480	1440
gat gtg ctt cct gcc ttt aat gca ctg ggt cag ctg agt tct ggc tcc Asp Val Leu Pro Ala Phe Asn Ala Leu Gly Gln Leu Ser Ser Gly Ser 485 490 495	1488
aca ccc agc ccc gag gtt tat gca ggg ctc att gat ctg tat aaa tcc Thr Pro Ser Pro Glu Val Tyr Ala Gly Leu Ile Asp Leu Tyr Lys Ser 500 505 510	1536
tcg gac ctc ccg gga gga gag ttt tct acc tgt ttc aca gtc ctg cag Ser Asp Leu Pro Gly Gly Glu Phe Ser Thr Cys Phe Thr Val Leu Gln 515 520 525	1584
cga aac ttc att cgc tcc cgg ccc acc aaa cta aag gat tta att cgc Arg Asn Phe Ile Arg Ser Arg Pro Thr Lys Leu Lys Asp Leu Ile Arg 530 535 540	1632
ctg gtg aag cac tgg tac aaa gag tgt gaa agg aaa ctg aag cca aag Leu Val Lys His Trp Tyr Lys Glu Cys Glu Arg Lys Leu Lys Pro Lys 545 550 555 560	1680
ggg tct ttg ccc cca aag tat gcc ttg gag ctg ctc acc atc tat gcc Gly Ser Leu Pro Pro Lys Tyr Ala Leu Glu Leu Leu Thr Ile Tyr Ala 565 570 575	1728
tgg gag cag ggg agt gga gtg ccg gat ttt gac act gca gaa ggt ttc Trp Glu Gln Gly Ser Gly Val Pro Asp Phe Asp Thr Ala Glu Gly Phe 580 585 590	1776
cgg aca gtc ctg gag ctg gtc aca caa tat cag cag ctc ggc atc ttc Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Gln Gln Leu Gly Ile Phe 595 600 605	1824
tgg aag gtc aat tac aac ttt gaa gat gag acc gtg agg aag ttt cta Trp Lys Val Asn Tyr Asn Phe Glu Asp Glu Thr Val Arg Lys Phe Leu 610 615 620	1872
ctg agc cag ttg cag aaa acc agg cct gtg atc ttg gac cca ggc gaa Leu Ser Gln Leu Gln Lys Thr Arg Pro Val Ile Leu Asp Pro Gly Glu 625 630 635 640	1920
ccc aca ggt gac gtg ggt gga ggg gac cgt tgg tgt tgg cat ctt ctg Pro Thr Gly Asp Val Gly Gly Gly Asp Arg Trp Cys Trp His Leu Leu 645 650 655	1968
gac aaa gaa gca aag gtt agg tta tcc tct ccc tgc ttc aag gat ggg Asp Lys Glu Ala Lys Val Arg Leu Ser Ser Pro Cys Phe Lys Asp Gly 660 665 670	2016
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<210> SEQ ID NO 6

<211> LENGTH: 687

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

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Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Cys Arg Asn Pro
35 40 45

Glu Gln Phe Pro Leu Val Gln Gly Val Ala Ile Gly Gly Ser Tyr Gly
50 55 60

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Arg	Lys	Thr	Val	Leu	Arg	Gly	Asn	Ser	Asp	Gly	Thr	Leu	Val	Leu	Phe	65	70	75	80
Phe	Ser	Asp	Leu	Lys	Gln	Phe	Gln	Asp	Gln	Lys	Arg	Ser	Gln	Arg	Asp	85	90	95	
Ile	Leu	Asp	Lys	Thr	Gly	Asp	Lys	Leu	Lys	Phe	Cys	Leu	Phe	Thr	Lys	100	105	110	
Trp	Leu	Lys	Asn	Asn	Phe	Glu	Ile	Gln	Lys	Ser	Leu	Asp	Gly	Ser	Thr	115	120	125	
Ile	Gln	Val	Phe	Thr	Lys	Asn	Gln	Arg	Ile	Ser	Phe	Glu	Val	Leu	Ala	130	135	140	
Ala	Phe	Asn	Ala	Leu	Ser	Leu	Asn	Asp	Asn	Pro	Ser	Pro	Trp	Ile	Tyr	145	150	155	160
Arg	Glu	Leu	Lys	Arg	Ser	Leu	Asp	Lys	Thr	Asn	Ala	Ser	Pro	Gly	Glu	165	170	175	
Phe	Ala	Val	Cys	Phe	Thr	Glu	Leu	Gln	Gln	Lys	Phe	Phe	Asp	Asn	Arg	180	185	190	
Pro	Gly	Lys	Leu	Lys	Asp	Leu	Ile	Leu	Leu	Ile	Lys	His	Trp	His	Gln	195	200	205	
Gln	Cys	Gln	Lys	Lys	Ile	Lys	Asp	Leu	Pro	Ser	Leu	Ser	Pro	Tyr	Ala	210	215	220	
Leu	Glu	Leu	Leu	Thr	Val	Tyr	Ala	Trp	Glu	Gln	Gly	Cys	Arg	Lys	Asp	225	230	235	240
Asn	Phe	Asp	Ile	Ala	Glu	Gly	Val	Arg	Thr	Val	Leu	Glu	Leu	Ile	Lys	245	250	255	
Cys	Gln	Glu	Lys	Leu	Cys	Ile	Tyr	Trp	Met	Val	Asn	Tyr	Asn	Phe	Glu	260	265	270	
Asp	Glu	Thr	Ile	Arg	Asn	Ile	Leu	Leu	His	Gln	Leu	Gln	Ser	Ala	Arg	275	280	285	
Pro	Val	Ile	Leu	Asp	Pro	Val	Asp	Pro	Thr	Asn	Asn	Val	Ser	Gly	Asp	290	295	300	
Lys	Ile	Cys	Trp	Gln	Trp	Leu	Lys	Lys	Glu	Ala	Gln	Thr	Trp	Leu	Thr	305	310	315	320
Ser	Pro	Asn	Leu	Asp	Asn	Glu	Leu	Pro	Ala	Pro	Ser	Trp	Asn	Val	Leu	325	330	335	
Pro	Ala	Pro	Leu	Phe	Thr	Thr	Pro	Gly	His	Leu	Leu	Asp	Lys	Phe	Ile	340	345	350	
Lys	Glu	Phe	Leu	Gln	Pro	Asn	Lys	Cys	Phe	Leu	Glu	Gln	Ile	Asp	Ser	355	360	365	
Ala	Val	Asn	Ile	Ile	Arg	Thr	Phe	Leu	Lys	Glu	Asn	Cys	Phe	Arg	Gln	370	375	380	
Ser	Thr	Ala	Lys	Ile	Gln	Ile	Val	Arg	Gly	Gly	Ser	Thr	Ala	Lys	Gly	385	390	395	400
Thr	Ala	Leu	Lys	Thr	Gly	Ser	Asp	Ala	Asp	Leu	Val	Val	Phe	His	Asn	405	410	415	
Ser	Leu	Lys	Ser	Tyr	Thr	Ser	Gln	Lys	Asn	Glu	Arg	His	Lys	Ile	Val	420	425	430	
Lys	Glu	Ile	His	Glu	Gln	Leu	Lys	Ala	Phe	Trp	Arg	Glu	Lys	Glu	Glu	435	440	445	
Glu	Leu	Glu	Val	Ser	Phe	Glu	Pro	Pro	Lys	Trp	Lys	Ala	Pro	Arg	Val	450	455	460	
Leu	Ser	Phe	Ser	Leu	Lys	Ser	Lys	Val	Leu	Asn	Glu	Ser	Val	Ser	Phe	465	470	475	480

