US007897744B2

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

(10) **Patent No.: US 7,897,744 B2**
(45) **Date of Patent: Mar. 1, 2011**

(54) **SARS VIRUS NUCLEOTIDE AND AMINO ACID SEQUENCES AND USES THEREOF**

(75) Inventors: **Frank Plummer**, Winnipeg (CA); **Heinz Feldmann**, Winnipeg (CA); **Steven Jones**, Winnipeg (CA); **Yan Li**, Winnipeg (CA); **Nathalie Bastien**, Winnipeg (CA); **Robert Conrad Brunham**, Vancouver (CA); **Angela Brooks-Wilson**, Richmond (CA); **Robert Holt**, North Vancouver (CA); **Christopher Upton**, Victoria (CA); **Rachel Roper**, Winterville, NC (US); **Caroline Astell**, Vancouver (CA); **Steven Jones**, Burnaby (CA)

(73) Assignee: **The Public Health Agency of Canada** (CA)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 906 days.

(21) Appl. No.: **10/555,073**

(22) PCT Filed: **Apr. 28, 2004**

(86) PCT No.: **PCT/CA2004/000626**

§ 371 (c)(1),
(2), (4) Date: **Dec. 19, 2006**

(87) PCT Pub. No.: **WO2004/096842**

PCT Pub. Date: **Nov. 11, 2004**

(65) **Prior Publication Data**

US 2007/0258999 A1 Nov. 8, 2007

Related U.S. Application Data

(60) Provisional application No. 60/465,783, filed on Apr. 28, 2003, provisional application No. 60/466,733, filed on May 1, 2003.

(51) **Int. Cl.**
C12N 15/50 (2006.01)
C12N 7/00 (2006.01)

(52) **U.S. Cl.** **536/23.72**; 435/235.1; 435/320.1; 514/44

(58) **Field of Classification Search** .... None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

4,554,101	A	11/1985	Hopp	
4,683,202	A	7/1987	Mullis	
4,708,871	A	11/1987	Geysen	
6,004,744	A	12/1999	Goelet et al.	
6,188,783	B1	2/2001	Balaban	
6,484,183	B1	11/2002	Balaban	
7,220,852	B1 *	5/2007	Rota et al.	536/23.72
2002/0132788	A1	9/2002	Lewis et al.	
2002/0173478	A1	11/2002	Gewirtz	

OTHER PUBLICATIONS

Marra, Marco A. et al. The Genome Sequence of the SARS-Associated Coronavirus *Science*. (2003) 300: 1399-404.

Rota, Paul A. et al. Characteriazation of a Novel Coronavirus Associated with Severe Acute Respiratory Syndrome. *Science*. (2003) 300: 1394-9.

Anand, Kanchan et. al. Coronavirus Main Proteinase (3CLpro) Structure: Basis for Design of anti-SARS Drugs. *Science*. (Jun. 2003) 300: 1763-7.

Altschul. S. F. et al., *Nucleic Acids Res* 25: 3389-3402 (Sep. 1, 1997).

Apweiler, R. et al., *Nucleic Acids Res* 29: 37-40 (Jan. 1, 2001).

Barry, M. A. et al., "Protection against mycoplasma infection using expression-library immunization", *Nature* 377: 632-635 (1995).

Bateman, A. et al., *Nucleic Acids Res* 30: 276-280 (Jan. 1, 2002).

Borrebaeck, C. A. et al., "Protein chips based on recombinant antibody fragments: a highly sensitive approach as detected by mass spectrometry", *Biotechniques* 30: 1126-1132 (2001).

Bowtell, D. D. L., *Nature Genetics Supplement* 21: 25-32 (1999).

Chen, J. et al., "MMDB: Entrez's 3D-structure database", *Nucleic Acids Research* 31(1): 474-477 (2003).

Cheung. V. G. et al., *Nature Genetics Supplement* 21:15-19 (1999).

Chiang, A. et al., "The Structure Superposition Database", *Nucleic Acids Research* 31(1): 505-510 (2003).

Eckert et al., *PCR Methods and Applications* 1: 17 (1991).

Eisenberg et al., *J. Mol. Bio*. 179:125-142 (1984).

Emili, A. Q. and Cagney, G., "Large-scale functional analysis using peptide or protein arrays", *Nature Biotechnol* 18: 393-397 (2000).

Evan et al., *Mol. Cell Biol*. 5: 3610-3616 (1985).

Ewing, B. and Green, P., *Genome Res* 8:186-194 (Mar. 1998).

Fynan, E. F. et al., "DNA vaccines: protective immunizations by parental, mucosal, and genegun inoculations", *Proc Natl Acad Sci USA* 90: 11478-11482 (1993).

Gibson, U. E. et al., "A novel method for real time quantitative RT-PCR", *Genome Research* 6(10): 995-1001 (Oct. 1996).

Gordon, D. et al., *Genome Res* 8: 195-202 (Mar. 1998).

Guatelli et al., *Proc. Nat. Acad. Sci. USA* 87: 1874 (1990).

Heid et al., "Real Time Quantitative PCT", *Genome Research*, pp. 986-994 (1996).

Higuchi, R. et al., "Kinetic PCR Analysis: Real-time Monitoring of DNA Amplification Reactions", *Bio/Technology* 11: 1026-1030 (1993).

Hofman, K. and Stoffel, W., *Biol. Chem. Hoope-Seyler* 374: 166 (1993).

Holland et al., *Proc. Natl. Acad. Sci*. 88: 7276-7280 (1991).

Holloway, A. J. et al., *Nature Genetics Supplement* 32: 481-489 (2002).

(Continued)

Primary Examiner—Bo Peng
(74) *Attorney, Agent, or Firm*—Nixon Peabody LLP

(57) **ABSTRACT**

The invention provides, in part, the genomic sequence of a putative coronavirus, the SARS virus, and provides novel nucleic acid and amino acid sequences that may be used, for example, for the diagnosis, prophylaxis, or therapy of a variety of SARS virus related disorders.

14 Claims, 55 Drawing Sheets

OTHER PUBLICATIONS

Huang, R. P., "Detection of multiple proteins in an antibody-based protein microarray system", *J Immunol Methods* 255:1-13 (2001).
Hung, L. H. and Samudrala, R., "PROTINFO: secondary and tertiary protein structure prediction", *Nucleic Acids Research* 31(13): 3296-3299 (2003).
Jonassen, C.M. et al., *J. Gen Virol* 79 (Pt. 4): 715-718 (Apr. 1998).
Kohler, et al., *Eur. J. Immunol*. 6:292 (1976).
Kohler, et al., *Eur. J. Immunol*. 6:511 (1976).
Kohler, et al., *Nature* 256: 495 (1975).
Kukar, T. et al., "Protein microarrays to detect protein-protein interactions using red and green fluorescent proteins", *Anal Biochem* 306:50-54 (2002).
Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86: 1173 (1989).
Lai, M.M.C. and Cavanagh, D., *Adv Virus Res*. 48: 1-100 (1997).
Landegren et al., *Science* 241: 1077 (1988).
Levit-Binnun, N. et al., "Quantitative detection of protein arrays", *Anal Chem* 75:1436-1441 (2003).
Lipshutz, R. J. et al., *Nature Genetics Supplement* 21:20-24 (1999).
Lueking, A. et al., "Protein Microarrays for Gene Expression and Antibody Screening", *Anal. Biochem*. 270: 103-111 (1999).
MacBeath, G. and Schreiber, S. L., *Science* 289: 1760-1763 (2000).
Martzen, M. R. et al., *Science* 286:1153 (1999).
Mattila et al., *Nucleic Acids Res*. 19: 4967 (1991).
Munch, R., *Microbes Infect* 5 69-74 (Jan. 2003).
Nielsen, H. et al., *Prot Engineer* 10:1-6 (1997).
Parsons, J. D., *Comput Appl Biosci* 11: 615-619 (Dec. 1995).
Pearson, W. R. and Lipman, D. J., *Proc Natl Acad Sci USA* 85: 2444-2448 (Apr. 1988).
Sawicki, D.L. et al., *J. Gen Virol* 82, 386 (2001).
Sawicki, S.G. and Sawicki, D.L., *Adv. Exp. Med Biol*. 440: 215-9 (1998).
Sawicki, S.G. and Sawicki, D.L., *J. Virol*. 64: 1050 (1990).
Schaad, M. and Baric, R.S.J., *J. Virol*. 68: 8169 (1994).
Schweitzer, B. et al., *Nature Biotechnol*. 20: 359-365 (2002).
Sethna, P.B. et al., *Proc. Natl. Acad. Sci. U.S.A*. 86: 5626 (1989).
Singh-Gasson, S. et al., *Nature Biotechnol*. 17: 974-978 (1999).
Smith et al., *Gene* 67: 31-40 (1988).
Sonnhammer, E.L. et al., *Proc Int Conf Intell Syst Mol Biol* 6: 175-182 (1998).
Templin, M. F. et al., "Protein microarray technology", *Drug Discov Today* 7: 815-822 (2002).
Thompson, J.E. et al., *Nucleic Acids Res* 22: 4673-80 (Nov. 11, 1994).
Whalen, R. G. et al., "DNA-mediated immunization and the energetic immune response to hepatitis B surface antigen", *Clin Immunol Immunopathol* 75: 1-12 (1995).
Wolff, J. A. et al., "Direct gene transfer into mouse muscle in vivo", *Science* 247: 1465-1468 (1990).
Wu and Wallace, *Genomics* 4: 560 (1989).
Yamaguchi, A. et al., "Enlarged FAMSBASE: protein 3D structure models of genome sequences for 41 species", *Nucleic Acids Research* 31(1): 463-468 (2003).
Zdobnov, E. M. and Apweiler, R., *Bioinformatics* 17: 847-848 (Sep. 2001).
Zhu, H. et al., "Analysis of yeast protein kinases using protein chips", *Nature Genet* 26: 283-289 (2000).
Ziebuhr, J. et al., *J. Gen Virol* 81: 853-79 (Apr. 2000).

* cited by examiner

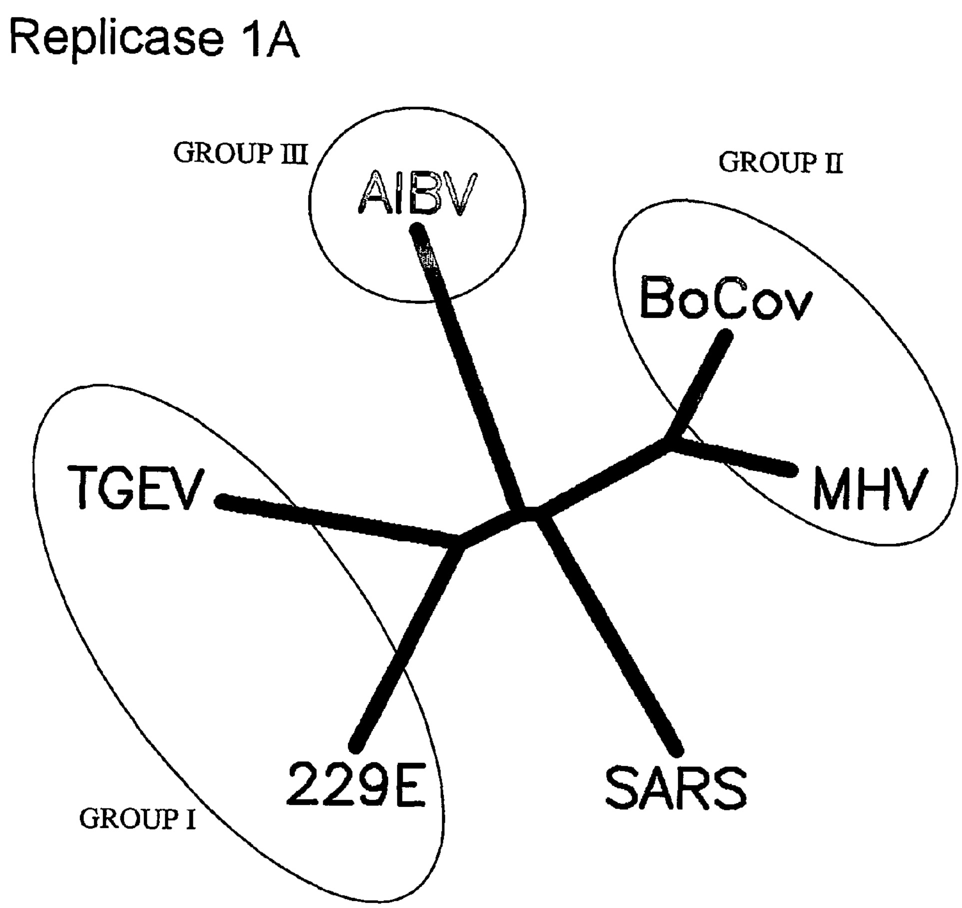

Replicase 1A
GROUP III
AIBV
GROUP II
BoCov
MHV
TGEV
229E
SARS
GROUP I

Figure 1A

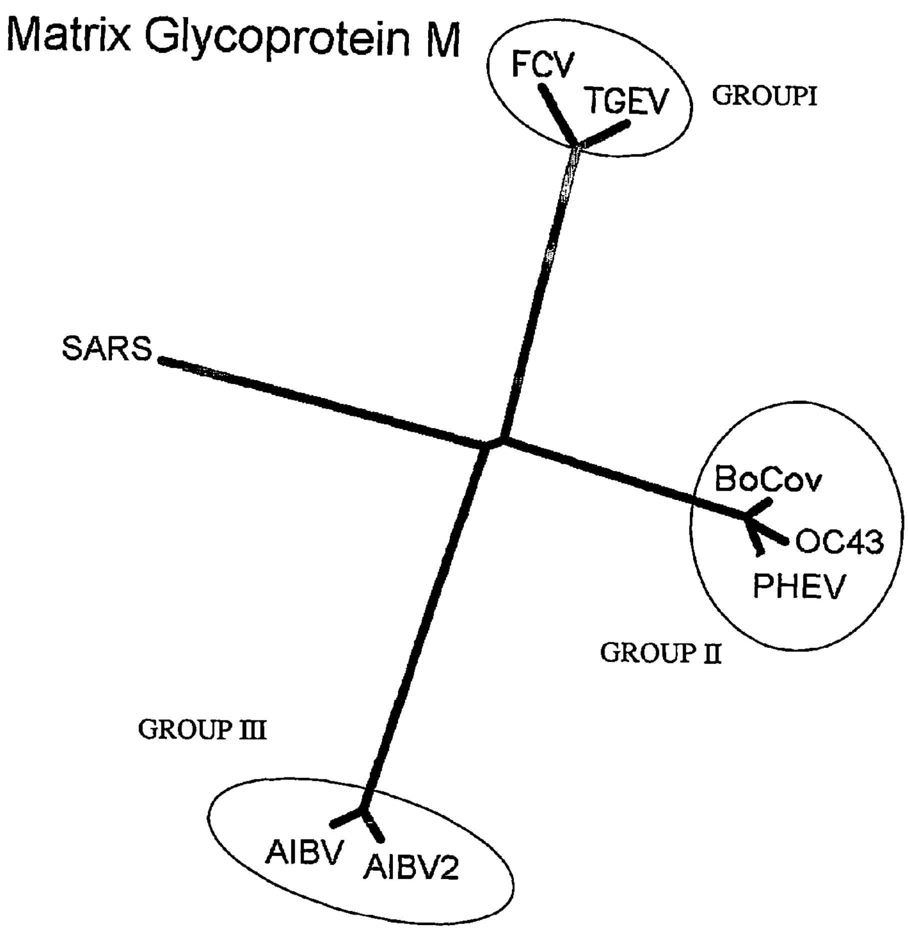

Matrix Glycoprotein M
FCV
TGEV
GROUPI
SARS
BoCov
OC43
PHEV
GROUP II
GROUP III
AIBV
AIBV2

Figure 1B

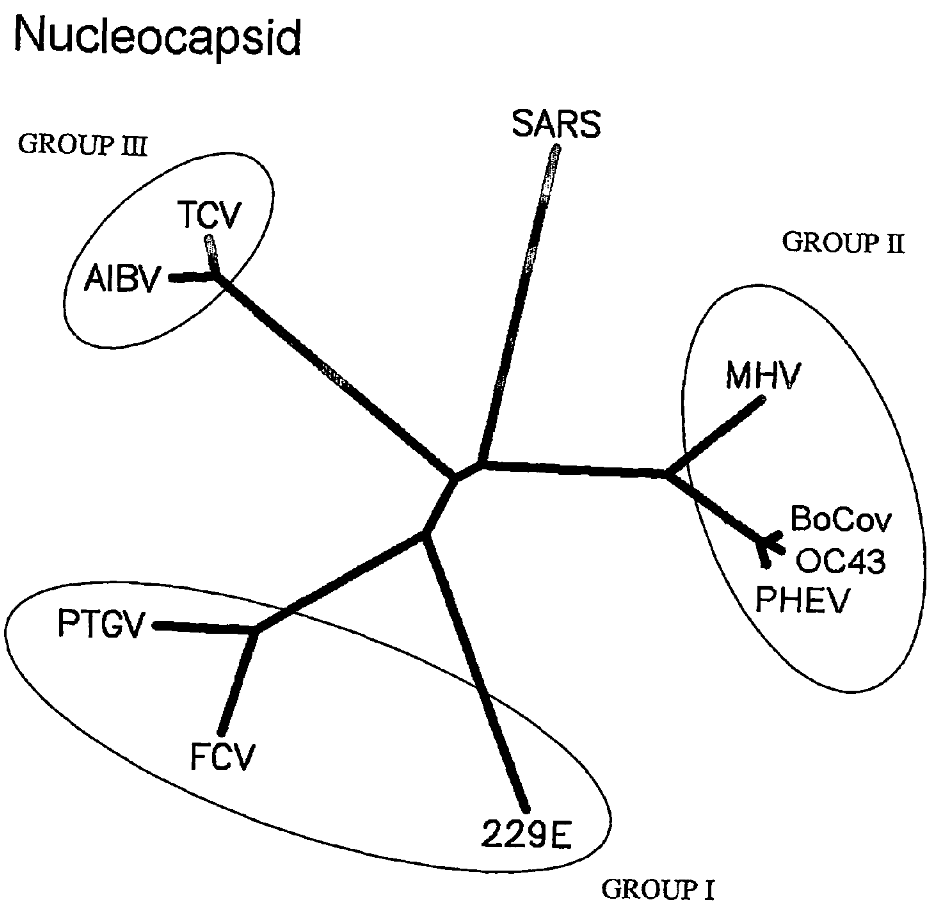

Nucleocapsid
SARS
GROUP III
TCV
AIBV
GROUP II
MHV
BoCov
OC43
PHEV
PTGV
FCV
229E
GROUP I

Figure 1C

S (Spike) Glycoprotein

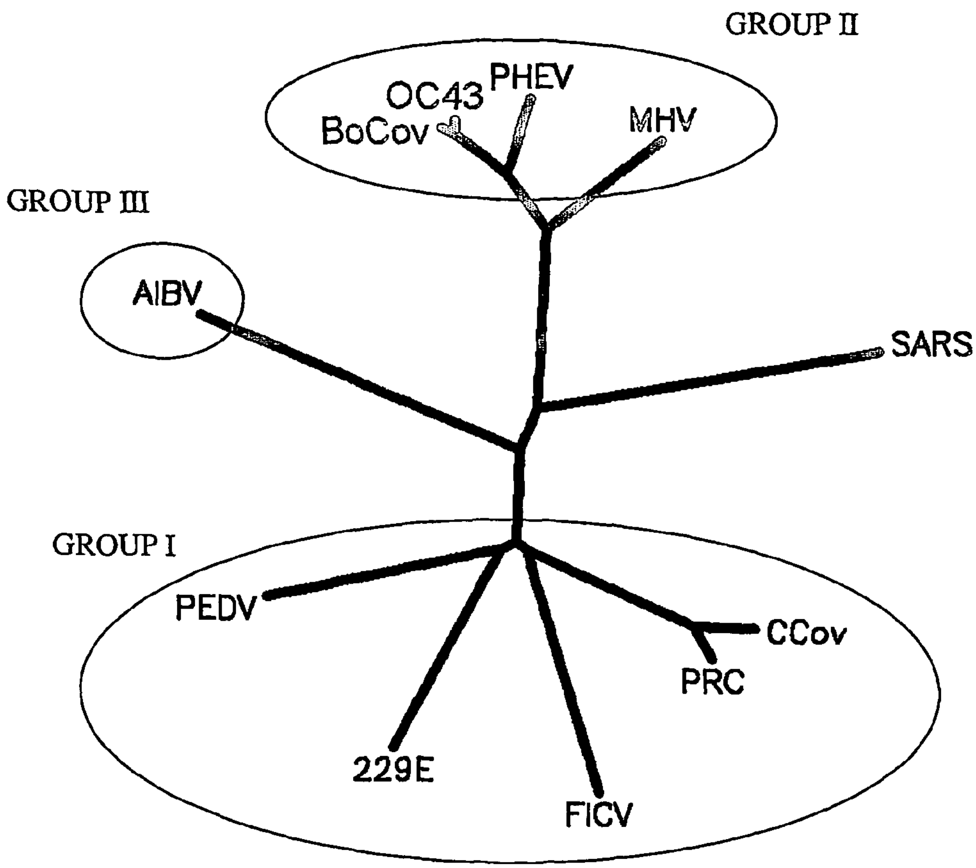


Figure 1D

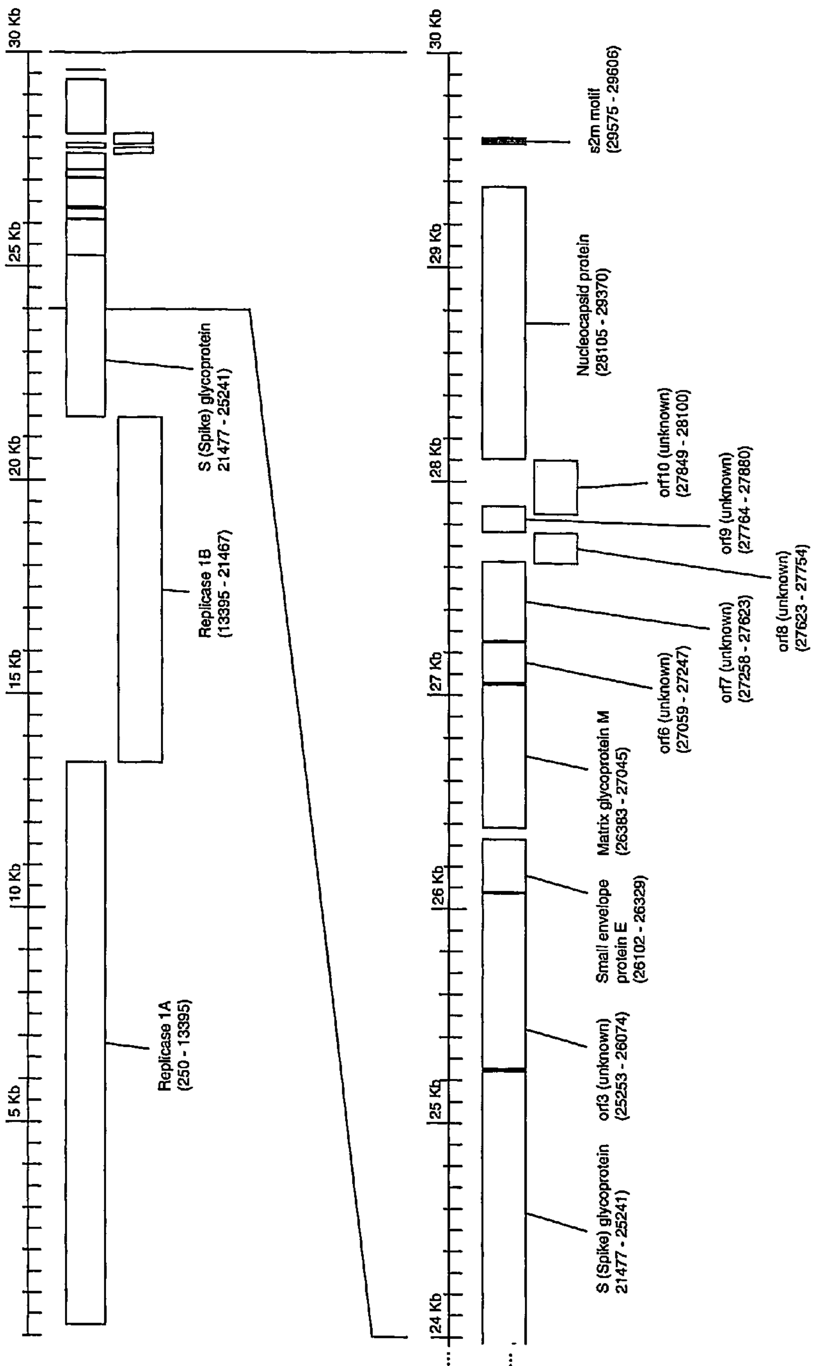

30 Kb
25 Kb
20 Kb
15 Kb
10 Kb
5 Kb
S (Spike) glycoprotein
21477 - 25241)
Replicase 1B
(13395 - 21467)
Replicase 1A
(250 - 13395)
30 Kb
29 Kb
28 Kb
27 Kb
26 Kb
25 Kb
24 Kb
s2m motif
(29575 - 29606)
Nucleocapsid protein
(28105 - 29370)
orf10 (unknown)
(27849 - 28100)
orf9 (unknown)
(27764 - 27880)
orf8 (unknown)
(27623 - 27754)
orf7 (unknown)
(27258 - 27623)
orf6 (unknown)
(27059 - 27247)
Matrix glycoprotein M
(26383 - 27045)
Small envelope
protein E
(26102 - 26329)
orf3 (unknown)
(25253 - 26074)
S (Spike) glycoprotein
21477 - 25241)

Figure 2

CTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTTCTCTAAACGAACTTTAAAATCTGTGT
AGCTGTCGCTCGGCTGCATGCCTAGTGCACCTACGCAGTATAAACAATAATAAATTTTACTGTCGTTGACA
AGAAACGAGTAACTCGTCCCTCTTCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCA
TACCTAGGTTTCGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAAC
ACACGTCCAACTCAGTTTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCGTGGCTTCGGGGACTCTGTGG
AAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAAAAAGGC
GTACTGCCCCAGCTTGAACAGCCCTATGTGTTCATTAAACGTTCTGATGCCTTAAGCACCAATCACGGCCA
CAAGGTCGTTGAGCTGGTTGCAGAAATGGACGGCATTCAGTACGGTCGTAGCGGTATAACACTGGGAGTAC
TCGTGCCACATGTGGGCGAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGA
GCCGGTGGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGATCCCAT
TGAAGATTATGAACAAAACTGGAACACTAAGCATGGCAGTGGTGCACTCCGTGAACTCACTCGTGAGCTCA
ATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGCCCAGATGGGTACCCTCTTGATTGCATC
AAAGATTTTCTCGCACGCGCGGGCAAGTCAATGTGCACTCTTTCCGAACAACTTGATTACATCGAGTCGAA
GAGAGGTGTCTACTGCTGCCGTGACCATGAGCATGAAATTGCCTGGTTCACTGAGCGCTCTGATAAGAGCT
ACGAGCACCAGACACCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG
TTTGTGTTTCCTCTTAACTCAAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAGACTGAGGGTTT
CATGGGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGTAACAATATGCACTTGTCTACCT
TGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAGACGTGCGACTTTCTGAAAGCCACTTGTGAACAT
TGTGGCACTGAAAATTTAGTTATTGAAGGACCTACTACATGTGGGTACCTACCTACTAATGCTGTAGTGAA
AATGCCATGTCCTGCCTGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTTGCAGATTATCACAACCACT
CAAACATTGAAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCCTATGTT
GGCTGCTATAATAAGCGTGCCTACTGGGTTCCTCGTGCTAGTGCTGATATTGGCTCAGGCCATACTGGCAT
TACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGAACGTGTTAACATTA
ACATTGTTGGCGATTTTCATTTGAATGAAGAGGTTGCCATCATTTTGGCATCTTTCTCTGCTTCTACAAGT
GCCTTTATTGACACTATAAAGAGTCTTGATTACAAGTCTTTCAAAACCATTGTTGAGTCCTGCGGTAACTA
TAAAGTTACCAAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGTTTTAACACCAC
TGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAAC
CACTCAATTCCTGATTTGCAAAGAGCAGCTGTCACCATACTTGATGGTATTTCTGAACAGTCATTACGTCT
TGTCGACGCCATGGTTTATACTTCAGACCTGCTCACCAACAGTGTCATTATTATGGCATATGTAACTGGTG
GTCTTGTACAACAGACTTCTCAGTGGTTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATC
TTTGAATGGATTGAGGCGAAACTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATT
TCTCATTACAGGTGTTTTTGACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAGGATTGTG
TAAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCGCTGGCGCA
AAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAAAGCAAGGGACTTTACCGTCAGTGTATACG
TGGCAAGGAGCAGCTGCAACTACTCATGCCTCTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATT
CACATGACACAGTACTTACCTCTGAGGAGGTTGTTCTCAAGAACGGTGAACTCGAAGCACTCGAGACGCCC
GTTGATAGCTTCACAAATGGAGCTATCGTCGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAGAT
TAAGGACAAAGAACAATACTGCGCATTGTCTCCTGGTTTACTGGCTACAAACAATGTCTTTCGCTTAAAAG
GGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGATACTGTTTGGGAAGTTCAAGGTTACAAGAATGTG
AGAATCACATTTGAGCTTGATGAACGTGTTGACAAAGTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGA
ATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTT
CTGATCTCCTTACCAACATGGGTATTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGAT
GCTGGTGAAGAAAACTTTTCATCACGTATGTATTGTTCCTTTTACCCTCCAGATGAGGAAGAAGAGGACGA
TGCAGAGTGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGTACAGAGGATGATTATCAAG
GTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGAGTTGAGGAAGAAGAAGAGGAAGACTGGCTG
GATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAGAACCTACACCTGAAGAACCAGTTAATCAGTT
TACTGGTTATTTAAAACTTACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTG
CTAATCCTATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCACTC
AACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGT
AGGAGGGTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGTCTGCATGTTGTTGGACCTAACCTAA
ATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCATATGAAAATTTCAATTCACAGGACATCTTACTTGCA
CCATTGTTGTCAGCAGGCATATTTGGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGACGGTTCG
TACACAGGTTTATATTGCAGTCAATGACAAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACC
TGAAGCCTAGAGTGGAAGCACCTAAACAAGAGGAGCCACCAAACACAGAAGATTCCAAAACTGAGGAGAAA
TCTGTCGTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATTGATGAGGTTACCACAACACT
GGAAGAAACTAAGTTTCTTACCAATAAGTTACTCTTGTTTGCTGATATCAATGGTAAGCTTTACCATGATT
CTCAGAACATGCTTAGAGGTGAAGATATGTCTTTCCTTGAGAAGGATGCACCTTACATGGTAGGTGATGTT

FIGURE 3A

ATCACTAGTGGTGATATCACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTC
AAGAGCTTTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGTTATA
CACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTACCTTCAGAAGCACCT
AATGCTAAGGAAGAGATTCTAGGAACTGTATCCTGGAATTTGAGAGAAATGCTTGCTCATGCTGAAGAGAC
AAGAAAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACCATCCAACGTAAGTATAAAGGAA
TTAAAATTCAAGAGGGCATCGTTGACTATGGTGTCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCT
TCTATTATTACGAAGCTGAACTCTCTAAATGAGCCGCTTGTCACAATGCCAATTGGTTATGTGACACATGG
TTTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTCAGTATCATCAC
CAGATGCTGTTACTACATATAATGGATACCTCACTTCGTCATCAAAGACATCTGAGGAGCACTTTGTAGAA
ACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCCTATTCAGGACAGCGTACAGAGTTAGGTGTTGAATT
TCTTAAGCGTGGTGACAAAATTGTGTACCACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGG
TTCTTTCACTTGACAAACTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAAAAGTGTTCACAACT
GTGGACAACACTAATCTCCACACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGTCCAAC
ATACTTGGATGGTGCTGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGTAAGACTTTCTTTGTAC
TACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTACCATACTCTTGATGAGAGTTTTCTTGGT
AGGTACATGTCTGCTTTAAACCACACAAAGAAATGGAAATTTCCTCAAGTTGGTGGTTTAACTTCAATTAA
ATGGGCTGATAACAATTGTTATTTGTCTAGTGTTTTATTAGCACTTCAACAGCTTGAAGTCAAATTCAATG
CACCAGCACTTCAAGAGGCTTATTATAGAGCCCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTC
GCTTACAGTAATAAAACTGTTGGCGAGCTTGGTGATGTCAGAGAAACTATGACCCATCTTCTACAGCATGC
TAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGTGGTCAGAAAACTACTACCTTAA
CGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCTTATGATAATCTTAAGACAGGTGTTTCCATTCCA
TGTGTGTGTGGTCGTGATGCTACACAATATCTAGTACAACAAGAGTCTTCTTTTGTTATGATGTCTGCACC
ACCTGCTGAGTATAAATTACAGCAAGGTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTG
GTCATTACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAGATGTCA
GAGTACAAAGGACCAGTGACTGATGTTTTCTACAAGGAAACATCTTACACTACAACCATCAAGCCTGTGTC
GTATAAACTCGATGGAGTTACTTACACAGAGATTGAACCAAAATTGGATGGGTATTATAAAAAGGATAATG
CTTACTATACAGAGCAGCCTATAGACCTTGTACCAACTCAACCATTACCAAATGCGAGTTTTGATAATTTC
AAACTCACATGTTCTAACACAAAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTC
ACGAGAGCTATCTGTCACATTCTTCCCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTATT
CAGCGAGTTTCAAGAAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAACCAGGCTACAACC
AAGACAACGTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGTACAAAGCCAGTAGATACTTCAAA
TTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGAATGGACAATCTTGCTTGTGAAAGTCAACAACCCA
CCTCTGAAGAAGTAGTGGAAAATCCTACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACTACCGAA
GTTGTAGGCAATGTCATACTTAAACCATCAGATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGA
TCTTATGGCTGCTTATGTGGAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTTCACTAGCCTTAG
GTTTAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGGAGTAAAATTTTGGCTTAT
GTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAATTGCGCTAAGAGATTAGCACAACGTGTGTT
TAACAATTATATGCCTTATGTGTTTACATTATTGTTCCAATTGTGTACTTTTACTAAAAGTACCAATTCTA
GAATTAGAGCTTCACTACCTACAACTATTGCTAAAAATAGTGTTAAGAGTGTTGCTAAATTATGTTTGGAT
GCCGGCATTAATTATGTGAAGTCACCCAAATTTTCTAAATTGTTCACAATCGCTATGTGGCTATTGTTGTT
AAGTATTTGCTTAGGTTCTCTAATCTGTGTAACTGCTGCTTTTGGTGTACTCTTATCTAATTTTGGTGCTC
CTTCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAACGTTACTACTATGGATTTCTGTGAA
GGTTCTTTTCCTTGCAGCATTTGTTTAAGTGGATTAGACTCCCTTGATTCTTATCCAGCTCTTGAAACCAT
TCAGGTGACGATTTCATCGTACAAGCTAGACTTGACAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCAT
ATATGTTGTTCACAAAATTCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTT
GCTAGTCATTTCATCAGCAATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCACCCGTTTC
TGCAATGGTTAGGATGTACATCTTCTTTGCTTCTTTCTACTACATATGGAAGAGCTATGTTCATATCATGG
ATGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGCAATCGTGCCACACGCGTTGAGTGTACAACT
ATTGTTAATGGCATGAAGAGATCTTTCTATGTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAA
TTGGAATTGTCTCAATTGTGACACATTTTGCACTGGTAGTACATTCATTAGTGATGAAGTTGCTCGTGATT
TGTCACTCCAGTTTAAAAGACCAATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTTGCTGTG
AAAAATGGCGCGCTTCACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCGCTCTCCCA
TTTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCACTGCCTATTAATGTCATAGTTTTTG
ATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAGTCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAA
CCTATTCTGTTGCTTGACCAAGCTCTTGTATCAGACGTTGGAGATAGTACTGAAGTTTCCGTTAAGATGTT
TGATGCTTATGTCGACACCTTTTCAGCAACTTTTAGTGTTCCTATGGAAAAACTTAAGGCACTTGTTGCTA
CAGCTCACAGCGAGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCCTTTCTACATTCGTGTCAGCTGCCCGA

FIGURE 3B

CAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTCAAACTTTCACATCACTCTGA
CTTAGAAGTGACAGGTGACAGTTGTAACAATTTCATGCTCACCTATAATAAGGTTGAAAACATGACGCCCA
GAGATCTTGGCGCATGTATTGACTGTAATGCAAGGCATATCAATGCCCAAGTAGCAAAAAGTCACAATGTT
TCACTCATCTGGAATGTAAAAGACTACATGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTAGTGCTGC
CAAGAAGAACAACATACCTTTTAGACTAACTTGTGCTACAACTAGACAGGTTGTCAATGTCATAACTACTA
AAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAGGCCACATTATTGTGC
GTTCTTGCTGCATTGGTTTGTTATATCGTTATGCCAGTACATACATTGTCAATCCATGATGGTTACACAAA
TGAAATCATTGGTTACAAAGCCATTCAGGATGGTGTCACTCGTGACATCATTTCTACTGATGATTGTTTTG
CAAATAAACATGCTGGTTTTGACGCATGGTTTAGCCAGCGTGGTGGTTCATACAAAAATGACAAAAGCTGC
CCTGTAGTAGCTGCTATCATTACAAGAGAGATTGGTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAG
AGCAATCAATGGTGACTTCTTGCATTTTCTACCTCGTGTTTTTAGTGCTGTTGGCAACATTTGCTACACAC
CTTCCAAACTCATTGAGTATAGTGATTTTGCTACCTCTGCTTGCGTTCTTGCTGCTGAGTGTACAATTTTT
AAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGACACTAATTTGCTAGAGGGTTCTATTTCTTATAG
TGAGCTTCGTCCAGACACTCGTTATGTGCTTATGGATGGTTCCATCATACAGTTTCCTAACACTTACCTGG
AGGGTTCTGTTAGAGTAGTAACAACTTTTGATGCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAA
GTAGGTATTTGCCTATCTACCAGTGGTAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCAGGAGT
TTTCTGTGGTGTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGTGCAACCTGTGGGTGCTT
TAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTATTATTGCCATATTGGTGACTTGTGCTGCCTACTACTTT
ATGAAATTCAGACGTGTTTTTGGTGAGTACAACCATGTTGTTGCTGCTAATGCACTTTTGTTTTTGATGTC
TTTCACTATACTCTGTCTGGTACCAGCTTACAGCTTTCTGCCGGGAGTCTACTCAGTCTTTTACTTGTACT
TGACATTCTATTTCACCAATGATGTTTCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT
GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGGTTCTTTAACAA
CTATCTTAGGAAAAGAGTCATGTTTAATGGAGTTACATTTAGTACCTTCGAGGAGGCTGCTTTGTGTACCT
TTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGCGAGACACTGTTGCCACTTACACAGTATAACAGG
TATCTTGCTCTATATAACAAGTACAAGTATTTCAGTGGAGCCTTAGATACTACCAGCTATCGTGAAGCAGC
TTGCTGCCACTTAGCAAAGGCTCTAAATGACTTTAGCAACTCAGGTGCTGATGTTCTCTACCAACCACCAC
AGACATCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTAGGAAAATGGCATTCCCGTCAGGCAAAGTTGAA
GGGTGCATGGTACAAGTAACCTGTGGAACTACAACTCTTAATGGATTGTGGTTGGATGACACAGTATACTG
TCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCTAACTATGAAGATCTGCTCATTCGCAAAT
CCAACCATAGCTTTCTTGTTCAGGCTGGCAATGTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGT
CTGCTTAGGCTTAAAGTTGATACTTCTAACCCTAAGACACCCAAGTATAAATTTGTCCGTATCCAACCTGG
TCAAACATTTTCAGTTCTAGCATGCTACAATGGTTCACCATCTGGTGTTTATCAGTGTGCCATGAGACCTA
ATCATACCATTAAAGGTTCTTTCCTTAATGGATCATGTGGTAGTGTTGGTTTTAACATTGATTATGATTGC
GTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACACGCTGGTACTGACTTAGAAGGTAA
ATTCTATGGTCCATTTGTTGACAGACAAACTGCACAGGCTGCAGGTACAGACACAACCATAACATTAAATG
TTTTGGCATGGCTGTATGCTGCTGTTATCAATGGTGATAGGTGGTTTCTTAATAGATTCACCACTACTTTG
AATGACTTTAACCTTGTGGCAATGAAGTACAACTATGAACCTTTGACACAAGATCATGTTGACATATTGGG
ACCTCTTTCTGCTCAAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTGCAGAATG
GTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACACCATTTGATGTTGTTAGA
CAATGCTCTGGTGTTACCTTCCAAGGTAAGTTCAAGAAAATTGTTAAGGGCACTCATCATTGGATGCTTTT
AACTTTCTTGACATCACTATTGATTCTTGTTCAAAGTACACAGTGGTCACTGTTTTTCTTTGTTTACGAGA
ATGCTTTCTTGCCATTTACTCTTGGTATTATGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAG
CACGCATTCTTGTGCTTGTTTCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATATGGTCTACATGCC
TGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCTGGTTATAGGCTTA
AGGATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTTTATGATGAT
GCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTTACAAAGTCTACTATGGTAATGCTTT
AGATCAAGCTATTTCCATGTGGGCCTTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTA
TCATGTTTTTAGCTAGAGCTATAGTGTTTGTGTGTGTTGAGTATTACCCATTGTTATTTATTACTGGCAAC
ACCTTACAGTGTATCATGCTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTG
TTTACTCAACCGTTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTCTCTACACAAGAATTTAGGT
ATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATTGATGCTTTCAAGCTTAACATTAAGTTGTTG
GGTATTGGAGGTAAACCATGTATCAAGGTTGCTACTGTACAGTCTAAAATGTCTGACGTAAAGTGCACATC
TGTGGTACTGCTCTCGGTTCTTCAACAACTTAGAGTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTAC
AACTCCACAATGATATTCTTCTTGCAAAAGACACAACTGAAGCTTTCGAGAAGATGGTTTCTCTTTTGTCT
GTTTTGCTATCCATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTCGATAACCGTGCTAC
TCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCCGCTTATGCCACTGCCCAGGAGGCCT
ATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCT

FIGURE 3C

AAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCA
AATGTACAAACAGGCAAGATCTGAGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCA
CTATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGTTGTGTTCCA
CTCAACATCATACCATTGACTACAGCAGCCAAACTCATGGTTGTTGTCCCTGATTATGGTACCTACAAGAA
CACTTGTGATGGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAAGTTGTTGATGCGGATA
GCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATTCACCAAATTTGGCTTGGCCTCTTATTGTTACA
GCTCTAAGAGCCAACTCAGCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGATGTC
CTGTGCGGCTGGTACCACACAAACAGCTTGTACTGATGACAATGCACTTGCCTACTATAACAATTCGAAGG
GAGGTAGGTTTGTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGAT
GGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTTGTTACAGACACACCAAAAGGGCCTAA
AGTGAAATACTTGTACTTCATCAAAGGCTTAAACAACCTAAATAGAGGTATGGTGCTGGGCAGTTTAGCTG
CTACAGTACGTCTTCAGGCTGGAAATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCTTCTGTGCT
TTTGCAGTAGACCCTGCTAAAGCATATAAGGATTACCTAGCAAGTGGAGGACAACCAATCACCAACTGTGT
GAAGATGTTGTGTACACACACTGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAACATGGACCAAG
AGTCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGACCATCCAAATCCTAAAGGATTC
TGTGACTTGAAAGGTAAGTACGTCCAAATACCTACCACTTGTGCTAATGACCCAGTGGGTTTTACACTTAG
AAACACAGTCTGTACCGTCTGCGGAATGTGGAAAGGTTATGGCTGTAGTTGTGACCAACTCCGCGAACCCT
TGATGCAGTCTGCGGATGCATCAACGTTTTTAAACGGGTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGT
GCGGCACAGGCACTAGTACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAAGTTGCTGGTTTT
GCAAAGTTCCTAAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCAATTTATTAGACTCTTA
CTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAGAGACTATTTATAACTTGGTTAAAGATT
GTCCAGCGGTTGCTGTCCATGACTTTTTCAAGTTTAGAGTAGATGGTGACATGGTACCACATATATCACGT
CAGCGTCTAACTAAATACACAATGGCTGATTTAGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGA
TACATTAAAAGAAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATG
ACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAACTTAGGTGAGCGTGTACGCCAATCATTATTA
AAGACTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCGTACTGACATTAGATAATCAGGA
TCTTAATGGGAACTGGTACGATTTCGGTGATTTCGTACAAGTAGCACCAGGCTGCGGAGTTCCTATTGTGG
ATTCATATTACTCATTGCTGATGCCCATCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGAT
GCTGATCTCGCAAAACCACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGAAGAGAGACTTTGTCT
CTTCGACCGTTATTTTAAATATTGGGACCAGACATACCATCCCAATTGTATTAACTGTTTGGATGATAGGT
GTATCCTTCATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTACAAGTTTTGGACCACTA
GTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTTGTTTCAACTGGATACCATTTTCGTGAGTTAGGAGT
CGTACATAATCAGGATGTAAACTTACATAGCTCGCGTCTCAGTTTCAAGGAACTTTTAGTGTATGCTGCTG
ATCCAGCTATGCATGCAGCTTCTGGCAATTTATTGCTAGATAAACGCACTACATGCTTTTCAGTAGCTGCA
CTAACAAACAATGTTGCTTTTCAAACTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTGT
GTCTAAAGGTTTCTTTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTCTTTGCTCAGGATGGCAACG
CTGCTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACAATGTGTGATATCAGACAACTCCTATTC
GTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACGATGGTGGCTGTATTAATGCCAACCAAGTAATCGT
TAACAATCTGGATAAATCAGCTGGTTTCCCATTTAATAAATGGGGTAAGGCTAGACTTTATTATGACTCAA
TGAGTTATGAGGATCAAGATGCACTTTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATG
AATCTTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTAGTACTAT
GACAAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAATTG
GAACAAGCAAGTTTTACGGTGGCTGGCATAATATGTTAAAAACTGTTTACAGTGATGTAGAAACTCCACAC
CTTATGGGTTGGGATTATCCAAAATGTGACAGAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGT
TCTTGCTCGCAAACATAACACTTGCTGTAACTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGC
AAGTATTAAGTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTGAT
GCTACAACTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATGTAAATGCACTTCT
TTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTACAACACAGGCTCTATGAGTGTCTCT
ATAGAAATAGGGATGTTGATCATGAATTCGTGGATGAGTTTTACGCTTACCTGCGTAAACATTTCTCCATG
ATGATTCTTTCTGATGATGCCGTTGTGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGCTAGCAT
TAAGAACTTTAAGGCAGTTCTTTATTATCAAAATAATGTGTTCATGTCTGAGGCAAAATGTTGGACTGAGA
CTGACCTTACTAAAGGACCTCACGAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAGATGATTAC
GTGTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTGTCGATGATATTGTCAAAAC
AGATGGTACACTTATGATTGAAAGGTTCGTGTCACTGGCTATTGATGCTTACCCACTTACAAAACATCCTA
ATCAGGAGTATGCTGATGTCTTTCACTTGTATTTACAATACATTAGAAAGTTACATGATGAGCTTACTGGC
CACATGTTGGACATGTATTCCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTTA
TGAGGCTATGTACACACCACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGACTT

FIGURE 3D

CACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAGTGCTGCTATGACCATGTCATTTCA
ACATCACACAAATTAGTGTTGTCTGTTAATCCCTATGTTTGCAATGCCCCAGGTTGTGATGTCACTGATGT
GACACAACTGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGCCTCCCATTAGTTTTCCATTAT
GTGCTAATGGTCAGGTTTTTGGTTTATACAAAAACACATGTGTAGGCAGTGACAATGTCACTGACTTCAAT
GCGATAGCAACATGTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAA
GCTTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTGCCACTGTAC
GCGAAGTACTCTCTGACAGAGAATTGCATCTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGAACAGA
AACTATGTCTTTACTGGTTACCGTGTAACTAAAAATAGTAAAGTACAGATTGGAGAGTACACCTTTGAAAA
AGGTGACTATGGTGATGCTGTTGTGTACAGAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTG
TGTTGACATCTCACACTGTAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATT
ACTGGCTTGTACCCAACACTCAACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAGGTCGG
CATGCAAAAGTACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACTTGCTC
TCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATGCAGCTGTTGATGCCCTATGTGAAAAG
GCATTAAAATATTTGCCCATAGATAAATGTAGTAGAATCATACCTGCGCGTGCGCGCGTAGAGTGTTTTGA
TAAATTCAAAGTGAATTCAACACTAGAACAGTATGTTTTCTGCACTGTAAATGCATTGCCAGAAACAACTG
CTGACATTGTAGTCTTTGATGAAATCTCTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTT
CGTGCAAAACACTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCCGCACATTGCTGACTAAAGG
CACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAATAGGTCCAGACATGTTCCTTG
GAACTTGTCGCCGTTGTCCTGCTGAAATTGTTGACACTGTGAGTGCTTTAGTTTATGACAATAAGCTAAAA
GCACACAAGGATAAGTCAGCTCAATGCTTCAAAATGTTCTACAAAGGTGTTATTACACATGATGTTTCATC
TGCAATCAACAGACCTCAAATAGGCGTTGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTG
TTTTTATCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTGCCTACGCAGACTGTT
GATTCATCACAGGGTTCTGAATATGACTATGTCATATTCACACAAACTACTGAAACAGCACACTCTTGTAA
TGTCAACCGCTTCAATGTGGCTATCACAAGGGCAAAAATTGGCATTTTGTGCATAATGTCTGATAGAGATC
TTTATGACAAACTGCAATTTACAAGTCTAGAAATACCACGTCGCAATGTGGCTACATTACAAGCAGAAAAT
GTAACTGGACTTTTTAAGGACTGTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCT
CAGCGTTGATATAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT
ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATC
ACCCGCGAAGAAGCTATTCGTCACGTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAG
AGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA
CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAG
TTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAAT
GCTCAGTGATACACTGAAAGGATTGTCAGACAGAGTCGTGTTCGTCCTTTGGGCGCATGGCTTTGAGCTTA
CATCAATGAAGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTTGC
TTTTCTACTTCATCAGATACTTATGCCTGCTGGAATCATTCTGTGGGTTTTGACTATGTCTATAACCCATT
TATGATTGATGTTCAGCAGTGGGGCTTTACGGTAACCTTCAGAGTAACCATGACCAACATTGCCAGGTAC
ATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTT
AAGCGCGTTGATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAGAAA
AGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATGACATTGGAAATC
CAAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGAC
AAAGCTTACAAAATAGAGGAACTCTTCTATTCTTATGCTACACATCACGATAAATTCACTGATGGTGTTTG
TTTGTTTTGGAATTGTAACGTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCT
TGTCAAACTTGAACTTACCAGGCTGTGATGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCA
GCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAATTGCCTTTCTTTTACTATTCTGATAGTCCTTGTGA
GTCTCATGGCAAACAAGTAGTGTCGGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACACGAT
GCAATTTAGGTGGTGCTGTTTGCAGACACCATGCAAATGAGTACCGACAGTACTTGGATGCATATAATATG
ATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATACATTTAC
CAGGTTACAGAGTTTAGAAAATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGGACACGCCGGCG
AAGCACCTGTTTCCATCATTAATAATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTGAA
AATAAGACAACACTTCCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTAAACCAGTGCCAGA
GATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTGTAATCTGGGACTACAAAAGAGAAG
CCCCAGCACATGTATCTACAATAGGTGTCTGCACAATGACTGACATTGCCAAGAAACCTACTGAGAGTGCT
TGTTCTTCACTTACTGTCTTGTTTGATGGTAGAGTGGAAGGACAGGTAGACCTTTTTAGAAACGCCCGTAA
TGGTGTTTTAATAACAGAAGGTTCAGTCAAAGGTCTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCA
ATGGAGTCACATTAATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACGGCATTATT
CAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTAAGCCCAGATCACAAATGGA
AACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGCGATATAAGCTCGAGGGCTATGCCTTCGAAC

FIGURE 3E

ACATCGTTTATGGAGATTTCAGTCATGGACAACTTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGC
TCACAAGATTCACCACTTAAATTAGAGGATTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAAC
AGATGCGCAAACAGGTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTCGAGA
TAATAAAGTCACAAGATTTGTCAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACTATGCTGAAATTTCA
TTCATGCTTTGGTGTAAGGATGGACATGTTGAAACCTTCTACCCAAAACTACAAGCAAGTCGAGCGTGGCA
ACCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAAGAATGCTTCTTGAAAAGTGTGACCTTCAGAATT
ATGGTGAAAATGCTGTTATACCAAAAGGAATAATGATGAATGTCGCAAAGTATACTCAACTGTGTCAATAC
TTAAATACACTTACTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGGTGCTGGCTCTGATAAAGG
AGTTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTCGATTCAGATCTTA
ATGACTTCGTCTCCGACGCATATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGCTAATAAATGG
GACCTTATTATTAGCGATATGTATGACCCTAGGACCAAACATGTGACAAAAGAGAATGACTCTAAAGAAGG
GTTTTTCACTTATCTGTGTGGATTTATAAAGCAAAAACTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAA
CAGAGCATTCTTGGAATGCTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTTACA
AATGTAAATGCATCATCATCGGAAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAAT
TGATGGCTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCCAGTTGTCTTCCTATT
CACTCTTTGACATGAGCAAATTTCCTCTTAAATTAAGAGGAACTGCTGTAATGTCTCTTAAGGAGAATCAA
ATCAATGATATGATTTATTCTCTTCTGGAAAAAGGTAGGCTTATCATTAGAGAAAACAACAGAGTTGTGGT
TTCAAGTGATATTCTTGTTAACAACTAAACGAACATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTG
GTAGTGACCTTGACCGGTGCACCACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCT
ATGAGGGGGGTTTACTATCCTGATGAAATTTTTAGATCAGACACTCTTTATTTAACTCAGGATTTATTTCT
TCCATTTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTGGCAACCCTGTCATACCTTTTA
AGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATGTTGTCCGTGGTTGGGTTTTTGGTTCTACCATG
AACAACAAGTCACAGTCGGTGATTATTATTAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTTGA
ATTGTGTGACAACCCTTTCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTCGATA
ATGCATTTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAAT
TTTAAACACTTACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACC
TATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGAAACCTATTTTTAAGTTGCCTCTTGGTA
TTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCT
GCAGCCTATTTTGTTGGCTATTTAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCAC
AGATGCTGTTGATTGTTCTCAAAATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA
AAGGAATTTACCAGACCTCTAATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACA
AACTTGTGTCCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCCTTCTGTCTATGCATGGGAGAGAAAAAA
AATTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACAACTCAACATTTTTTTCAACCTTTAAGTGCTATG
GCGTTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGA
GATGATGTAAGACAAATAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGA
TTTCATGGGTTGTGTCCTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATA
AATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCCCT
GATGGCAAACCTTGCACCCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATGGTTTTTACACCAC
TACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGG
TTTGTGGACCAAAATTATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACT
GGTACTGGTGTGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGA
TTTCACTGATTCCGTTCGAGATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCGCTTTTGGGGGTG
TAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACT
GATGTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATATATTCTACTGGAAACAATGT
ATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTA
TTGGAGCTGGCATTTGTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTG
GCTTATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAA
CTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATATGT
ACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTTGCACACAACTAAAT
CGTGCACTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTGAAGTGTTCGCTCAAGTCAAACAAAT
GTACAAAACCCCAACTTTGAAATATTTTGGTGGTTTTAATTTTTCACAAATATTACCTGACCCTCTAAAGC
CAACTAAGAGGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAG
CAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTTAC
AGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTGCTGCTCTAGTTAGTGGTACTGCCA
CTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTATGCAAATGGCATATAGGTTC
AATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAACAAATCGCCAACCAATTTAACAAGGC
GATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGCAAGCTGCAAGACGTTGTTAACC

FIGURE 3F

AGAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTA
AATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACT
TCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCTTG
CTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCAC
CTTATGTCCTTCCCACAAGCAGCCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTGCCATCCCAGGA
GAGGAACTTCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTTTTG
TGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAATTACTACAGACAAT
ACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTATGATCCTCTGCAACC
TGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATACATCACCAGATGTTGATCTTG
GCGACATTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCT
AAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTG
GTATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTGTTGCATGA
CTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAAGTTTGATGAGGATGACTCT
GAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAACGAACTTATGGATTTGTTTATGAGATTTTTT
ACTCTTGGATCAATTACTGCACAGCCAGTAAAAATTGACAATGCTTCTCCTGCAAGTACTGTTCATGCTAC
AGCAACGATACCGCTACAAGCCTCACTCCCTTTCGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTT
TTCAGAGCGCTACCAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCAGTTC
ATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGCTTGTCGCTGCAGGTATGGAGGC
GCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCATCAACGCATGTAGAATTATTATGAGAT
GTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCCATTACTTTATGATGCCAACTACTTTGTTTGCTGGCAC
ACACATAACTATGACTACTGTATACCATATAACAGTGTCACAGATACAATTGTCGTTACTGAAGGTGACGG
CATTTCAACACCAAAACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACTCAGGTGTTA
AAGACTATGTCGTTGTACATGGCTATTTCACCGAAGTTTACTACCAGCTTGAGTCTACACAAATTACTACA
GACACTGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAAAGACCCACCGAATGTGCAAAT
ACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGCAATGGATCCAATTTATGATGAGCCGACGACGA
CTACTAGCGTGCCTTTGTAAGCACAAGAAAGTGAGTACGAACTTATGTACTCATTCGTTTCGGAAGAAACA
GGTACGTTAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTCGTGGTATTCTTGCTAGTCACACTAGCCAT
CCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAACGGTTT
ACGTCTACTCGCGTGTTAAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCTGGTCTAAACGAACTAA
CTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATGGCAGACAACGGTACTATTACCGTTGAG
GAGCTTAAACAACTCCTGGAACAATGGAACCTAGTAATAGGTTTCCTATTCCTAGCCTGGATTATGTTACT
ACAATTTGCCTATTCTAATCGGAACAGGTTTTTGTACATAATAAAGCTTGTTTTCCTCTGGCTCTTGTGGC
CAGTAACACTTGCTTGTTTTGTGCTTGCTGCTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT
GCAATGGCTTGTATTGTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCCTTCAGGCTGTTTGCTCGTAC
CCGCTCAATGTGGTCATTCAACCCAGAAACAAACATTCTTCTCAATGTGCCTCTCCGGGGGACAATTGTGA
CCAGACCGCTCATGGAAAGTGAACTTGTCATTGGTGCTGTGATCATTCGTGGTCACTTGCGAATGGCCGGA
CACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTC
TTATTACAAATTAGGAGCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTA
TTGGAAACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAGTAAGTG
ACAACAGATGTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGATTATCATTATGAGGACTT
TCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATTTAAGCCTCTAACT
AAGAAGAATTATTCGGAGTTAGATGATGAAGAACCTATGGAGTTAGATTATCCATAAAACGAACATGAAAA
TTATTCTCTTCCTGACATTGATTGTATTTACATCTTGCGAGCTATATCACTATCAGGAGTGTGTTAGAGGT
ACGACTGTACTACTAAAAGAACCTTGCCCATCAGGAACATACGAGGGCAATTCACCATTTCACCCTCTTGC
TGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGCTTGTGCTGACGGTACTCGACATA
CCTATCAGCTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGACAAGAGGAGGTTCAACAAGAGCTC
TACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTATTTTTAATACTTTGCTTCACCATTAAGAGAAAGAC
AGAATGAATGAGCTCACTTTAATTGACTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCCTTGTTTTAAT
AATGCTTATTATATTTTGGTTTTCACTCGAAATCCAGGATCTAGAAGAACCTTGTACCAAAGTCTAAACGA
ACATGAAACTTCTCATTGTTTTGACTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACAGCGCTGT
GCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGGGTAATACTTATAGCACTG
CTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGATGGCACACTATGGTTCAAACATGCACACCT
AATGTTACTATCAACTGTCAAGATCCAGCTGGTGGTGCGCTTATAGCTAGGTGTTGGTACCTTCATGAAGG
TCACCAAACTGCTGCATTTAGAGACGTACTTGTTGTTTTAAATAAACGAACAAATTAAAATGTCTGATAAT
GGACCCCAATCAAACCAACGTAGTGCCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAATAA
CCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCCAATAATACTGCGT
CTTGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAACTTAGATTCCCTCGAGGCCAGGGCGTTCCAATC

FIGURE 3G

AACACCAATAGTGGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGA
CGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTC
CCTACGGCGCTAACAAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCAC
ATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAACTTCCTCAAGGAACAACATTGCCAAA
AGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTA
ATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAATGGCTAGCGGAGGTGGTGAA
ACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACA
ACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTG
CCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTTCGGG
GACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAATTTGCTCCAAGTGC
CTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTGACTTATCATG
GAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGAC
GCATACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTT
GCCGCAGAGACAAAAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGAC
AACTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAA
GGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTACGATACATAGTCTACTCTTGTGCAGAATGAAT
TCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTA
ACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGT
GAATAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCC
CCATGTGATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAAA

GenBank Accession No. AY274119.1; SEQ ID NO: 1

FIGURE 3H

CTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTTCTCTAAACGAACTTTAAAATCTGTGT
AGCTGTCGCTCGGCTGCATGCCTAGTGCACCTACGCAGTATAAACAATAATAAATTTTACTGTCGTTGACA
AGAAACGAGTAACTCGTCCCTCTTCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCA
TACCTAGGTTTCGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAAC
ACACGTCCAACTCAGTTTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCGTGGCTTCGGGGACTCTGTGG
AAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAAAAAGGC
GTACTGCCCCAGCTTGAACAGCCCTATGTGTTCATTAAACGTTCTGATGCCTTAAGCACCAATCACGGCCA
CAAGGTCGTTGAGCTGGTTGCAGAAATGGACGGCATTCAGTACGGTCGTAGCGGTATAACACTGGGAGTAC
TCGTGCCACATGTGGGCGAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGA
GCCGGTGGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGATCCCAT
TGAAGATTATGAACAAAACTGGAACACTAAGCATGGCAGTGGTGCACTCCGTGAACTCACTCGTGAGCTCA
ATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGCCCAGATGGGTACCCTCTTGATTGCATC
AAAGATTTTCTCGCACGCGCGGGCAAGTCAATGTGCACTCTTTCCGAACAACTTGATTACATCGAGTCGAA
GAGAGGTGTCTACTGCTGCCGTGACCATGAGCATGAAATTGCCTGGTTCACTGAGCGCTCTGATAAGAGCT
ACGAGCACCAGACACCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG
TTTGTGTTTCCTCTTAACTCAAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAGACTGAGGGTTT
CATGGGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGTAACAATATGCACTTGTCTACCT
TGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAGACGTGCGACTTTCTGAAAGCCACTTGTGAACAT
TGTGGCACTGAAAATTTAGTTATTGAAGGACCTACTACATGTGGGTACCTACCTACTAATGCTGTAGTGAA
AATGCCATGTCCTGCCTGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTTGCAGATTATCACAACCACT
CAAACATTGAAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCCTATGTT
GGCTGCTATAATAAGCGTGCCTACTGGGTTCCTCGTGCTAGTGCTGATATTGGCTCAGGCCATACTGGCAT
TACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGAACGTGTTAACATTA
ACATTGTTGGCGATTTTCATTTGAATGAAGAGGTTGCCATCATTTTGGCATCTTTCTCTGCTTCTACAAGT
GCCTTTATTGACACTATAAAGAGTCTTGATTACAAGTCTTTCAAAACCATTGTTGAGTCCTGCGGTAACTA
TAAAGTTACCAAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGTTTTAACACCAC
TGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAAC
CACTCAATTCCTGATTTGCAAAGAGCAGCTGTCACCATACTTGATGGTATTTCTGAACAGTCATTACGTCT
TGTCGACGCCATGGTTTATACTTCAGACCTGCTCACCAACAGTGTCATTATTATGGCATATGTAACTGGTG
GTCTTGTACAACAGACTTCTCAGTGGTTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATC
TTTGAATGGATTGAGGCGAAACTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATT
TCTCATTACAGGTGTTTTTGACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAGGATTGTG
TAAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCGCTGGCGCA
AAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAAAGCAAGGGACTTTACCGTCAGTGTATACG
TGGCAAGGAGCAGCTGCAACTACTCATGCCTCTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATT
CACATGACACAGTACTTACCTCTGAGGAGGTTGTTCTCAAGAACGGTGAACTCGAAGCACTCGAGACGCCC
GTTGATAGCTTCACAAATGGAGCTATCGTTGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAGAT
TAAGGACAAAGAACAATACTGCGCATTGTCTCCTGGTTTACTGGCTACAAACAATGTCTTTCGCTTAAAAG
GGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGATACTGTTTGGGAAGTTCAAGGTTACAAGAATGTG
AGAATCACATTTGAGCTTGATGAACGTGTTGACAAAGTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGA
ATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTT
CTGATCTCCTTACCAACATGGGTATTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGAT
GCTGGTGAAGAAAACTTTTCATCACGTATGTATTGTTCCTTTTACCCTCCAGATGAGGAAGAAGAGGACGA
TGCAGAGTGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGTACAGAGGATGATTATCAAG
GTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGAGTTGAGGAAGAAGAAGAGGAAGACTGGCTG
GATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAGAACCTACACCTGAAGAACCAGTTAATCAGTT
TACTGGTTATTTAAAACTTACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTG
CTAATCCTATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCACTC
AACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGT
AGGAGGGTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGTCTGCATGTTGTTGGACCTAACCTAA
ATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCATATGAAAATTTCAATTCACAGGACATCTTACTTGCA
CCATTGTTGTCAGCAGGCATATTTGGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGACGGTTCG
TACACAGGTTTATATTGCAGTCAATGACAAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACC
TGAAGCCTAGAGTGGAAGCACCTAAACAAGAGGAGCCACCAAACACAGAAGATTCCAAAACTGAGGAGAAA
TCTGTCGTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATTGATGAGGTTACCACAACACT
GGAAGAAACTAAGTTTCTTACCAATAAGTTACTCTTGTTTGCTGATATCAATGGTAAGCTTTACCATGATT
CTCAGAACATGCTTAGAGGTGAAGATATGTCTTTCCTTGAGAAGGATGCACCTTACATGGTAGGTGATGTT

FIGURE 3I

ATCACTAGTGGTGATATCACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTC
AAGAGCTTTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGTTATA
CACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTACCTTCAGAAGCACCT
AATGCTAAGGAAGAGATTCTAGGAACTGTATCCTGGAATTTGAGAGAAATGCTTGCTCATGCTGAAGAGAC
AAGAAAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACCATCCAACGTAAGTATAAAGGAA
TTAAAATTCAAGAGGGCATCGTTGACTATGGTGTCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCT
TCTATTATTACGAAGCTGAACTCTCTAAATGAGCCGCTTGTCACAATGCCAATTGGTTATGTGACACATGG
TTTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTCAGTATCATCAC
CAGATGCTGTTACTACATATAATGGATACCTCACTTCGTCATCAAAGACATCTGAGGAGCACTTTGTAGAA
ACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCCTATTCAGGACAGCGTACAGAGTTAGGTGTTGAATT
TCTTAAGCGTGGTGACAAAATTGTGTACCACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGG
TTCTTTCACTTGACAAACTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAAAAGTGTTCACAACT
GTGGACAACACTAATCTCCACACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGTCCAAC
ATACTTGGATGGTGCTGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGTAAGACTTTCTTTGTAC
TACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTACCATACTCTTGATGAGAGTTTTCTTGGT
AGGTACATGTCTGCTTTAAACCACACAAAGAAATGGAAATTTCCTCAAGTTGGTGGTTTAACTTCAATTAA
ATGGGCTGATAACAATTGTTATTTGTCTAGTGTTTTATTAGCACTTCAACAGCTTGAAGTCAAATTCAATG
CACCAGCACTTCAAGAGGCTTATTATAGAGCCCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTC
GCTTACAGTAATAAAACTGTTGGCGAGCTTGGTGATGTCAGAGAAACTATGACCCATCTTCTACAGCATGC
TAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGTGGTCAGAAAACTACTACCTTAA
CGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCTTATGATAATCTTAAGACAGGTGTTTCCATTCCA
TGTGTGTGTGGTCGTGATGCTACACAATATCTAGTACAACAAGAGTCTTCTTTTGTTATGATGTCTGCACC
ACCTGCTGAGTATAAATTACAGCAAGGTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTG
GTCATTACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAGATGTCA
GAGTACAAAGGACCAGTGACTGATGTTTTCTACAAGGAAACATCTTACACTACAACCATCAAGCCTGTGTC
GTATAAACTCGATGGAGTTACTTACACAGAGATTGAACCAAAATTGGATGGGTATTATAAAAAGGATAATG
CTTACTATACAGAGCAGCCTATAGACCTTGTACCAACTCAACCATTACCAAATGCGAGTTTTGATAATTTC
AAACTCACATGTTCTAACACAAAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTC
ACGAGAGCTATCTGTCACATTCTTCCCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTATT
CAGCGAGTTTCAAGAAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAACCAGGCTACAACC
AAGACAACGTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGTACAAAGCCAGTAGATACTTCAAA
TTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGAATGGACAATCTTGCTTGTGAAAGTCAACAACCCA
CCTCTGAAGAAGTAGTGGAAAATCCTACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACTACCGAA
GTTGTAGGCAATGTCATACTTAAACCATCAGATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGA
TCTTATGGCTGCTTATGTGGAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTTCACTAGCCTTAG
GTTTAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGGAGTAAAATTTTGGCTTAT
GTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAATTGCGCTAAGAGATTAGCACAACGTGTGTT
TAACAATTATATGCCTTATGTGTTTACATTATTGTTCCAATTGTGTACTTTTACTAAAAGTACCAATTCTA
GAATTAGAGCTTCACTACCTACAACTATTGCTAAAAATAGTGTTAAGAGTGTTGCTAAATTATGTTTGGAT
GCCGGCATTAATTATGTGAAGTCACCCAAATTTTCTAAATTGTTCACAATCGCTATGTGGCTATTGTTGTT
AAGTATTTGCTTAGGTTCTCTAATCTGTGTAACTGCTGCTTTTGGTGTACTCTTATCTAATTTTGGTGCTC
CTTCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAACGTTACTACTATGGATTTCTGTGAA
GGTTCTTTTCCTTGCAGCATTTGTTTAAGTGGATTAGACTCCCTTGATTCTTATCCAGCTCTTGAAACCAT
TCAGGTGACGATTTCATCGTACAAGCTAGACTTGACAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCAT
ATATGTTGTTCACAAAATTCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTT
GCTAGTCATTTCATCAGCAATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCACCCGTTTC
TGCAATGGTTAGGATGTACATCTTCTTTGCTTCTTTCTACTACATATGGAAGAGCTATGTTCATATCATGG
ATGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGCAATCGTGCCACACGCGTTGAGTGTACAACT
ATTGTTAATGGCATGAAGAGATCTTTCTATGTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAA
TTGGAATTGTCTCAATTGTGACACATTTTGCACTGGTAGTACATTCATTAGTGATGAAGTTGCTCGTGATT
TGTCACTCCAGTTTAAAAGACCAATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTTGCTGTG
AAAAATGGCGCGCTTCACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCGCTCTCCCA
TTTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCACTGCCTATTAATGTCATAGTTTTTG
ATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAGTCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAA
CCTATTCTGTTGCTTGACCAAGCTCTTGTATCAGACGTTGGAGATAGTACTGAAGTTTCCGTTAAGATGTT
TGATGCTTATGTCGACACCTTTTCAGCAACTTTTAGTGTTCCTATGGAAAAACTTAAGGCACTTGTTGCTA
CAGCTCACAGCGAGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCCTTTCTACATTCGTGTCAGCTGCCCGA