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<210> SEQ ID NO 8

<211> LENGTH: 727

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

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20           25           30
Leu Ile Asp Glu Met Val Asn Thr Ile Cys Asp Val Cys Arg Asn Pro
35           40           45
Glu Gln Phe Pro Leu Val Gln Gly Val Ala Ile Gly Gly Ser Tyr Gly
50           55           60
Arg Lys Thr Val Leu Arg Gly Asn Ser Asp Gly Thr Leu Val Leu Phe
65           70           75           80
Phe Ser Asp Leu Lys Gln Phe Gln Asp Gln Lys Arg Ser Gln Arg Asp
85           90           95

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Ile	Leu	Asp	Lys 100	Thr	Gly	Asp	Lys	Leu 105	Lys	Phe	Cys	Leu	Phe 110	Thr	Lys
Trp	Leu	Lys 115	Asn	Asn	Phe	Glu	Ile 120	Gln	Lys	Ser	Leu	Asp 125	Gly	Ser	Thr
Ile	Gln	Val 130	Phe	Thr	Lys	Asn 135	Gln	Arg	Ile	Ser	Phe 140	Glu	Val	Leu	Ala
Ala 145	Phe	Asn	Ala	Leu	Ser 150	Leu	Asn	Asp	Asn	Pro 155	Ser	Pro	Trp	Ile	Tyr 160
Arg	Glu	Leu	Lys 165	Arg	Ser	Leu	Asp	Lys 170	Thr	Asn	Ala	Ser	Pro	Gly 175	Glu
Phe	Ala	Val	Cys 180	Phe	Thr	Glu	Leu	Gln 185	Gln	Lys	Phe	Phe 190	Asp	Asn	Arg
Pro	Gly	Lys 195	Leu	Lys	Asp	Leu	Ile 200	Leu	Leu	Ile	Lys	His 205	Trp	His	Gln
Gln	Cys 210	Gln	Lys	Lys	Ile	Lys 215	Asp	Leu	Pro	Ser	Leu 220	Ser	Pro	Tyr	Ala
Leu 225	Glu	Leu	Leu	Thr	Val 230	Tyr	Ala	Trp	Glu	Gln 235	Gly	Cys	Arg	Lys	Asp 240
Asn	Phe	Asp	Ile 245	Ala	Glu	Gly	Val	Arg	Thr 250	Val	Leu	Glu	Leu	Ile	Lys
Cys	Gln	Glu	Lys 260	Leu	Cys	Ile	Tyr	Trp 265	Met	Val	Asn	Tyr	Asn 270	Phe	Glu
Asp	Glu	Thr 275	Ile	Arg	Asn	Ile	Leu 280	Leu	His	Gln	Leu	Gln 285	Ser	Ala	Arg
Pro	Val 290	Ile	Leu	Asp	Pro	Val 295	Asp	Pro	Thr	Asn	Asn 300	Val	Ser	Gly	Asp
Lys 305	Ile	Cys	Trp	Gln	Trp 310	Leu	Lys	Lys	Glu	Ala 315	Gln	Thr	Trp	Leu	Thr 320
Ser	Pro	Asn	Leu 325	Asp	Asn	Glu	Leu	Pro	Ala 330	Pro	Ser	Trp	Asn	Val 335	Leu
Pro	Ala	Pro	Leu 340	Phe	Thr	Thr	Pro	Gly 345	His	Leu	Leu	Asp	Lys 350	Phe	Ile
Lys	Glu	Phe 355	Leu	Gln	Pro	Asn	Lys 360	Cys	Phe	Leu	Glu	Gln 365	Ile	Asp	Ser
Ala 370	Val	Asn	Ile	Ile	Arg	Thr 375	Phe	Leu	Lys	Glu	Asn 380	Cys	Phe	Arg	Gln
Ser 385	Thr	Ala	Lys	Ile	Gln 390	Ile	Val	Arg	Gly	Gly 395	Ser	Thr	Ala	Lys	Gly 400
Thr	Ala	Leu	Lys 405	Thr	Gly	Ser	Asp	Ala 410	Asp	Leu	Val	Val	Phe	His 415	Asn
Ser	Leu	Lys 420	Ser	Tyr	Thr	Ser	Gln	Lys 425	Asn	Glu	Arg	His 430	Lys	Ile	Val
Lys	Glu	Ile 435	His	Glu	Gln	Leu	Lys 440	Ala	Phe	Trp	Arg	Glu 445	Lys	Glu	Glu
Glu 450	Leu	Glu	Val	Ser	Phe	Glu 455	Pro	Pro	Lys	Trp	Lys 460	Ala	Pro	Arg	Val
Leu 465	Ser	Phe	Ser	Leu	Lys 470	Ser	Lys	Val	Leu	Asn 475	Glu	Ser	Val	Ser	Phe 480
Asp	Val	Leu	Pro 485	Ala	Phe	Asn	Ala	Leu	Gly 490	Gln	Leu	Ser	Ser	Gly 495	Ser
Thr	Pro	Ser 500	Pro	Glu	Val	Tyr	Ala	Gly 505	Leu	Ile	Asp	Leu	Tyr 510	Lys	Ser
Ser	Asp	Leu	Pro	Gly	Gly	Glu	Phe	Ser	Thr	Cys	Phe	Thr	Val	Leu	Glu

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Arg Asn Phe Ile Arg Ser Arg Pro Thr Lys Leu Lys Asp Leu Ile Arg		
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Leu Val Lys His Trp Tyr Lys Glu Cys Glu Arg Lys Leu Lys Pro Lys		
545	550	555
Gly Ser Leu Pro Pro Lys Tyr Ala Leu Glu Leu Leu Thr Ile Tyr Ala		
565	570	575
Trp Glu Gln Gly Ser Gly Val Pro Asp Phe Asp Thr Ala Glu Gly Phe		
580	585	590
Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Gln Gln Leu Gly Ile Phe		
595	600	605
Trp Lys Val Asn Tyr Asn Phe Glu Asp Glu Thr Val Arg Lys Phe Leu		
610	615	620
Leu Ser Gln Leu Gln Lys Thr Arg Pro Val Ile Leu Asp Pro Gly Glu		
625	630	635
Pro Thr Gly Asp Val Gly Gly Gly Asp Arg Trp Cys Trp His Leu Leu		
645	650	655
Asp Lys Glu Ala Lys Val Arg Leu Ser Ser Pro Cys Phe Lys Asp Gly		
660	665	670
Thr Gly Asn Pro Ile Pro Pro Trp Lys Val Pro Thr Met Gln Thr Pro		
675	680	685
Gly Ser Cys Gly Ala Arg Ile His Pro Ile Val Asn Glu Met Phe Ser		
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Ser Arg Ser His Arg Ile Leu Asn Asn Asn Ser Lys Arg Asn Phe Thr		
705	710	715
Arg Ser Ser Gly Asn Arg Phe		
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<210> SEQ ID NO 9
 <211> LENGTH: 3264
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(3264)
 <223> OTHER INFORMATION:
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Rebouillat, D., et al.
 <302> TITLE: The 100-kDa 2',5'-oligoadenylate synthetase catalyzing preferentially the synthesis of dimeric pppA2'p5'A molecules
 <303> JOURNAL: J. Biol. Chem.
 <304> VOLUME: 274
 <305> ISSUE: 3
 <306> PAGES: 1557-1565
 <307> DATE: 1999
 <308> DATABASE ACCESSION NUMBER: NCBI/AF_063613
 <309> DATABASE ENTRY DATE: 1999-05-04
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Rebouillat, D. and Hovanessian, A.G.
 <302> TITLE: Direct Submission
 <303> JOURNAL: Submitted (07-May-1998) Dept.of Aids and Retroviruses, Institut Pasteur
 <304> VOLUME: 0
 <305> ISSUE: 0
 <306> PAGES: 0
 <307> DATE: 1998
 <308> DATABASE ACCESSION NUMBER: NCBI/AF_063613
 <309> DATABASE ENTRY DATE: 1999-05-04
 <400> SEQUENCE: 9

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Leu Gly Ala Leu Ala Ala Ala Leu Arg Glu Arg Gly Gly Arg Leu Gly	
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gct gct gcc ccg cgg gtg ctg aaa act gtc aag gga gcc tcc tcg ggc	192
Ala Ala Ala Pro Arg Val Leu Lys Thr Val Lys Gly Gly Ser Ser Gly	
50 55 60	
cgg gcc aca gct ctg aag ggt gcc tgt gat tct gaa ctt gtc atc ttc	240
Arg Gly Thr Ala Leu Lys Gly Gly Cys Asp Ser Glu Leu Val Ile Phe	
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ctc gac tgc ttc aag agc tat gtg gac cag agg gcc cgc cgt gca gag	288
Leu Asp Cys Phe Lys Ser Tyr Val Asp Gln Arg Ala Arg Arg Ala Glu	
85 90 95	
atc ctg agt gag atg cgg gca tgc ctg gaa tcc tgg tgg cag aac cca	336
Ile Leu Ser Glu Met Arg Ala Ser Leu Glu Ser Trp Trp Gln Asn Pro	
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gtc cct ggt ctg aga ctc acg ttt cct gag cag agc gtg cct ggg gcc	384
Val Pro Gly Leu Arg Leu Thr Phe Pro Glu Gln Ser Val Pro Gly Ala	
115 120 125	
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Leu Gln Phe Arg Leu Thr Ser Val Asp Leu Glu Asp Trp Met Asp Val	
130 135 140	
agc ctg gtg cct gcc ttc aat gtc ctg ggt cag gcc gcc tcc gcg gtc	480
Ser Leu Val Pro Ala Phe Asn Val Leu Gly Gln Ala Gly Ser Ala Val	
145 150 155 160	
aaa ccc aag cca caa gtc tac tct acc ctg ctg aac agt gcc tgc caa	528
Lys Pro Lys Pro Gln Val Tyr Ser Thr Leu Leu Asn Ser Gly Cys Gln	
165 170 175	
ggg gcc gag cat gcg gcc tgc ttc aca gag ctg cgg agg aac ttt gtg	576
Gly Gly Glu His Ala Ala Cys Phe Thr Glu Leu Arg Arg Asn Phe Val	
180 185 190	
aac att cgc cca gcc aag ttg aag aac cta atc ttg ctg gtg aag cac	624
Asn Ile Arg Pro Ala Lys Leu Lys Asn Leu Ile Leu Leu Val Lys His	
195 200 205	
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Trp Tyr His Gln Val Cys Leu Gln Gly Leu Trp Lys Glu Thr Leu Pro	
210 215 220	
ccg gtc tat gcc ctg gaa ttg ctg acc atc ttc gcc tgg gag cag gcc	720
Pro Val Tyr Ala Leu Glu Leu Leu Thr Ile Phe Ala Trp Glu Gln Gly	
225 230 235 240	
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Cys Lys Lys Asp Ala Phe Ser Leu Gly Glu Gly Leu Arg Thr Val Leu	
245 250 255	
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Gly Leu Ile Gln Gln His Gln His Leu Cys Val Phe Trp Thr Val Asn	
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tat ggc ttc gag gac cct gca gtt ggg cag ttc ttg cag cgg cac gtt	864
Tyr Gly Phe Glu Asp Pro Ala Val Gly Gln Phe Leu Gln Arg His Val	
275 280 285	
aag aga ccc agg cct gtg atc ctg gac cca gct gac ccc aca tgg gac	912
Lys Arg Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro Thr Trp Asp	
290 295 300	
ctg ggg aat ggg gca gcc tgg cac tgg gat ttg cat gcc cag gag gca	960
Leu Gly Asn Gly Ala Trp His Trp Asp Leu His Ala Gln Glu Ala	
305 310 315 320	
gca tcc tgc tat gac cac cca tgc ttt ctg agg ggg atg ggg gac cca	1008
Ala Ser Cys Tyr Asp His Pro Cys Phe Leu Arg Gly Met Gly Asp Pro	
325 330 335	