FIGURE 3J

CAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTCAAACTTTCACATCACTCTGA
CTTAGAAGTGACAGGTGACAGTTGTAACAATTTCATGCTCACCTATAATAAGGTTGAAAACATGACGCCCA
GAGATCTTGGCGCATGTATTGACTGTAATGCAAGGCATATCAATGCCCAAGTAGCAAAAAGTCACAATGTT
TCACTCATCTGGAATGTAAAAGACTACATGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTAGTGCTGC
CAAGAAGAACAACATACCTTTTAGACTAACTTGTGCTACAACTAGACAGGTTGTCAATGTCATAACTACTA
AAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAGGCCACATTATTGTGC
GTTCTTGCTGCATTGGTTTGTTATATCGTTATGCCAGTACATACATTGTCAATCCATGATGGTTACACAAA
TGAAATCATTGGTTACAAAGCCATTCAGGATGGTGTCACTCGTGACATCATTTCTACTGATGATTGTTTTG
CAAATAAACATGCTGGTTTTGACGCATGGTTTAGCCAGCGTGGTGGTTCATACAAAAATGACAAAAGCTGC
CCTGTAGTAGCTGCTATCATTACAAGAGAGATTGGTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAG
AGCAATCAATGGTGACTTCTTGCATTTTCTACCTCGTGTTTTAGTGCTGTTGGCAACATTTGCTACACAC
CTTCCAAACTCATTGAGTATAGTGATTTTGCTACCTCTGCTTGCGTTCTTGCTGCTGAGTGTACAATTTTT
AAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGACACTAATTTGCTAGAGGGTTCTATTTCTTATAG
TGAGCTTCGTCCAGACACTCGTTATGTGCTTATGGATGGTTCCATCATACAGTTTCCTAACACTTACCTGG
AGGGTTCTGTTAGAGTAGTAACAACTTTTGATGCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAA
GTAGGTATTTGCCTATCTACCAGTGGTAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCAGGAGT
TTTCTGTGGTGTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGTGCAACCTGTGGGTGCTT
TAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTATTATTGCCATATTGGTGACTTGTGCTGCCTACTACTTT
ATGAAATTCAGACGTGTTTTTGGTGAGTACAACCATGTTGTTGCTGCTAATGCACTTTTGTTTTTGATGTC
TTTCACTATACTCTGTCTGGTACCAGCTTACAGCTTTCTGCCGGGAGTCTACTCAGTCTTTTACTTGTACT
TGACATTCTATTTCACCAATGATGTTTCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT
GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGGTTCTTTAACAA
CTATCTTAGGAAAAGAGTCATGTTTAATGGAGTTACATTTAGTACCTTCGAGGAGGCTGCTTTGTGTACCT
TTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGCGAGACACTGTTGCCACTTACACAGTATAACAGG
TATCTTGCTCTATATAACAAGTACAAGTATTTCAGTGGAGCCTTAGATACTACCAGCTATCGTGAAGCAGC
TTGCTGCCACTTAGCAAAGGCTCTAAATGACTTTAGCAACTCAGGTGCTGATGTTCTCTACCAACCACCAC
AGACATCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTAGGAAAATGGCATTCCCGTCAGGCAAAGTTGAA
GGGTGCATGGTACAAGTAACCTGTGGAACTACAACTCTTAATGGATTGTGGTTGGATGACACAGTATACTG
TCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCTAACTATGAAGATCTGCTCATTCGCAAAT
CCAACCATAGCTTTCTTGTTCAGGCTGGCAATGTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGT
CTGCTTAGGCTTAAAGTTGATACTTCTAACCCTAAGACACCCAAGTATAAATTTGTCCGTATCCAACCTGG
TCAAACATTTTCAGTTCTAGCATGCTACAATGGTTCACCATCTGGTGTTTATCAGTGTGCCATGAGACCTA
ATCATACCATTAAAGGTTCTTTCCTTAATGGATCATGTGGTAGTGTTGGTTTTAACATTGATTATGATTGC
GTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACACGCTGGTACTGACTTAGAAGGTAA
ATTCTATGGTCCATTTGTTGACAGACAAACTGCACAGGCTGCAGGTACAGACACAACCATAACATTAAATG
TTTTGGCATGGCTGTATGCTGCTGTTATCAATGGTGATAGGTGGTTTCTTAATAGATTCACCACTACTTTG
AATGACTTTAACCTTGTGGCAATGAAGTACAACTATGAACCTTTGACACAAGATCATGTTGACATATTGGG
ACCTCTTTCTGCTCAAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTGCAGAATG
GTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACACCATTTGATGTTGTTAGA
CAATGCTCTGGTGTTACCTTCCAAGGTAAGTTCAAGAAAATTGTTAAGGGCACTCATCATTGGATGCTTTT
AACTTTCTTGACATCACTATTGATTCTTGTTCAAAGTACACAGTGGTCACTGTTTTTCTTTGTTTACGAGA
ATGCTTTCTTGCCATTTACTCTTGGTATTATGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAG
CACGCATTCTTGTGCTTGTTTCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATATGGTCTACATGCC
TGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCTGGTTATAGGCTTA
AGGATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTTTATGATGAT
GCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTTACAAAGTCTACTATGGTAATGCTTT
AGATCAAGCTATTTCCATGTGGGCCTTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTA
TCATGTTTTTAGCTAGAGCTATAGTGTTTGTGTGTGTTGAGTATTACCCATTGTTATTTATTACTGGCAAC
ACCTTACAGTGTATCATGCTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTG
TTTACTCAACCGTTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTCTCTACACAAGAATTTAGGT
ATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATTGATGCTTTCAAGCTTAACATTAAGTTGTTG
GGTATTGGAGGTAAACCATGTATCAAGGTTGCTACTGTACAGTCTAAAATGTCTGACGTAAAGTGCACATC
TGTGGTACTGCTCTCGGTTCTTCAACAACTTAGAGTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTAC
AACTCCACAATGATATTCTTCTTGCAAAAGACACAACTGAAGCTTTCGAGAAGATGGTTTCTCTTTTGTCT
GTTTTGCTATCCATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTCGATAACCGTGCTAC
TCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCCGCTTATGCCACTGCCCAGGAGGCCT
ATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCT

FIGURE 3K

AAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCA
AATGTACAAACAGGCAAGATCTGAGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCA
CTATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGTTGTGTTCCA
CTCAACATCATACCATTGACTACAGCAGCCAAACTCATGGTTGTTGTCCCTGATTATGGTACCTACAAGAA
CACTTGTGATGGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAAGTTGTTGATGCGGATA
GCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATTCACCAAATTTGGCTTGGCCTCTTATTGTTACA
GCTCTAAGAGCCAACTCAGCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGATGTC
CTGTGCGGCTGGTACCACACAAACAGCTTGTACTGATGACAATGCACTTGCCTACTATAACAATTCGAAGG
GAGGTAGGTTTGTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGAT
GGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTTGTTACAGACACACCAAAAGGGCCTAA
AGTGAAATACTTGTACTTCATCAAAGGCTTAAACAACCTAAATAGAGGTATGGTGCTGGGCAGTTTAGCTG
CTACAGTACGTCTTCAGGCTGGAAATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCTTCTGTGCT
TTTGCAGTAGACCCTGCTAAAGCATATAAGGATTACCTAGCAAGTGGAGGACAACCAATCACCAACTGTGT
GAAGATGTTGTGTACACACACTGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAACATGGACCAAG
AGTCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGACCATCCAAATCCTAAAGGATTC
TGTGACTTGAAAGGTAAGTACGTCCAAATACCTACCACTTGTGCTAATGACCCAGTGGGTTTTACACTTAG
AAACACAGTCTGTACCGTCTGCGGAATGTGGAAAGGTTATGGCTGTAGTTGTGACCAACTCCGCGAACCCT
TGATGCAGTCTGCGGATGCATCAACGTTTTTAAACGGGTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGT
GCGGCACAGGCACTAGTACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAAGTTGCTGGTTTT
GCAAAGTTCCTAAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCAATTTATTAGACTCTTA
CTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAGAGACTATTTATAACTTGGTTAAAGATT
GTCCAGCGGTTGCTGTCCATGACTTTTTCAAGTTTAGAGTAGATGGTGACATGGTACCACATATATCACGT
CAGCGTCTAACTAAATACACAATGGCTGATTTAGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGA
TACATTAAAAGAAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATG
ACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAACTTAGGTGAGCGTGTACGCCAATCATTATTA
AAGACTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCGTACTGACATTAGATAATCAGGA
TCTTAATGGGAACTGGTACGATTTCGGTGATTTCGTACAAGTAGCACCAGGCTGCGGAGTTCCTATTGTGG
ATTCATATTACTCATTGCTGATGCCCATCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGAT
GCTGATCTCGCAAAACCACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGAAGAGAGACTTTGTCT
CTTCGACCGTTATTTTAAATATTGGGACCAGACATACCATCCCAATTGTATTAACTGTTTGGATGATAGGT
GTATCCTTCATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTACAAGTTTTGGACCACTA
GTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTTGTTTCAACTGGATACCATTTTCGTGAGTTAGGAGT
CGTACATAATCAGGATGTAAACTTACATAGCTCGCGTCTCAGTTTCAAGGAACTTTTAGTGTATGCTGCTG
ATCCAGCTATGCATGCAGCTTCTGGCAATTTATTGCTAGATAAACGCACTACATGCTTTTCAGTAGCTGCA
CTAACAAACAATGTTGCTTTTCAAACTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTGT
GTCTAAAGGTTTCTTTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTCTTTGCTCAGGATGGCAACG
CTGCTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACAATGTGTGATATCAGACAACTCCTATTC
GTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACGATGGTGGCTGTATTAATGCCAACCAAGTAATCGT
TAACAATCTGGATAAATCAGCTGGTTTCCCATTTAATAAATGGGGTAAGGCTAGACTTTATTATGACTCAA
TGAGTTATGAGGATCAAGATGCACTTTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATG
AATCTTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTAGTACTAT
GACAAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAATTG
GAACAAGCAAGTTTTACGGTGGCTGGCATAATATGTTAAAAACTGTTTACAGTGATGTAGAAACTCCACAC
CTTATGGGTTGGGATTATCCAAAATGTGACAGAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGT
TCTTGCTCGCAAACATAACACTTGCTGTAACTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGC
AAGTATTAAGTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTGAT
GCTACAACTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATGTAAATGCACTTCT
TTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTACAACACAGGCTCTATGAGTGTCTCT
ATAGAAATAGGGATGTTGATCATGAATTCGTGGATGAGTTTTACGCTTACCTGCGTAAACATTTCTCCATG
ATGATTCTTTCTGATGATGCCGTTGTGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGCTAGCAT
TAAGAACTTTAAGGCAGTTCTTTATTATCAAAATAATGTGTTCATGTCTGAGGCAAAATGTTGGACTGAGA
CTGACCTTACTAAAGGACCTCACGAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAGATGATTAC
GTGTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTGTCGATGATATTGTCAAAAC
AGATGGTACACTTATGATTGAAAGGTTCGTGTCACTGGCTATTGATGCTTACCCACTTACAAAACATCCTA
ATCAGGAGTATGCTGATGTCTTTCACTTGTATTTACAATACATTAGAAAGTTACATGATGAGCTTACTGGC
CACATGTTGGACATGTATTCCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTTA
TGAGGCTATGTACACACCACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGACTT

FIGURE 3L

CACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAGTGCTGCTATGACCATGTCATTTCA
ACATCACACAAATTAGTGTTGTCTGTTAATCCCTATGTTTGCAATGCCCCAGGTTGTGATGTCACTGATGT
GACACAACTGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGCCTCCCATTAGTTTTCCATTAT
GTGCTAATGGTCAGGTTTTTGGTTTATACAAAAACACATGTGTAGGCAGTGACAATGTCACTGACTTCAAT
GCGATAGCAACATGTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAA
GCTTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTGCCACTGTAC
GCGAAGTACTCTCTGACAGAGAATTGCATCTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGAACAGA
AACTATGTCTTTACTGGTTACCGTGTAACTAAAAATAGTAAAGTACAGATTGGAGAGTACACCTTTGAAAA
AGGTGACTATGGTGATGCTGTTGTGTACAGAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTG
TGTTGACATCTCACACTGTAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATT
ACTGGCTTGTACCCAACACTCAACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAGGTCGG
CATGCAAAAGTACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACTTGCTC
TCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATGCAGCTGTTGATGCCCTATGTGAAAAG
GCATTAAAATATTTGCCCATAGATAAATGTAGTAGAATCATACCTGCGCGTGCGCGCGTAGAGTGTTTTGA
TAAATTCAAAGTGAATTCAACACTAGAACAGTATGTTTTCTGCACTGTAAATGCATTGCCAGAAACAACTG
CTGACATTGTAGTCTTTGATGAAATCTCTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTT
CGTGCAAAACACTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCCGCACATTGCTGACTAAAGG
CACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAATAGGTCCAGACATGTTCCTTG
GAACTTGTCGCCGTTGTCCTGCTGAAATTGTTGACACTGTGAGTGCTTTAGTTTATGACAATAAGCTAAAA
GCACACAAGGATAAGTCAGCTCAATGCTTCAAAATGTTCTACAAAGGTGTTATTACACATGATGTTTCATC
TGCAATCAACAGACCTCAAATAGGCGTTGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTG
TTTTTATCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTGCCTACGCAGACTGTT
GATTCATCACAGGGTTCTGAATATGACTATGTCATATTCACACAAACTACTGAAACAGCACACTCTTGTAA
TGTCAACCGCTTCAATGTGGCTATCACAAGGGCAAAAATTGGCATTTTGTGCATAATGTCTGATAGAGATC
TTTATGACAAACTGCAATTTACAAGTCTAGAAATACCACGTCGCAATGTGGCTACATTACAAGCAGAAAAT
GTAACTGGACTTTTTAAGGACTGTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCT
CAGCGTTGATATAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT
ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATC
ACCCGCGAAGAAGCTATTCGTCACGTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAG
AGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA
CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAG
TTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAAT
GCTCAGTGATACACTGAAAGGATTGTCAGACAGAGTCGTGTTCGTCCTTTGGGCGCATGGCTTTGAGCTTA
CATCAATGAAGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTTGC
TTTTCTACTTCATCAGATACTTATGCCTGCTGGAATCATTCTGTGGGTTTTGACTATGTCTATAACCCATT
TATGATTGATGTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAGTAACCATGACCAACATTGCCAGGTAC
ATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTT
AAGCGCGTTGATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAGAAA
AGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATGACATTGGAAATC
CAAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGAC
AAAGCTTACAAAATAGAGGAACTCTTCTATTCTTATGCTACACATCACGATAAATTCACTGATGGTGTTTG
TTTGTTTTGGAATTGTAACGTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCT
TGTCAAACTTGAACTTACCAGGCTGTGATGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCA
GCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAATTGCCTTTCTTTTACTATTCTGATAGTCCTTGTGA
GTCTCATGGCAAACAAGTAGTGTCGGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACACGAT
GCAATTTAGGTGGTGCTGTTTGCAGACACCATGCAAATGAGTACCGACAGTACTTGGATGCATATAATATG
ATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATACATTTAC
CAGGTTACAGAGTTTAGAAAATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGGACACGCCGGCG
AAGCACCTGTTTCCATCATTAATAATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTGAA
AATAAGACAACACTTCCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTAAACCAGTGCCAGA
GATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTGTAATCTGGGACTACAAAAGAGAAG
CCCCAGCACATGTATCTACAATAGGTGTCTGCACAATGACTGACATTGCCAAGAAACCTACTGAGAGTGCT
TGTTCTTCACTTACTGTCTTGTTTGATGGTAGAGTGGAAGGACAGGTAGACCTTTTTAGAAACGCCCGTAA
TGGTGTTTTAATAACAGAAGGTTCAGTCAAAGGTCTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCA
ATGGAGTCACATTAATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACGGCATTATT
CAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTAAGCCCAGATCACAAATGGA
AACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGCGATATAAGCTCGAGGGCTATGCCTTCGAAC

FIGURE 3M

ACATCGTTTATGGAGATTTCAGTCATGGACAACTTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGC
TCACAAGATTCACCACTTAAATTAGAGGATTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAAC
AGATGCGCAAACAGGTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTCGAGA
TAATAAAGTCACAAGATTTGTCAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACTATGCTGAAATTTCA
TTCATGCTTTGGTGTAAGGATGGACATGTTGAAACCTTCTACCCAAAACTACAAGCAAGTCAAGCGTGGCA
ACCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAAGAATGCTTCTTGAAAAGTGTGACCTTCAGAATT
ATGGTGAAAATGCTGTTATACCAAAAGGAATAATGATGAATGTCGCAAAGTATACTCAACTGTGTCAATAC
TTAAATACACTTACTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGGTGCTGGCTCTGATAAAGG
AGTTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTCGATTCAGATCTTA
ATGACTTCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGCTAATAAATGG
GACCTTATTATTAGCGATATGTATGACCCTAGGACCAAACATGTGACAAAAGAGAATGACTCTAAAGAAGG
GTTTTTCACTTATCTGTGTGGATTTATAAAGCAAAAACTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAA
CAGAGCATTCTTGGAATGCTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTTACA
AATGTAAATGCATCATCATCGGAAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAAT
TGATGGCTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCCAGTTGTCTTCCTATT
CACTCTTTGACATGAGCAAATTTCCTCTTAAATTAAGAGGAACTGCTGTAATGTCTCTTAAGGAGAATCAA
ATCAATGATATGATTTATTCTCTTCTGGAAAAAGGTAGGCTTATCATTAGAGAAAACAACAGAGTTGTGGT
TTCAAGTGATATTCTTGTTAACAACTAAACGAACATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTG
GTAGTGACCTTGACCGGTGCACCACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCT
ATGAGGGGGGTTTACTATCCTGATGAAATTTTTAGATCAGACACTCTTTATTTAACTCAGGATTTATTTCT
TCCATTTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTGGCAACCCTGTCATACCTTTTA
AGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATGTTGTCCGTGGTTGGGTTTTTGGTTCTACCATG
AACAACAAGTCACAGTCGGTGATTATTATTAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTTGA
ATTGTGTGACAACCCTTTCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTCGATA
ATGCATTTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAAT
TTTAAACACTTACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACC
TATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGAAACCTATTTTTAAGTTGCCTCTTGGTA
TTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCT
GCAGCCTATTTTGTTGGCTATTTAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCAC
AGATGCTGTTGATTGTTCTCAAAATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA
AAGGAATTTACCAGACCTCTAATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACA
AACTTGTGTCCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCCTTCTGTCTATGCATGGGAGAGAAAAAA
AATTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACAACTCAACATTTTTTTCAACCTTTAAGTGCTATG
GCGTTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGA
GATGATGTAAGACAAATAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGA
TTTCATGGGTTGTGTCCTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATA
AATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCCCT
GATGGCAAACCTTGCACCCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATGGTTTTTACACCAC
TACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGG
TTTGTGGACCAAAATTATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACT
GGTACTGGTGTGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGA
TTTCACTGATTCCGTTCGAGATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCGCTTTTGGGGGTG
TAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACT
GATGTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATATATTCTACTGGAAACAATGT
ATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTA
TTGGAGCTGGCATTTGTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTG
GCTTATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAA
CTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATATGT
ACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTTGCACACAACTAAAT
CGTGCACTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTGAAGTGTTCGCTCAAGTCAAACAAAT
GTACAAAACCCCAACTTTGAAATATTTTGGTGGTTTTAATTTTTCACAAATATTACCTGACCCTCTAAAGC
CAACTAAGAGGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAG
CAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTTAC
AGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTGCTGCTCTAGTTAGTGGTACTGCCA
CTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTATGCAAATGGCATATAGGTTC
AATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAACAAATCGCCAACCAATTTAACAAGGC
GATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACC

FIGURE 3N

AGAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTA
AATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACT
TCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCTTG
CTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCAC
CTTATGTCCTTCCCACAAGCAGCCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTGCCATCCCAGGA
GAGGAACTTCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTTTTG
TGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAATTACTACAGACAAT
ACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTATGATCCTCTGCAACC
TGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATACATCACCAGATGTTGATCTTG
GCGACATTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCT
AAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTG
GTATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTGTTGCATGA
CTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAAGTTTGATGAGGATGACTCT
GAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAACGAACTTATGGATTTGTTTATGAGATTTTTT
ACTCTTAGATCAATTACTGCACAGCCAGTAAAAATTGACAATGCTTCTCCTGCAAGTACTGTTCATGCTAC
AGCAACGATACCGCTACAAGCCTCACTCCCTTTCGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTT
TTCAGAGCGCTACCAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCAGTTC
ATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGCTTGTCGCTGCAGGTATGGAGGC
GCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCATCAACGCATGTAGAATTATTATGAGAT
GTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCCATTACTTTATGATGCCAACTACTTTGTTTGCTGGCAC
ACACATAACTATGACTACTGTATACCATATAACAGTGTCACAGATACAATTGTCGTTACTGAAGGTGACGG
CATTTCAACACCAAAACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACTCAGGTGTTA
AAGACTATGTCGTTGTACATGGCTATTTCACCGAAGTTTACTACCAGCTTGAGTCTACACAAATTACTACA
GACACTGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAAAGACCCACCGAATGTGCAAAT
ACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGCAATGGATCCAATTTATGATGAGCCGACGACGA
CTACTAGCGTGCCTTTGTAAGCACAAGAAAGTGAGTACGAACTTATGTACTCATTCGTTTCGGAAGAAACA
GGTACGTTAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTCGTGGTATTCTTGCTAGTCACACTAGCCAT
CCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAACGGTTT
ACGTCTACTCGCGTGTTAAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCTGGTCTAAACGAACTAA
CTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATGGCAGACAACGGTACTATTACCGTTGAG
GAGCTTAAACAACTCCTGGAACAATGGAACCTAGTAATAGGTTTCCTATTCCTAGCCTGGATTATGTTACT
ACAATTTGCCTATTCTAATCGGAACAGGTTTTTGTACATAATAAAGCTTGTTTTCCTCTGGCTCTTGTGGC
CAGTAACACTTGCTTGTTTTGTGCTTGCTGCTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT
GCAATGGCTTGTATTGTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCCTTCAGGCTGTTTGCTCGTAC
CCGCTCAATGTGGTCATTCAACCCAGAAACAAACATTCTTCTCAATGTGCCTCTCCGGGGGACAATTGTGA
CCAGACCGCTCATGGAAAGTGAACTTGTCATTGGTGCTGTGATCATTCGTGGTCACTTGCGAATGGCCGGA
CACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTC
TTATTACAAATTAGGAGCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTA
TTGGAAACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAGTAAGTG
ACAACAGATGTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGATTATCATTATGAGGACTT
TCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATTTAAGCCTCTAACT
AAGAAGAATTATTCGGAGTTAGATGATGAAGAACCTATGGAGTTAGATTATCCATAAAACGAACATGAAAA
TTATTCTCTTCCTGACATTGATTGTATTTACATCTTGCGAGCTATATCACTATCAGGAGTGTGTTAGAGGT
ACGACTGTACTACTAAAAGAACCTTGCCCATCAGGAACATACGAGGGCAATTCACCATTTCACCCTCTTGC
TGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGCTTGTGCTGACGGTACTCGACATA
CCTATCAGCTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGACAAGAGGAGGTTCAACAAGAGCTC
TACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTATTTTTAATACTTTGCTTCACCATTAAGAGAAAGAC
AGAATGAATGAGCTCACTTTAATTGACTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCCTTGTTTTAAT
AATGCTTATTATATTTTGGTTTTCACTCGAAATCCAGGATCTAGAAGAACCTTGTACCAAAGTCTAAACGA
ACATGAAACTTCTCATTGTTTTGACTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACAGCGCTGT
GCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGGGTAATACTTATAGCACTG
CTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGATGGCACACTATGGTTCAAACATGCACACCT
AATGTTACTATCAACTGTCAAGATCCAGCTGGTGGTGCGCTTATAGCTAGGTGTTGGTACCTTCATGAAGG
TCACCAAACTGCTGCATTTAGAGACGTACTTGTTGTTTTAAATAAACGAACAAATTAAAATGTCTGATAAT
GGACCCCAATCAAACCAACGTAGTGCCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAATAA
CCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCCAATAATACTGCGT
CTTGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAACTTAGATTCCCTCGAGGCCAGGGCGTTCCAATC

FIGURE 3O

AACACCAATAGTGGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGA
CGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTC
CCTACGGCGCTAACAAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCAC
ATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAACTTCCTCAAGGAACAACATTGCCAAA
AGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTA
ATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAATGGCTAGCGGAGGTGGTGAA
ACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACA
ACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTG
CCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTTCGGG
GACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAATTTGCTCCAAGTGC
CTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTGACTTATCATG
GAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGAC
GCATACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTT
GCCGCAGAGACAAAAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGAC
AACTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAA
GGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTACGATACATAGTCTACTCTTGTGCAGAATGAAT
TCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTA
ACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGT
GAATAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCC
CCATGTGATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAAA

GenBank Accession No. AY274119.2.; SEQ ID NO: 2

FIGURE 3P

```
ERV-2    ------------------------------------------------------------
TOR2     ACACTCATGATGACCACACAAGGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTA
AIBV     ------------------------------------------------------------

ERV-2    ------------------------------------------------------------
TOR2     CGATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAGTAGGTT
AIBV     ------------------------------------------------------------

ERV-2    ------------------------------------ACCCGTTACCCTAAAATTCCCTCC
TOR2     TAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTG
AIBV     -------------------------------------TAGTTTAGTTTAAGTTAGTTTAG
                                                  * *   **      *

ERV-2    CCTTTCTCTTCAC------TCGCCGAGGCCACGCCGAGTAGGACCGAGGGTACAGC----
TOR2     AAAGAGCCACCACATTT--TCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGT----
AIBV     AGTAGGTATAAAGATGCCAGTGCCGGGGCCACGCGGAGTACGATCGAGGGTACAGCACTA
                     *            ** ******** ***** ** ***********

ERV-2    -GAGTCTTT-TAGTTTAAGGTGT-TAGATGTAAGGTACGTGGGCTTTCT--TTTGGTTTA
TOR2     -GAATAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTA
AIBV     GGACGCCCATTAGGGGAAGA-GCTAAATTTTAGTTTAAGTTAAGTTTAA---TTGGCTAA
          **      ***    **  *   *  *  *         *   * *     *   * *

ERV-2    CTTCTTC--------------------------------------- GenBank: AF361253 (SEQ ID NO: 31)
TOR2     GTAGTGCTATCCCCATGTGATTTTAATAGCTTCTTAGGAGAATGAC (SEQ ID NO: 18)
AIBV     GTATAGTTAAAATTTATAGGCTAGTATAGAGTTAGAGCA------- GenBank: NC_001451 (SEQ ID NO: 32)
          *
```

Figure 4

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSD
TLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRG
WVFGSTMNNKSQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMGTQTHT
MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGY
QPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAA
AYFVGYLKPTTFMLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIY
QTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVA
DYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPG
QTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRP
FERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLS
FELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQ
FGRDVSDFTDSVRDPKTSEILDISPCAFGGVSVITPGTNASSEVAVLYQD
VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDI
PIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNF
SISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALS
GIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFI
EDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDD
MIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE
NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS
NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI
RASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYV
PSQERNFTTAPAICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITTD
NTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGD
ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL
GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGV
KLHYT (SEQ ID NO: 33)

Figure 5

MADNGTITVEELKQLLEQWNLVIGFLFLAWIMLLQFAYSNRNRFLYIIKL
VFLWLLWPVTLACFVLAAVYRINWVTGGIAIAMACIVGLMWLSYFVASFR
LFARTRSMWSFNPETNILLNVPLRGTIVTRPLMESELVIGAVIIRGHLRM
AGHSLGRCDIKDLPKEITVATSRTLSYYKLGASQRVGTDSGFAAYNRYRI
GNYKLNTDHAGSNDNIALLV (SEQ ID NO: 34)

Figure 6

MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVS
LVKPTVYVYSRVKNLNSSEGVPDLLV (SEQ ID NO: 35)

Figure 7

MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNT
ASWFTALTQHGKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDG
KMKELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTR
NPNNNAATVLQLPQGTTLPKGFYAEGSRGGSQASSRSSSRSRGNSRNSTP
GSSRGNSPARMASGGGETALALLLLDRLNQLESKVSGKGQQQQGQTVTKK
SAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGTDYK
HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDN
VILLNKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLLPAAD
MDDFSRQLQNSMSGASADSTQA (SEQ ID NO: 36)

Figure 8

```
BoCov           -----------------------------MSSVTTPAP--VYTWTADEAIKFLKEWNFSL
OC43            -----------------------------MSSKTTPAP--VYIWTADEAIKFLKEWNFSL
PHEV            -----------------------------MSSPTTPVP--VISWTADEAIKFLKEWNFSL
FCV             MKILLILACAVACVYGEQIRYCAMQ-ETGLSCRNGTASDCESCFNGGDLIWHLANWNFSW
TGEV            MKILLILACVIACACGE--RYCAMKSDTDLSCRNSTASDCESCFNGGDLIWHLANWNFSW
TOR2_M          -----------------------------------MAD--NGTITVEELKQLLEQWNLVI
ORF5            -----------------------------------MAD--NGTITVEELKQLLEQWNLVI
AIBV2           ----------------------------------MMEN---CTLNLEQATLLFKEYNLFI
AIBV            -------------------------------MSNGTEN---CTLSTQQAAELFKEYNLFI
                                                             .  :   : ::*:

BoCov           GIILLFITVILQFGYTSRSMFVYVIKMVILWLMWPLTIILTIFNCV--YALNN-VYLGFS
OC43            GIILLFITIILQFGYTSRSMFVYVIKMIILWLMWPLTIILTIFNCV--YALNN-VYLGLS
PHEV            GIIVLFITIILQFGYTSRSMFVYVIKMVILWLMWPLTIILTIFNCV--YALNN-VYLGFS
FCV             SIILIVFITVLQYGRPQFSWFVYGIKMLIMWLLWPIVLALTIFNAYSEYEVSRYVMFGFS
TGEV            SIILIVFITVLQYGRPQFSWFVYGIKMLIMWLLWPVVLALTIFNAYSEYQVSRYVMFGFS
TOR2_M          GFLFLAWIMLLQFAYSNRNRFLYIIKLVFLWLLWPVTLACFVLAAV--YRINW-VTGGIA
ORF5            GFLFLAWIMLLQFAYSNRNRFLYIIKLVFLWLLWPVTLACFVLAAV--YRINW-VTGGIA
AIBV2           TAFLLFLTILLQYGYATRSRFIYILKMIVLWCFWPLNIAVGVISCI--YPPNT-GGLVAA
AIBV            TAFLLFLTILLQYGYATRSRFIYILKMIVLWCFWPLNIAVGIISCI--YPPNT-GGLVAA
                  :.:    :**:. .  . *:* :*::.:* :**: :   :: .   *   .      :

BoCov           IVFTIVAIIMWIVYFVNSIRLFIRTGSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYHTL
OC43            IVFTIVAIIMWIVYFVNSIRLFIRTGSFWSFNPETNNLMCIDMK-GTMYVRPIIEDYHTL
PHEV            IVFTIVAIIMWVVYFVNSIRLFIRTGSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYHTL
FCV             VAGAVVTFALWMMYFVRSIQLYRRTKSWWSFNPETNAILCVNAL-GRSYVLPLDGTPTGV
TGEV            IAGAIVTFVLWIMYFVRSIQLYRRTKSWWSFNPETKAILCVSAL-GRSYVLPLEGVPTGV
TOR2_M          IAMACIVGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLR-GTIVTRPLMESELVI
ORF5            IAMACIVGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLR-GTIVTRPLMESELVI
AIBV2           IILTVFACLSFVGYWIQSCRLFKRCRSWWSFNPESNAVGSILLTNGQQCNFAIESVPMVL
AIBV            IILTVFACLSFVGYWIQSFRLFKRCRSWWSFNPESNAVGSILLTNGQQCNFAIESVPMVL
                :  : ..   :: *:: * :*: *  * ******:: :  :    *     .:      :

BoCov           TVTIIRGHLYMQGIKLGTGYSLSDLPAYVTVAKVSHLLTYKR---GFLDKIGDTSGFAVY
OC43            TVTIIRGHLYIQGIKLGTGYSWADLPAYMTVAKVTHLCTYKR---GFLDRISDTSGFAVY
PHEV            TATIIRGHLYIQGIKLGTGYSLSDLPAYVTVAKVTHLCTYKR---GFLDRIGDTSGFAVY
FCV             TLTLLSGNLYAEGFKMAGGLTIEHLPKYVMIRTPNRTIVYTLV--GKQLKATTATGWAYY
TGEV            TLTLLSGNLYAEGFKIAGGMNIDNLPKYVMVALPSRTIVYTLV--GKKLKASSATGWAYY
TOR2_M          GAVIIRGHLRMAGHSLGR-CDIKDLPKEITVAT-SRTLSYYKL--GASQRVGTDSGFAAY
ORF5            GAVIIRGHLRMAGHSLGR-CDIKDLPKEITVAT-SRTLSYYKL--GASQRVGTDSGFAAY
AIBV2           APIIKNGVLYCEGQWLAK-CEPDHLPKDIFVCTPDRRNIYRMVQKYTGDQSGNKKRVATF
AIBV            SPIIKNGALYCEGQWLAK-CEPDHLPKDIFVCTPDRRNIYRMVQKYTGDQSGNKKRFATF
                    :  * *   *  :.      .**  : :   :   *         :    .  * :

BoCov           VKSKVGNYRLPSTQKGSGLDTALLRNNI
OC43            VKSKVGNYRLPSTQKGSGMDTALLRNNI
PHEV            VKSKVGNYRLPSTHKGSGMDTALLRNNI
FCV             VKSKAGDYSTEARTDNLSEHEKLLHMV-
TGEV            VKSKAGDYSTEARTDNLSEQEKLLHMV-
TOR2_M          NRYRIGNYKLNTDHAGSNDNIALLVQ--
ORF5            NRYRIGNYKLNTDHAGSNDNIALLVQ--
AIBV2           VYAKQSVDTGELESVPTGGSSLYT----
AIBV            VYAKQSVDTGELGSVATGGSSLYT----
                   : .              .
```

Key	Name	Genbank	%ID	
PHEV	Porcine hemagglutinating encephalomyelitis virus	AAL80035	40.4%	(SEQ ID NO: 37)
BoCov	matrix protein [Bovine coronavirus].	NP_150082	40.0%	(SEQ ID NO: 38)
AIBV	membrane protein [Avian infectious bronchitis virus].	AAF35863	31.3%	(SEQ ID NO: 39)
TGEV	membrane protein [Transmissible gastroenteritis virus].	NP_058427	28.5%	(SEQ ID NO: 40)
FCV	membrane [feline coronavirus].	BAC01160	27.7%	(SEQ ID NO: 41)
OC43	membrane glycoprotein [Human coronavirus OC43].	AAA45462	39.1%	(SEQ ID NO: 42)
AIBV2	membrane protein [Avian infectious bronchitis virus].	AAK83027	32.0%	(SEQ ID NO: 43)
TOR2_M/ORF 5	Sars associated coronavirus M glycoprotein			(SEQ ID NO: 34)