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gtg cag tct tgg aag ggg ccg ggc ctt cca cgt gct gga tgc tca ggt Val Gln Ser Trp Lys Gly Pro Gly Leu Pro Arg Ala Gly Cys Ser Gly 340 345 350	1056
ttg ggc cac ccc atc cag cta gac cct aac cag aag acc cct gaa aac Leu Gly His Pro Ile Gln Leu Asp Pro Asn Gln Lys Thr Pro Glu Asn 355 360 365	1104
agc aag agc ctc aat gct gtg tac cca aga gca ggg agc aaa cct ccc Ser Lys Ser Leu Asn Ala Val Tyr Pro Arg Ala Gly Ser Lys Pro Pro 370 375 380	1152
tca tgc cca gct cct ggc ccc act gcg gag cca gca tgc tac ccc tct Ser Cys Pro Ala Pro Gly Pro Thr Ala Glu Pro Ala Ser Tyr Pro Ser 385 390 395 400	1200
gtg ccg gga atg gcc ttg gac ctg tct cag atc ccc acc aag gag ctg Val Pro Gly Met Ala Leu Asp Leu Ser Gln Ile Pro Thr Lys Glu Leu 405 410 415	1248
gac cgc ttc atc cag gac cac ctg aag ccg agc ccc cag ttc cag gag Asp Arg Phe Ile Gln Asp His Leu Lys Pro Ser Pro Gln Phe Gln Glu 420 425 430	1296
cag gtg aaa aag gcc atc gac atc atc ttg cgc tgc ctc cat gag aac Gln Val Lys Lys Ala Ile Asp Ile Ile Leu Arg Cys Leu His Glu Asn 435 440 445	1344
tgt gtt cac aag gcc tca aga gtc agt aaa ggg ggc tca ttt ggc ccg Cys Val His Lys Ala Ser Arg Val Ser Lys Gly Gly Ser Phe Gly Arg 450 455 460	1392
ggc aca gac cta agg gat ggc tgt gat gtt gaa ctc atc atc ttc ctc Gly Thr Asp Leu Arg Asp Gly Cys Asp Val Glu Leu Ile Ile Phe Leu 465 470 475 480	1440
aac tgc ttc acg gac tac aag gac cag ggg ccc cgc cgc gca gag atc Asn Cys Phe Thr Asp Tyr Lys Asp Gln Gly Pro Arg Arg Ala Glu Ile 485 490 495	1488
ctt gat gag atg cga gcg cac gta gaa tcc tgg tgg cag gac cag gtg Leu Asp Glu Met Arg Ala His Val Glu Ser Trp Trp Gln Asp Gln Val 500 505 510	1536
ccc agc ctg agc ctt cag ttt cct gag cag aat gtg cct gag gct ctg Pro Ser Leu Ser Leu Gln Phe Pro Glu Gln Asn Val Pro Glu Ala Leu 515 520 525	1584
cag ttc cag ctg gtg tcc aca gcc ctg aag agc tgg acg gat gtt agc Gln Phe Gln Leu Val Ser Thr Ala Leu Lys Ser Trp Thr Asp Val Ser 530 535 540	1632
ctg ctg cct gcc ttc gat gct gtg ggg cag ctc agt tct ggc acc aaa Leu Leu Pro Ala Phe Asp Ala Val Gly Gln Leu Ser Ser Gly Thr Lys 545 550 555 560	1680
cca aat ccc cag gtc tac tcg agg ctc ctc acc agt ggc tgc cag gag Pro Asn Pro Gln Val Tyr Ser Arg Leu Leu Thr Ser Gly Cys Gln Glu 565 570 575	1728
ggc gag cat aag gcc tgc ttc gca gag ctg ccg agg aac ttc atg aac Gly Glu His Lys Ala Cys Phe Ala Glu Leu Arg Arg Asn Phe Met Asn 580 585 590	1776
att cgc cct gtc aag ctg aag aac ctg att ctg ctg gtg aag cac tgg Ile Arg Pro Val Lys Leu Lys Asn Leu Ile Leu Leu Val Lys His Trp 595 600 605	1824
tac cgc cag gtt gcg gct cag aac aaa gga aaa gga cca gcc cct gcc Tyr Arg Gln Val Ala Ala Gln Asn Lys Gly Lys Gly Pro Ala Pro Ala 610 615 620	1872
tct ctg ccc cca gcc tat gcc ctg gag ctc ctc acc atc ttt gcc tgg Ser Leu Pro Pro Ala Tyr Ala Leu Glu Leu Leu Thr Ile Phe Ala Trp 625 630 635 640	1920
gag cag ggc tgc agg cag gat tgt ttc aac atg gcc caa ggc ttc ccg Glu Gln Gly Cys Arg Gln Asp Cys Phe Asn Met Ala Gln Gly Phe Arg	1968

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acg	gtg	ctg	ggg	ctc	gtg	caa	cag	cat	cag	cag	ctc	tgt	gtc	tac	tgg	2016																																																															
Thr	Val	Leu	Gly	Leu	Val	Gln	Gln	His	Gln	Gln	Leu	Cys	Val	Tyr	Trp																																																																
																660																665																670																															
acg	gtc	aac	tat	agc	act	gag	gac	cca	gcc	atg	aga	atg	cac	ctt	ctt	2064																																																															
Thr	Val	Asn	Tyr	Ser	Thr	Glu	Asp	Pro	Ala	Met	Arg	Met	His	Leu	Leu																																																																
																675																680																685																															
ggc	cag	ctt	cga	aaa	ccc	aga	ccc	ctg	gtc	ctg	gac	ccc	gct	gat	ccc	2112																																																															
Gly	Gln	Leu	Arg	Lys	Pro	Arg	Pro	Leu	Val	Leu	Asp	Pro	Ala	Asp	Pro																																																																
																690																695																700																															
acc	tgg	aac	gtg	ggc	cac	ggg	agc	tgg	gag	ctg	tgg	gcc	cag	gaa	gca	2160																																																															
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																705																710																715																720															
gca	gcg	ctg	ggg	atg	cag	gcc	tgc	ttt	ctg	agt	aga	gac	ggg	aca	tct	2208																																																															
Ala	Ala	Leu	Gly	Met	Gln	Ala	Cys	Phe	Leu	Ser	Arg	Asp	Gly	Thr	Ser																																																																
																725																730																735																															
gtg	cag	ccc	tgg	gat	gtg	atg	cca	gcc	ctc	ctt	tac	caa	acc	cca	gct	2256																																																															
Val	Gln	Pro	Trp	Asp	Val	Met	Pro	Ala	Leu	Leu	Tyr	Gln	Thr	Pro	Ala																																																																
																740																745																750																															
ggg	gac	ctt	gac	aag	ttc	atc	agt	gaa	ttt	ctc	cag	ccc	aac	cgc	cag	2304																																																															
Gly	Asp	Leu	Asp	Lys	Phe	Ile	Ser	Glu	Phe	Leu	Gln	Pro	Asn	Arg	Gln																																																																
																755																760																765																															
ttc	ctg	gcc	cag	gtg	aac	aag	gcc	gtt	gat	acc	atc	tgt	tca	ttt	ttg	2352																																																															
Phe	Leu	Ala	Gln	Val	Asn	Lys	Ala	Val	Asp	Thr	Ile	Cys	Ser	Phe	Leu																																																																
																770																775																780																															
aag	gaa	aac	tgc	ttc	cgg	aat	tct	ccc	atc	aaa	gtg	atc	aag	gtg	gtc	2400																																																															
Lys	Glu	Asn	Cys	Phe	Arg	Asn	Ser	Pro	Ile	Lys	Val	Ile	Lys	Val	Val																																																																
																785																790																795																800															
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Lys	Gly	Gly	Ser	Ser	Ala	Lys	Gly	Thr	Ala	Leu	Arg	Gly	Arg	Ser	Asp																																																																
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gcc	gac	ctc	gtg	gtg	ttc	ctc	agc	tgc	ttc	agc	cag	ttc	act	gag	cag	2496																																																															
Ala	Asp	Leu	Val	Val	Phe	Leu	Ser	Cys	Phe	Ser	Gln	Phe	Thr	Glu	Gln																																																																
																820																825																830																															
ggc	aac	aag	cgg	gcc	gag	atc	atc	tcc	gag	atc	cga	gcc	cag	ctg	gag	2544																																																															
Gly	Asn	Lys	Arg	Ala	Glu	Ile	Ile	Ser	Glu	Ile	Arg	Ala	Gln	Leu	Glu																																																																
																835																840																845																															
gca	tgt	caa	cag	gag	cgg	cag	ttc	gag	gtc	aag	ttt	gaa	gtc	tcc	aaa	2592																																																															
Ala	Cys	Gln	Gln	Glu	Arg	Gln	Phe	Glu	Val	Lys	Phe	Glu	Val	Ser	Lys																																																																
																850																855																860																															
tgg	gag	aat	ccc	cgc	gtg	ctg	agc	ttc	tca	ctg	aca	tcc	cag	acg	atg	2640																																																															
Trp	Glu	Asn	Pro	Arg	Val	Leu	Ser	Phe	Ser	Leu	Thr	Ser	Gln	Thr	Met																																																																
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Lys Gly Arg Gly Ser Leu Pro Pro Gln His Gly Leu Glu Leu Leu Thr	
965 970 975	
gtg tat gcc tgg gag cag ggc ggg aag gac tcc cag ttc aac atg gct	2976
Val Tyr Ala Trp Glu Gln Gly Gly Lys Asp Ser Gln Phe Asn Met Ala	
980 985 990	
gag ggc ttc cgc acg gtc ctg gag ctg gtc acc cag tac cgc cag ctg	3024
Glu Gly Phe Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Arg Gln Leu	
995 1000 1005	
tgt atc tac tgg acc atc aac tac aac gcc aag gac aag act gtt	3069
Cys Ile Tyr Trp Thr Ile Asn Tyr Asn Ala Lys Asp Lys Thr Val	
1010 1015 1020	
gga gac ttc ctg aaa cag cag ctt cag aag ccc agg cct atc atc	3114
Gly Asp Phe Leu Lys Gln Gln Leu Gln Lys Pro Arg Pro Ile Ile	
1025 1030 1035	
ctg gat ccg gct gac ccg aca ggc aac ctg ggc cac aat gcc cgc	3159
Leu Asp Pro Ala Asp Pro Thr Gly Asn Leu Gly His Asn Ala Arg	
1040 1045 1050	
tgg gac ctg ctg gcc aag gaa gct gca gcc tgc aca tct gcc ctg	3204
Trp Asp Leu Leu Ala Lys Glu Ala Ala Ala Cys Thr Ser Ala Leu	
1055 1060 1065	
tgc tgc atg gga cgg aat ggc atc ccc atc cag cca tgg cca gtg	3249
Cys Cys Met Gly Arg Asn Gly Ile Pro Ile Gln Pro Trp Pro Val	
1070 1075 1080	
aag gct gct gtg tga	3264
Lys Ala Ala Val	
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<210> SEQ ID NO 10