Figure 9

```
BoCov      MSFTPGKQSS-SRASSGNRSGNGILK---WADQSDQSRNVQTRGRRAQP--KQTATSQQP
OC43       MSFTPGKQSS-SRASSGNRSGNGILK---WADQSDQVRNVQTRGRRAQP--KQTATSQQP
PHEV       MSFTPGKQSS-SRASSGNRSGNGILK---WADQSDQSRNVQTRGRRVQS--KQTATSQQP
MHV        MSFVPGQENAGSRSSSVNRAGNGILKKTTWADQTERGPNNQNRGRRNQP--KQTATTQ-P
AIBV2      ----------------MASGKAAGK---TDAPAPVIK----LGGPKPP--KVGSSGN--
TCV        ----------------MASGKATGK---TDAPAPIIK----LGGPKPP--KVGSSGN--
AIBV       ----------------MASGKAAGK---TDAPAPVIK----LGGPKPP--KVGSSGN--
FCV        ----------------MATQGQRVN---WGDEPSKRR-----GRSNSR--GRKNNDIP-
PTGV       ----------------MANQGQRVS---WGDESTKTR-----GRSNSR--GRKNNNIP-
229E       --------------------MATVK---WADASEPQR-----GRQ-----GRIPYSL--
TOR2_N     -----------MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPN
                                              .        *

BoCov      SGGNVVPYYSWFSGITQFQKGKEFEFAEGQGVPIAPGVPATEAKGYWYRHNRRSFKTADG
OC43       SGGNVVPYYSWFSGITQFQKGKEFEFVEGQGPPIAPGVPATEAKGYWYRHNRGSFKTADG
PHEV       SGGTVVPYYSWFSGITQFQKGKEFEFAEGQGVPIAPGVPSTEAKGYWYRHNRRSFKTADG
MHV        NSGSVVPHYSWFSGITQFQKGKEFQFAQGQGVPIANGIPASEQKGYWYRHNRRSFKTPDG
AIBV2      AS--------WFQAIKAKKLNTPPPKFEGSGVPDNENIKPSQQHGYWRRQAR--FKPGKG
TCV        AS--------WFQSIKAKKLNSPQPKFEGSGVPDNENIKTSQQHGYWRRQAR--FKPGKG
AIBV       AS--------WFQALKAKKLNAPAPKFEGSGVPDNENLKISQQHGYWRRQAR--YKPGKG
FCV        LS--------YFNPITLDQGSKFWNLCPRDFVPKGIGNK-DQQIGYWNRQAR--YRIVKG
PTGV       LS--------FFNPITLQQGSKFWNLCPRDFVPKGIGNR-DQQIGYWNRQTR--YRMVKG
229E       -Y----------SPLLVDS-EQPWKVIPRNLVPINKKDK-NKLIGYWNVQKR--FRTRKG
TOR2_N     NTAS------WFTALTQHG-KEELRFPRGQGVPINTNSGPDDQIGYYRRATRR-VRGGDG
                     :            .  *        .  **:     *    :  .*

BoCov      NQRQLLPRWYFYYLGTGPHAKDQYGTDIDGVYWVASNQADVNTPADILDRDPSSDEAIPT
OC43       NQRQLLPRWYFYYLGTGPHAKDQYGTDIDGVYWVASNQADVNTPADIVDRDPSSDEAIPT
PHEV       NQRQLLPRWYFYYLGTGPHAKDQYGTDIDGVFWVASNQADINTPADIVDRDPSSDEAIPT
MHV        QQKQLLPRWYFYYLGTGPHAGAEYGDDIDGVVWVASQQADTKTTADIVERDPSSHEAIPT
AIBV2      GRKPVPDAWYFYYTGTGPAADLNWGDTQDGIVWVAAKGADTKSRSNQGTRDPDKFDQYPL
TCV        GRKPVPDAWYFYYTGTGPAADLNWGDTQDGIVWVAAKGADVKSRSNQGTRDPDKFDQYPL
AIBV       GRKPVPDAWYFYYTGTGPAADLNWGDSQDGIVWVAAKGADVKSRSNQGTRDPDKFDQYPL
FCV        QRVELPERWFFYFLGTGPHADAKFKAKIDGVFWVARDGAMN-KPTSLGTRG-TNNESKPL
PTGV       QRKELPERWFFYYLGTGPHADAKFKDKLDGVVWVAKDGAMN-KPTTLGSRG-ANNESKAL
229E       KRVDLSPKLHFYYLGTGPHKDAKFRERVEGVVWVAVDGAKT-EPTGYGVRR-KNSEPEIP
TOR2_N     KMKELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
              :      .**: ****     :     :*: *** . *        *    .

BoCov      RFPPGTVLPQGYYIEGS-GRSAPNSRSTSRASSRASSA---GSRSRANSGNR---TPTSG
OC43       RFPPGTVLPQGYYIEGS-GRSAPNSRSTSRTSSRASSA---GSRSRANSGNR---TPTSG
PHEV       RFPPGTVLPQGYYIEGS-GRSAPNSRSTSRAPNRAPSA---GSRSRANSGNR---TSTPG
MHV        RFAPGTVLPQGFYVEGS-GRSAPASRSGSRSQSRGP-----NNRARSSSNQR---QPAST
AIBV2      RFSDG--GPDGNFRWDF-IPLKNRGRSG-RSTAASSAA---ASRAPSREGSR---GRRSD
TCV        RFSDG--GPDSNFRWDF-IPLH-RGRSG-RSTAASSAA---SSRAPSRDGSR---GRRSG
AIBV       RFSDG--GPDGNFRWDF-IPLN-RGRSG-RSTAASSAA---SSRAPSREGSR---GRLNG
FCV        KFDGK-IPPQFQLEVNR-SRNNSRSGSQSRSVSRNRS----QSRGRQQSNNQ--NTNVED
PTGV       KFDGK-VPGEFQLEVNQ-SRDNSRLRSQSRSRSRNRS----QSRGRQQSNNKK-DDSVEQ
229E       HFNQK--LPNGVTVVEE-PDSRAPSRSQSRSQSRGRGESKPQSRNPSSDRNHNSQDDIMK
TOR2_N     QLPQGTTLPKGFYAEGSRGGSQASSRSSSRSRGNSRNSTPGSSRGNSPARMAS-GGGETA
           ::        .                *   *:            .*

BoCov      VTPDMADQIASLVLAKLGKDAAKP-----------------QQVTKQTAKEIRQK--IL
OC43       VTPDMADQIASLVLAKLGKDATKP-----------------QQVTKHTAKEVRQK--IL
PHEV       VTPDMADQIASLVLAKLGKDATKP-----------------QQVTKQTAKEVRQK--IL
MHV        VKPDMAEEIAALVLAKLGKDAGQP-----------------KQVTKQSAKEVRQK--IL
AIBV2      SGDDLIARAAKIIQDQQKKGS--------------------RITKAKADEMAHR--RY
TCV        SEDDLIARAAKIIQDQQKKGS--------------------RITKAKADEMAHR--RY
AIBV       AEDDLIARAAKIIQDQQKKGS--------------------RITKAKAEEMIHR--RY
FCV        TIVAVLQKLGVTDK---QRSRSKS-----------------GERSQSKSRDTTPK--NA
PTGV       AVLAALKKLGVYTEKQQQRSRSKS-----------------KERSNSKIRDTTPK--NE
229E       AVAAALKSLGFDKPQEKDKKSAKTGTPKPSRNQSPASSQTSAKSLARSQSSETKEQKHEM
TOR2_N     LALLLLDRLNQLESKVSGKGQQQQG----------------QTVTKKSAAEASKK--PR
                          :                           :.    :    :
```

FIGURE 10A

```
BoCov      NKPRQKRSPNKQCT--VQQCFGKR---GPNQNFGGGEMLKLGTSDPQFPILAELAPTAGA
OC43       NKPRQKRSPNKQCT--VQQCFGKR---GPNQNFGGGEMLKLGTSDPQFPILAELAPTAGA
PHEV       NKPRQKRSPNKQCT--VQQCFGKR---GPNQNFGGGEMLKLGTSDPQFPILAELAPTAGA
MHV        NKPRQKRTPNKQCP--VQQCFGKR---GPNQNFGGSEMLKLGTSDPQFPILAELAPTPSA
AIBV2      CK----RTIPPNYR--VDQVFGPRT-KGKEGNFGDDKMNEEGIKDGRVTAMLNLVPSSHA
TCV        CK----RTVPPGYK--VDQVFGPRT-KGKEGNFGDDKMNEEGIKDGRVTAMLNLVPSSHA
AIBV       CK----RTVPPGVS--IDKVFGPRT-KGKEGNFGDDKMNEEGIKDGRVTAMLNLVPSSHA
FCV        NKHTWKKTAGKGD---VTNFYGAR---SSSANFGDSDLVANGNAAKCYPQIAECVPSVSS
PTGV       NKHTWKRTAGKGD---VTRFYGTR---SNSANFGDSDLVANGSSAKHYPQLAECVPSVSS
229E       QKPRWKRQPNDDVTSNVTQCFGPR---DLDHNFGSAGVVANGVKAKGYPQFAELVPSTAA
TOR2_N     QK----RTATKQYN--VTQAFGRRGPEQTQGNFGDQDLIRQGTDYKHWPQIAQFAPSASA
            *    :         : . :* *     . ***.  :   *      . : : .*:  :

BoCov      FFFGSRLELAKVQNLSGNLDEPQKDVYELRYNGAIR-----FDSTLSGFETIMKVLNENL
OC43       FFFGSRLELAKVQNLSGNPDEPQKDVYELRYNGAIR-----FDSTLSGFETIMKVLNENL
PHEV       FFFGSRLELAKVQNLSGNPDEPQKDVYELRYNGAIR-----FDSTLSGFETIMKVLNQNL
MHV        FFFGSKLELVKKN--SGGADDPTKDVYELQYSGAIR-----FDSTLPGFETIMKVLNENL
AIBV2      CLFGSRVTPKLQL--DGLHLRFEFTTVVPCDDPQFDNYVKICDQCVDGVGTRPKDDEPKP
TCV        CLFGSRVTPKLQP--DGLHLRFEFTTVVPRDDPQFDNYVTICDQCVDGIGTRPKDNEPRP
AIBV       CLFGSQVTPKLQP--DGLHLTFRFTTVVSRDDPQFDNYVKICDECVDGVGTRPKDEVVRP
FCV        ILFGSQWSAEEAG--DQVKVTLTHNYYLPKDDAKTS------------------QFLEQI
PTGV       ILFGSYWTSKEDG--DQIEVTFTHKYHLPKDDPKTG------------------QFLQQI
229E       MLFDSHIVSKESG--NTVVLTFTTRVTVPKDHPHLG------------------KFLEEL
TOR2_N     FFGMSRIGMEVTP--SGTWLTYHGAIKLDDKDPQFK------DN--------VILLNKHI
            :  *          .                                          .

BoCov      NAYQQQ-DGTMNMSPKPQRQRG----QKNGQGENDNISVAAPKSRVQQNKIRELTAEDIS
OC43       NAYQQQ-DGMMNMSPKPQRQRG----HKNGQGENDNISVAVPKSRVQQNKSRELTAEDIS
PHEV       NAYQHQEDGMMNISPKPQRQRG----QKNGQVENDNVSVAAPKSRVQQNKSRELTAEDIS
MHV        DAYQDQAGGADVVSPKPQRKRGT--KQKALKGEVDNVSVAKPKSSVQRNVSRELTPEDRS
AIBV2      KSRSSSRPATRGNSPAPRQQRPK--KEKKLKKQDDEADKALTSDEERNNAQLEFYDEP-K
TCV        KSRPSSRPATRGNSPAPRQQRPK--KEKKPKKQDDEVDKALTSDEERNNAQLEFDDEP-K
AIBV       KSRSSSRPATRGTSPAPKQQRPK--KEKKPKKQDDEVDKALTSDEERNNAQLEFDDEP-K
FCV        DAYKRP-------SEVAKDQRQ----RKSRSKSADKKPEELS--VTLEAYTDVFDDTQVE
PTGV       NAYARP-------SEVAKEQRK----RKSRSKSAERSEQEVVPDALIENYTDVFDDTQVE
229E       NAPTRE-----------MQQHP------LLNPSALEFNPSQTSPATAEPVRDEVSIET-D
TOR2_N     DAYKTFPP----TEPKKDKKKKTDEAQPLPQRQKKQPTVTLLPAADMDDFSRQLQNSMSG
           .:                 ::         . .  .                 .

BoCov      LLKKMDEP-----FTEDTSEI
OC43       LLKKMDEP-----YTEDTSEI
PHEV       LLKKMDEP-----YTEDTSEI
MHV        LLAQILDDGVVPDGLEDDSNV
AIBV2      VINWGDAA-----LGENEL--
TCV        VINWGDSA-----LGENHL--
AIBV       VINWGDSA-----LGENEL--
FCV        MIDEVTN--------------
PTGV       MIDEVTN--------------
229E       IIDEVN---------------
TOR2_N     ASADSTQA-------------
```

Key

		Genbank	*%ID	
MHV	NUCLEOCAPSID PROTEIN	P18446	34.3%	(SEQ ID NO: 44)
BoCov	nucleocapsid protein [Bovine coronavirus].	NP_150083	34.4%	(SEQ ID NO: 45)
AIBV	nucleocapsid protein [Avian infectious bronchitis virus].	AAK27162	28.3%	(SEQ ID NO: 46)
FCV	nucleocapsid [Feline coronavirus].	CAA74230	29.4%	(SEQ ID NO: 47)
PTGV	nucleoprotein [porcine transmissible gastroenteritis virus].	AAM97563	28.0%	(SEQ ID NO: 48)
229E	nucleocapsid protein [Human coronavirus 229E].	NP_073556	24.6%	(SEQ ID NO: 49)
OC43	NUCLEOCAPSID PROTEIN.	P33469	33.9%	(SEQ ID NO: 50)
PHEV	nucleocapsid protein [porcine hemagglutinating encephalomyelitis]	AAL80036	33.3%	(SEQ ID NO: 51)
TCV	nucleocapsid protein [turkey coronavirus].	AAP23873	28.2%	(SEQ ID NO: 52)
TOR_N	SARS associated virus nucleocapsid protein (SEQ ID NO: 36)			

FIGURE 10B

ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTG
TAGATCTGTTCTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGC
TGCATGCCTAGTGCACCTACGCAGTATAAACAATAATAAATTTTACTGTC
GTTGACAAGAAACGAGTAACTCGTCCCTCTTCTGCAGACTGCTTACGGTT
TCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTCGTCCGGGTGT
GACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA
CACGTCCAACTCAGTTTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCG
TGGCTTCGGGGACTCTGTGGAAGAGGCCCTATCGGAGGCACGTGAACACC
TCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAAAAAGGCGTACTGCCC
CAGCTTGAACAGCCCTATGTGTTCATTAAACGTTCTGATGCCTTAAGCAC
CAATCACGGCCACAAGGTCGTTGAGCTGGTTGCAGAAATGGACGGCATTC
AGTACGGTCGTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGC
GAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAA
GGGAGCCGGTGGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAG
GTGACGAGCTTGGCACTGATCCCATTGAAGATTATGAACAAAACTGGAAC
ACTAAGCATGGCAGTGGTGCACTCCGTGAACTCACTCGTGAGCTCAATGG
AGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGCCCAGATGGGT
ACCCTCTTGATTGCATCAAAGATTTTCTCGCACGCGCGGGCAAGTCAATG
TGCACTCTTTCCGAACAACTTGATTACATCGAGTCGAAGAGAGGTGTCTA
CTGCTGCCGTGACCATGAGCATGAAATTGCCTGGTTCACTGAGCGCTCTG
ATAAGAGCTACGAGCACCAGACACCCTTCGAAATTAAGAGTGCCAAGAAA
TTTGACACTTTCAAAGGGGAATGCCCAAAGTTTGTGTTTCCTCTTAACTC
AAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAGACTGAGGGTT
TCATGGGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGT
AACAATATGCACTTGTCTACCTTGATGAAATGTAATCATTGCGATGAAGT
TTCATGGCAGACGTGCGACTTTCTGAAAGCCACTTGTGAACATTGTGGCA
CTGAAAATTTAGTTATTGAAGGACCTACTACATGTGGGTACCTACCTACT
AATGCTGTAGTGAAAATGCCATGTCCTGCCTGTCAAGACCCAGAGATTGG
ACCTGAGCATAGTGTTGCAGATTATCACAACCACTCAAACATTGAAACTC
GACTCCGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCC
TATGTTGGCTGCTATAATAAGCGTGCCTACTGGGTTCCTCGTGCTAGTGC
TGATATTGGCTCAGGCCATACTGGCATTACTGGTGACAATGTGGAGACCT
TGAATGAGGATCTCCTTGAGATACTGAGTCGTGAACGTGTTAACATTAAC
ATTGTTGGCGATTTTCATTTGAATGAAGAGGTTGCCATCATTTTGGCATC
TTTCTCTGCTTCTACAAGTGCCTTTATTGACACTATAAAGAGTCTTGATT
ACAAGTCTTTCAAAACCATTGTTGAGTCCTGCGGTAACTATAAAGTTACC
AAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGT
TTTAACACCACTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGAT
CAATTTTTGCGCGCACACTTGATGCAGCAAACCACTCAATTCCTGATTTG
CAAAGAGCAGCTGTCACCATACTTGATGGTATTTCTGAACAGTCATTACG
TCTTGTCGACGCCATGGTTTATACTTCAGACCTGCTCACCAACAGTGTCA
TTATTATGGCATATGTAACTGGTGGTCTTGTACAACAGACTTCTCAGTGG
TTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATCTTTGA
ATGGATTGAGGCGAAACTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTT
GGGAGATTCTCAAATTTCTCATTACAGGTGTTTTTGACATCGTCAAGGGT
CAAATACAGGTTGCTTCAGATAACATCAAGGATTGTGTAAAATGCTTCAT
TGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCG
CTGGCGCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAA
AGCAAGGGACTTTACCGTCAGTGTATACGTGGCAAGGAGCAGCTGCAACT
ACTCATGCCTCTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATT
CACATGACACAGTACTTACCTCTGAGGAGGTTGTTCTCAAGAACGGTGAA
CTCGAAGCACTCGAGACGCCCGTTGATAGCTTCACAAATGGAGCTATCGT
TGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAGATTAAGGACA
AAGAACAATACTGCGCATTGTCTCCTGGTTTACTGGCTACAAACAATGTC
TTTCGCTTAAAAGGGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGA
TACTGTTTGGGAAGTTCAAGGTTACAAGAATGTGAGAATCACATTTGAGC
TTGATGAACGTGTTGACAAAGTGCTTAATGAAAAGTGCTCTGTCTACACT

FIGURE 11A

GTTGAATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCAGAGGC
TGTTGTGAAGACTTTACAACCAGTTTCTGATCTCCTTACCAACATGGGTA
TTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCT
GGTGAAGAAAACTTTTCATCACGTATGTATTGTTCCTTTTACCCTCCAGA
TGAGGAAGAAGAGGACGATGCAGAGTGTGAGGAAGAAGAAATTGATGAAA
CCTGTGAACATGAGTACGGTACAGAGGATGATTATCAAGGTCTCCCTCTG
GAATTTGGTGCCTCAGCTGAAACAGTTCGAGTTGAGGAAGAAGAAGAGGA
AGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAG
AACCTACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAAACTT
ACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAG
TGCTAATCCTATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATG
GTGGTGGTGTAGCAGGTGCACTCAACAAGGCAACCAATGGTGCCATGCAA
AAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGTAGGAGG
GTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGTCTGCATGTTG
TTGGACCTAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCA
TATGAAAATTTCAATTCACAGGACATCTTACTTGCACCATTGTTGTCAGC
AGGCATATTTGGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGA
CGGTTCGTACACAGGTTTATATTGCAGTCAATGACAAAGCTCTTTATGAG
CAGGTTGTCATGGATTATCTTGATAACCTGAAGCCTAGAGTGGAAGCACC
TAAACAAGAGGAGCCACCAAACACAGAAGATTCCAAAACTGAGGAGAAAT
CTGTCGTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATT
GATGAGGTTACCACAACACTGGAAGAAACTAAGTTTCTTACCAATAAGTT
ACTCTTGTTTGCTGATATCAATGGTAAGCTTTACCATGATTCTCAGAACA
TGCTTAGAGGTGAAGATATGTCTTTCCTTGAGAAGGATGCACCTTACATG
GTAGGTGATGTTATCACTAGTGGTGATATCACTTGTGTTGTAATACCCTC
CAAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCTTTGAAGAAAG
TGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGT
TATACACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATT
TTATGTACTACCTTCAGAAGCACCTAATGCTAAGGAAGAGATTCTAGGAA
CTGTATCCTGGAATTTGAGAGAAATGCTTGCTCATGCTGAAGAGACAAGA
AAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACCATCCA
ACGTAAGTATAAAGGAATTAAAATTCAAGAGGGCATCGTTGACTATGGTG
TCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACG
AAGCTGAACTCTCTAAATGAGCCGCTTGTCACAATGCCAATTGGTTATGT
GACACATGGTTTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTA
AAGCTCCTGCCGTAGTGTCAGTATCATCACCAGATGCTGTTACTACATAT
AATGGATACCTCACTTCGTCATCAAAGACATCTGAGGAGCACTTTGTAGA
AACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCCTATTCAGGACAGC
GTACAGAGTTAGGTGTTGAATTTCTTAAGCGTGGTGACAAAATTGTGTAC
CACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGGTTCTTTC
ACTTGACAAACTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAA
AAGTGTTCACAACTGTGGACAACACTAATCTCCACACACAGCTTGTGGAT
ATGTCTATGACATATGGACAGCAGTTTGGTCCAACATACTTGGATGGTGC
TGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGTAAGACTTTCT
TTGTACTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTAC
CATACTCTTGATGAGAGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCA
CACAAAGAAATGGAAATTTCCTCAAGTTGGTGGTTTAACTTCAATTAAAT
GGGCTGATAACAATTGTTATTTGTCTAGTGTTTTATTAGCACTTCAACAG
CTTGAAGTCAAATTCAATGCACCAGCACTTCAAGAGGCTTATTATAGAGC
CCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTCGCTTACAGTA
ATAAAACTGTTGGCGAGCTTGGTGATGTCAGAGAAACTATGACCCATCTT
CTACAGCATGCTAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTG
TAAACATTGTGGTCAGAAAACTACTACCTTAACGGGTGTAGAAGCTGTGA
TGTATATGGGTACTCTATCTTATGATAATCTTAAGACAGGTGTTTCCATT
CCATGTGTGTGTGGTCGTGATGCTACACAATATCTAGTACAACAAGAGTC
TTCTTTTGTTATGATGTCTGCACCACCTGCTGAGTATAAATTACAGCAAG
GTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTGGTCAT

FIGURE 11B

TACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCA
CCTTACAAAGATGTCAGAGTACAAAGGACCAGTGACTGATGTTTTCTACA
AGGAAACATCTTACACTACAACCATCAAGCCTGTGTCGTATAAACTCGAT
GGAGTTACTTACACAGAGATTGAACCAAAATTGGATGGGTATTATAAAAA
GGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTACCAACTCAAC
CATTACCAAATGCGAGTTTTGATAATTTCAAACTCACATGTTCTAACACA
AAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTC
ACGAGAGCTATCTGTCACATTCTTCCCAGACTTGAATGGCGATGTAGTGG
CTATTGACTATAGACACTATTCAGCGAGTTTCAAGAAAGGTGCTAAATTA
CTGCATAAGCCAATTGTTTGGCACATTAACCAGGCTACAACCAAGACAAC
GTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGTACAAAGCCAG
TAGATACTTCAAATTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGA
ATGGACAATCTTGCTTGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGT
GGAAAATCCTACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACTA
CCGAAGTTGTAGGCAATGTCATACTTAAACCATCAGATGAAGGTGTTAAA
GTAACACAAGAGTTAGGTCATGAGGATCTTATGGCTGCTTATGTGGAAAA
CACAAGCATTACCATTAAGAAACCTAATGAGCTTTCACTAGCCTTAGGTT
TAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGG
AGTAAAATTTTGGCTTATGTCAAACCATTCTTAGGACAAGCAGCAATTAC
AACATCAAATTGCGCTAAGAGATTAGCACAACGTGTGTTTAACAATTATA
TGCCTTATGTGTTTACATTATTGTTCCAATTGTGTACTTTTACTAAAAGT
ACCAATTCTAGAATTAGAGCTTCACTACCTACAACTATTGCTAAAAATAG
TGTTAAGAGTGTTGCTAAATTATGTTTGGATGCCGGCATTAATTATGTGA
AGTCACCCAAATTTTCTAAATTGTTCACAATCGCTATGTGGCTATTGTTG
TTAAGTATTTGCTTAGGTTCTCTAATCTGTGTAACTGCTGCTTTTGGTGT
ACTCTTATCTAATTTTGGTGCTCCTTCTTATTGTAATGGCGTTAGAGAAT
TGTATCTTAATTCGTCTAACGTTACTACTATGGATTTCTGTGAAGGTTCT
TTTCCTTGCAGCATTTGTTTAAGTGGATTAGACTCCCTTGATTCTTATCC
AGCTCTTGAAACCATTCAGGTGACGATTTCATCGTACAAGCTAGACTTGA
CAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCATATATGTTGTTCACA
AAATTCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGG
CTATTTTGCTAGTCATTTCATCAGCAATTCTTGGCTCATGTGGTTTATCA
TTAGTATTGTACAAATGGCACCCGTTTCTGCAATGGTTAGGATGTACATC
TTCTTTGCTTCTTTCTACTACATATGGAAGAGCTATGTTCATATCATGGA
TGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGCAATCGTGCCA
CACGCGTTGAGTGTACAACTATTGTTAATGGCATGAAGAGATCTTTCTAT
GTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAATTGGAATTG
TCTCAATTGTGACACATTTTGCACTGGTAGTACATTCATTAGTGATGAAG
TTGCTCGTGATTTGTCACTCCAGTTTAAAAGACCAATCAACCCTACTGAC
CAGTCATCGTATATTGTTGATAGTGTTGCTGTGAAAAATGGCGCGCTTCA
CCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCGCTCT
CCCATTTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCA
CTGCCTATTAATGTCATAGTTTTTGATGGCAAGTCCAAATGCGACGAGTC
TGCTTCTAAGTCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAACCTA
TTCTGTTGCTTGACCAAGCTCTTGTATCAGACGTTGGAGATAGTACTGAA
GTTTCCGTTAAGATGTTTGATGCTTATGTCGACACCTTTTCAGCAACTTT
TAGTGTTCCTATGGAAAAACTTAAGGCACTTGTTGCTACAGCTCACAGCG
AGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCCTTTCTACATTCGTGTCA
GCTGCCCGACAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTAT
TGAATGTCTCAAACTTTCACATCACTCTGACTTAGAAGTGACAGGTGACA
GTTGTAACAATTTCATGCTCACCTATAATAAGGTTGAAAACATGACGCCC
AGAGATCTTGGCGCATGTATTGACTGTAATGCAAGGCATATCAATGCCCA
AGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTAAAAGACTACA
TGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTAGTGCTGCCAAGAAG
AACAACATACCTTTTAGACTAACTTGTGCTACAACTAGACAGGTTGTCAA
TGTCATAACTACTAAAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTT
GTTTTAAACTTATGCTTAAGGCCACATTATTGTGCGTTCTTGCTGCATTG

FIGURE 11C

GTTTGTTATATCGTTATGCCAGTACATACATTGTCAATCCATGATGGTTA
CACAAATGAAATCATTGGTTACAAAGCCATTCAGGATGGTGTCACTCGTG
ACATCATTTCTACTGATGATTGTTTTGCAAATAAACATGCTGGTTTTGAC
GCATGGTTTAGCCAGCGTGGTGGTTCATACAAAAATGACAAAAGCTGCCC
TGTAGTAGCTGCTATCATTACAAGAGAGATTGGTTTCATAGTGCCTGGCT
TACCGGGTACTGTGCTGAGAGCAATCAATGGTGACTTCTTGCATTTTCTA
CCTCGTGTTTTTAGTGCTGTTGGCAACATTTGCTACACACCTTCCAAACT
CATTGAGTATAGTGATTTTGCTACCTCTGCTTGCGTTCTTGCTGCTGAGT
GTACAATTTTTAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGAC
ACTAATTTGCTAGAGGGTTCTATTTCTTATAGTGAGCTTCGTCCAGACAC
TCGTTATGTGCTTATGGATGGTTCCATCATACAGTTTCCTAACACTTACC
TGGAGGGTTCTGTTAGAGTAGTAACAACTTTTGATGCTGAGTACTGTAGA
CATGGTACATGCGAAAGGTCAGAAGTAGGTATTTGCCTATCTACCAGTGG
TAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCAGGAGTTTTCT
GTGGTGTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGTG
CAACCTGTGGGTGCTTTAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTAT
TATTGCCATATTGGTGACTTGTGCTGCCTACTACTTTATGAAATTCAGAC
GTGTTTTTGGTGAGTACAACCATGTTGTTGCTGCTAATGCACTTTTGTTT
TTGATGTCTTTCACTATACTCTGTCTGGTACCAGCTTACAGCTTTCTGCC
GGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTATTTCACCAATG
ATGTTTCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT
GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCA
CTGCCATTGGTTCTTTAACAACTATCTTAGGAAAAGAGTCATGTTTAATG
GAGTTACATTTAGTACCTTCGAGGAGGCTGCTTTGTGTACCTTTTTGCTC
AACAAGGAAATGTACCTAAAATTGCGTAGCGAGACACTGTTGCCACTTAC
ACAGTATAACAGGTATCTTGCTCTATATAACAAGTACAAGTATTTCAGTG
GAGCCTTAGATACTACCAGCTATCGTGAAGCAGCTTGCTGCCACTTAGCA
AAGGCTCTAAATGACTTTAGCAACTCAGGTGCTGATGTTCTCTACCAACC
ACCACAGACATCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTAGGAAAA
TGGCATTCCCGTCAGGCAAAGTTGAAGGGTGCATGGTACAAGTAACCTGT
GGAACTACAACTCTTAATGGATTGTGGTTGGATGACACAGTATACTGTCC
AAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCTAACTATGAAG
ATCTGCTCATTCGCAAATCCAACCATAGCTTTCTTGTTCAGGCTGGCAAT
GTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGTCTGCTTAGGCT
TAAAGTTGATACTTCTAACCCTAAGACACCCAAGTATAAATTTGTCCGTA
TCCAACCTGGTCAAACATTTTCAGTTCTAGCATGCTACAATGGTTCACCA
TCTGGTGTTTATCAGTGTGCCATGAGACCTAATCATACCATTAAAGGTTC
TTTCCTTAATGGATCATGTGGTAGTGTTGGTTTTAACATTGATTATGATT
GCGTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACAC
GCTGGTACTGACTTAGAAGGTAAATTCTATGGTCCATTTGTTGACAGACA
AACTGCACAGGCTGCAGGTACAGACACAACCATAACATTAAATGTTTTGG
CATGGCTGTATGCTGCTGTTATCAATGGTGATAGGTGGTTTCTTAATAGA
TTCACCACTACTTTGAATGACTTTAACCTTGTGGCAATGAAGTACAACTA
TGAACCTTTGACACAAGATCATGTTGACATATTGGGACCTCTTTCTGCTC
AAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTG
CAGAATGGTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGA
TGAGTTTACACCATTTGATGTTGTTAGACAATGCTCTGGTGTTACCTTCC
AAGGTAAGTTCAAGAAAATTGTTAAGGGCACTCATCATTGGATGCTTTTA
ACTTTCTTGACATCACTATTGATTCTTGTTCAAAGTACACAGTGGTCACT
GTTTTTCTTTGTTTACGAGAATGCTTTCTTGCCATTTACTCTTGGTATTA
TGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAGCACGCATTC
TTGTGCTTGTTTCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATAT
GGTCTACATGCCTGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAAT
TGGCTGACACTAGCTTGTCTGGTTATAGGCTTAAGGATTGTGTTATGTAT
GCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTTTATGA
TGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTT
ACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCC

FIGURE 11D

TTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTATCAT
GTTTTTAGCTAGAGCTATAGTGTTTGTGTGTGTTGAGTATTACCCATTGT
TATTTATTACTGGCAACACCTTACAGTGTATCATGCTTGTTTATTGTTTC
TTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTGTTTACTCAACCG
TTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTCTCTACACAAG
AATTTAGGTATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATT
GATGCTTTCAAGCTTAACATTAAGTTGTTGGGTATTGGAGGTAAACCATG
TATCAAGGTTGCTACTGTACAGTCTAAAATGTCTGACGTAAAGTGCACAT
CTGTGGTACTGCTCTCGGTTCTTCAACAACTTAGAGTAGAGTCATCTTCT
AAATTGTGGGCACAATGTGTACAACTCCACAATGATATTCTTCTTGCAAA
AGACACAACTGAAGCTTTCGAGAAGATGGTTTCTCTTTTGTCTGTTTTGC
TATCCATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTC
GATAACCGTGCTACTCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACC
ATCATATGCCGCTTATGCCACTGCCCAGGAGGCCTATGAGCAGGCTGTAG
CTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTAAAGAAATCTTTGAAT
GTGGCTAAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAGTTGGA
AAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAGGCAAGATCTG
AGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCACT
ATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGC
GCGTGATGGTTGTGTTCCACTCAACATCATACCATTGACTACAGCAGCCA
AACTCATGGTTGTTGTCCCTGATTATGGTACCTACAAGAACACTTGTGAT
GGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAAGTTGT
TGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATT
CACCAAATTTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACTCA
GCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGAT
GTCCTGTGCGGCTGGTACCACACAAACAGCTTGTACTGATGACAATGCAC
TTGCCTACTATAACAATTCGAAGGGAGGTAGGTTTGTGCTGGCATTACTA
TCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGATGGTAC
AGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTTGTTACAGACA
CACCAAAAGGGCCTAAAGTGAAATACTTGTACTTCATCAAAGGCTTAAAC
AACCTAAATAGAGGTATGGTGCTGGGCAGTTTAGCTGCTACAGTACGTCT
TCAGGCTGGAAATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCT
TCTGTGCTTTTGCAGTAGACCCTGCTAAAGCATATAAGGATTACCTAGCA
AGTGGAGGACAACCAATCACCAACTGTGTGAAGATGTTGTGTACACACAC
TGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAACATGGACCAAG
AGTCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGAC
CATCCAAATCCTAAAGGATTCTGTGACTTGAAAGGTAAGTACGTCCAAAT
ACCTACCACTTGTGCTAATGACCCAGTGGGTTTTACACTTAGAAACACAG
TCTGTACCGTCTGCGGAATGTGGAAAGGTTATGGCTGTAGTTGTGACCAA
CTCCGCGAACCCTTGATGCAGTCTGCGGATGCATCAACGTTTTTAAACGG
GTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGTGCGGCACAGGCACTAG
TACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAAGTTGCTG
GTTTTGCAAAGTTCCTAAAAACTAATTGCTGTCGCTTCCAGGAGAAGGAT
GAGGAAGGCAATTTATTAGACTCTTACTTTGTAGTTAAGAGGCATACTAT
GTCTAACTACCAACATGAAGAGACTATTTATAACTTGGTTAAAGATTGTC
CAGCGGTTGCTGTCCATGACTTTTTCAAGTTTAGAGTAGATGGTGACATG
GTACCACATATATCACGTCAGCGTCTAACTAAATACACAATGGCTGATTT
AGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGATACATTAAAAG
AAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAG
GATTGGTATGACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAA
CTTAGGTGAGCGTGTACGCCAATCATTATTAAAGACTGTACAATTCTGCG
ATGCTATGCGTGATGCAGGCATTGTAGGCGTACTGACATTAGATAATCAG
GATCTTAATGGGAACTGGTACGATTTCGGTGATTTCGTACAAGTAGCACC
AGGCTGCGGAGTTCCTATTGTGGATTCATATTACTCATTGCTGATGCCCA
TCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGATGCTGAT
CTCGCAAAACCACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGA
AGAGAGACTTTGTCTCTTCGACCGTTATTTTAAATATTGGGACCAGACAT

FIGURE 11E

ACCATCCCAATTGTATTAACTGTTTGGATGATAGGTGTATCCTTCATTGT
GCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTACAAGTTTTGG
ACCACTAGTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTTGTTTCAA
CTGGATACCATTTTCGTGAGTTAGGAGTCGTACATAATCAGGATGTAAAC
TTACATAGCTCGCGTCTCAGTTTCAAGGAACTTTTAGTGTATGCTGCTGA
TCCAGCTATGCATGCAGCTTCTGGCAATTTATTGCTAGATAAACGCACTA
CATGCTTTTCAGTAGCTGCACTAACAAACAATGTTGCTTTTCAAACTGTC
AAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTGTGTCTAAAGG
TTTCTTTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTCTTTGCTC
AGGATGGCAACGCTGCTATCAGTGATTATGACTATTATCGTTATAATCTG
CCAACAATGTGTGATATCAGACAACTCCTATTCGTAGTTGAAGTTGTTGA
TAAATACTTTGATTGTTACGATGGTGGCTGTATTAATGCCAACCAAGTAA
TCGTTAACAATCTGGATAAATCAGCTGGTTTCCCATTTAATAAATGGGGT
AAGGCTAGACTTTATTATGACTCAATGAGTTATGAGGATCAAGATGCACT
TTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATC
TTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTC
TCTATCTGTAGTACTATGACAAATAGACAGTTTCATCAGAAATTATTGAA
GTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAATTGGAACAAGCAAGT
TTTACGGTGGCTGGCATAATATGTTAAAAACTGTTTACAGTGATGTAGAA
ACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACAGAGCCATGCC
TAACATGCTTAGGATAATGGCCTCTCTTGTTCTTGCTCGCAAACATAACA
CTTGCTGTAACTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCG
CAAGTATTAAGTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACC
AGGTGGAACATCATCCGGTGATGCTACAACTGCTTATGCTAATAGTGTCT
TTAACATTTGTCAAGCTGTTACAGCCAATGTAAATGCACTTCTTTCAACT
GATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTACAACACAGGCT
CTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG
AGTTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATTCTTTCTGAT
GATGCCGTTGTGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGC
TAGCATTAAGAACTTTAAGGCAGTTCTTTATTATCAAAATAATGTGTTCA
TGTCTGAGGCAAAATGTTGGACTGAGACTGACCTTACTAAAGGACCTCAC
GAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAGATGATTACGT
GTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTG
TCGATGATATTGTCAAAACAGATGGTACACTTATGATTGAAAGGTTCGTG
TCACTGGCTATTGATGCTTACCCACTTACAAAACATCCTAATCAGGAGTA
TGCTGATGTCTTTCACTTGTATTTACAATACATTAGAAAGTTACATGATG
AGCTTACTGGCCACATGTTGGACATGTATTCCGTAATGCTAACTAATGAT
AACACCTCACGGTACTGGGAACCTGAGTTTTATGAGGCTATGTACACACC
ACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGA
CTTCACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAG
TGCTGCTATGACCATGTCATTTCAACATCACACAAATTAGTGTTGTCTGT
TAATCCCTATGTTTGCAATGCCCCAGGTTGTGATGTCACTGATGTGACAC
AACTGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGCCTCCC
ATTAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTTTATACAAAAA
CACATGTGTAGGCAGTGACAATGTCACTGACTTCAATGCGATAGCAACAT
GTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAG
AGACTCAAGCTTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATT
TAAGCTGTCATATGGTATTGCCACTGTACGCGAAGTACTCTCTGACAGAG
AATTGCATCTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGAACAGA
AACTATGTCTTTACTGGTTACCGTGTAACTAAAAATAGTAAAGTACAGAT
TGGAGAGTACACCTTTGAAAAAGGTGACTATGGTGATGCTGTTGTGTACA
GAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTGTGTTGACA
TCTCACACTGTAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCA
CTATGTGAGAATTACTGGCTTGTACCCAACACTCAACATCTCAGATGAGT
TTTCTAGCAATGTTGCAAATTATCAAAAGGTCGGCATGCAAAAGTACTCT
ACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACT
TGCTCTCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATG

FIGURE 11F

CAGCTGTTGATGCCCTATGTGAAAAGGCATTAAAATATTTGCCCATAGAT
AAATGTAGTAGAATCATACCTGCGCGTGCGCGCGTAGAGTGTTTGATAA
ATTCAAAGTGAATTCAACACTAGAACAGTATGTTTTCTGCACTGTAAATG
CATTGCCAGAAACAACTGCTGACATTGTAGTCTTTGATGAAATCTCTATG
GCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTTCGTGCAAAACA
CTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCCGCACATTGC
TGACTAAAGGCACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTT
ATGAAAACAATAGGTCCAGACATGTTCCTTGGAACTTGTCGCCGTTGTCC
TGCTGAAATTGTTGACACTGTGAGTGCTTTAGTTTATGACAATAAGCTAA
AAGCACACAAGGATAAGTCAGCTCAATGCTTCAAAATGTTCTACAAAGGT
GTTATTACACATGATGTTTCATCTGCAATCAACAGACCTCAAATAGGCGT
TGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTGTTTTTA
TCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTG
CCTACGCAGACTGTTGATTCATCACAGGGTTCTGAATATGACTATGTCAT
ATTCACACAAACTACTGAAACAGCACACTCTTGTAATGTCAACCGCTTCA
ATGTGGCTATCACAAGGGCAAAAATTGGCATTTTGTGCATAATGTCTGAT
AGAGATCTTTATGACAAACTGCAATTTACAAGTCTAGAAATACCACGTCG
CAATGTGGCTACATTACAAGCAGAAAATGTAACTGGACTTTTTAAGGACT
GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTC
AGCGTTGATATAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGG
CATACCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCA
AAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAA
GAAGCTATTCGTCACGTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTG
TCATGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGAT
TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACT
GAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGA
CCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATG
TAGTGCGTATTAAGATAGTACAAATGCTCAGTGATACACTGAAAGGATTG
TCAGACAGAGTCGTGTTCGTCCTTTGGGCGCATGGCTTTGAGCTTACATC
AATGAAGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTG
ACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGG
AATCATTCTGTGGGTTTTGACTATGTCTATAACCCATTTATGATTGATGT
TCAGCAGTGGGGCTTTACGGGTAACCTTCAGAGTAACCATGACCAACATT
GCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACT
AGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGT
TGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAGAA
AAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCA
GTTCTTCATGACATTGGAAATCCAAAGGCTATCAAGTGTGTGCCTCAGGC
TGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGACAAAGCTT
ACAAAATAGAGGAACTCTTCTATTCTTATGCTACACATCACGATAAATTC
ACTGATGGTGTTTGTTTGTTTTGGAATTGTAACGTTGATCGTTACCCAGC
CAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACTTGAACT
TACCAGGCTGTGATGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCAC
ACTCCAGCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAATTGCCTTT
CTTTTACTATTCTGATAGTCCTTGTGAGTCTCATGGCAAACAAGTAGTGT
CGGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACACGATGC
AATTTAGGTGGTGCTGTTTGCAGACACCATGCAAATGAGTACCGACAGTA
CTTGGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTT
ACAAACAATTTGATACTTATAACCTGTGGAATACATTTACCAGGTTACAG
AGTTTAGAAAATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGG
ACACGCCGGCGAAGCACCTGTTTCCATCATTAATAATGCTGTTTACACAA
AGGTAGATGGTATTGATGTGGAGATCTTTGAAAATAAGACAACACTTCCT
GTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTAAACCAGTGCC
AGAGATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTG
TAATCTGGGACTACAAAAGAGAAGCCCCAGCACATGTATCTACAATAGGT
GTCTGCACAATGACTGACATTGCCAAGAAACCTACTGAGAGTGCTTGTTC
TTCACTTACTGTCTTGTTTGATGGTAGAGTGGAAGGACAGGTAGACCTTT

FIGURE 11G

TTAGAAACGCCCGTAATGGTGTTTTAATAACAGAAGGTTCAGTCAAAGGT
CTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCAATGGAGTCACATT
AATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACG
GCATTATTCAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTA
GAGGATTTTAAGCCCAGATCACAAATGGAAACTGACTTTCTCGAGCTCGC
TATGGATGAATTCATACAGCGATATAAGCTCGAGGGCTATGCCTTCGAAC
ACATCGTTTATGGAGATTTCAGTCATGGACAACTTGGCGGTCTTCATTTA
ATGATAGGCTTAGCCAAGCGCTCACAAGATTCACCACTTAAATTAGAGGA
TTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGC
AAACAGGTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGAT
GACTTTGTCGAGATAATAAAGTCACAAGATTTGTCAGTGATTTCAAAAGT
GGTCAAGGTTACAATTGACTATGCTGAAATTTCATTCATGCTTTGGTGTA
AGGATGGACATGTTGAAACCTTCTACCCAAAACTACAAGCAAGTCAAGCG
TGGCAACCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAAGAATGCT
TCTTGAAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTATACCAA
AAGGAATAATGATGAATGTCGCAAAGTATACTCAACTGTGTCAATACTTA
AATACACTTACTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGG
TGCTGGCTCTGATAAAGGAGTTGCACCAGGTACAGCTGTGCTCAGACAAT
GGTTGCCAACTGGCACACTACTTGTCGATTCAGATCTTAATGACTTCGTC
TCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGC
TAATAAATGGGACCTTATTATTAGCGATATGTATGACCCTAGGACCAAAC
ATGTGACAAAAGAGAATGACTCTAAAGAAGGGTTTTTCACTTATCTGTGT
GGATTTATAAAGCAAAAACTAGCCCTGGGTGGTTCTATAGCTGTAAAGAT
AACAGAGCATTCTTGGAATGCTGACCTTTACAAGCTTATGGGCCATTTCT
CATGGTGGACAGCTTTTGTTACAAATGTAAATGCATCATCATCGGAAGCA
TTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAATTGATGG
CTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCC
AGTTGTCTTCCTATTCACTCTTTGACATGAGCAAATTTCCTCTTAAATTA
AGAGGAACTGCTGTAATGTCTCTTAAGGAGAATCAAATCAATGATATGAT
TTATTCTCTTCTGGAAAAAGGTAGGCTTATCATTAGAGAAAACAACAGAG
TTGTGGTTTCAAGTGATATTCTTGTTAACAACTAAACGAACATGTTTATT
TTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCAC
CACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTA
TGAGGGGGTTTACTATCCTGATGAAATTTTTAGATCAGACACTCTTTAT
TTAACTCAGGATTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCA
TACTATTAATCATACGTTTGGCAACCCTGTCATACCTTTTAAGGATGGTA
TTTATTTTGCTGCCACAGAGAAATCAAATGTTGTCCGTGGTTGGGTTTTT
GGTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTATTAACAATTC
TACTAATGTTGTTATACGAGCATGTAACTTTGAATTGTGTGACAACCCTT
TCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTC
GATAATGCATTTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCT
TGATGTTTCAGAAAAGTCAGGTAATTTTAAACACTTACGAGAGTTTGTGT
TTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACCTATA
GATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGAAACCTATTTT
TAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAG
CCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTT
GTTGGCTATTTAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGG
TACAATCACAGATGCTGTTGATTGTTCTCAAAATCCACTTGCTGAACTCA
AATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGACCTCT
AATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTAC
AAACTTGTGTCCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCCTTCTG
TCTATGCATGGGAGAGAAAAAAAATTTCTAATTGTGTTGCTGATTACTCT
GTGCTCTACAACTCAACATTTTTTTCAACCTTTAAGTGCTATGGCGTTTC
TGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTT
TTGTAGTCAAGGGAGATGATGTAAGACAAATAGCGCCAGGACAAACTGGT
GTTATTGCTGATTATAATTATAAATTGCCAGATGATTTCATGGGTTGTGT
CCTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATA

FIGURE 11H

ATTATAAATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGA
GACATATCTAATGTGCCTTTCTCCCCTGATGGCAAACCTTGCACCCCACC
TGCTCTTAATTGTTATTGGCCATTAAATGATTATGGTTTTTACACCACTA
CTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACTT
TTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCACTGACCTTAT
TAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTG
TGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGT
GATGTTTCTGATTTCACTGATTCCGTTCGAGATCCTAAAACATCTGAAAT
ATTAGACATTTCACCTTGCGCTTTTGGGGGTGTAAGTGTAATTACACCTG
GAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGC
ACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCG
CATATATTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTA
TAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGA
GCTGGCATTTGTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAG
CCAAAAATCTATTGTGGCTTATACTATGTCTTTAGGTGCTGATAGTTCAA
TTGCTTACTCTAATAACACCATTGCTATACCTACTAACTTTTCAATTAGC
ATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTG
TAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCC
AATATGGTAGCTTTTGCACACAACTAAATCGTGCACTCTCAGGTATTGCT
GCTGAACAGGATCGCAACACACGTGAAGTGTTCGCTCAAGTCAAACAAAT
GTACAAAACCCCAACTTTGAAATATTTTGGTGGTTTTAATTTTTCACAAA
TATTACCTGACCCTCTAAAGCCAACTAAGAGGTCTTTTATTGAGGACTTG
CTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAGCAATATGG
CGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGT
TCAATGGACTTACAGTGTTGCCACCTCTGCTCACTGATGATATGATTGCT
GCCTACACTGCTGCTCTAGTTAGTGGTACTGCCACTGCTGGATGGACATT
TGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTATGCAAATGGCATATA
GGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAA
CAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACT
TACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGA
ATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGT
GCAATTTCAAGTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGA
GGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTTC
AAACCTATGTAACACAACAACTAATCAGGGCTGCTGAAATCAGGGCTTCT
GCTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAA
AAGAGTTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAG
CAGCCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTGCCATCCCAG
GAGAGGAACTTCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATA
CTTCCCTCGTGAAGGTGTTTTTGTGTTTAATGGCACTTCTTGGTTTATTA
CACAGAGGAACTTCTTTTCTCCACAAATAATTACTACAGACAATACATTT
GTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTA
TGATCCTCTGCAACCTGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGT
ACTTCAAAAATCATACATCACCAGATGTTGATCTTGGCGACATTTCAGGC
ATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGA
GGTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAA
AATATGAGCAATATATTAAATGGCCTTGGTATGTTTGGCTCGGCTTCATT
GCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTGTTGCATGAC
TAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCA
AGTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACAT
TACACATAAACGAACTTATGGATTTGTTTATGAGATTTTTTACTCTTAGA
TCAATTACTGCACAGCCAGTAAAAATTGACAATGCTTCTCCTGCAAGTAC
TGTTCATGCTACAGCAACGATACCGCTACAAGCCTCACTCCCTTTCGGAT
GGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTTTCAGAGCGCTACCAAA
ATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCA
GTTCATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTCACATCTTT
TGCTTGTCGCTGCAGGTATGGAGGCGCAATTTTTGTACCTCTATGCCTTG
ATATATTTTCTACAATGCATCAACGCATGTAGAATTATTATGAGATGTTG

FIGURE 11I

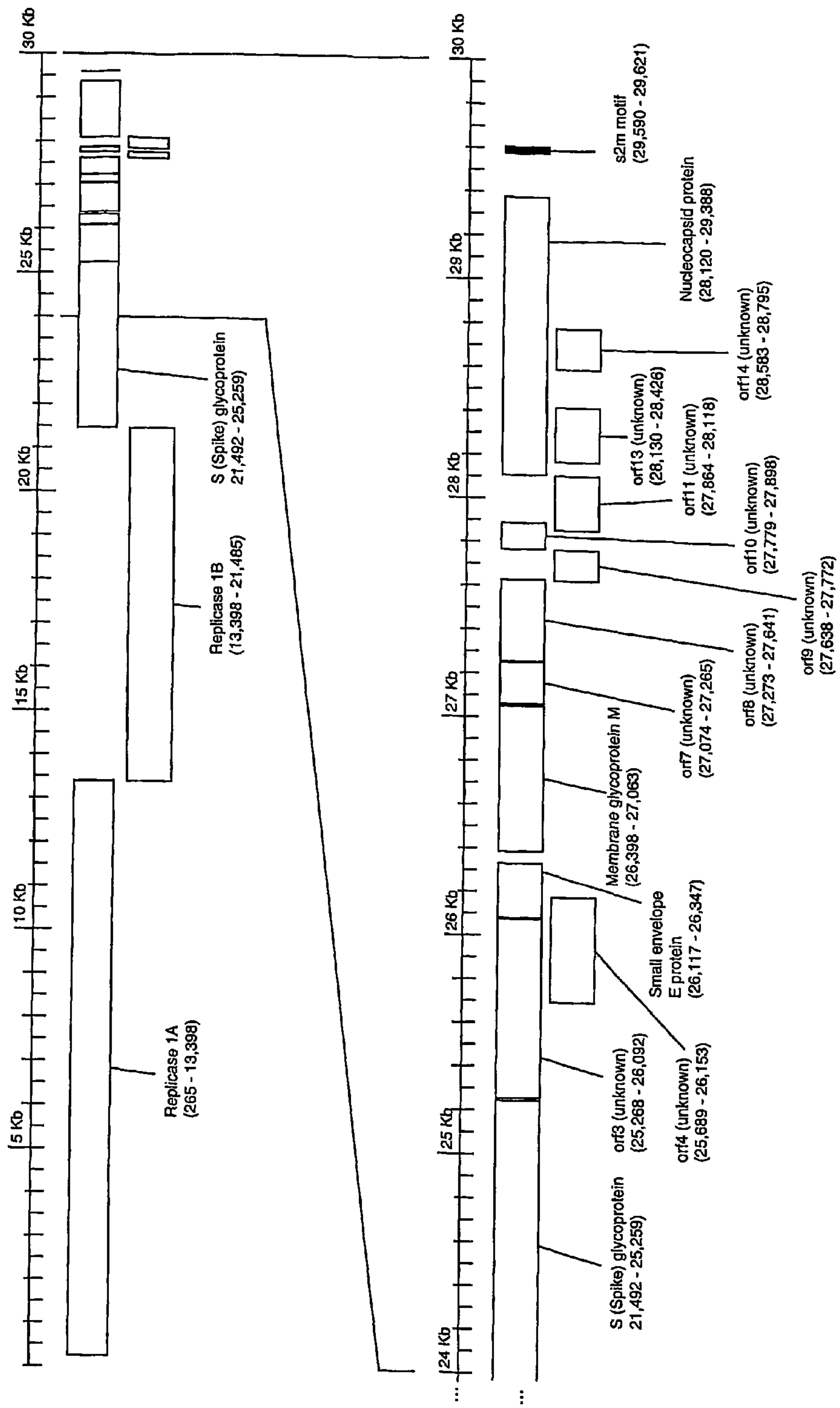
GCTTTGTTGGAAGTGCAAATCCAAGAACCCATTACTTTATGATGCCAACT
ACTTTGTTTGCTGGCACACACATAACTATGACTACTGTATACCATATAAC
AGTGTCACAGATACAATTGTCGTTACTGAAGGTGACGGCATTTCAACACC
AAAACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACT
CAGGTGTTAAAGACTATGTCGTTGTACATGGCTATTTCACCGAAGTTTAC
TACCAGCTTGAGTCTACACAAATTACTACAGACACTGGTATTGAAAATGC
TACATTCTTCATCTTTAACAAGCTTGTTAAAGACCCACCGAATGTGCAAA
TACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGCAATGGATCCA
ATTTATGATGAGCCGACGACGACTACTAGCGTGCCTTTGTAAGCACAAGA
AAGTGAGTACGAACTTATGTACTCATTCGTTTCGGAAGAAACAGGTACGT
TAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTCGTGGTATTCTTGCTA
GTCACACTAGCCATCCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAA
TATTGTTAACGTGAGTTTAGTAAAACCAACGGTTTACGTCTACTCGCGTG
TTAAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCTGGTCTAAACG
AACTAACTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATG
GCAGACAACGGTACTATTACCGTTGAGGAGCTTAAACAACTCCTGGAACA
ATGGAACCTAGTAATAGGTTTCCTATTCCTAGCCTGGATTATGTTACTAC
AATTTGCCTATTCTAATCGGAACAGGTTTTTGTACATAATAAAGCTTGTT
TTCCTCTGGCTCTTGTGGCCAGTAACACTTGCTTGTTTTGTGCTTGCTGC
TGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATTGCAATGGCTT
GTATTGTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCCTTCAGGCTG
TTTGCTCGTACCCGCTCAATGTGGTCATTCAACCCAGAAACAAACATTCT
TCTCAATGTGCCTCTCCGGGGGACAATTGTGACCAGACCGCTCATGGAAA
GTGAACTTGTCATTGGTGCTGTGATCATTCGTGGTCACTTGCGAATGGCC
GGACACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAGATCAC
TGTGGCTACATCACGAACGCTTTCTTATTACAAATTAGGAGCGTCGCAGC
GTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTATTGGA
AACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTT
GCTAGTACAGTAAGTGACAACAGATGTTTCATCTTGTTGACTTCCAGGTT
ACAATAGCAGAGATATTGATTATCATTATGAGGACTTTCAGGATTGCTAT
TTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATTTAAGC
CTCTAACTAAGAAGAATTATTCGGAGTTAGATGATGAAGAACCTATGGAG
TTAGATTATCCATAAAACGAACATGAAAATTATTCTCTTCCTGACATTGA
TTGTATTTACATCTTGCGAGCTATATCACTATCAGGAGTGTGTTAGAGGT
ACGACTGTACTACTAAAAGAACCTTGCCCATCAGGAACATACGAGGGCAA
TTCACCATTTCACCCTCTTGCTGACAATAAATTTGCACTAACTTGCACTA
GCACACACTTTGCTTTTGCTTGTGCTGACGGTACTCGACATACCTATCAG
CTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGACAAGAGGAGGT
TCAACAAGAGCTCTACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTAT
TTTTAATACTTTGCTTCACCATTAAGAGAAAGACAGAATGAATGAGCTCA
CTTTAATTGACTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCCTTGTT
TTAATAATGCTTATTATATTTTGGTTTTCACTCGAAATCCAGGATCTAGA
AGAACCTTGTACCAAAGTCTAAACGAACATGAAACTTCTCATTGTTTTGA
CTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACAGCGCTGTGCA
TCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGG
GTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAAGGTTTTACCT
TTTCATAGATGGCACACTATGGTTCAAACATGCACACCTAATGTTACTAT
CAACTGTCAAGATCCAGCTGGTGGTGCGCTTATAGCTAGGTGTTGGTACC
TTCATGAAGGTCACCAAACTGCTGCATTTAGAGACGTACTTGTTGTTTTA
AATAAACGAACAAATTAAAATGTCTGATAATGGACCCCAATCAAACCAAC
GTAGTGCCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAAT
AACCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCA
AGGTTTACCCAATAATACTGCGTCTTGGTTCACAGCTCTCACTCAGCATG
GCAAGGAGGAACTTAGATTCCCTCGAGGCCAGGGCGTTCCAATCAACACC
AATAGTGGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACCCGACG
AGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACT
TCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTCCCTACGGCGCTAAC

FIGURE 11J

AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAA
AGACCACATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTAC
AACTTCCTCAAGGAACAACATTGCCAAAAGGCTTCTACGCAGAGGGAAGC
AGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTAA
TTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAA
TGGCTAGCGGAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGACAGA
TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAACAAGG
CCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCC
AAAAACGTACTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGA
CGTGGTCCAGAACAAACCCAAGGAAATTTCGGGGACCAAGACCTAATCAG
ACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAATTTGCTCCAA
GTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT
TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGA
TCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCAT
ACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACT
GATGAAGCTCAGCCTTTGCCGCAGAGACAAAAGAAGCAGCCCACTGTGAC
TCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAACTTCAAAATT
CCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATG
ACCACACAAGGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTACG
ATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACA
AGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGT
AACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGC
GGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAGCTGCCTATAT
GGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG
ATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAA A

GenBank Accession No. AY274119.3, SEQ ID NO: 15

FIGURE 11K



30 Kb
25 Kb
20 Kb
15 Kb
10 Kb
5 Kb
S (Spike) glycoprotein 21,492 - 25,259
Replicase 1B (13,398 - 21,465)
Replicase 1A (265 - 13,398)
30 Kb
29 Kb
28 Kb
27 Kb
26 Kb
25 Kb
24 Kb
s2m motif (29,590 - 29,621)
Nucleocapsid protein (28,120 - 29,388)
orf14 (unknown) (28,583 - 28,795)
orf13 (unknown) (28,130 - 28,426)
orf11 (unknown) (27,864 - 28,118)
orf10 (unknown) (27,779 - 27,898)
orf9 (unknown) (27,638 - 27,772)
orf8 (unknown) (27,273 - 27,641)
orf7 (unknown) (27,074 - 27,265)
Membrane glycoprotein M (26,398 - 27,063)
Small envelope E protein (26,117 - 26,347)
orf4 (unknown) (25,689 - 26,153)
orf3 (unknown) (25,268 - 26,092)
S (Spike) glycoprotein 21,492 - 25,259

Figure 12

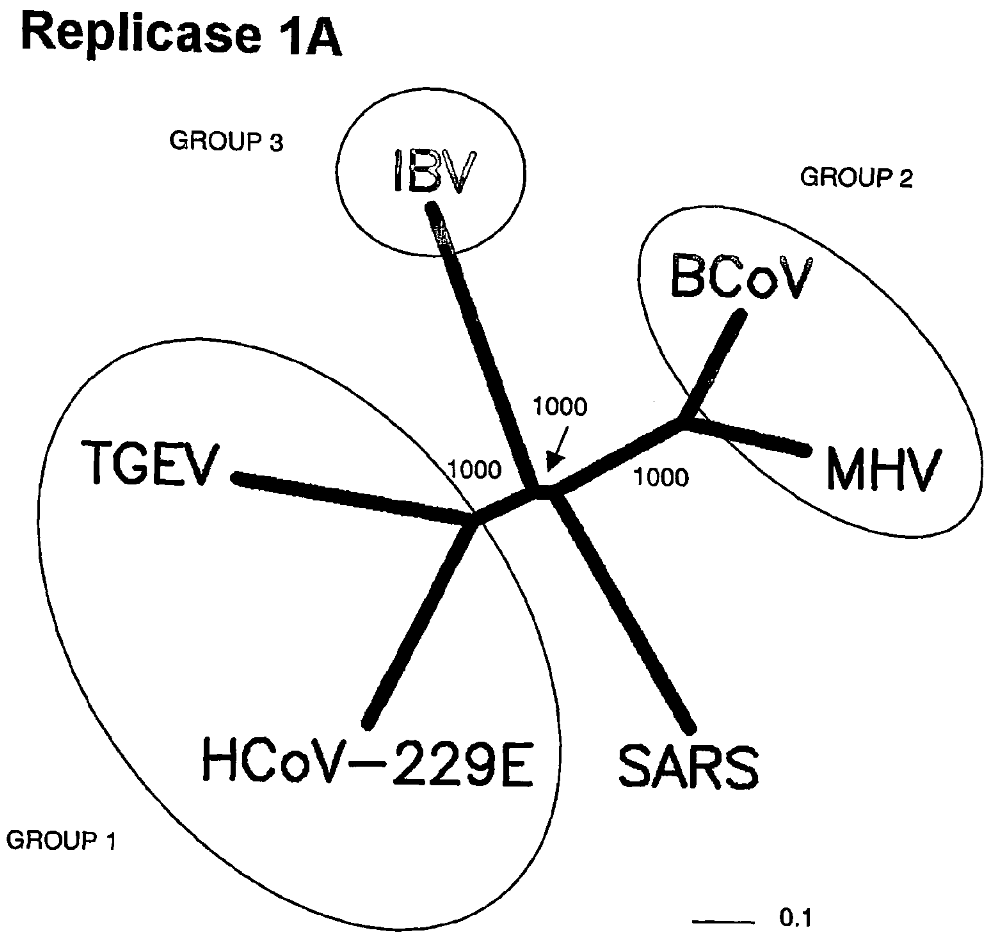

Replicase 1A
GROUP 3
IBV
GROUP 2
BCoV
1000
TGEV
1000
1000
MHV
HCoV-229E
SARS
GROUP 1
0.1

Figure 13A

Membrane Glycoprotein

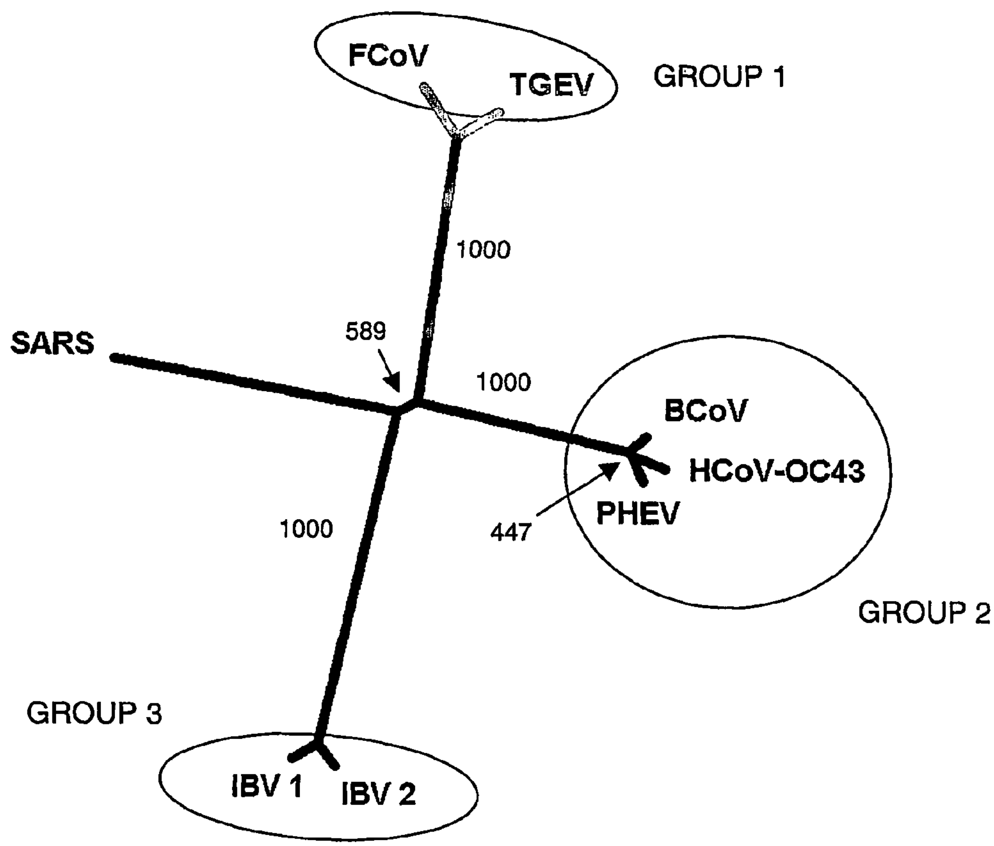


Figure 13B

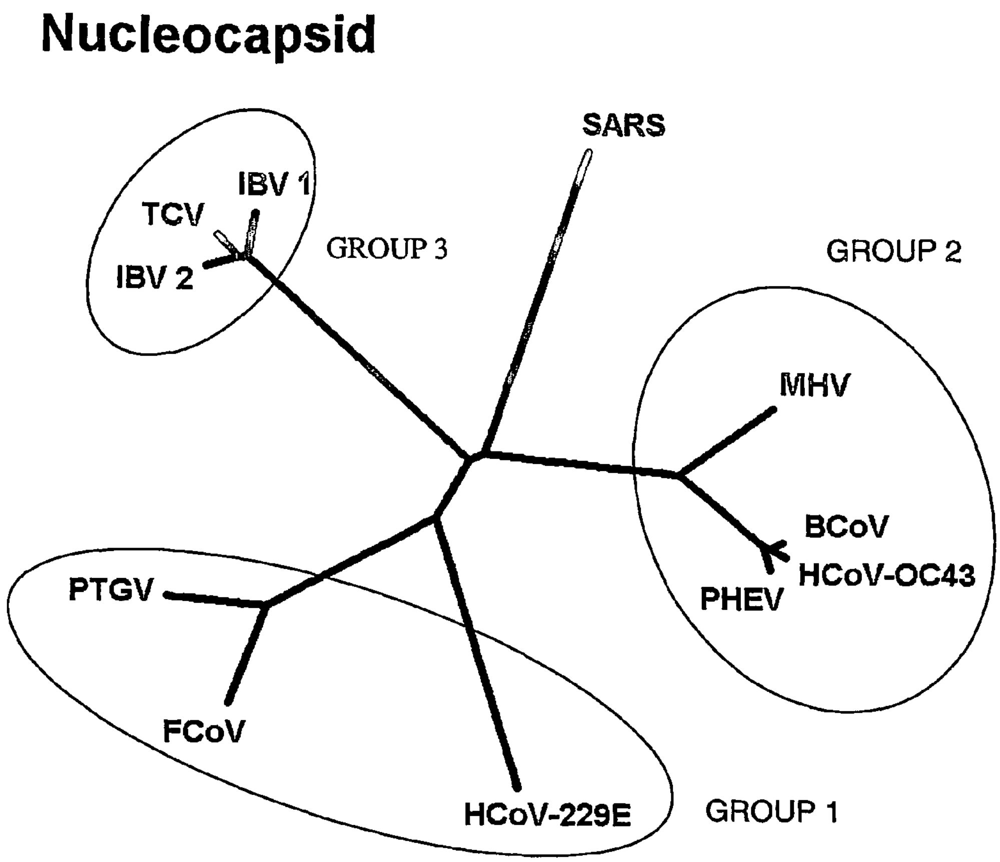

Nucleocapsid
SARS
IBV 1
TCV
IBV 2
GROUP 3
GROUP 2
MHV
BCoV
HCoV-OC43
PHEV
PTGV
FCoV
HCoV-229E
GROUP 1

Figure 13C

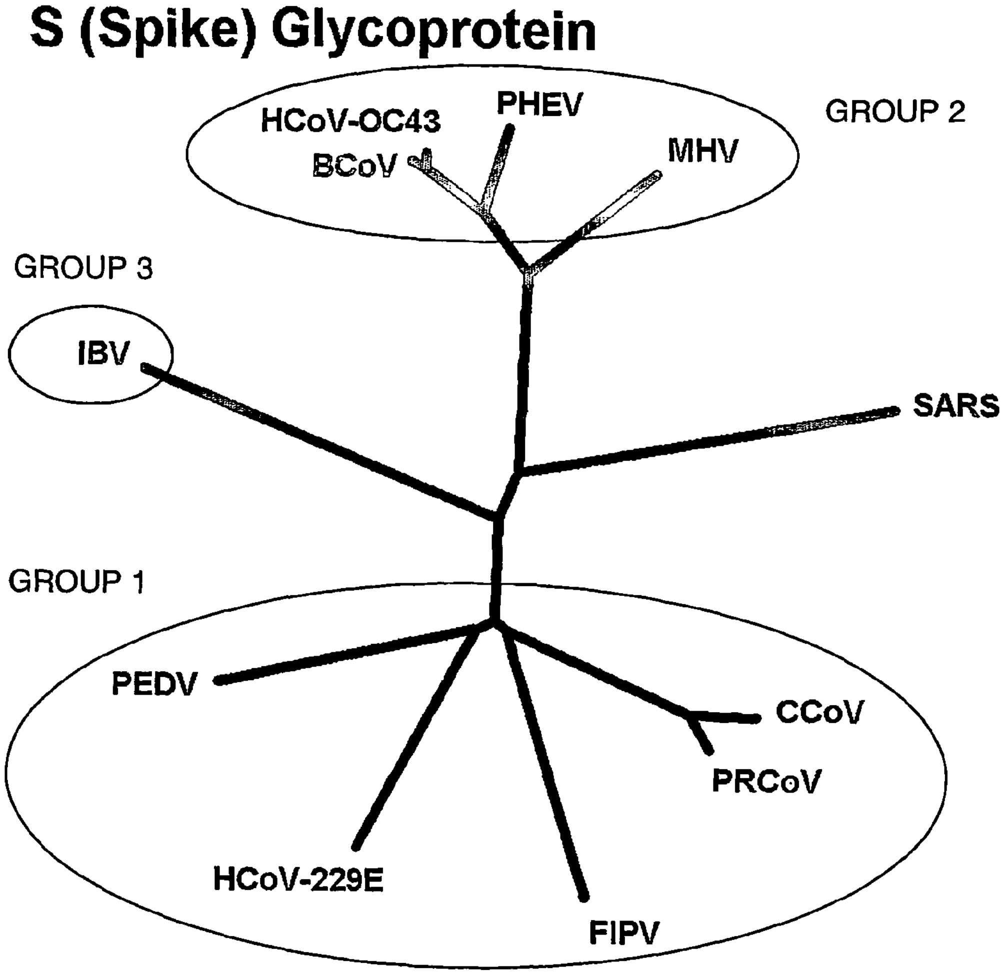

S (Spike) Glycoprotein
HCoV-OC43
PHEV
BCoV
MHV
GROUP 2
GROUP 3
IBV
SARS
GROUP 1
PEDV
CCoV
PRCoV
HCoV-229E
FIPV