<211> LENGTH: 1087

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

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

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

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610	615	620
Ser Leu Pro Pro Ala Tyr Ala Leu Glu Leu Leu Thr Ile Phe Ala Trp		
625	630	635 640
Glu Gln Gly Cys Arg Gln Asp Cys Phe Asn Met Ala Gln Gly Phe Arg		
645	650	655
Thr Val Leu Gly Leu Val Gln Gln His Gln Gln Leu Cys Val Tyr Trp		
660	665	670
Thr Val Asn Tyr Ser Thr Glu Asp Pro Ala Met Arg Met His Leu Leu		
675	680	685
Gly Gln Leu Arg Lys Pro Arg Pro Leu Val Leu Asp Pro Ala Asp Pro		
690	695	700
Thr Trp Asn Val Gly His Gly Ser Trp Glu Leu Leu Ala Gln Glu Ala		
705	710	715 720
Ala Ala Leu Gly Met Gln Ala Cys Phe Leu Ser Arg Asp Gly Thr Ser		
725	730	735
Val Gln Pro Trp Asp Val Met Pro Ala Leu Leu Tyr Gln Thr Pro Ala		
740	745	750
Gly Asp Leu Asp Lys Phe Ile Ser Glu Phe Leu Gln Pro Asn Arg Gln		
755	760	765
Phe Leu Ala Gln Val Asn Lys Ala Val Asp Thr Ile Cys Ser Phe Leu		
770	775	780
Lys Glu Asn Cys Phe Arg Asn Ser Pro Ile Lys Val Ile Lys Val Val		
785	790	795 800
Lys Gly Gly Ser Ser Ala Lys Gly Thr Ala Leu Arg Gly Arg Ser Asp		
805	810	815
Ala Asp Leu Val Val Phe Leu Ser Cys Phe Ser Gln Phe Thr Glu Gln		
820	825	830
Gly Asn Lys Arg Ala Glu Ile Ile Ser Glu Ile Arg Ala Gln Leu Glu		
835	840	845
Ala Cys Gln Gln Glu Arg Gln Phe Glu Val Lys Phe Glu Val Ser Lys		
850	855	860
Trp Glu Asn Pro Arg Val Leu Ser Phe Ser Leu Thr Ser Gln Thr Met		
865	870	875 880
Leu Asp Gln Ser Val Asp Phe Asp Val Leu Pro Ala Phe Asp Ala Leu		
885	890	895
Gly Gln Leu Val Ser Gly Ser Arg Pro Ser Ser Gln Val Tyr Val Asp		
900	905	910
Leu Ile His Ser Tyr Ser Asn Ala Gly Glu Tyr Ser Thr Cys Phe Thr		
915	920	925
Glu Leu Gln Arg Asp Phe Ile Ile Ser Arg Pro Thr Lys Leu Lys Ser		
930	935	940
Leu Ile Arg Leu Val Lys His Trp Tyr Gln Gln Cys Thr Lys Ile Ser		
945	950	955 960
Lys Gly Arg Gly Ser Leu Pro Pro Gln His Gly Leu Glu Leu Leu Thr		
965	970	975
Val Tyr Ala Trp Glu Gln Gly Gly Lys Asp Ser Gln Phe Asn Met Ala		
980	985	990
Glu Gly Phe Arg Thr Val Leu Glu Leu Val Thr Gln Tyr Arg Gln Leu		
995	1000	1005
Cys Ile Tyr Trp Thr Ile Asn Tyr Asn Ala Lys Asp Lys Thr Val		
1010	1015	1020
Gly Asp Phe Leu Lys Gln Gln Leu Gln Lys Pro Arg Pro Ile Ile		
1025	1030	1035

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Leu Asp Pro Ala Asp Pro Thr Gly Asn Leu Gly His Asn Ala Arg
 1040 1045 1050