Figure 13D

```
229E      ------------------------------------------------------------
PEDV      ------MRSLIYFWLLLPVLPTLSLPQDVTRCQSTT---------NFRRFFSKFNVQAPA
CCov      MIVLILCLLLFSYNSVICTSNNDCVQGNVTQLPGNE---------NIIKDFLFHTFKEEP
PRC       ------------------------------------------------------------
FICV      --------MIFIILTLLSVAKSEDAPHGVTLPQFNTSHNNERFELNFYNFLQTWDIPPNT
BoCov     ------------------------------------------------------------
OC43      ------------------------------------------------MFLILLISLPMA
PHEV      ------------------------------------------------MFLILLISLPMA
MHV       ------------------------------------------------MFFILLISLPSA
TOR2_S    ------------------------------------------------MLFVFILLLPSC
AIBV      ------------------------------------------------------------

229E      ------------------------------------------------------------
PEDV      VVVLGGYLP-----------------SMNSSSWYCGTGIETASGVHGIFLSYIDSGQGFE
CCov      SVVVGGYYPTE--------------VWYNCSRSATTTAYKDFSNIHAFYFDMEAMENSTG
PRC       ------------------------------------------------------------
FICV      ETILGGYLPYCGAGVNCGWYNFSQSVGQNGKYAYINTQNLNIPNVHGVYFDVREHNNDGE
BoCov     FAVIGDLKCT------------------------TVSINDVDTGAPSISTDIVDVTNGLG
OC43      LAVIGDLKCT------------------------TVAINDVDTGVPSTSTDIVDVTNGLG
PHEV      FAVIGDLKCT------------------------TSLINDVDTGVPSISSEVVDVTNGLG
MHV       LGYIGDFRCIQ-----------------------TVNYNGNNASAPSISTEAVDVSKGRG
TOR2_S    ----------------------------MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQ
AIBV      ------------------------------------------------------------

229E      ------------------------------------------------------------
PEDV      IG-----ISQEPFDPSGYQLYLHKATNGNTNATARLR--ICQFPDNKTLGPTVNDVTTG-
CCov      NARGKPLLVHVHGDPVSIIIYISAYRDDVQPRPLLKHGLLCITKNKIIDYNTFTSAQWS-
PRC       ------------------------------------------------------------
FICV      WDDRDKVGLLIAIHGNSKYSLLMVLQDAVEANQPHVAVKICHWKPGNISSYHAFSVNLGD
BoCov     TY-----YVLDRVYLNTTLLLNGYYPTSGSTYRNMALKGTLLLSRLWFKPPFLSDFING-
OC43      TY-----YVLDRVYLNTTLLLNGYYPTSGSTYRNMALKGTLLLSRLWFKPPFLSDFING-
PHEV      TF-----YVLDRVYLNTTLLLNGYYPISGATFRNMALKGTRLLSTLWFKPPFLSPFNDG-
MHV       TY-----YVLDRVYLNATLLLTGYYPVDGSNYRNLALTGTNTLSLTWFKPPFLSEFNDG-
TOR2_S    HT-----SSMRGVYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDG-
AIBV      ------------------------------------------------------------

229E      ------------------------------------------------------------
PEDV      -RNCLFNKAIP---AYMRDGKDIVVGITWDNDRVT-VFADKIYHFYLKNDWSR-------
CCov      -AICLGDDRKIPFSVIPTDNGTKIFGLEWNDDYVTAYISDRSHHLNINNNWFNNVTILYS
PRC       ------------------------------------------------------------
FICV      GGQCVFNQRFS---LDTVLTTNDFYGFQWTDTYVDIYLGGTITKVWVDNDWSIVEAS---
BoCov     ----IFAKVKN-----TKVIKKGVMYSEFPAITIGSTFVNTSYSVVVQPHTTN-------
OC43      ----IFAKVKN-----TKVIKHGVMYSEFPAITIGSTFVNTSYSVVVQPHTTN-------
PHEV      ----IFAKVKN-----SRFSKDGVIYSEFPAITIGSTFVNTSYSIVVEPHTSL-------
MHV       ----IFAKVQN-----LKTNTPTGATSYFPTIVIGSLFGNTSYTVVLEPYNN--------
TOR2_S    ---IYFAATEK-----SNVVRGWVFGSTMNNKSQSVIIINNSTNVVIRACNFELCDN---
AIBV      -----------------MLGKSLFLVTILCALCSANLFDPANYVYYYQSAFRP-------

229E      -----------MFVLLVAYALLHIAGCQTTNGLN--TSYSVCNG---CVGYSENVFAVES
PEDV      --VATRCYNRRSCAMQYVYTPTYYMLNVTSAGEDG-IYYEPCTAN--CTGYAANVFATDS
CCov      RSSSATWQKSAAYVYQGVSNFTYYKLNNTNGLKS----YELCEDYEYCTGYATNVFAPTV
PRC       --------MKKLFVVLVVMPLIYGDKFPTSVVSN-------CTD--QCASYVANVFTTQP
FICV      -ISYHWNRINYGYYMQFVNRTTYYAYNNTGGANYTQLQLSECHTD-YCAGYAKNVFVP-I
BoCov     -LDNKLQGLLEISVCQYTMCEYPHTICHPKL-GNKRVELWHWDTGVVSCLYKRNFTYDVN
OC43      -LDNKLQGLLEISVCQYTMCEYPNTICHPNL-GNRRVELWHWDTGVVSCLYKRNFTYDVN
PHEV      -INGNLQGLLQISVCQYTMCEYPHTICHPNL-GNQRIELWHYDTDVVSCLYRRNFTYDVN
MHV       --------IIMASVCTYTICQLPYTPCKPNTNGNRVIGFWHTDVKPPICLLKRNFTFNVN
TOR2_S    ---PFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDG
AIBV      ----SNGWHLQGGAYAVVNSSNYANNAGSASECT---VGVIKDVYNQSAASIAMTAPLQG
```

FIGURE 14A

```
229E            GGYIPSDFAFNN--WFLLTNTSSVVDGVVRSFQPLLLNCLWSVSGLRFTTGFVYFNGTGR
PEDV            NGHIPEGFSFNN--WFLLSNDSTLLHGKVVSNQPLLVNCLLAIPKIYGLGQFFSFNHTMD
CCov            GGYIPHGFSFNN--WFMRTNSSTFVSGRFVTNQPLLVNCLWPVPSFGVAAQQFCFEGAQF
PRC             GGFIPSDFSFNN--WFLLTNSSTLVSGKLVTKQPLLVNCLWPVPSFEEAASTFCFEGADF
FICV            DGKIPEDFSFSN--WFLLSDKSTLVQGRVLSSQPVFVQCLRPVPSWSNNTAVVHFKN-D
BoCov           ADYLYFHFYQEGGTFYAYFTDTGVVTKFLFNVYLGTVLSHYYVLPLTCS----SAMTLEY
OC43            ADYLYFHFYQEGGIFYAYFTDTGVVTKFLFNVYLGTVLSYYYVMPLTCN----SAMTLEY
PHEV            ADYLYFHFYQEGGTFYAYFTDTGFVTKFLFKLYLGTVLSHYYVMPLTCN----SALSLEY
MHV             APWLYFHFYQQGGTFYAYYADKPSATTFLFSVYIGDILTQYFVLPFICTPTAGSTLAPLY
TOR2_S          FLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAAY
AIBV            MAWSKSQFCSAHCDFSEITVFVTHCYSSGSGSCPITGMIARGHIRISAMKNGSLFYNLTV
                       :

229E            GDCKGFSSDVLSDVIRYNLN-FEENLRRGT-----ILFKTSYGV-VVFYCTNNT------
PEDV            GVCNGAAVDRAPEALRFNINDTSVILAEGS-----IVLHTALGTNLSFVCSNSSD-----
CCov            SQCNGVSLNNTVDVIRFNLN-FTALVQSGMGATV-FSLNTTGGVILEISCYNDTVS---E
PRC             DQCNGAVLNNTVDVIRFNLN-FTTNVQSGKGATV-FSLNTTGGVTLEISCYNDTVS---D
FICV            AFCP----NVTADVLRFNLNFSDTDVYTDSTNDEQLFFTFEDNTTASIACYSSANVTDFQ
BoCov           WVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMS---EIKCKTLSIAPSTGVYELNG-----
OC43            WVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMS---EIKCKTLSIAPSTGVYELNG-----
PHEV            WVTPLTTRQFLLAFDQDGVLYHAVDCASDFMS---EIMCKTSSITPPTGVYELNG-----
MHV             WVTPLLKRQYLFNFNEKGVITSAVDCASSYIS---EIKCKTQSLLPSTGVYDLSG-----
TOR2_S          FVGYLKPTTFMLKYDENGTITDAVDCSQNPLA---ELKCSVKSFEIDKGIYQTSN-----
AIBV            SVSKYPNFKSFQCVNNFTSVYLNGDLVFTSNKTTDVTSAGVYFKAGGPVNYSIMK-----
                                .                                  .

229E            -LVSGDAHIPFGTVLGNFYCFVNTTIGTETTSAFVGALPKTVREFVISRTGHFYINGYRY
PEDV            -PHLAIFAIPLGATEVPYYCFLKVDTYNSTVYKFLAVLPSTVREIVITKYGDVYVNGFGY
CCov            SSFYSYGEISFGVTDGPRYCFA---LYNGTALKYLGTLPPSVKEIAISKWGHFYINGYNF
PRC             SSFSSYGEIPFGVTNGPRYCYV---LYNGTALKYLGTLPPSVKEIAISKWGHFYINGYNF
FICV            PANNSVSHIPFGKT--AHFCFAN-FSHSIVSRQFLGILPPTVREFAFGRDGSIFVNGYKY
BoCov           -YTVQPIADVYRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSNCNFNMSSLMSFIQADS
OC43            -YTVQPIADVYRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSNCNFNMSSLMSFIQADS
PHEV            -YTVQPVATVYRRIPDLPNCDIEAWLNSKTVSSPLNWERKIFSNCNFNMGRLMSFIQADS
MHV             -YTVQPVGVVYRRVPNLPDCKIEEWLTAKSVPSPLNWERRTFQNCNFNLSSLLRYVQAES
TOR2_S          -FRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFST
AIBV            -EFKVLAYFVNGTAQDVILCDNSPKGLLACQYNTGNFSDGFYPFTNSTLVREKFIVYRES
                                   *

229E            FTLGNVEAVNFNVTTAETTD----FFTVALASYADVLVNVSQTSIANIIYCNSVINRLRC
PEDV            LHLGLLDAVTIYFTGHGTDDDVSGFWTIASTNFVDALIEVQGTSIQRILYCDDPVSQLKC
CCov            FSTFPIDCISFNLTTGDSGA----FWTIAYTSYTDALVQVENTAIKKVTYCNSHINNIKC
PRC             FSTFPIDCISFNLTTGDSDV----FWTIAYTSYTEALVQVENTAITNVTYCNSYVNNIKC
FICV            FSLPAIRSVNFSISSVEEYG----FWTIAYTNYTDVMVDVNGTAITRLFYCDSPLNRIKC
BoCov           FTCNNIDAAKIYGMCFSSIT----IDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSC
OC43            FTCNNIDAAKIYGMCFSSIT----IDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSC
PHEV            FGCNNIDASRLYGMCFGSIT----IDKFAIPNSRKVDLQVGKSGYLQSFNYKIDTAVSSC
MHV             LSCNNIDASKVYGMCFGSVS----VDKFAIPRSRQIDLQIGNSGFLQTANYKIDTAATSC
TOR2_S          FKCYGVSATKLNDLCFSNVY----ADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGC
AIBV            SVNTTLALTNFTFTNVSNAQ----PNSGGVHTFHLYQTQTAQSGYYNFNLSFLSQFVYKA
                     :    .               .                .                .

229E            DQLSFYVPDGFYSTSP--IQSVELPVSIVSLP--------VYHKHMFIVLYVDFKPQ---
PEDV            SQVAFDLDDGFYPISSRNLLSHEQPISFVTLP--------SFNDHSFVNITVSAA-----
CCov            SQLTANLQNGFYPVAS--SEVGLVNKSVVLLP--------SFYSHTSVNITIDLGMKR--
PRC             SQLTANLNNGFYPVSS--SEVGSVNKSVVLLP--------SFLTHTIVNITIGLGMKR--
FICV            QQLKHELPDGFYSASM--LVKKDLPKTFVTMP--------QFYHWMNVTLHVVLNDTEKK
BoCov           -QLYYNLPAANVSVSRFNPSTWNRRFGFTEQFVFKPQPVGVFTHHDVVYAQHCFKAPKNF
OC43            -QLYYNLPAANVSVSRFNPSIWNRRFGFTEQSVFKPQPAGVFTDHDVVYAQHCFKAPTNF
PHEV            -QLYYSLPAANVSVTHYNPSSWNRRYGFNNQS------FGSRGLHDAVYSQQCFNTPNTY
MHV             -QLYYSLPKNNVTINNYNPSSWNRRYGFKVND----------------------------
TOR2_S          -VLAWNTRNIDATSTG----NYNYKYRYLRHG----------------------------
AIBV            SDYMYGSYHPICAFRP---ETINSGLWFNSLS----------------------------
                            .
```

FIGURE 14B

```
229E      ---SGGGKCFNCYPAGVNITLANFNETKG---PLCVDTSHFT---------TKYVAVYAN
PEDV      ---FGGLSSANLVAS--DTTINGFSS-------FCVDTRQFTI--------TLFYNVTNS
CCov      ---SGYGQPIASTLS--NITLPMQDNNTD---VYCIRSNRFSVYFHSTCKSSLWDDVFNS
PRC       ---SGYGQPIASTLS--NITLPMQDNNTD---VYCVRSDQFSVYVHSTCKSALWDNVFKR
FICV      YDIILAKAPELAALADVHFEIAQANGSVTNVTSLCVQARQLA----------LFYKYTSL
BoCov     --CPCKLDGSLCVGNGPGIDAGYKNSGIG----TCPAGTNYLT----CHNAA----QCDC
OC43      --CPCKLDGSLCVGNGPGIDAGYKNSGIG----TCPAGTNYLT----CHNAV----QCNC
PHEV      --CPCRT--SQCIG---G-------AGTG----TCPVGTTVRK----CFAAVTKATKCTC
MHV       ------------------------------------------------------------
TOR2_S    ------------------------------------------------------------
AIBV      ------------------------------------------------------------

229E      ----VGRWSASINTGNCPFSFGKVNNFVKFGSVCFSLKDIPGG-CAMPIVANWAYSKYYT
PEDV      ----YGYVSKSQDS-NCPFTLQSVNDYLSFSKFCVSTSLLAGA-CTIDLFGYPAFGSGVK
CCov      DCTDVLYATAVIKTGTCPFSFDKLNNYLTFNKFCLSLNPVGAN-CKFDVAARTRTNEQVV
PRC       NCTDVLDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGAN-CKFDVAARTRTNEQVV
FICV      QGLYTYSNLVELQNYDCPFSPQQFNNYLQFETLCFDVNPAVAG-CKWSLVHDVQWRTQFA
BoCov     LCTPDPITSKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQAFLGWSVDSC
OC43      LCTPDPITSKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQAFLGWSVDSC
PHEV      WCQPDPSTYKGVNAWTCPQSKVSIQPGQHCPGLGLVEDDCSGNPCTCKPQAFIGWSSETC
MHV       ------------------------------------------------------------
TOR2_S    --------KLR------PFERDISN--VPFSPDGKPCTPPALN-CYWPLNDYGFYTTTGI
AIBV      ----------VSLTYGPLQGGYKQSVFSGKATCCYAYSYNGPRACKGVYSGELSRDFECG

229E      IG----TLYVSWSDGDGITGVPQ-PVEGVSSFMNVTLDKCTKYNIYDVSGVGVIRVSNDT
PEDV      LT----SLYFQFTKGELITGTPK-PLEGITDVSFMTLDVCTKYTIYGFKGEGIITLTNSS
CCov      R-----SLYVIYEEGDNIVGVPS-DNSGLHDLSVLHLDSCTDYNIYGITGVGIIRQTNST
PRC       R-----SLYVIYEEGDSIVGVPS-DNSGLHDLSVLHLDSCTDYNIYGRTGVGIIRQTNRT
FICV      T------ITVSYKHGSMITTHAKGHSWGFQDTSVLVKDECTDYNIYGFQGTGIIRNTTSR
BoCov     LQGDRCNIFANFIFHDVNSGTTC-STDLQKSNTDIILGVCVNYDLYGITGQGIFVEVNAT
OC43      LQGDRCNIFANFILHDVNSGTTC-STDLQKSNTDIILGVCVNYDLYGITGQGIFVEVNAP
PHEV      LQNGRCNIFANFILNDVNSGTTC-STDLQQGNTIITTDVCVNYDLYGITGQGILIEVNAT
MHV       ----RCQIFANILLNGINSGTTC-STDLQLPNTEVATGVCVRYDLYGITGQGVFKEVKAD
TOR2_S    G----YQPYRVVVLSFELLNAPA-TVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKR
AIBV      L-----LVYVTKSDGSRIQTRTEPLVLTQHNYNNITLDKCVAYNIYGRVGQGFITNVTDS
                          .                  :  . *. : : .   * *.:    .

229E      FLN---------GITYTSTSGNLLGFKDVTKGTIYSITPCNP---PDQLVVYQQAVVGAM
PEDV      ILA---------GVYYTSDSGQLLAFKNVTSGAVYSVTPCSF---SEQAAYVNDDIVGVI
CCov      LLS---------GLYYTSLSGDLLGFKNVSDGVIYSVTPCDV---SAHAAVIDGAIVGAM
PRC       LLS---------GLYYTSLSGDLLGFKNVSDGVIYSVTPCDV---SAQAAVIDGTIVGAI
FICV      LVA---------GLYYTSISGDLLAFKNSTTGEIFTVVPCDL---TAQVAVINDEIVGAI
BoCov     YYNS-------WQNLLYDSNGNLYGFRDYLTNRTFMIRSCYSG--RVSAAFHANSSEPAL
OC43      YYNS-------WQNLLYDSNGNLYGFRDYLTNRTFMIRSCYSG--RVSAAFHANSSEPAL
PHEV      YYNS-------WQNLLYDSSGNLYGFRDYLSNRTFLIRSCYSG--RVSAVFHANSSEPAL
MHV       YYNS-------WQALLYDVNGNLNGFRDLTTNKTYTIRSCYSG--RVSAAYHKEAPEPAL
TOR2_S    FQP--------FQQFGRDVSDFTDSVRDPKTSEILDISPCAFGGVSVITPGTNASSEVAV
AIBV      VANFSYLADGGLAILDTSGAIDVFVVQGSYGLNYYKVNPCEDVN--QQFVVSGGNIVGIL
                        .        .:.        : .*                    :

229E      LSENFTSY-----------------GFSNVVELPKFFYASNGTYN---------------
PEDV      SSLSNST-------------------FNNTRELPGFFYHSNDGSN---------------
CCov      TSINSELL-----------------GLTHWTTTPNFYYYSIYNYTNERTRGTAID--SND
PRC       TSINSELL-----------------GLTHWTITPNFYYYSIYNYTNDKTRGTPID--SND
FICV      TAVNQTDLFEFVNNTQARRSRSSTPNFVTSYTMPQFYYITKWNNDTS-S-----------
BoCov     LFRNIKCN--------------YVFNNTLSRQLQPINYFDSYLGCVVNADN------STS
OC43      LFRNIKCN--------------YVFNNTLSRQLQPINYFDSYLGCVVNADN------STA
PHEV      MFRNLKCS--------------HVFNNTILRQIQLVNYFDSYLGCVVNAYN------NTA
MHV       LYRNINCS--------------YVFTNNISREENPLNYFDSYLGCVVNADN------RTD
TOR2_S    LYQDVNCT--------------DVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV
AIBV      TSRNETGS---------------------E-QVENQFYVKLTNSSHRRRRS-------IG
             .

229E      -CTDAVLTYSSFGVCADGSIIAVQ-----PRNVSYDSVSAIVTANLS-------------
PEDV      -CTEPVLVYSNIGVCKSGSIGYV------PSQYGQVKIAPTVTGNIS-------------
CCov      VDCEPIITYSNIGVCKNGALVFI------NVTHSDGDVQPISTGNVT-------------
PRC       VGCEPVITYSNIGVCKNGALVFI------NVTHSDGDVQPISTGNVT-------------
FICV      -NCTSAITYSSFAICNTGEIKYVNVTHVEIVDDSIGVIKPVSTGNIS-------------
BoCov     SVVQTCDLTVGSGYCVDYSTKRRSR-RAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQ
```

FIGURE 14C

```
OC43      SAVQTCDLTVGSGYCVDYSTKRRSR-RAITTGYRFTNFEPFTVNSVNDSLEHVGGLYEIQ
PHEV      SAVSTCDLTVGSGYCVDYVTALRSR-RSFTTGYRFTNFEPFAANLVNDSIEPVGGLYEIQ
MHV       EALPNCNLRMGAGLCVDYSKSRRAR-RSVSTGYRLTTFEPYMPMLVNDSVQSVGGLYEMQ
TOR2_S    DTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNN-------TIA
AIBV      QNVTSCPYVSYGRFCIEPDGSLKMI----VPEELKQFVAPLLNITES-----------VL
                         *

229E      IPSNWTISVQVEYLQITSTPIVVDCSTYVCNGNVRCVELLKQYTSACKTIEDALRNSARL
PEDV      IPTNFSMSIRTEYLQLYNTPVSVDCATYVCNGNSRCKQLLTQYTAACKTIESALQLSARL
CCov      IPTNFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARL
PRC       IPTNFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARL
FICV      IPKNFTVAVQAEYIQIQVKPVVVDCATYVCNGNTHCLKLLTQYTSACQTIENALNLGARL
BoCov     IPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNEL
OC43      IPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDCAACKSQLVEYGSFCDNINAILTEVNEL
PHEV      IPSEFTIGNLEEFIQTRSPKVTIDCATFVCGDYAACRQQLAEYGSFCENINAILTEVNEL
MHV       IPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLVEYGSFCDNVNAILNEVNNL
TOR2_S    IPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAE
AIBV      IPNSFNLTVTDEYIQTRMDKVQINCLQYVCGNSLECRKLFQQYGPVCDNILSVVNSVSQK
          **..:.:     * :         ::*  ::*..   * . : :* . *  :   :

229E      ESADVSEMLTFDKKAFTLANVSSF-GD-------YNLSSVIPS--------LPTSGSR--
PEDV      ESVEVNSMLTISEEALQLATISSFNGDG------YNFTNVLGASVY-----DPASGRV--
CCov      ENMEIDSMLFVSENALKLASVEAFNSTETLDPIYKEWPNIGGSWLGGLKDILPSHNSK--
PRC       ENMEVDSMLFVSENALKLASVEAFNSSETLDPIYTQWPNIGGFWLEGLKYILPSDNSK--
FICV      ESLMLNDMITVSDRGLELATVERFNATA------LGGEKLGGLYFDG---LSSLLPPK--
BoCov     LDTTQLQVANSLMNGVTLSTKLKDGVN-------FNVDDINFSPVLG---CLGSACNK--
OC43      LDTTQLQVANSLMNGVTLSTKLKDGVN-------FNVDDVNFSPVLG---CLGSECNK--
PHEV      LDTTQLQVANSLMNGVTLSTKIKDGIN-------FNVDDINFSPVLG---CLGSECNR--
MHV       LDNMQLQVASALMQGVTISSRLPDGIS-------GPIDDINFSPLLG---CIGSTCAEDG
TOR2_S    QDRNTREVFAQVKQMYKTPTLKYFGGF--------NFSQILPDPLKP-------------
AIBV      EDMELLSFYSSTKPKGYDTPVLSNVSTG-----EFNISLLLTPPSSP-------------
            .     ..          .                         :

229E      -----VAGRSAIEDILFSKIVTSGLGTVDADYKNCTKGLS--IADLACAQYYNGIMVLPG
PEDV      -----VQKRSVIEDLLFNKVVTNGLGTVDEDYKRCSNGRS--VADLVCAQYYSGVMVLPG
CCov      -----RKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGYD--IADLVCAQYYNGIMVLPG
PRC       -----RKYRSAIEDLLFSKVVTSGLGTVDEDYKRCTGGYD--IADLVCAQYYNGIMVLPG
FICV      -----IGKRSAVEDLLFNKVVTSGLGTVDDDYKKCSSGTD--VADLVCAQYYNGIMVLPG
BoCov     -----VSSRSAIEDLLFSKVKLSDVG-FVEAYNNCTGGAE--IRDLICVQSYNGIKVLPP
OC43      -----VSSRSAIEDLLFSKVRLSDVG-FVEAYNNCTGGAG--IRDLICVQSYNGIKVLPP
PHEV      -----ASTRSAIEDLLFDKVKLSDVG-FVQAYNNCTGGAE--IRDLICVQSYNGIKVLPP
MHV       NGPSAIRGRSAIEDLLFDKVKLSDVG-FVEAYNNCTGGQE--VRDLLCVQSFNGIKVLPP
TOR2_S    ------TKRSFIEDLLFNKVTLADAG-FMKQYGECLGDIN--ARDLICAQKFNGLTVLPP
AIBV      ------SGRSFVEDLLFTSVETVGLP-TDAEYKKCTAGPLGTLKDLICAREYNGLLVLPP
                  ** :**:**  .:    .       * .*  .      ** *.: :.*: ***

229E      VADAERMAMYTGSLIGGIALGGLT----SAVSIPFSLAIQARLNYVALQTDVLQENQKIL
PEDV      VVDAEKLHMYSASLIGGMALGGIT----AAAALPFSYAVQARLNYLALQTDVLQRNQQLL
CCov      VANDDKMAMYTASLAGGITLGSLGG---GAVSIPFAIAVQARLNYVALQTDVLNKNQQIL
PRC       VANADKMTMYTASLAGGITLGAFGG---GAVSIPFAVAVQARLNYVALQTDVLNKNQQIL
FICV      VVDGNKMSMYTASLIGGMALGSIT----SAVAVPFAMQVQARLNYVALQTDVLQENQKIL
BoCov     LLSVNQISGYTLAATSASLFPPLS----AAVGVPFYLNVQYRINGIGVTMDVLSQNQKLI
OC43      LLSDNQISGYTLAATSANLFPPWS----AAAGVPFYLNVQYRINGIGVTMDVLSQNQKLI
PHEV      LLSENQISGYTLAATAASLFPPWT----AAAGVPFYLNVQYRINGLGVTMDVLSQNQKLI
MHV       VLSESQISGYTAGATAAAMFPPWT----AAAGVPFSLNVQYRINGLGVTMNVLSENQKMI
TOR2_S    LLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQI
AIBV      IITADMQTMYTASLVGAMAFGGIT----SAAAIPFATQIQARINHLGIAQSLLMKNQEKI
          :    .    *: .  ..            .*  :**    :   *:* :.:   .:* .**: :

229E      AASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQN
PEDV      AESFNSAIGNITSAFESVKEAISQTSKGLNTVAHALTKVQEVVNSQGSALNQLTVQLQHN
CCov      ANAFNQAIGNITQAFGKVNDAIHQTSQGLATVAKVLAKVQDVVNTQGQALSHLTLQLQNN
PRC       ASAFNQAIGNITQSFGKVNDAIHQTSRGLTTVAKALAKVQDVVNTQGQALRHLTVQLQNN
FICV      ANAFNNAIGNITLALGKVSNAITTTSDGFNSMASALTKIQSVVNQQGEALSQLTSQLQKN
BoCov     ANAFNNALDAIQEGFDATN-------------S-ALVKIQAVVNANAEALNNLLQQLSNR
OC43      ANAFNNALDAIQEGFDATN-------------S-ALVKIQAVVNADAEALNNLLQQLSNR
PHEV      ASAFNNALDAIQEGFDATN-------------S-ALVKIQAVVNANAEALNNLLQQLSNR
MHV       ASAFNNALGAIQEGFDATN-------------S-ALGKIQSVVNANAEALNNLLNQLSNR
TOR2_S    ANQFNKAISQIQESLTTTS--------------TALGKLQDVVNQNAQALNTLVKQLSSN
AIBV      AASFNKAIGHMQEGFRSTS--------------LALQQVQDVVNKQSAILTETMNSLNKN
          *   **.*:  :  .:  ..                .* ::* *** :.  *     .*  .
```

FIGURE 14D

```
229E          FQAISSSIQAIYDRLDTIQADQQVDRLITGRLAALNVFVSHTLTKYTEVRASRQLAQQKV
PEDV          FQAISSSIDDIYSRLDILLADVQVDRLITGRLSALNAFVAQTLTKYTEVQASRKLAQQKV
CCov          FQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKDKV
PRC           FQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKDKV
FICV          FQAISSSIAEIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYAEVKASRQIALEKV
BoCov         FGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNVYVSQQLSDSTLVKFSAAQAMEKV
OC43          FGAISSSLQEILSRLDALEAQAQIDRLINGRLTALDAYVSQQLSDSTLVKFSAAQAMEKV
PHEV          FGAISASLQEILSRLDALEAKAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAIEKV
MHV           FGAISASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKFSAAQAIEKV
TOR2_S        FGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
AIBV     >      FGAISSVIQDIYAQLDAIQADAQVDRLITGRLSSLSVLASAKQSEYIRVSQQRELATQKI
              * ***: :   *   :*: : *. *:****.*** :*..   :           :   .    *   *:

229E          NECVKSQSKRYGFCG-NGTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAWSGLCV-DG--
PEDV          NECVKSQSQRYGFCGGDGEHIFSLVQAAPQGLLFLHTVLVPGDFVNVLAIAGLCV-NG--
CCov          NECVRSQSQRFGFCG-NGTHLFSLANAAPNGMIFFHTVLLPTAYETVTAWSGICASDGDR
PRC           NECVRSQSQRFGFCG-NGTHLFSLANAAPNGMIFFHTVLLPTAYETVTAWSGICALDGDR
FICV          NECVKSQSNRYGFCG-NGTHLFSLVNSAPEGLLFFHTVLLPTEWEEVTAWSGICVNDT--
BoCov         NECVKSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCI-----
OC43          NECVKSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCI-----
PHEV          NECVKSQSSRINFCG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCI-----
MHV           NECVKSQTTRINFCG-NGNHILSLVQNAPYGLCFIHFSYVPTSFKTANVSPGLCI-----
TOR2_S        SECVLGQSKRVDFCG-KGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICH-----
AIBV     >      NECVKSQSNRYGFCG-SGRHVLSIPQNAPNGIVFIHFTYTPETFVNVTAIVGFCVNPLNA
              .***  .*: *  .***  .*  *::*:  : ** *: *:*      *          .   .:*

229E          TNGYVLRQPNLALYK------EGNYYRITSRIMFEPRIPTMADFVQIENCNVTFVNISRS
PEDV          EIALTLREPGLVLFTHELQTYTATEYFVSSRRMFEPRKPTVSDFVQIESCVVTYVNLTSD
CCov          TFGLVVKDVQLTLFRN-----LDDKFYLTPRTMYQPIVATSSDFVQIEGCDVLFVNATVI
PRC           TFGLVVKDVQLTLFRN-----LDDKFYLTPRTMYQPRVATSSDFVQIEGCDVLFVNTTVS
FICV          -YAYVLKDFDHSIFS------YNGTYMVTPRNMFQPRKPQMSDFVQITSCEVTFLNMTYT
BoCov         -AGDRGIAPKSGYFVN-----VNNTWMFTGSGYYYPEPITGNNVVVMSTCAVNYTKAPDV
OC43          -AGDRGIAPKSGYFVN-----VNNTWMFTGSRYYYPEPITGNNVVVMSTCAVNYTKAPDV
PHEV          -AGDIGISPKSGYFIN-----VNNSWMFTGSSYYYPEPITQNNVVVMSTCAVNYTKAPDL
MHV           -SGDRGLAPKAGYFVQ-----DNGEWKFTGSNYYYPEPITDKNSVAMISCAVNYTKAPEV
TOR2_S        -EGKAYFPREGVFVFN------GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNT
AIBV     >      SQYAIVPANGRGIFIQ-----VNGTYYITSRDMYMPRDITAGDIVTLTSCQANYVNVNKT
                                  :  .:      : *        :  .      *  .

229E          ELQTIVP-EYIDVNKTLQELSYKL-PNYTVPDLV---VEQYNQTILNLTSEISTLENKSA
PEDV          QLPDVIP-DYIDVNKTLDEILASL-PNRTGPSLP---LDVFNATYLNLTGEIADLEQRSE
CCov          DLPSIIP-DYIDINQTVQDILENFRPNWTVPELP---LDIFNATYLNLTGEINDLEFRSE
PRC           DLPSIIP-DYIDINQTVQDILENFRPNWTVPELT---LDVFNATYLNLTGEIDDLEFRSE
FICV          TFQEIVI-DYIDINKTIADMLEQYNPNYTTPELNL-LLDIFNQTKLNLTAEIDQLEQRAD
BoCov         MLNISTP-NLHDFKEELDQWFKNQ--TSVAPDLSL-DY--INVTFLDLQDEMN-------
OC43          MLNISTP-NLPDFKEELDQWFKNQ--TLVAPDLSL-DY--INVTFLDLQDEMN-------
PHEV          MLNTSTP-NLPDFKEELYQWFKNQ--SSVAPDLSL-DY--INVTFLDLQDEMN-------
MHV           FLNNSIP-NLPDFKEELDKWFKNQ--TSIAPDLSL-DFEKLNVTFLDLTYEMN-------
TOR2_S        VYDPLQP-ELDSFKEELDKYFKNH----TSPDVDLGDISGINASVVNIQKEID-------
AIBV     >      VITTFVEDDDFNFDDELSKWWNDT--KHGLPDFD---DFNYTVPILNISGEID-------
                    :   .... : .    .         *..         . . :::    *:

229E          ELNYTVQKLQTLIDNINSTLVDLKWLNRVETYIKWPWWVWLCISVVLIFVVSMLLLCCCS
PEDV          SLRNTTEELRSLINNINNTLVDLEWLNRVETYIKWPWWVWLIIVIVLIFVVSLLVFCCIS
CCov          KLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIFCIPILLFCCCS
PRC           KLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIFCIPLLLFCCCS
FICV          NLTTIAHELQQYIDNLNKTLVDLDWLNRIETYVKWPWYVWLLIGLVVVFCIPLLLFCCLS
BoCov         -------RLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVAMLVLLFFICCC
OC43          -------RLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVAMLVLLFFICCC
PHEV          -------RLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGLAGVAMLVLLFFICCC
MHV           -------RIQDAIKKLNESYINLKEVGTYEMYVKWPWYVWLLIGLAGVAVCVLLFFICCC
TOR2_S        -------RLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCM
AIBV     >      -------NIQGVIQGLNDSLINLEELSIIKTYIKWPWYVWLAIGFAIIIFILILGWVFFM
                     .:     . :*.: ::*. :.   : *:****:***  :       :      :
```

FIGURE 14E

```
229E            TGCCG-FFSCFASSIRGCCESTKL-PYYDVEKIHIQ---------
PEDV            TGCCG-CCGCCGACFSGCCRGPRLQPYEAFEKVHVQ---------
CCov            TGCCG-CIGCLGSCCHSICSRRQFESYEPIEKVHVH---------
PRC             TGCCG-CIGCLGSCCHSIFSRRQFENYEPIEKVHVH---------
FICV            TGFCG-CFGCVGSCCHSLCSRRQFETYEPIEKVHIH---------
BoCov           TGCGTSCFKICGGCCD-DYTGHQELVIK---TSHDD---------
OC43            TGCGTSCFKKCGGCCD-DYTGHQELVIK---TSHEG---------
PHEV            TGCGTSCFKKCGGCCD-DYTGHQEFVIK---TSHDD---------
MHV             TGCGSCCFRKCGSCCD-EYGGHQDSIVIHNISAHED---------
TOR2_S          TSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT---------
AIBV    >          TGCCGCCCGCFGIIPLISKCGKKSSYYTTFDNDVVTEQYRPKKSV
                *.         .                  .
```

Key	Name	Genbank	% ID*	
229E	spike glycoprotein [Human coronavirus 229E].	AAK32191	28.6%	(SEQ ID NO: 53)
AIBV	spike glycoprotein [Avian infectious bronchitis virus].	AA034396	27.6%	(SEQ ID NO: 54)
BoCov	E2 glycoprotein precursor (Spike glycoprotein)	P25193	30.5%	(SEQ ID NO: 55)
CCoV	spike protein - canine coronavirus	S41453	26.1%	(SEQ ID NO: 56)
FICV	peplomer protein [Feline infectious peritonitis virus].	BAA06805	25.4%	(SEQ ID NO: 57)
MHV	E2 glycoprotein precursor (Spike glycoprotein)	P11225	31.9%	(SEQ ID NO: 58)
OC43	surface protein - human coronavirus	S44241	30.7%	(SEQ ID NO: 59)
PEDV	spike protein [Porcine epidemic diarrhea virus].	CAA80971	26.0%	(SEQ ID NO: 60)
PHEV	spike glycoprotein [porcine hemagglutinating encephalomyelitis virus]	AAL80031	30.5%	(SEQ ID NO: 61)
PRC	S protein [Porcine respiratory coronavirus].	AAA46905	27.5%	(SEQ ID NO: 62)
TOR2_S	Sars associated virus S glycoprotein (SEQ ID NO: 33)			

FIGURE 14F

```
10          20          30          40          50
TOR2_E      MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVSLVKPTV
                    : ...: ...: .. :: .....:...:.:. ..::  :::.  . .. :.
PGV     MTFPRALTVIDDNG-MVINIIFWFLLIIILILLSIALLNIIKLCMVCCNLGRTVIIVPAQ
                  10          20          30          40          50

          60          70
TOR2_E YVYSRVKNLNSSEGVPDLLV    (SEQ ID NO: 35)
       ..:.  ::.
PGV    HAYDAYKNFMRIKAYNPDGALLA  (SEQ ID NO: 63)
      60          70          80
```