Trp Asp Leu Leu Ala Lys Glu Ala Ala Ala Cys Thr Ser Ala Leu
 1055 1060 1065

Cys Cys Met Gly Arg Asn Gly Ile Pro Ile Gln Pro Trp Pro Val
 1070 1075 1080

Lys Ala Ala Val
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<210> SEQ ID NO 11
 <211> LENGTH: 1104
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1104)
 <223> OTHER INFORMATION:
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Coccia, E.M., et al.
 <302> TITLE: A full-length murine 2-5A synthetase cDNA transfected in
 NIH-3T3 cells
 <303> JOURNAL: Virology
 <304> VOLUME: 179
 <305> ISSUE: 1
 <306> PAGES: 228-233
 <307> DATE: 1990
 <308> DATABASE ACCESSION NUMBER: NCBI/M33863
 <309> DATABASE ENTRY DATE: 1993-06-11

<400> SEQUENCE: 11

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ata gag gat tac ctc ctt ccc gac acc acc ttt ggt gct gat gtc aaa	96
Ile Glu Asp Tyr Leu Leu Pro Asp Thr Thr Phe Gly Ala Asp Val Lys	
20 25 30	
tca gcc gtc aat gtc gtg tgt gat ttc ctg aag gag aga tgc ttc caa	144
Ser Ala Val Asn Val Val Cys Asp Phe Leu Lys Glu Arg Cys Phe Gln	
35 40 45	
ggt gct gcc cac cca gtg agg gtc tcc aag gtg gtg aag ggt ggc tcc	192
Gly Ala Ala His Pro Val Arg Val Ser Lys Val Val Lys Gly Gly Ser	
50 55 60	
tca ggc aaa ggc acc aca ctc aag ggc agg tca gac gct gac ctg gtg	240
Ser Gly Lys Gly Thr Thr Leu Lys Gly Arg Ser Asp Ala Asp Leu Val	
65 70 75 80	
gtg ttc ctt aac aat ctc acc agc ttt gag gat cag tta aac cga cgg	288
Val Phe Leu Asn Asn Leu Thr Ser Phe Glu Asp Gln Leu Asn Arg Arg	
85 90 95	
gga gag ttc atc aag gaa att aag aaa cag ctg tac gag gtt cag cat	336
Gly Glu Phe Ile Lys Glu Ile Lys Lys Gln Leu Tyr Glu Val Gln His	
100 105 110	
gag aga cgt ttt aga gtc aag ttt gag gtc cag agt tca tgg tgg ccc	384
Glu Arg Arg Phe Arg Val Lys Phe Glu Val Gln Ser Ser Trp Trp Pro	
115 120 125	
aac gcc cgg tct ctg agc ttc aag ctg agc gcc ccc cat ctg cat cag	432
Asn Ala Arg Ser Leu Ser Phe Lys Leu Ser Ala Pro His Leu His Gln	
130 135 140	
gag gtg gag ttt gat gtg ctg cca gcc ttt gat gtc ctg ggt cat gtt	480
Glu Val Glu Phe Asp Val Leu Pro Ala Phe Asp Val Leu Gly His Val	
145 150 155 160	
aat act tcc agc aag cct gat ccc aga atc tat gcc atc ctc atc gag	528
Asn Thr Ser Ser Lys Pro Asp Pro Arg Ile Tyr Ala Ile Leu Ile Glu	
165 170 175	

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ctc atc cgc ctg gtc aag cac tgg tac caa ctg tgt aag gag aag ctg Leu Ile Arg Leu Val Lys His Trp Tyr Gln Leu Cys Lys Glu Lys Leu 210 215 220	672
ggg aag cca ttg cct cca cag tac gcc cta gag ttg ctc act gtc ttt Gly Lys Pro Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Phe 225 230 235 240	720
gcc tgg gaa caa ggg aat gga tgt tat gag ttc aac aca gcc cag ggc Ala Trp Glu Gln Gly Asn Gly Cys Tyr Glu Phe Asn Thr Ala Gln Gly 245 250 255	768
ttc cgg acc gtc ttg gaa ctg gtc atc aat tat cag cat ctt cga atc Phe Arg Thr Val Leu Glu Leu Val Ile Asn Tyr Gln His Leu Arg Ile 260 265 270	816
tac tgg aca aag tat tat gac ttt caa cac cag gag gtc tcc aaa tac Tyr Trp Thr Lys Tyr Tyr Asp Phe Gln His Gln Glu Val Ser Lys Tyr 275 280 285	864
ctg cac aga cag ctc aga aaa gcc agg cct gtg atc ctg gac cca gct Leu His Arg Gln Leu Arg Lys Ala Arg Pro Val Ile Leu Asp Pro Ala 290 295 300	912
gac cca aca ggg aat gtg gcc ggt ggg aac cca gag ggc tgg agg cgg Asp Pro Thr Gly Asn Val Ala Gly Gly Asn Pro Glu Gly Trp Arg Arg 305 310 315 320	960
ttg gct gaa gag gct gat gtg tgg cta tgg tac cca tgt ttt att aaa Leu Ala Glu Glu Ala Asp Val Trp Leu Trp Tyr Pro Cys Phe Ile Lys 325 330 335	1008
aag gat ggt tcc cga gtg agc tcc tgg gat gtg ccg acg gtg gtt cct Lys Asp Gly Ser Arg Val Ser Ser Trp Asp Val Pro Thr Val Val Pro 340 345 350	1056
gta cct ttt gag cag gta gaa gag aac tgg aca tgt atc ctg ctg tga Val Pro Phe Glu Gln Val Glu Glu Asn Trp Thr Cys Ile Leu Leu 355 360 365	1104

<210> SEQ ID NO 12

<211> LENGTH: 367

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 12

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Ile Glu Asp Tyr Leu Leu Pro Asp Thr Thr Phe Gly Ala Asp Val Lys 20 25 30
Ser Ala Val Asn Val Val Cys Asp Phe Leu Lys Glu Arg Cys Phe Gln 35 40 45
Gly Ala Ala His Pro Val Arg Val Ser Lys Val Val Lys Gly Gly Ser 50 55 60
Ser Gly Lys Gly Thr Thr Leu Lys Gly Arg Ser Asp Ala Asp Leu Val 65 70 75 80
Val Phe Leu Asn Asn Leu Thr Ser Phe Glu Asp Gln Leu Asn Arg Arg 85 90 95
Gly Glu Phe Ile Lys Glu Ile Lys Lys Gln Leu Tyr Glu Val Gln His 100 105 110
Glu Arg Arg Phe Arg Val Lys Phe Glu Val Gln Ser Ser Trp Trp Pro

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 <301> AUTHORS: Aissouni, Y. et al.
 <302> TITLE: The cleavage/polyadenylation activity triggered by a U-rich motif sequence
 <303> JOURNAL: J. Biol. Chem.
 <304> VOLUME: 277
 <305> ISSUE: 39
 <306> PAGES: 35808-35814
 <307> DATE: 2002
 <308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
 <309> DATABASE ENTRY DATE: 2003-04-06
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Behera, A.K., et al.
 <302> TITLE: 2'-5' Oligoadenylate synthetase plays a critical role in interferon-gamma inhibition
 <303> JOURNAL: J. Biol. Chem.
 <304> VOLUME: 277
 <305> ISSUE: 28
 <306> PAGES: 25601-25608
 <307> DATE: 2002
 <308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
 <309> DATABASE ENTRY DATE: 2003-04-06
 <300> PUBLICATION INFORMATION:
 <301> AUTHORS: Sarkar, S.N., et al.
 <302> TITLE: Identification of the substrate-binding sites of 2'-5'-oligoadenylate synthetase
 <303> JOURNAL: J. Biol. Chem.