FIGURE 15

MESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVEEALSEAREHLKNGT
CGLVELEKGVLPQLEQPYVFIKRSDALSTNHGHKVVELVAEMDGIQYGRS
GITLGVLVPHVGETPIAYRNVLLRKNGNKGAGGHSYGIDLKSYDLGDELG
TDPIEDYEQNWNTKHGSGALRELTRELNGGAVTRYVDNNFCGPDGYPLDC
IKDFLARAGKSMCTLSEQLDYIESKRGVYCCRDHEHEIAWFTERSDKSYE
HQTPFEIKSAKKFDTFKGECPKFVFPLNSKVKVIQPRVEKKKTEGFMGRI
RSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFLKATCEHCGTENLV
IEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRLRKG
GRTRCFGGCVFAYVGCYNKRAYWVPRASADIGSGHTGITGDNVETLNEDL
LEILSRERVNINIVGDFHLNEEVAIILASFSASTSAFIDTIKSLDYKSFK
TIVESCGNYKVTKGKPVKGAWNIGQQRSVLTPLCGFPSQAAGVIRSIFAR
TLDAANHSIPDLQRAAVTILDGISEQSLRLVDAMVYTSDLLTNSVIIMAY
VTGGLVQQTSQWLSNLLGTTVEKLRPIFEWIEAKLSAGVEFLKDAWEILK
FLITGVFDIVKGQIQVASDNIKDCVKCFIDVVNKALEMCIDQVTIAGAKL
RSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVTFLEGDSHDTV
LTSEEVVLKNGELEALETPVDSFTNGAIVGTPVCVNGLMLLEIKDKEQYC
ALSPGLLATNNVFRLKGGAPIKGVTFGEDTVWEVQGYKNVRITFELDERV
DKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLQPVSDLLTNMGIDLDE
WSVATFYLFDDAGEENFSSRMYCSFYPPDEEEEDDAECEEEEIDETCEHE
YGTEDDYQGLPLEFGASAETVRVEEEEEEDWLDDTTEQSEIEPEPEPTPE
EPVNQFTGYLKLTDNVAIKCVDIVKEAQSANPMVIVNAANIHLKHGGGVA
GALNKATNGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVVGPNL
NAGEDIQLLKAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQ
VYIAVNDKALYEQVVMDYLDNLKPRVEAPKQEEPPNTEDSKTEEKSVVQK
PVDVKPKIKACIDEVTTTLEETKFLTNKLLLFADINGKLYHDSQNMLRGE
DMSFLEKDAPYMVGDVITSGDITCVVIPSKKAGGTTEMLSRALKKVPVDE
YITTYPGQGCAGYTLEEAKTALKKCKSAFYVLPSEAPNAKEEILGTVSWN
LREMLAHAEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRFFF
YTSKEPVASIITKLNSLNEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAV
VSVSSPDAVTTYNGYLTSSSKTSEEHFVETVSLAGSYRDWSYSGQRTELG
VEFLKRGDKIVYHTLESPVEFHLDGEVLSLDKLKSLLSLREVKTIKVFTT
VDNTNLHTQLVDMSMTYGQQFGPTYLDGADVTKIKPHVNHEGKTFFVLPS
DDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWKFPQVGGLTSIKWADNN
CYLSSVLLALQQLEVKFNAPALQEAYYRARAGDAANFCALILAYSNKTVG
ELGDVRETMTHLLQHANLESAKRVLNVVCKHCGQKTTTLTGVEAVMYMGT
LSYDNLKTGVSIPCVCGRDATQYLVQQESSFVMMSAPPAEYKLQQGTFLC
ANEYTGNYQCGHYTHITAKETLYRIDGAHLTKMSEYKGPVTDVFYKETSY
TTTIKPVSYKLDGVTYTEIEPKLDGYYKKDNAYYTEQPIDLVPTQPLPNA
SFDNFKLTCSNTKFADDLNQMTGFTKPASRELSVTFFPDLNGDVVAIDYR
HYSASFKKGAKLLHKPIVWHINQATTKTTFKPNTWCLRCLWSTKPVDTSN
SFEVLAVEDTQGMDNLACESQQPTSEEVVENPTIQKEVIECDVKTTEVVG
NVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIA
THGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRLAQRVFNNYMPYVF
TLLFQLCTFTKSTNSRIRASLPTTIAKNSVKSVAKLCLDAGINYVKSPKF
SKLFTIAMWLLLLSICLGSLICVTAAFGVLLSNFGAPSYCNGVRELYLNS
SNVTTMDFCEGSFPCSICLSGLDSLDSYPALETIQVTISSYKLDLTILGL
AAEWVLAYMLFTKFFYLLGLSAIMQVFFGYFASHFISNSWLMWFIISIVQ
MAPVSAMVRMYIFFASFYYIWKSYVHIMDGCTSSTCMMCYKRNRATRVEC
TTIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDTFCTGSTFISDEVARDL
SLQFKRPINPTDQSSYIVDSVAVKNGALHLYFDKAGQKTYERHPLSHFVN
LDNLRANNTKGSLPINVIVFDGKSKCDESASKSASVYYSQLMCQPILLLD
QALVSDVGDSTEVSVKMFDAYVDTFSATFSVPMEKLKALVATAHSELAKG
VALDGVLSTFVSAARQGVVDTDVDTKDVIECLKLSHHSDLEVTGDSCNNF
MLTYNKVENMTPRDLGACIDCNARHINAQVAKSHNVSLIWNVKDYMSLSE
QLRKQIRSAAKKNNIPFRLTCATTRQVVNVITTKISLKGGKIVSTCFKLM
LKATLLCVLAALVCYIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDIIST
DDCFANKHAGFDAWFSQRGGSYKNDKSCPVVAAIITREIGFIVPGLPGTV
LRAINGDFLHFLPRVFSAVGNICYTPSKLIEYSDFATSACVLAAECTIFK
DAMGKPVPYCYDTNLLEGSISYSELRPDTRYVLMDGSIIQFPNTYLEGSV
RVVTTFDAEYCRHGTCERSEVGICLSTSGRWVLNNEHYRALSGVFCGVDA
MNLIANIFTPLVQPVGALDVSASVVAGGIIAILVTCAAYYFMKFRRVFGE
YNHVVAANALLFLMSFTILCLVPAYSFLPGVYSVFYLYLTFYFTNDVSFL
AHLQWFAMFSPIVPFWITAIYVFCISLKHCHWFFNNYLRKRVMFNGVTFS
TFEEAALCTFLLNKEMYLKLRSETLLPLTQYNRYLALYNKYKYFSGALDT
TSYREAACCHLAKALNDFSNSGADVLYQPPQTSITSAVLQSGFRKMAFPS
GKVEGCMVQVTCGTTTLNGLWLDDTVYCPRHVICTAEDMLNPNYEDLLIR
KSNHSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPKTPKYKFVRIQPGQ
TFSVLACYNGSPSGVYQCAMRPNHTIKGSFLNGSCGSVGFNIDYDCVSFC
YMHHMELPTGVHAGTDLEGKFYGPFVDRQTAQAAGTDTTITLNVLAWLYA
AVINGDRWFLNRFTTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQTGIA
VLDMCAALKELLQNGMNGRTILGSTILEDEFTPFDVVRQCSGVTFQGKFK

FIGURE 16A

KIVKGTHHWMLLTFLTSLLILVQSTQWSLFFFVYENAFLPFTLGIMAIAA
CAMLLVKHKHAFLCLFLLPSLATVAYFNMVYMPASWVMRIMTWLELADTS
LSGYRLKDCVMYASALVLLILMTARTVYDDAARRVWTLMNVITLVYKVYY
GNALDQAISMWALVISVTSNYSGVVTTIMFLARAIVFVCVEYYPLLFITG
NTLQCIMLVYCFLGYCCCCYFGLFCLLNRYFRLTLGVYDYLVSTQEFRYM
NSQGLLPPKSSIDAFKLNIKLLGIGGKPCIKVATVQSKMSDVKCTSVVLL
SVLQQLRVESSSKLWAQCVQLHNDILLAKDTTEAFEKMVSLLSVLLSMQG
AVDINRLCEEMLDNRATLQAIASEFSSLPSYAAYATAQEAYEQAVANGDS
EVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMADQAMTQMYKQARSEDKRA
KVTSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLNIIPLTTAAKLMVV
VPDYGTYKNTCDGNTFTYASALWEIQQVVDADSKIVQLSEINMDNSPNLA
WPLIVTALRANSAVKLQNNELSPVALRQMSCAAGTTQTACTDDNALAYYN
NSKGGRFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGP
KVKYLYFIKGLNNLNRGMVLGSLAATVRLQAGNATEVPANSTVLSFCAFA
VDPAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQESFGG
ASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRNTVCTVC
GMWKGYGCSCDQLREPLMQSADASTF

(SEQ ID NO: 64)

FIGURE 16B

FKRVCG
VSAARLTPCGTGTSTDVVYRAFDIYNEKVAGFAKFLKTNCCRFQEKDEEG
NLLDSYFVVKRHTMSNYQHEETIYNLVKDCPAVAVHDFFKFRVDGDMVPH
ISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWY
DFVENPDILRVYANLGERVRQSLLKTVQFCDAMRDAGIVGVLTLDNQDLN
GNWYDFGDFVQVAPGCGVPIVDSYYSLLMPILTLTRALAAESHMDADLAK
PLIKWDLLKYDFTEERLCLFDRYFKYWDQTYHPNCINCLDDRCILHCANF
NVLFSTVFPPTSFGPLVRKIFVDGVPFVVSTGYHFRELGVVHNQDVNLHS
SRLSFKELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNVAFQTVKPG
NFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTM
CDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKAR
LYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISAKNRARTVAGVSIC
STMTNRQFHQKLLKSIAATRGATVVIGTSKFYGGWHNMLKTVYSDVETPH
LMGWDYPKCDRAMPNMLRIMASLVLARKHNTCCNLSHRFYRLANECAQVL
SEMVMCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGN
KIADKYVRNLQHRLYECLYRNRDVDHEFVDEFYAYLRKHFSMMILSDDAV
VCYNSNYAAQGLVASIKNFKAVLYYQNNVFMSEAKCWTETDLTKGPHEFC
SQHTMLVKQGDDYVYLPYPDPSRILGAGCFVDDIVKTDGTLMIERFVSLA
IDAYPLTKHPNQEYADVFHLYLQYIRKLHDELTGHMLDMYSVMLTNDNTS
RYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRCGACIRRPFLCCKCCY
DHVISTSHKLVLSVNPYVCNAPGCDVTDVTQLYLGGMSYYCKSHKPPISF
PLCANGQVFGLYKNTCVGSDNVTDFNAIATCDWTNAGDYILANTCTERLK
LFAAETLKATEETFKLSYGIATVREVLSDRELHLSWEVGKPRPPLNRNYV
FTGYRVTKNSKVQIGEYTFEKGDYGDAVVYRGTTTYKLNVGDYFVLTSHT
VMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQKYSTLQ
GPPGTGKSHFAIGLALYYPSARIVYTACSHAAVDALCEKALKYLPIDKCS
RIIPARARVECFDKFKVNSTLEQYVFCTVNALPETTADIVVFDEISMATN
YDLSVVNARLRAKHYVYIGDPAQLPAPRTLLTKGTLEPEYFNSVCRLMKT
IGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVIT
HDVSSAINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTQ
TVDSSQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDL
YDKLQFTSLEIPRRNVATLQAENVTGLFKDCSKIITGLHPTQAPTHLSVD
IKFKTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAI
RHVRAWIGFDVEGCHATRDAVGTNLPLQLGFSTGVNLVAVPTGYVDTENN
TEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIKIVQMLSDTLKGLSDR
VVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNHS
VGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCL
AVHECFVKRVDWSVEYPIIGDELRVNSACRKVQHMVVKSALLADKFPVLH
DIGNPKAIKCVPQAEVEWKFYDAQPCSDKAYKIEELFYSYATHHDKFTDG
VCLFWNCNVDRYPANAIVCRFDTRVLSNLNLPGCDGGSLYVNKHAFHTPA
FDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDIDYVPLKSATCITRCNLG
GAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQSLE
NVAYNVVNKGHFDGHAGEAPVSIINNAVYTKVDGIDVEIFENKTTLPVNV
AFELWAKRNIKPVPEIKILNNLGVDIAANTVIWDYKREAPAHVSTIGVCT
MTDIAKKPTESACSSLTVLFDGRVEGQVDLFRNARNGVLITEGSVKGLTP
SKGPAQASVNGVTLIGESVKTQFNYFKKVDGIIQQLPETYFTQSRDLEDF
KPRSQMETDFLELAMDEFIQRYKLEGYAFEHIVYGDFSHGQLGGLHLMIG
LAKRSQDSPLKLEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFV
EIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVETFYPKLQASQAWQP
GVAMPNLYKMQRMLLEKCDLQNYGENAVIPKGIMMNVAKYTQLCQYLNTL
TLAVPYNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVDSDLNDFVSDA
DSTLIGDCATVHTANKWDLIISDMYDPRTKHVTKENDSKEGFFTYLCGFI
KQKLALGGSIAVKITEHSWNADLYKLMGHFSWWTAFVTNVNASSSEAFLI
GANYLGKPKEQIDGYTMHANYIFWRNTNPIQLSSYSLFDMSKFPLKLRGT
AVMSLKENQINDMIYSLLEKGRLIIRENNRVVVSSDILVNN

(SEQ ID NO: 65)

FIGURE 17

MDLFMRFFTLRSITAQPVKIDNASPASTVHATATIPLQASLPFGWLVIGV
AFLAVFQSATKIIALNKRWQLALYKGFQFICNLLLLFVTIYSHLLLVAAG
MEAQFLYLYALIYFLQCINACRIIMRCWLCWKCKSKNPLLYDANYFVCWH
THNYDYCIPYNSVTDTIVVTEGDGISTPKLKEDYQIGGYSEDRHSGVKDY
VVVHGYFTEVYYQLESTQITTDTGIENATFFIFNKLVKDPPNVQIHTIDG
SSGVANPAMDPIYDEPTTTTSVPL (SEQ ID NO: 66)

FIGURE 18

MMPTTLFAGTHITMTTVYHITVSQIQLSLLKVTAFQHQNSKKTTKLVVIL
RIGTQVLKTMSLYMAISPKFTTSLSLHKLLQTLVLKMLHSSSLTSLLKTH
RMCKYTQSTALQELLIQQWIQFMMSRRRLLACLCKHKKVSTNLCTHSFRK
KQVR (SEQ ID NO: 67)

FIGURE 19

MFHLVDFQVTIAEILIIIMRTFRIAIWNLDVIISSIVRQLFKPLTKKNYS
ELDDEEPMELDYP (SEQ ID NO: 68)

FIGURE 20

MKIILFLTLIVFTSCELYHYQECVRGTTVLLKEPCPSGTYEGNSPFHPLA
DNKFALTCTSTHFAFACADGTRHTYQLRARSVSPKLFIRQEEVQQELYSP
LFLIVAALVFLILCFTIKRKTE (SEQ ID NO: 69)

FIGURE 21

MNELTLIDFYLCFLAFLLFLVLIMLIIFWFSLEIQDLEEPCTKV

(SEQ ID NO: 70)

FIGURE 22

MKLLIVLTCISLCSCICTVVQRCASNKPHVLEDPCKVQH

(SEQ ID NO: 71)

FIGURE 23

MCLKILVRYNTRGNTYSTAWLCALGKVLPFHRWHTMVQTCTPNVTINCQD
PAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN (SEQ ID NO: 72)

FIGURE 24

```
MDPNQTNVVPPALHLVDPQIQLTITRMEDAMGQGQNSADPKVYPIILRLG
SQLSLSMARRNLDSLEARAFQSTPIVVQMTKLATTEELPDEFVVVTAK

(SEQ ID NO: 73)
```

FIGURE 25

```
MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQLLAAVG
EILLLEWLAEVVKLPSRYCC   (SEQ ID NO: 74)
```

FIGURE 26

```
CIAVGQLCVFWNIGRPCCSGLCVFA--CTVKL     conotoxin
CISLCS-CICTVVQRCASNKPHVLEDPCKVQH      sars
**::.  *:   : * ...   *:   *.*:
```

FIGURE 27

SARS VIRUS NUCLEOTIDE AND AMINO ACID SEQUENCES AND USES THEREOF

Seguence Listing

The instant application contains a Seguence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Jan. 18, 2010, is named 308410US.txt and is 462,420 bytes in size.

FIELD OF THE INVENTION

The invention is in the field of virology. More specifically, the invention is in the field of coronaviruses.

BACKGROUND OF THE INVENTION

Severe acute respiratory syndrome (SARS), a worldwide outbreak of atypical pneumonia with an overall mortality rate of about 3 to 6%, has been attributed to a coronavirus following tests of causation according to Koch's postulates, including monkey inoculation (R. Munch, *Microbes Infect* 5, 69-74, January 2003). The coronaviruses are members of a family of enveloped viruses that replicate in the cytoplasm of animal host cells (B. N. Fields et al., *Fields virology*, Lippincott Williams & Wilkins, Philadelphia, 4th ed., 2001). They are distinguished by the presence of a single-stranded plus sense RNA genome, approximately 30 kb in length, that has a 5' cap structure and 3' polyA tract. Hence the genome is essentially a very large mRNA. Upon infection of an appropriate host cell, the 5'-most open reading frame (ORF) of the viral genome is translated into a large polyprotein that is cleaved by viral-encoded proteases to release several nonstructural proteins including an RNA-dependent RNA polymerase (Pol) and an ATPase helicase (Hel). These proteins in turn are responsible for replicating the viral genome as well as generating nested transcripts that are used in the synthesis of the viral proteins. The mechanism by which these subgenomic mRNAs are made is not fully understood, however transcription regulating sequences (TRSs) at the 5'end of each gene may represent signals that regulate the discontinuous transcription of subgenomic mRNAs (sgmRNAs). The TRSs include a partially conserved core sequence (CS) that in some coronaviruses is 5'-CUAAAC-3'. Two major models have been proposed to explain the discontinuous transcription in coronaviruses and arterioviruses (M. M. C. Lai, D. Cavanagh, Adv Virus Res. 48, 1 (1997); S. G. Sawicki, D. L. Sawicki, Adv. Exp. Med Biol. 440, 215 (1998)). The discovery of transcriptionally active, subgenomic-size minus strands containing the antileader sequence and transcription intermediates active in the synthesis of mRNAs (D. L. Sawicki et al., J. Gen Virol 82, 386 (2001); S. G. Sawicki, D. L. Sawicki, J. Virol. 64, 1050 (1990); M. Schaad, R. S. J. Baric, J. Virol. 68, 8169 (1994); P. B. Sethna et al., Proc. Natl. Acad. Sci. U.S.A. 86, 5626 (1989)) favors the model of discontinuous transcription during the minus strand synthesis (S. G. Sawicki, D. L. Sawicki, Adv. Exp. Med Biol. 440, 215 (1998)).

The coronaviral membrane proteins, including the major proteins S (Spike) and M (Membrane), are inserted into the endoplasmic reticulum Golgi intermediate compartment (ERGIC) while full length replicated RNA (+ strands) assemble with the N (nucleocapsid) protein. This RNA-protein complex then associates with the M protein embedded in the membranes of the ER and virus particles form as the nucleocapsid complex buds into the ER. The virus then migrates through the Golgi complex and eventually exits the

cell, likely by exocytosis (B. N. Fields et al., *Fields virology*, Lippincott Williams & Wilkins, Philadelphia, 4th ed., 2001). The site of viral attachment to the host cell resides within the S protein.

The coronaviruses include a large number of viruses that infect different animal species. The predominant diseases associated with these viruses are respiratory and enteric infections, although hepatic and neurological diseases also occur with some viruses. Coronaviruses are divided into three serotypes, Types I, II and III. Phylogenetic analysis of coronavirus sequences also identifies three main classes of these viruses, corresponding to each of the three serotypes. Type II coronaviruses contain a hemagglutinin esterase (HE) gene homologous to that of Influenza C virus. It is presumed that the precursor of the Type II coronaviruses acquired HE as a result of a recombination event within a doubly infected host cell.

In view of the rapid worldwide dissemination of SARS, which has the potential of creating a pandemic, along with its alarming morbidity and mortality rates, it would be useful to have a better understanding of this coronavirus agent at the molecular level to provide diagnostics, vaccines, and therapeutics, and to support public health control measures.

SUMMARY OF THE INVENTION

In general, the invention provides the genomic sequence of a novel coronavirus, the SARS virus, and provides novel nucleic acid molecules encoding novel proteins that may be used, for example, for the diagnosis or therapy of a variety of SARS virus-related disorders.

In one aspect, the invention provides a substantially pure SARS virus nucleic acid molecule or fragment thereof, for example, a genornic RNA or DNA, cDNA, synthetic DNA, or mRNA molecule. In some embodiments, the nucleic acid molecule includes a sequence substantially identical to any of the sequences of SEQ ID NOs: 1-13, 15-18, 20-30, 90-159, 208, 209. In some embodiments, the nucleic acid molecule includes a sequence from SEQ ID NO: 1, SEQ ID NO:2, or SEQ ID NO: 15 or a fragment of these sequences. In alternative embodiments, the nucleic acid molecule may include a sequence substantially identical to SEQ ID NO: 1, SEQ ID NO:2, or SEQ ID NO: 15, or a fragment thereof In alternative embodiments, the nucleic acid molecule may include a s2m motif (for example, a s2m sequence substantially identical to any of the sequence of SEQ ID NOs: 16, 17, and 18), a leader sequence (for example, a sequence substantially identical to the sequence of SEQ ID NO: 3), or a transcriptional regulatory sequence (for example, a sequence substantially identical to any of the sequence of SEQ ID NOs: 4-13 and 20-30). In alternative embodiments, the nucleic acid molecule includes a sequence substantially identical to any of the sequences of nucleotides 265-13,398; 13,398-21,485; 21,492-25,259; 25,268-26,092; 25,689-26,153; 26,117-26,347; 26,398-27,063; 27,074-27,265; 27,273-27,641; 27,638-27,772; 27,779-27,898; 27,864-28,118; 28,120-29,388; 28,130-28,426; 28,583-28,795; and 29,590-29,621 of SEQ ID NO: 15. In alternative embodiments, the nucleic acid molecule may encode a polyprotein or a polypeptide. In alternative embodiments, the invention provides a nucleic acid molecule including a sequence complementary to a SARS virus nucleotide sequence.

In an alternative aspect, the invention provides a substantially pure SARS virus polypeptide or fragment thereof, for example, a polyprotein, glycoprotein (for example, a matrix glycoprotein that may include a sequence substantially identical to the sequence of SEQ ID NO: 34), a transmembrane protein (for example, a multitransmembrane protein, a type I transmembrane protein, or a type II transmembrane protein), a RNA binding protein, or a viral envelope protein. In alternative embodiments, the invention provides a replicase 1a protein, replicase 1b protein, a spike glycoprotein, a small envelope protein, a matrix glycoprotein, or a nucleocapsid protein. In alternative embodiments, the invention provides a nucleic acid molecule encoding a SARS virus polypeptide. In alternative embodiments, the SARS virus polypeptide includes an identifiable signal sequence (for example, a signal sequence substantially identical to the sequence of SEQ ID NOs: 76 or 85), a transmembrane domain (for example, a transmembrane domain substantially identical to any of the sequences of SEQ ID NOs: 77-86), a transmembrane anchor, a transmembrane helix, an ATP-binding domain, a nuclear localization signal, a hydrophilic domain, (for example, a hydrophilic domain substantially identical to the sequence of SEQ ID NOs: 87), or a lysine-rich sequence (for example, a sequence substantially identical to the sequence of SEQ ID NO: 14). In alternative embodiments, the SARS virus polypeptide may include a sequence substantially identical to any of the sequences of SEQ ID NOs: 14, 33-36, 64-74, and 76-87.

In alternative embodiments, the invention provides a vector (for example, a gene therapy vector or a cloning vector) including a SARS virus nucleic acid molecule (for example, a molecule including a sequence substantially identical to any of the sequences of SEQ ID NOs: 1-13, 15-18, 20-30, 90-159, 208, 209), or a host cell (for example, a mammalian cell, a yeast, a bacterium, or a nematode cell) including the vector.

In alternative embodiments, the invention provides a nucleic acid molecule having substantial nucleotide sequence identity (for example, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% complementarity) to a sequence encoding a SARS virus polypeptide or fragment thereof, for example where the fragment includes at least six amino acids, and where the nucleic acid molecule hybridizes under high stringency conditions to at least a portion of a SARS virus nucleic acid molecule.

In alternative embodiments, the invention provides a nucleic acid molecule having substantial nucleotide sequence identity (for example, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% complementarity) to a SARS virus nucleotide sequence, for example where the nucleic acid molecule includes at least ten nucleotides, and where the nucleic acid molecule hybridizes under high stringency conditions to at least a portion of a SARS virus nucleic acid molecule.

In alternative embodiments, the invention provides a nucleic acid molecule comprising a sequence that is antisense to a SARS virus nucleic acid molecule, or an antibody (for example, a neutralizing antibody) that specifically binds to a SARS virus polypeptide.

In alternative embodiments, the invention provides a method for detecting a SARS epitope, such as a virion or polypeptide in a sample, by contacting the sample with an antibody that specifically binds a SARS epitope, such as a virus polypeptide, and determining whether the antibody specifically binds to the polypeptide. In alternative embodiments, the invention provides a method for detecting a SARS virus genome, gene, or homolog or fragment thereof in a sample by contacting a SARS virus nucleic acid molecule, for example where the nucleic acid molecule includes at least ten nucleotides, with a preparation of genomic DNA from the sample, under hybridization conditions providing detection of DNA sequences having nucleotide sequence identity to a SARS virus nucleic acid molecule. In alternative embodiments, the invention provides a method of targeting a protein for secretion from a cell, by attaching a signal sequence from a SARS virus polypeptide to the protein, such that the protein is secreted from the cell.

In alternative aspects, the invention provides a method for eliciting an immune response in an animal, by identifying an animal infected with or at risk for infection with a SARS virus and administering a SARS virus polypeptide or fragment thereof or fragment thereof, or administering a SARS virus nucleic acid molecule encoding a SARS virus polypeptide or fragment thereof to the animal. In alternative embodiments, the administering results in the production of an antibody in the mammal, or results in the generation of cytotoxic or helper T-lymphocytes in the mammal.

In alternative embodiments, the invention provides a kit for detecting the presence of a SARS virus nucleic acid molecule or polypeptide in a sample, where the kit includes a SARS virus nucleic acid molecule, or an antibody that specifically binds a SARS virus polypeptide.

In alternative aspects the invention provides a method for treating or preventing a SARS virus infection by identifying an animal (e.g., a human) infected with or at risk for infection with a SARS virus, and administering a SARS virus nucleic acid molecule or polypeptide, or administering a compound that inhibits pathogenicity or replication of a SARS virus, to the animal. In alternative embodiments, the invention provides the use of a SARS virus nucleic acid molecule or polypeptide for treating or preventing a SARS virus infection.

In alternative aspects the invention provides a method of identifying a compound for treating or preventing a SARS virus infection, by contacting sample including a SARS virus nucleic acid molecule or contacting a SARS virus polypeptide with the compound, where an increase or decrease in the expression or activity of the nucleic acid molecule or the polypeptide identifies a compound for treating or preventing a SARS virus infection.

In alternative aspects the invention provides a vaccine (e.g., a DNA vaccine) including a SARS virus nucleic acid molecule or polypeptide.

In alternative aspects the invention provides a microarray including a plurality of elements, wherein each element includes one or more distinct nucleic acid or amino acid sequences, and where the sequences are selected from a SARS virus nucleic acid molecule or polypeptide, or a antibody that specifically binds a SARS virus nucleic acid molecule or polypeptide.

In alternative aspects the invention provides a computer readable record (e.g., a database) including distinct SARS virus nucleic acid or amino acid sequences.

A "SARS virus" is a virus putatively belonging to the coronavirus family and identified as the causative agent for sudden acute respiratory syndrome (SARS). A SARS virus nucleic acid molecule may include a sequence substantially identical to the nucleotide sequences described herein or fragments thereof. A SARS virus polypeptide may include a sequence substantially identical to a sequence encoded by a SARS virus nucleic acid molecule, or may include a sequence substantially identical to the polypeptide sequences described herein, or fragments thereof.

A compound is "substantially pure" when it is separated from the components that naturally accompany it. Typically, a compound is substantially pure when it is at least 60%, more generally 75% or over 90%, by weight, of the total material in a sample. Thus, for example, a polypeptide that is chemically synthesized or produced by recombinant technology will be generally be substantially free from its naturally associated components. A nucleic acid molecule may be substantially pure when it is not immediately contiguous with (i.e., covalently linked to) the coding sequences with which it is normally contiguous in the naturally occurring genome of the organism from which the DNA of the invention is derived. A nucleic acid molecule may also be substantially pure when it is isolated from the organism in which it is normally found. A substantially pure compound can be obtained, for example, by extraction from a natural source; by expression of a recombinant nucleic acid molecule encoding a polypeptide compound; or by chemical synthesis. Purity can be measured using any appropriate method such as column chromatography, gel electrophoresis, HPLC, etc.

A "substantially identical" sequence is an amino acid or nucleotide sequence that differs from a reference sequence only by one or more conservative substitutions, as discussed herein, or by one or more non-conservative substitutions, deletions, or insertions located at positions of the sequence that do not destroy the biological function of the amino acid or nucleic acid molecule. Such a sequence can be at least 10%, 20%, 30%, 40%, 50%, 52.5%, 55% or 60% or 75%, or more generally at least 80%, 85%, 90%, or 95%, or as much as 99% or 100% identical at the amino acid or nucleotide level to the sequence used for comparison using, for example, the Align Program (Myers and Miller, CABIOS, 1989, 4:11-17) or FASTA. For polypeptides, the length of comparison sequences maybe at least 4, 5, 10, or 15 amino acids, or at least 20, 25, or 30 amino acids. In alternate embodiments, the length of comparison sequences may be at least 35, 40, or 50 amino acids, or over 60, 80, or 100 amino acids. For nucleic acid molecules, the length of comparison sequences may be at least 15, 20, or 25 nucleotides, or at least 30, 40, or 50 nucleotides. In alternate embodiments, the length of comparison sequences may be at least 60, 70, 80, or 90 nucleotides, or over 100, 200, or 500 nucleotides. Sequence identity can be readily measured using publicly available sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wis. 53705, or BLAST software available from the National Library of Medicine, or as described herein). Examples of useful software include the programs Pile-up and PrettyBox. Such software matches similar sequences by assigning degrees of homology to various substitutions, deletions, insertions, and other modifications.

Alternatively, or additionally, two nucleic acid sequences may be "substantially identical" if they hybridize under high stringency conditions. In some embodiments, high stringency conditions are, for example, conditions that allow hybridization comparable with the hybridization that occurs using a DNA probe of at least 500 nucleotides in length, in a buffer containing 0.5 M $NaHPO_4$, pH 7.2, 7% SDS, 1 mM EDTA, and 1% BSA (fraction V), at a temperature of 65° C., or a buffer containing 48% formamide, 4.8×SSC, 0.2 M Tris-Cl, pH 7.6, 1× Denhardt's solution, 10% dextran sulfate, and 0.1% SDS, at a temperature of 42° C. (These are typical conditions for high stringency northern or Southern hybridizations.) Hybridizations may be carried out over a period of about 20 to 30 minutes, or about 2 to 6 hours, or about 10 to 15 hours, or over 24 hours or more. High stringency hybridization is also relied upon for the success of numerous techniques routinely performed by molecular biologists, such as high stringency PCR, DNA sequencing, single strand conformational polymorphism analysis, and in situ hybridization. In contrast to northern and Southern hybridizations, these techniques are usually performed with relatively short probes (e.g., usually about 16 nucleotides or longer for PCR or sequencing and about 40 nucleotides or longer for in situ hybridization). The high stringency conditions used in these techniques are well known to those skilled in the art of molecular biology, and examples of them can be found, for example, in Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y., 1998, which is hereby incorporated by reference.

The terms "nucleic acid" or "nucleic acid molecule" encompass both RNA (plus and minus strands) and DNA, including cDNA, genomic DNA, and synthetic (e.g., chemically synthesized) DNA. The nucleic acid may be double-stranded or single-stranded. Where single-stranded, the nucleic acid may be the sense strand or the antisense strand. A nucleic acid molecule may be any chain of two or more covalently bonded nucleotides, including naturally occurring or non-naturally occurring nucleotides, or nucleotide analogs or derivatives. By "RNA" is meant a sequence of two or more covalently bonded, naturally occurring or modified ribonucleotides. One example of a modified RNA included within this term is phosphorothioate RNA. By "DNA" is meant a sequence of two or more covalently bonded, naturally occurring or modified deoxyribonucleotides. By "cDNA" is meant complementary or copy DNA produced from an RNA template by the action of RNA-dependent DNA polymerase (reverse transcriptase). Thus a "cDNA clone" means a duplex DNA sequence complementary to an RNA molecule of interest, carried in a cloning vector.

An "isolated nucleic acid" is a nucleic acid molecule that is free of the nucleic acid molecules that normally flank it in the genome or that is free of the organism in which it is normally found. Therefore, an "isolated" gene or nucleic acid molecule is in some cases intended to mean a gene or nucleic acid molecule which is not flanked by nucleic acid molecules which normally (in nature) flank the gene or nucleic acid molecule (such as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (as in a cDNA or RNA library). In some cases, an isolated nucleic acid molecule is intended to mean the genome of an organism such as a virus. An isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. The term therefore includes, e.g., a genome; a recombinant nucleic acid incorporated into a vector, such as an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other sequences. It also includes a recombinant nucleic acid which is part of a hybrid gene encoding additional polypeptide sequences. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Thus, an isolated gene or nucleic acid molecule can include a gene or nucleic acid molecule which is synthesized chemically or by recombinant means. Recombinant DNA contained in a vector are included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. In vivo and in vitro RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleic acid molecules. Such isolated nucleic acid molecules are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (e.g., from other species), for gene mapping (e.g., by in situ hybridization with chromosomes), or for detecting expression of the nucleic acid molecule in tissue (e.g., human tissue, such as peripheral blood), such as by Northern blot analysis.

Various genes and nucleic acid sequences of the invention may be recombinant sequences. The term "recombinant" means that something has been recombined, so that when made in reference to a nucleic acid construct the term refers to a molecule that is comprised of nucleic acid sequences that are joined together or produced by means of molecular biological techniques. The term "recombinant" when made in reference to a protein or a polypeptide refers to a protein or polypeptide molecule which is expressed using a recombinant nucleic acid construct created by means of molecular biological techniques. The term "recombinant" when made in reference to genetic composition refers to a gamete or progeny with new combinations of alleles that did not occur in the parental genomes. Recombinant nucleic acid constructs may include a nucleotide sequence which is ligated to, or is manipulated to become ligated to, a nucleic acid sequence to which it is not ligated in nature, or to which it is ligated at a different location in nature. Referring to a nucleic acid construct as "recombinant" therefore indicates that the nucleic acid molecule has been manipulated using genetic engineering, i.e. by human intervention. Recombinant nucleic acid constructs may for example be introduced into a host cell by transformation. Such recombinant nucleic acid constructs may include sequences derived from the same host cell species or from different host cell species, which have been isolated and reintroduced into cells of the host species. Recombinant nucleic acid construct sequences may become integrated into a host cell genome, either as a result of the original transformation of the host cells, or as the result of subsequent recombination and/or repair events.

As used herein, "heterologous" in reference to a nucleic acid or protein is a molecule that has been manipulated by human intervention so that it is located in a place other than the place in which it is naturally found. For example, a nucleic acid sequence from one species may be introduced into the genome of another species, or a nucleic acid sequence from one genomic locus may be moved to another genomic or extrachromasomal locus in the same species. A heterologous protein includes, for example, a protein expressed from a heterologous coding sequence or a protein expressed from a recombinant gene in a cell that would not naturally express the protein.

By "antisense," as used herein in reference to nucleic acids, is meant a nucleic acid sequence that is complementary to one strand of a nucleic acid molecule. In some embodiments, an antisense sequence is complementary to the coding strand of a gene, preferably, a SARS virus gene. The preferred antisense nucleic acid molecule is one which is capable of lowering the level of polypeptide encoded by the complementary gene when both are expressed in a cell. In some embodiments, the polypeptide level is lowered by at least 10%, or at least 25%, or at least 50%, as compared to the polypeptide level in a cell expressing only the gene, and not the complementary antisense nucleic acid molecule.