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<304> VOLUME: 277
<305> ISSUE: 27
<306> PAGES: 24321-24330
<307> DATE: 2002
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<300> PUBLICATION INFORMATION:
<301> AUTHORS: Hovnanian, A., et al.
<302> TITLE: The human 2',5'-oligoadenylate synthetase locus is composed of three distinct genes
<303> JOURNAL: Genomics
<304> VOLUME: 52
<305> ISSUE: 3
<306> PAGES: 267-277
<307> DATE: 1998
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<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Renault, B.
<302> TITLE: A sequence-ready physical map of a region of 12q24.1
<303> JOURNAL: Genomics
<304> VOLUME: 45
<305> ISSUE: 2
<306> PAGES: 271-278
<307> DATE: 1997
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Nechiporuk, T., et al.
<302> TITLE: A high-resolution PAC and BAC map of the SCA2 region
<303> JOURNAL: Genomics
<304> VOLUME: 44
<305> ISSUE: 3
<306> PAGES: 321-329
<307> DATE: 1997
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<301> AUTHORS: Wathélet, M.G., et al.
<302> TITLE: Cloning and chromosomal location of human genes inducible by type I interferon
<303> JOURNAL: Somat. Cell Mol. Genet.
<304> VOLUME: 14
<305> ISSUE: 5
<306> PAGES: 415-426
<307> DATE: 1988
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Rutherford, M.N., et al.
<302> TITLE: Interferon-induced binding of nuclear factors to promoter elements of the 2-5A synthetase gene
<303> JOURNAL: EMBO J.
<304> VOLUME: 7
<305> ISSUE: 3
<306> PAGES: 751-759
<307> DATE: 1988
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
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<300> PUBLICATION INFORMATION:
<301> AUTHORS: Wathélet, M.G., et al.
<302> TITLE: New inducers revealed by the promoter sequence analysis of two interferon-activated human genes
<303> JOURNAL: Eur. J. Biochem.
<304> VOLUME: 169
<305> ISSUE: 2
<306> PAGES: 313-321
<307> DATE: 1987
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Benech, P., et al.
<302> TITLE: Interferon-responsive regulatory elements in the promoter of the human 2',5'-oligo(A) synthetase gene
<303> JOURNAL: Mol. Cell. Biol.
<304> VOLUME: 7
<305> ISSUE: 12
<306> PAGES: 4498-4504
<307> DATE: 1987

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<301> AUTHORS: Hovanessian, A.G., et al.
<302> TITLE: Identification of 69-kd and 100-kd forms of 2-5A synthetase
<303> JOURNAL: EMBO J.
<304> VOLUME: 6
<305> ISSUE: 5
<306> PAGES: 1273-1280
<307> DATE: 1987
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<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Williams, B.R., et al.
<302> TITLE: Interferon-regulated human 2-5A synthetase gene maps to chromosome
<303> JOURNAL: Somat. Cell Mol. Genet.
<304> VOLUME: 12
<305> ISSUE: 4
<306> PAGES: 403-408
<307> DATE: 1986
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Shiojiri, S., et al.
<302> TITLE: Structure and expression of a cloned cDNA
<303> JOURNAL: J. Biochem.
<304> VOLUME: 99
<305> ISSUE: 5
<306> PAGES: 1455-1464
<307> DATE: 1986
<308> DATABASE ACCESSION NUMBER: NCBI/NM_016816
<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Wathelet, M., et al.
<302> TITLE: Full-length sequence and expression of the 42 kDa 2-5A synthetase
<303> JOURNAL: FEBS Lett.
<304> VOLUME: 196
<305> ISSUE: 1
<306> PAGES: 113-120
<307> DATE: 1986
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<300> PUBLICATION INFORMATION:
<301> AUTHORS: Benech, P., et al.
<302> TITLE: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase
<303> JOURNAL: EMBO J.
<304> VOLUME: 4
<305> ISSUE: 9
<306> PAGES: 2249-2256
<307> DATE: 1985
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<300> PUBLICATION INFORMATION:
<301> AUTHORS: Saunders, M.E., et al.
<302> TITLE: Human 2-5A synthetase: characterization of a novel cDNA and corresponding gene structure
<303> JOURNAL: EMBO J.
<304> VOLUME: 4
<305> ISSUE: 7
<306> PAGES: 1761-1768
<307> DATE: 1985
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<309> DATABASE ENTRY DATE: 2003-04-06
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Merlin, G., et al.
<302> TITLE: Molecular cloning and sequence of partial cDNA for interferon-induced (2'-5') oligo(A) synthetase mRNA from human cells
<303> JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
<304> VOLUME: 80
<305> ISSUE: 16
<306> PAGES: 4904-4908
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<300> PUBLICATION INFORMATION:

<301> AUTHORS: Hovnanian, A., et al.

<302> TITLE: The human 2',5'-oligoadenylate synthetase locus is composed of three distinct genes

<303> JOURNAL: Genomics

<304> VOLUME: 52

<305> ISSUE: 3

<306> PAGES: 267-277

<307> DATE: 1998

<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535

<309> DATABASE ENTRY DATE: 2003-04-03

<300> PUBLICATION INFORMATION:

<301> AUTHORS: Marie, I. and Hovanessian, A.G.

<302> TITLE: The 69-kDa 2-5A synthetase is composed of two homologous and adjacent functional domains

<303> JOURNAL: J. Biol. Chem.

<304> VOLUME: 267

<305> ISSUE: 14

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<306> PAGES: 9933-9939
<307> DATE: 1992
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<309> DATABASE ENTRY DATE: 2003-04-03
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<301> AUTHORS: Marie, I., et al.
<302> TITLE: Differential expression and distinct structure of 69- and 100-kDa forms of 2-5A synthetase
<303> JOURNAL: J. Biol. Chem.
<304> VOLUME: 265
<305> ISSUE: 30
<306> PAGES: 18601-18607
<307> DATE: 1990
<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
<309> DATABASE ENTRY DATE: 2003-04-03
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Marie, I., et al.
<302> TITLE: Preparation and characterization of polyclonal antibodies
<303> JOURNAL: Biochem. Biophys. Res. Commun.
<304> VOLUME: 160
<305> ISSUE: 2
<306> PAGES: 580-587
<307> DATE: 1989
<308> DATABASE ACCESSION NUMBER: NCBI/NM_002535
<309> DATABASE ENTRY DATE: 2003-04-03
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<301> AUTHORS: Hovanessian, A.G., et al.
<302> TITLE: Characterization of 69- and 100-kDa forms of 2-5A-synthetase
<303> JOURNAL: J. Biol. Chem.
<304> VOLUME: 263
<305> ISSUE: 10
<306> PAGES: 4959
<307> DATE: 1988
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<309> DATABASE ENTRY DATE: 2003-04-03
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<301> AUTHORS: Hovanessian, A.G., et al.
<302> TITLE: Identification of 69-kd and 100-kd forms of 2-5A synthetase
<303> JOURNAL: EMBO J.
<304> VOLUME: 6
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<306> PAGES: 1273-1280
<307> DATE: 1987
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<302> TITLE: The 100-kDa 2',5'-oligoadenylate synthetase catalyzing
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<303> JOURNAL: J. Biol. Chem.
<304> VOLUME: 274
<305> ISSUE: 3
<306> PAGES: 1557-1565
<307> DATE: 1999
<308> DATABASE ACCESSION NUMBER: NCBI/AF063613
<309> DATABASE ENTRY DATE: 1999-05-04
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Rebouillat, D., and Hovanessian, A.G.
<302> TITLE: Direct Submission
<303> JOURNAL: Submitted (07-May-1998) Dept. of AIDS and Retroviruses,
        Institut Pasteur
<304> VOLUME: 0
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 <303> JOURNAL: Virology
 <304> VOLUME: 179
 <305> ISSUE: 1
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What is claimed is:

1. A method of increasing expression of 2'-5' oligoadenylate synthetase in a mammal, said method comprising administering to the mammal a nucleotide sequence encoding a 2'-5' oligoadenylate synthetase, or at least one enzymatically active fragment thereof, wherein the nucleotide sequence is expressed in the mammal.

2. The method of claim 1, wherein the enzymatically active fragment comprises an enzymatically active subunit of 2'-5' oligoadenylate synthetase selected from the group consisting of p40, p69, and p100.

3. The method according to claim 1, wherein the nucleotide sequence is administered to the mammal within a viral vector.

4. The method of claim 1, wherein the nucleotide sequence is administered to the mammal intranasally.

5. The method of claim 1, wherein the expression of 2'-5' oligoadenylate synthetase is increased to treat infection of the mammal by an RNA virus, and wherein the RNA virus is a type that transiently produces double-stranded RNA during intermediate replication.

6. The method of claim 5, wherein the mammal is a human.

7. The method of claim 6, wherein the human is a child.

8. The method of claim 6, wherein the human is elderly.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 8,802,647 B2
APPLICATION NO. : 13/621470
DATED : August 12, 2014
INVENTOR(S) : Shyam S. Mohapatra and Aruna K. Behera

Page 1 of 2

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Specification

Column 3, Line 47 through Column 4, Line 10:

“**Figure 10** shows results of treatment with adenoviral vector (Ad)- 2-5AS (p40) results in attenuation of RSV replication. BALB/c mice were intranasally administered with Ad-p40 and then infected with RSV. Lungs were harvested five days post RSV infection and RSV replication was assayed by RT-PCR analysis of RSV- N gene. GAPDH was used as internal control.

Figure 11 shows that Ad-p40 attenuates RSV lung titers. Mice were intranasally given Ad-p40 and then infected with RSV. Lungs were harvested five days post RSV infection and lung homogenate was used for RSV plaque assay. Ad-LacZ was used as control.

Figure 12 shows that Ad-p40 inhibits RSV induced airway reactivity. BALB/c mice were intranasally administered with Ad-p40 and subsequently infected with RSV. AHR was measured on day 4 post-RSV infection. Ad-p40 treatment significantly decreased pulmonary inflammation.

Figures 13A-13H show that Ad-p40 overexpression normalizes macrophage and lymphocyte numbers in the lung in RSV infected mice. BAL cell differential was performed and percentages of macrophage, lymphocytes and neutrophils was determined. Both Ad-IFN γ and Ad-p40 treatment reduced the lymphocyte population to normal, compared to RSV-infected mice. Histological sections from lungs were stained with hematoxylin and eosin and representative photomicrographs are shown. Sections shown are as follows: Naive mice (Figure 13A; with magnified inset Figure 13B); RSV infected mice (Figure 13C; with magnified inset, Figure 13D); Ad-p40 treated mice (Figure 13E; with magnified inset, Figure 13F); and Ad-lacZ treated mice (Figure 13G; with magnified inset, Figure 13H).”

SHOULD READ

--**Figure 10** shows that Ad-p40 attenuates RSV lung titers. Mice were intranasally given Ad-p40 and then infected with RSV. Lungs were harvested five days post RSV infection and lung homogenate was used for RSV plaque assay. Ad-LacZ was used as control. RSV replication was also assayed by RT-PCR analysis of RSV- N gene. GAPDH was used as internal control (data not shown).

Signed and Sealed this
Fifth Day of May, 2015



Michelle K. Lee
Director of the United States Patent and Trademark Office

Figure 11 shows that Ad-p40 inhibits RSV induced airway reactivity. BALB/c mice were intranasally administered with Ad-p40 and subsequently infected with RSV. AHR was measured on day 4 post-RSV infection. Ad-p40 treatment significantly decreased pulmonary inflammation.

Figure 12 shows that Ad-p40 overexpression normalizes macrophage and lymphocyte numbers in the lung in RSV infected mice. BAL cell differential was performed and percentages of macrophage, lymphocytes and neutrophils was determined. Both Ad-IFN γ and Ad-p40 treatment reduced the lymphocyte population to normal, compared to RSV-infected mice.

Figures 13A-13H show histological sections from lungs were stained with hematoxylin and eosin and representative photomicrographs are shown. Sections shown are as follows: Naive mice (Figure 13A; with magnified inset Figure 13B); RSV infected mice (Figure 13C; with magnified inset, Figure 13D); Ad-p40 treated mice (Figure 13E; with magnified inset, Figure 13F); and Ad-lacZ treated mice (Figure 13G; with magnified inset, Figure 13H).--

Column 18,

Line 51, "Pennsylvavania" should read --Pennsylvania--

Column 20,

Line 65, "pH7.4" should read --pH 7.4--

Column 21,

Line 40, "50 M" should read --50 μ M--

Column 23,

Line 16, "25 AS" should read --2-5 AS--

Column 27,

Line 20, "log 10 PFU/ml" should read --log₁₀ PFU/ml--

Line 22, "log 10 PFU/ml" should read --log₁₀ PFU/ml--

Column 30,

Line 3, "(FIG. 10)" should read --(FIG. 11)--

Line 39, "(FIGS. 12A-12H)" should read --(FIGS. 13A-13H)--

Column 31,

Line 38, "*J. Pedaiar.*" should read --*J. Pediatr.*--