A "probe" or "primer" is a single-stranded DNA or RNA molecule of defined sequence that can base pair to a second DNA or RNA molecule that contains a complementary sequence (the target). The stability of the resulting hybrid molecule depends upon the extent of the base pairing that occurs, and is affected by parameters such as the degree of complementarity between the probe and target molecule, and the degree of stringency of the hybridization conditions. The degree of hybridization stringency is affected by parameters such as the temperature, salt concentration, and concentration of organic molecules, such as formamide, and is determined by methods that are known to those skilled in the art. Probes or primers specific for SARS virus nucleic acid sequences or molecules may vary in length from at least 8 nucleotides to over 500 nucleotides, including any value in between, depending on the purpose for which, and conditions under which, the probe or primer is used. For example, a probe or primer may be 8, 10, 15, 20, or 25 nucleotides in length, or may be at least 30, 40, 50, or 60 nucleotides in length, or maybe over 100, 200, 500, or 1000 nucleotides in length. Probes or primers specific for SARS virus nucleic acid molecules may have greater than 20-30% sequence identity, or at least 55-75% sequence identity, or at least 75-85% sequence identity, or at least 85-99% sequence identity, or 100% sequence identity to the nucleic acid sequences described herein. In various embodiments of the invention, probes having the sequences: 5'-ATg AAT TAC CAA gTC AAT ggT TAC-3', SEQ ID NO: 160; 5'-gAA gCT ATT CgT CAC gTT Cg-3', SEQ ID NO: 161; 5'-CTg TAg AAA ATC CTA gCT ggA g-3', SEQ ID NO: 162; 5'-CAT AAC CAg TCg gTA CAg CTA-3', SEQ ID NO: 163; 5'-TTA TCA CCC gCgAAg AAg CT-3', SEQ ID NO: 164; 5'-CTC TAg TTg CATGAC AgC CCT C-3', SEQ ID NO: 165; 5'-TCg TgC gTg gAT TggCTT TgA TgT-3', SEQ ID NO: 166; 5'-ggg TTg ggA CTA TCC TAA gTg TgA-3', SEQ ID NO: 167; 5'-TAA CAC ACA AAC ACC ATC ATC A-3', SEQ ID NO: 168; 5'-ggT Tgg gAC TAT CCT AAg TgT gA-3', SEQ ID NO: 169; 5'-CCA TCA TCA gAT AgA ATC ATC ATA-3', SEQ ID NO: 170; 5'-CCT CTC TTg TTC TTg CTC gCA-3', SEQ ID NO: 171; 5'-TAT AgT gAg CCg CCA CAC Atg-3', SEQ ID NO: 172; 5'-TAACACACAACICCATCATCA-3', SEQ ID NO: 173; 5'-CTAACATGCTTAGGATAATGG-3', SEQ ID NO: 174; 5'-GCCTCTCTTGTTCTTGCTCGC-3', SEQ ID NO: 175; 5'-CAGGTAAGCGTAAAACTCATC-3', SEQ ID NO: 176; 5'-TACACACCTCAGCGTTG-3', SEQ ID NO: 177; 5'-CACGAACGTGACGAAT-3', SEQ ID NO: 178; 5'-GCCGGAGCTCTGCAGAATTC-3', SEQ ID NO: 179; 5'-CAGGAAACAGCTATGAC TTGCATCACCACTAGTTGTGCCACCAGGTT-3', SEQ ID NO: 180; 5'-TGTAAAACGACGGCCAGTTGATGGGATGGGACTATCCTAAGTGTGA-3', SEQ ID NO: 181; 5'-GCATAGGCAGTAGTTGCATC-3', SEQ ID NO: 182, as well as sequences amplified by specific combinations of these probes, may be excluded from specific uses according to the invention. Probes can be detectably-labeled, either radioactively or non-radioactively, by methods that are known to those skilled in the art. Probes can be used for methods involving nucleic acid hybridization, such as nucleic acid sequencing, nucleic acid amplification by the polymerase chain reaction, single stranded conformational polymorphism (SSCP) analysis, restriction fragment polymorphism (RFLP) analysis, Southern hybridization, northern hybridization, in situ hybridization, electrophoretic mobility shift assay (EMSA), and other methods that are known to those skilled in the art.

By "complementary" is meant that two nucleic acid molecules, e.g., DNA or RNA, contain a sufficient number of nucleotides that are capable of forming Watson-Crick base pairs to produce a region of double-strandedness between the two nucleic acids. Thus, adenine in one strand of DNA or RNA pairs with thymine in an opposing complementary DNA strand or with uracil in an opposing complementary RNA strand. It will be understood that each nucleotide in a nucleic acid molecule need not form a matched Watson-Crick base pair with a nucleotide in an opposing complementary strand to form a duplex.

By "vector" is meant a DNA molecule derived, e.g., from a plasmid, bacteriophage, or mammalian or insect virus, or artificial chromosome, that may be used to introduce a polypeptide, for example a SARS virus polypeptide, into a host cell by means of replication or expression of an operably linked heterologous nucleic acid molecule. By "operably linked" is meant that a nucleic acid molecule such as a gene and one or more regulatory sequences (e.g., promoters, ribosomal binding sites, terminators in prokaryotes; promoters, terminators, enhancers in eukaryotes; leader sequences, etc.) are connected in such a way as to permit the desired function e.g. gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences. A vector may contain one or more unique restriction sites and may be capable of autonomous replication in a defined host or vehicle organism such that the cloned sequence is reproducible. By "DNA expression vector" is meant any autonomous element capable of directing the synthesis of a recombinant peptide. Such DNA expression vectors include bacterial plasmids and phages and mammalian and insect plasmids and viruses. A "shuttle vector" is understood as meaning a vector which can be propagated in at least two different cell types, or organisms, for example vectors which are first propagated or replicated in prokaryotes in order for, for example, subsequent transfection into eukaryotic cells. A "replicon" is a unit that is capable of autonomous replication in a cell and may includes plasmids, chromosomes (e.g., mini-chromosomes), cosmids, viruses, etc. A replicon may be a vector.

A "host cell" is any cell, including a prokaryotic or eukaryotic cell, into which a replicon, such as a vector, has been introduced by for example transformation, transfection, or infection.

An "open reading frame" or "ORF" is a nucleic acid sequence that encodes a polypeptide. An ORF may include a coding sequence having i.e., a sequence that is capable of being transcribed into mRNA and/or translated into a protein when combined with the appropriate regulatory sequences. In general, a coding sequence includes a 5' translation start codon and a 3' translation stop codon.

A "leader sequence" is a relatively short nucleotide sequence located at the 5' end of an RNA molecule that acts as a primer for transcription.

A "transcriptional regulatory sequence" "TRS" or "intergenic sequence" is a nucleotide sequence that lies upstream of an open reading frame (ORF) and serves as a template for the reassociation of a nascent RNA strand-polymerase complex.

A "frameshift mutation" is caused by a shift in a open reading frame, generally due to a deletion or addition of at least one nucleotide, such that an alternative polypeptide is ultimately translated.

By "detectably labeled" is meant any means for marking and identifying the presence of a molecule, e.g., an oligonucleotide probe or primer, a gene or fragment thereof, a cDNA molecule, a polypeptide, or an antibody. Methods for detectably-labeling a molecule are well known in the art and include, without limitation, radioactive labeling (e.g., with an isotope such as ^{32}P or ^{35}S) and nonradioactive labeling such as, enzymatic labeling (for example, using horseradish peroxidase or alkaline phosphatase), chemiluminescent labeling, fluorescent labeling (for example, using fluorescein), bioluminescent labeling, antibody detection of a ligand attached to the probe, or detection of double-stranded nucleic acid. Also included in this definition is a molecule that is detectably labeled by an indirect means, for example, a molecule that is bound with a first moiety (such as biotin) that is, in turn, bound to a second moiety that may be observed or assayed (such as fluorescein-labeled streptavidin). Labels also include digoxigenin, luciferases, and aequorin.

A "peptide," "protein," "polyprotein" or "polypeptide" is any chain of two or more amino acids, including naturally occurring or non-naturally occurring amino acids or amino acid analogues, regardless of post-translational modification (e.g., glycosylation or phosphorylation). An "polyprotein", "polypeptide", "peptide" or "protein" of the invention may include peptides or proteins that have abnormal linkages, cross links and end caps, non-peptidyl bonds or alternative modifying groups. Such modified peptides are also within the scope of the invention. The term "modifying group" is intended to include structures that are directly attached to the peptidic structure (e.g., by covalent coupling), as well as those that are indirectly attached to the peptidic structure (e.g., by a stable non-covalent association or by covalent coupling to additional amino acid residues, or mimetics, analogues or derivatives thereof, which may flank the core peptidic structure). For example, the modifying group can be coupled to the amino-terminus or carboxy-terminus of a peptidic structure, or to a peptidic or peptidomimetic region flanling the core domain. Alternatively, the modifying group can be coupled to a side chain of at least one amino acid residue of a peptidic structure, or to a peptidic or peptidomimetic region flanking the core domain (e.g., through the epsilon amino group of a lysyl residue(s), through the carboxyl group of an aspartic acid residue(s) or a glutamic acid residue(s), through a hydroxy group of a tyrosyl residue(s), a serine residue(s) or a threonine residue(s) or other suitable reactive group on an amino acid side chain). Modifying groups covalently coupled to the peptidic structure can be attached by means and using methods well known in the art for linking chemical structures, including, for example, amide, alkylamino, carbamate or urea bonds.

A "polyprotein" is the polypeptide that is initially translated from the genome of a plus-stranded RNA virus, for example, a SARS virus. Accordingly, a polyprotein has not been subjected to post-translational processing by proteolytic cleavage into its processed protein products, and therefore, retains its cleavage sites. In some embodiments of the invention, the protease cleavage sites of a polyprotein may be modified, for example, by amino acid substitution, to result in a polyprotein that is incapable of being cleaved into its processed protein products.

An antibody "specifically binds" or "selectively binds" an antigen when it recognizes and binds the antigen, but does not substantially recognize and bind other molecules in a sample, having for example an affinity for the antigen which is 10, 100, 1000 or 10000 times greater than the affinity of the antibody for another reference molecule in a sample. A "neutralizing antibody" is an antibody that selectively interferes with any of the biological activities of a SARS virus polypeptide or polyprotein, for example, replication of the SARS virus, or infection of host cells. A neutralizing antibody may reduce the ability of a SARS virus polypeptide to carry out its specific biological activity by about 50%, or by about 70%, or by about 90% or more, or may completely abolish the ability of a SARS virus polypeptide to carry out its specific biological activity. Any standard assay for the biological activity of any SARS virus polypeptide, for example, assays determining expression levels, ability to infect host cells, or ability to replicate DNA, including those assays described herein or known to those of skill in the art, may be used to assess potentially neutralizing antibodies that are specific for SARS virus polypeptides.

A "signal sequence" is a sequence of amino acids that may be identified, for example by homology or biological activity to a peptide sequence with the known function of targeting a polypeptide to a particular region of the cell. A signal sequence or signal peptide may be a peptide of any length, that is capable of targeting a polypeptide to a particular region of the cell. In some embodiments, the signal sequence may direct the polypeptide to the cellular membrane so that the polypeptide may be secreted. In alternate embodiments, the signal sequence may direct the polypeptide to an intracellular compartment or organelle, such as the Golgi apparatus, or to the surface of a virus, such as the SARS virus. In alternate embodiments, a signal sequence may range from about 13 or 15 amino acids in length to about 60 amino acids in length.

A "transmembrane protein" is an amphipathic protein having a hydrophobic region ("transmembrane domain") that spans the lipid bilayer of the cell membrane from the cytoplasm to the cell surface, or spans the viral envelope, interspersed between hydrophilic regions on both sides of the membrane. The number of hydrophobic regions in an amphipathic protein is often proportional to the number of times that proteins spans the lipid bilayer. Thus, a single transmembrane protein spans the lipid bilayer once, and has a single transmembrane domain, while a multi-transmembrane protein spans the lipid bilayer multiple times. Multi-transmembrane proteins may enable virus entry into a host cell, or act to initiate transduction of a signal from the cell surface to the interior of the cell, for example, by a conformational change upon ligand binding. A "transmembrane anchor" is a transmembrane domain that maintains a polypeptide in its position in the cell membrane or viral envelope and is generally hydrophobic. A transmembrane anchor may generally be in the structure of an alpha helix, i.e., a "transmembrane helix". Multi-transmembrane proteins may have multiple transmembrane alpha-helices.

A "nuclear localization signal" is an amino acid sequence that permits the entry of a polypeptide into the nucleus of a cell through nuclear pores. A nuclear localization signal generally has a cluster of positively charged residues, for example, lysines. A "lysine-rich sequence" is a sequence having at least two contiguous lysine residues, or at least three contiguous lysine residues. In some embodiments, a lysine-rich sequence may be a nuclear localization signal.

An "ATP binding domain" is a consensus domain that is found in many ATP or GTP-binding proteins, and that forms a flexible loop (P-loop) between alpha-helical and beta pleated sheet domains. The general consensus for an ATP binding domain may be (A or G)-XXXXGK-(S or T).

A "RNA binding protein" is a protein that is capable of binding to a RNA molecule (see, for example, "RNA Binding Proteins: New Concepts in Gene Regulation" 1st ed, eds. K. Sandberg and S. E. Mulroney, Kluwers Academic Publishers, 2001). RNA binding proteins may contain common structural features such as arginine-rich tracts, for example, arginines alternating with aspartates, serines, or glycines, or zinc finger regions. RNA binding proteins may also have a common ribonucleotide sequence domain. RNA binding proteins are believed to play diverse roles in modulating post-transcriptional gene expression.

An "immune response" includes, but is not limited to, one or more of the following responses in a mammal: induction of antibodies, B cells, T cells (including helper T cells, suppressor T cells, cytotoxic T cells, γδ T cells) directed specifically to the antigen(s) in a composition or vaccine, following administration of the composition or vaccine. An immune response to a composition or vaccine thus generally includes the development in the host mammal of a cellular and/or antibody-mediated response to the composition or vaccine of interest. In general, the immune response will result in prevention or reduction of infection by a SARS virus.

An "immunogenic fragment" of a polypeptide or nucleic acid molecule refers to an amino acid or nucleotide sequence that elicits an immune response. Thus, an immunogenic fragment may include, without limitation, any portion of any of the SARS virus sequences described herein, or a sequence substantially identical thereto, that includes one or more epitopes (the antigenic determinant i.e., site recognized by a specific immune system cell, such as a T cell or a B cell). An "epitope" may include amino acids in a spatial orientation that they are non-contiguous in the amino acid sequence but are near each other due to the three dimensional conformation of the polypeptide. A epitope may include at least 3, 5, 8, or 10 or more amino acids. Immunogenic fragments or epitopes may be identified using standard methods known to those of skill in the art, such as epitope mapping techniques or antigenicity or hydropathy plots using, for example, the Omiga version 1.0 program from Oxford Molecular Group (see, for example, U.S. Pat. No. 4,708,871). Immunogenic fragments or epitopes may also be identified using methods for determining three dimensional molecule structure such as X-ray crystallography or nuclear magnetic resonance.

A "sample" may be a tissue biopsy, amniotic fluid, cell, blood, serum, plasma, urine, stool, sputum, conjunctiva, or any other specimen, or any extract thereof, obtained from a patient (human or animal), test subject, or experimental animal. A "sample" may also be a cell or cell line created under experimental conditions, and constituents thereof (such as cell culture supematants, cell fractions, infected cells, etc.). The sample may be analyzed to detect the presence of a SARS virus gene, genome, polypeptide, nucleic acid molecule or virion, or to detect a mutation in a SARS virus gene, expression levels of a SARS virus gene or polypeptide, or the biological function of a SARS virus polypeptide, using methods that are known in the art. For example, methods such as sequencing, single-strand conformational polymorphism (SSCP) analysis, or restriction fragment length polymorphism (RFLP) analysis of PCR products derived from a sample can be used to detect a mutation in a SARS virus gene; ELISA or western blotting can be used to measure levels of SARS virus polypeptide or antibody affinity; northern blotting can be used to measure SARS mRNA levels, or PCR can be used to measure the level of a SARS virus nucleic acid molecule.

Other features and advantages of the invention will be apparent from the following description of the drawings and the invention, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. **1**A-D show phylogenetic analyses of SARS proteins. Unrooted phylogenetic trees were generated by clustalw (Thompson, J. D. et al., *Nucleic Acids Res* 22, 4673-80, Nov. 11, 1994) bootstrap analysis using 1000 iterations. Genbank accessions for protein sequences are as follows: FIG. **1**A: Replicase 1A: BoCov (Bovine Coronavirus): AAL40396, 229E (Human Coronavirus): NP_07355, MHV (Mouse Hepatitis Virus): NP_045298, AIBV (Avian Infectious bronchitis virus): CAC39113, TGEV (Transmissible Gastroenteritis Virus): NP_058423. FIG. **1**B: Matrix Glycoprotein: PHEV (Porcine hemagglutinating encephalomyelitis virus): AAL80035, BoCov (Bovine Coronavirus):

NP_150082, AIBV & AIBV2 (Avian infectious bronchitis virus): AAF35863 & AAK83027, MHV (Mouse hepatitis virus): AAF36439, TGEV (Transmissible gastroenteritis virus): NP_058427, 229E & OC43 (Human Coronavirus): NP_073555 & AAA45462, FCV (Feline coronavirus): BAC01160. FIG. **1**C: Nucleocapsid: MHV (Mouse hepatitis virus): P18446, BoCov (Bovine coronavirus): NP_150083, AIBV (Avian infectious bronchitis virus): AAK27162, FCV (Feline coronavirus): CAA74230, PTGV (Porcine transmissible gastroenteritis virus): AAM97563, 229E & OC43 (Human coronavirus): NP_073556 & P33469, PHEV (porcine hemagglutinating encephalomyelitis virus): AAL80036, TCV (Turkey coronavirus): AAF23873. FIG. **1**D: S (Spike) Protein: BoCov (Bovine coronavirus): AAL40400, MHV (Mouse hepatitis virus): P11225, OC43 & 229E (Human coronavirus): S44241 & AAK32191, PHEV (Porcine hemagglutinating encephalomyelitis virus): AAL80031, PRC (Porcine respiratory coronavirus): AAA46905, PEDV (Porcine epidemic diarrhea virus): CAA80971, CCov (Canine coronavirus): S41453, FICV (Feline infectious peritonitis virus): BAA06805, AIBV (Avian infectious bronchitis virus): AA034396.

FIG. **2** shows a schematic representation of the ORFs and s2m motif in the 29,736-base SARS virus genome.

FIGS. **3**A-P show nucleotide sequences of the 29,736-base genome of the SARS virus (SEQ ID NOs: 1 and 2).

FIG. **4** shows an alignment of the s2m regions from Avian infectious bronchitis virus (AIBV; SEQ ID NO: 32) and equine rhinovirus serotype 2 (ERV-2; SEQ ID NO: 31) with the 3' untranslated region (UTR; SEQ ID NO: 18) of the SARS virus (TOR2). The conserved areas in the s2m region are indicated by asterisks.

FIG. **5** shows the amino acid sequence of the SARS virus S (Spike) Glycoprotein (SEQ ID NO: 33).

FIG. **6** shows the amino acid sequence of the SARS virus M (Matrix) Glycoprotein (residues 1-220 of SEQ ID NO: 34).

FIG. **7** shows the amino acid sequence of the SARS virus E (Small envelope) protein (SEQ ID NO: 35).

FIG. **8** shows the amino acid sequence of the SARS virus N (Nucleocapsid) Protein (SEQ ID NO: 36).

FIG. **9** shows an alignment of the matrix glycoprotein M from the SARS virus (Tor2_M or ORF5; SEQ ID NO: 34) and various other matrix glycoproteins (SEQ ID NOs: 37-43). Asterisks (*) indicate percentage identity to the SARS matrix protein as calculated by Align (Myers and Miller, CABIOS (1989) 4:11-17).

FIGS. **10**A-B show an alignment of the nucleocapsid protein N from tehj SARS virus (Tor2_N; SEQ ID NO: 36) and various other nucleocapsid proteins (SEQ ID NOs: 44-52; and SEQ ID NO: 199 of AIBV**2** nucleocapsid protein [Avian infectious bronchitis virus 2]). Asterisks (*) indicate percentage identity to the SARS nucleocapsid protein calculated by Align (Myers and Miller, CABIOS (1989) 4:11-17).

FIGS. **11**A-K show the nucleotide sequence of the 29,751-base genome of the SARS virus (SEQ ID NO: 15).

FIG. **12** shows a schematic representation of the ORFs and s2m motif in the 29,751-base SARS virus genome.

FIGS. **13**A-D show phylogenetic analyses of SARS proteins. Unrooted phylogenetic trees were generated by clustalw 1.74 (J. D. Thompson, D. G. Higgins, T. J. Gibson, Nucleic Acids Res 22, 4673-80 (Nov. 11, 1994) using the BLOSUM comparison matrix and a bootstrap analysis of 1000 iterations. Numbers indicate bootstrap replicates supporting each node. Phylogenetic trees were drawn with the Phylip Drawtree program 3.6a3 (Felsenstein, J. 1993. PHYLIP (Phylogeny Inference Package) version 3.5c. Distributed by the author. Department of Genetics, University of Washington, Seattle). Branch lengths indicate the number of substitutions per residue. Genbank accessions for protein sequences: A: Replicase **1**A: BoCoV (Bovine Coronavirus): AAL40396, HCoV-229E (Human Coronavirus):NP_07355, MHV (Mouse Hepatitis Virus): NP_045298, IBV (Avian Infectious bronchitis virus): CAC39113, TGEV (Transmissible Gastroenteritis Virus): NP_058423. B: Membrane Glycoprotein: PHEV (Porcine hemagglutinating encephalomyelitis virus): AAL80035, BoCoV (Bovine Coronavirus):NP_150082, IBV & IBV2 (Avian infectious bronchitis virus): AAF35863 & AAK83027, MHV (Mouse hepatitis virus): AAF36439, TGEV (Transmissible gastroenteritis virus): NP_058427, HCoV-229E & HCoV-OC43 (Human Coronavirus): NP_073555 & AAA45462, FCoV (Feline coronavirus): BAC01160. C: Nucleocapsid: MHV (Mouse hepatitis virus): P18446, BoCoV (Bovine coronavirus): NP_150083, IBV 1 & 2 (Avian infectious bronchitis virus): AAK27162 & NP_040838, FCoV (Feline coronavirus): CAA74230, PTGV (Porcine transmissible gastroenteritis virus): AAM97563, HCoV-229E & HCoV-OC43 (Human coronavirus): NP_073556 & P33469, PHEV (porcine hemagglutinating encephalomyelitis virus): AAL80036, TCV (Turkey coronavirus): AAF23873. D: S (Spike) Protein: BoCoV (Bovine coronavirus): AAL40400, MHV (Mouse hepatitis virus): P11225, HCoV-OC43 & HCoV-229E (Human coronavirus): S44241 & AAK32191, PHEV (Porcine hemagglutinating encephalomyelitis virus): AAL80031, PRCOV (Porcine respiratory coronavirus): AAA46905, PEDV (Porcine epidemic diarrhea virus): CAA80971, CCoV (Canine coronavirus): S41453, FIPV (Feline infectious peritonitis virus): BAA06805, IBV (Avian infectious bronchitis virus): AAO34396.

FIGS. **14**A-F show an alignment of the spike glycoprotein S from the SARS virus (Tor2_S; SEQ ID NO: 33) and various other spike glycoproteins (SEQ ID NOs: 53-62). Asterisks (*) indicate percentage identity to the SARS spike protein as calculated by Align (Myers and Miller, CABIOS (1989) 4:11-17).

FIG. **15** shows an alignment between the SARS virus Small envelope protein E (TOR2_E; SEQ ID NO: 35) and the Envelope protein (Protein 4) (X1 protein) (ORF 3) from Porcine transmissible gastroenteritis coronavirus (strain Purdue). Swissprot accession number P09048 (PGV; SEQ ID NO: 63), as calculated by FASTA (world wide web at ebi "dot" ac "dot" uk "forward slash" fasta33).

FIGS. **16**A-B show the amino acid sequence of the SARS virus Replicase 1A protein (SEQ ID NO: 64).

FIG. **17** shows the amino acid sequence of the SARS virus Replicase 1B protein (SEQ ID NO: 65).

FIG. **18** shows the amino acid sequence of ORF3 of SARS virus (SEQ ID NO: 66).

FIG. **19** shows the amino acid sequence of ORF4 of SARS virus (SEQ ID NO: 67).

FIG. **20** shows the amino acid sequence (SEQ ID NO: 68) of ORF6 (nucleotides 27059-27247 of the 29,736-base genome sequence) or ORF 7 (nucleotides 27,074-27,265 of the 29,751-base genome sequence) of SARS virus.

FIG. **21** shows the amino acid sequence (SEQ ID NO: 69) of ORF7 (nucleotides 27258-27623 of the 29,736-base genome sequence) or ORF 8 (nucleotides 27,273-27,641 of the 29,751-base genome sequence), of SARS virus.

FIG. **22** shows the amino acid sequence (SEQ ID NO: 70) of ORF8 (nucleotides 27623-27754 of the 29,736-base genome sequence) or ORF9 8 (nucleotides 27,638-27,772 of the 29,751-base genome sequence) of SARS virus.

FIG. **23** shows the amino acid sequence (SEQ ID NO: 71) of ORF9 (nucleotides 27764-27880 of the 29,736-base genome sequence) or ORF10 (nucleotides 27,779-27,898 of the 29,751-base genome sequence) of SARS virus.

FIG. **24** shows the amino acid sequence (SEQ ID NO: 72) of ORF10 (nucleotides 27849-28100 of the 29,736-base genome sequence) or ORF11 (nucleotides 27,864-28118 of the 29,751-base genome sequence) of SARS virus.

FIG. **25** shows the amino acid sequence of ORF13 of SARS virus (SEQ ID NO: 73).

FIG. **26** shows the amino acid sequence of ORF14 of SARS virus (SEQ ID NO: 74).

FIG. **27** shows an alignment of the secreted region of the SARS virus ORF 10 (SEQ ID NO: 201) of the 29,751-base genome sequence (sars) with the conotoxin from *Conus ventricosus* (conotoxin) (SEQ ID NO: 200). Sequence identity is indicated by asterisks and sequence homology is indicated by dots.

DETAILED DESCRIPTION OF THE INVENTION

In general, the invention provides nucleic acid molecules, polypeptides, and other reagents derived from a SARS virus, as well as methods of using such nucleic acid molecules, polypeptides, and other reagents.

The genome sequence (FIGS. **3**A-P, **11**A-K, SEQ ID NOs: 1, 2, and 15) reveals that the SARS coronavirus is only moderately related to other known coronaviruses, including two human coronaviruses, OC43 and 229E. Thus, the SARS virus is a previously unknown virus. The 5' end of the SARS genome contains a 5' leader sequence (Table 1; SEQ ID NO: 3) with sequence similarity to the highly conserved coronavirus core leader sequence, 5'-CUAAAC-3 (SEQ ID NO: 75; Sawicki, S. G., et al., *Adv Exp Med Biol* 440, 215-9, 1998; Lai, M. M. and D. Cavanagh, *Adv Virus Res* 48, 1-100, 1997). Transcriptional regulatory sequences (TRSs) were identified upstream of all open reading frames (ORFs) (Tables 1 and 2; SEQ ID NOs: 3-13 and 20-30). ORF9 and ORF10 of the 29,736-base SARS genome (ORF 10 and ORF 11 of the 29,751 base genome) overlap by 12 amino acids, and have matches to the TRS consensus in close proximity to their respective initiating methionine codons.

The 3 ' UTR sequence (SEQ ID NO: 18) of SARS virus contains a s2m region having the sequence ACATTTTCATCGAGGCCACGCGGAGTACGAT CGAGGGTACAGTGAAT; SEQ ID NO: 16) that includes a conserved, discontinuous 32 base-pair s2m motif. The conserved 32 base-pair motif is a universal feature of astroviruses that has also been identified in avian coronavirus (AIBV) and the ERV-2 equine rhinovirus. This motif has been identified by Jonassen C. M. et al. (J Gen Virol 1998 April; 79 (Pt 4):715-8) as GCCGNGGCCACGC(G/C)GAGTA(C/G)GANCGAGGGTACAG(G/C) (SEQ ID NO: 19), where N is generally not part of the conserved motif, and can be any nucleotide. The region corresponding to the 32 base-pair motif in SARS virus includes the sequence: CGAGGCCACGCGGAGTACGATCGAGGGTACAG (SEQ ID NO: 17), and spans positions 29590-29621 of the 29,751 base genome. FIG. **4** shows an alignment of the s2m regions from Avian infectious bronchitis virus (AIBV; SEQ ID NO: 32) and equine rhinovirus serotype 2 (ERV-2; SEQ ID NO: 31), as defined in Jonassen C. M. et al. (J Gen Virol 1998 April; 79 (Pt 4):715-8), with the entire 3' untranslated region (UTR) of the SARS virus (TOR2) (SEQ ID NO: 18).

TABLE 1

Listing of the transcription regulatory sequences of the 29,736-base SARS genome, showing the nucleotide position (base) and associated open-reading frames (ORF). An asterisk (*) indicates consensus sequence.

Base	ORF	TRS Sequence	
45	Leader	TCTCTAAACGAAACTTTAAAATCTGTG	(SEQ ID NO: 3)
21464	S	CAACTAAACGAACATG	(SEQ ID NO: 4)
25238	ORF3	CACATAAACGAACTTATG	(SEQ ID NO: 5)
26089	E	TGAGTACGAACTTATG	(SEQ ID NO: 6)
26326	M	GGTCTAAACGAACTAACT 40 ATG	(SEQ ID NO: 7)
26986	ORF6	AACTATAAATT 62 ATG	(SEQ ID NO: 8)
27244	ORF7	TCCATAAAACGAACATG	(SEQ ID NO: 9)
27575	ORF8	TGCTCTA---GTATTTTTAACTTTG 24 ATG	(SEQ ID NO: 10)
27751	ORF9	AGTCTAAACGAACATG	(SEQ ID NO: 11)
27837	ORF10	CTAATAAACCTCATG	(SEQ ID NO: 12)
28084	N	TAAAATAAACGAACAAATTAAAATG	(SEQ ID NO: 13)
		********	

TABLE 2

Listing of the transcription regulatory sequences of the 29,751-base SARS genome, showing the nucleotide position (base), associated open-reading frames (ORF), and identified transcription regulatory sequences. Numbers in parentheses within the alignment indicate distance to the putative initiating codon. The conserved core sequence is indicated in bold in the putative leader sequence. Contigous sequences identical to region of the leader sequence containing the core sequence are shaded. No putative TRSs were detected for ORFs 4, 13 and 14, although ORF 13 may share the TRS associated with the N protein.

Base	ORF	TRS Sequence	
60	Leader	UCUCUAAACGAACUUUAAAAUCUGUG	(SEQ ID NO: 20)
21479	S (Spike)	CAACUAAACGAACAUG	(SEQ ID NO: 21)
25252	ORF3	CACAUAAACGAACUUAUG	(SEQ ID NO: 22)
26104	Envelope	UGAGUACGAACUUAUG	(SEQ ID NO: 23)
26341	M	GGUCUAAACGAACUAACU (40)AUG	(SEQ ID NO: 24)
27001	ORF7	AACUAUAAAUU (62)AUG	(SEQ ID NO: 25)
27259	ORF8	UCCAUAAAACGAACAUG	(SEQ ID NO: 26)
27590	ORF9	UGCUCUA---GUAUUUUUAAUACUUUG (24)AUG	(SEQ ID NO: 27)
27766	ORF10	AGUCUAAACGAACAUG	(SEQ ID NO: 28)
27852	ORF11	CUAAUAAACCUCAUG	(SEQ ID NO: 29)
28099	NUCLEOCAPSID	UAAAUAAACGAACAAAUUAAAAUG	(SEQ ID NO: 30)

The coding potentials of the 29,736-base and 29,751-base genomes are depicted in FIGS. **2** and **12**, respectively. Open reading frames (ORFs) include the Replicase 1a and 1b translation products, the Spike glycoprotein, the small Envelope protein, the Membrane and the Nucleocapsid protein. Construction of unrooted phylogenetic trees using this set of known proteins from representatives of the three known coronaviral groups reveals that the proteins encoded by the SARS virus do not readily cluster more closely with any known group than with any other (FIGS. **1**A-D and **13**A-D). In addition, nine novel ORFs have been analyzed.

The Replicase 1a ORF located at nucleotides 250-13395 of the 29,736-base genome, and nucleotides 265-13,398 of the 29,751-base genome, and replicase 1b ORF located at nucleotides 13395-21467 of the 29,736-base genome, and nucleotides 13,398-21,485 of the 29,751-base genome, occupy 21.2 kb of the SARS virus genome (FIGS. **2** and **12**). These genes encode a number of proteins that are produced by proteolytic cleavage of a large polyprotein (Ziebuhr, J. et al., *J Gen Virol* 81, 853-79, April, 2000). A frame shift mutation interrupts the protein-coding region, separating the 1a and 1b open-reading frames. The proteins encoded by the Replicase 1a and 1b ORFs are depicted in FIGS. **16**A-B and **17**, SEQ ID NOs: 64 and 65).

The Spike glycoprotein (S) (E2 glycoprotein gene; FIGS. **2** and **12**; nucleotides 21477 to 25241 of the 29,736-base genome, and nucleotides 21,492 to 25,259 of the 29,751-base genome) encodes a surface projection glycoprotein precursor of about 1,255 amino acids in length (FIG. **5**; SEQ ID NO: 33), which may be significant in the virulence of the SARS virus. Mutations in this gene are correlated with altered pathogenesis and virulence in other coronaviruses (B. N. Fields et al., *Fields virology* (Lippincott Williams & Wilkins, Philadelphia, ed. 4th, 2001). In other coronaviruses, the mature spike protein is inserted in the viral envelope with the majority of the protein exposed on the surface of the particles. Three molecules of the Spike protein form the characteristic peplomers or corona-like structures of this virus family. Analysis of the spike glycoprotein with SignalP (Nielson, H. et al., *Prot Engineer.* 10:1-6 (1997) indicates a signal peptide (MFIFLLFLTLTSG; SEQ ID NO: 76)(probability 0.996) with cleavage between residues 13 and 14. TMHMM (Sonnhammer, E. L. et al., *Proc Int Conf Intell Syst Mol Biol* 6, 175-82 (1998)) indicates a transmembrane domain near the C-terminal end (WYVWLGFIAGLIAIVMVTILLCC; SEQ ID NO: 183). Together these data indicate a type I membrane protein with N-terminus and the majority of the protein (residues 14-1195) on the outside of the cell-surface or virus particle, which may be responsible for binding to a cellular receptor. The SARS virus Spike glycoprotein has limited sequence identity to other, known Spike glycoproteins (FIGS. **14**A-F).

ORF 3 (FIGS. **2** and **12**; nucleotides 25253-26074 of the 29,736-base genome and nucleotides 25,268-26,092 of the 29,751-base genome) encodes a protein of 274 amino acids (FIG. **18**; SEQ ID NO: 66) that lacks significant similarities to any known protein when analyzed with BLAST (Altschul, S. F. et al., *Nucleic Acids Res* 25, 3389-402, Sep. 1, 1997), FASTA (Pearson, W. R. and D. J. Lipman, *Proc Natl Acad Sci USA* 85, 2444-8, April, 1988) or PFAM (Bateman, A. et al., *Nucleic Acids Res* 30, 276-80, Jan. 1, 2002). Analysis of the N-terminal 70 amino acids with SignalP indicates the existence of a signal peptide (MDLFMRFFTLRSITAQ; SEQ ID NO: 184) and a cleavage site (probability 0.540). Both TMpred (Hofinan, K. and W. Stoffel, *Biol. Chem. Hoppe-Seyler* 374, 166 (1993) and TMHMM indicate three transmembrane regions spanning approximately residues 34-56 (TIPLQASLPFGWLVIGVAFLAVF, SEQ ID NO: 77), 77-99 (FQFICNLLLLFVTIYSHLLLVAA, SEQ ID NO: 78), and 103-125 (AQFLYLYALIYFLQCINACRIIM, SEQ ID NO: 79). Both TMpred and TMHMM indicate that the C-terminus and a large 149 amino acid domain is located inside the viral or cellular membrane. The C-terminal (interior) region of the protein, corresponding to about amino acids 124-274 (MRCWLCWKCKSKNPLLYDANYFVCWHTH-NYDYCIPYNSVTDTIVVTEGDGI STPKLKEDYQIGGY-SEDRHSGVKDYVVVHGYFTEVYYQLEST-QITTDTGIENAT FFIFNKLVKDPPNVQIHTIDGSSGVAN-PAMDPIYDEPTTTTSVPL; SEQ ID NO: 185) may encode a protein domain with ATP-binding properties (PD037277).

ORF 4 (FIG. **12**; nucleotides 25,689-26,153 of the 29,751-base genome) encodes a predicted protein of 154 amino acids (FIG. **19**; SEQ ID NO: 67). This ORF overlaps entirely with ORF 3 and the E protein. ORF4 may be expressed from the ORF mRNA using an internal ribosomal entry site. BLAST analyses failed to identify matching sequences. Analysis with TMPred predicts a single transmembrane helix, amino acids 1-20 MMPTTLFAGTHITMTTVYHI, SEQ ID NO: 186.

The small envelope protein E (FIGS. **2** and **12**; nucleotides 26102-26329 of the 29,736-base genome and nucleotides 26,117-26,347, ORF 5, of the 29,751-genome) encodes a protein of 76 amino acids (FIG. **7**; SEQ ID NO: 35). BLAST and FASTA comparisons indicate that the protein, while novel, is homologous to multiple envelope proteins (alternatively known as small membrane proteins) from several coronaviruses. An alignment of the SARS virus E protein with the envelope protein of Porcine transmissible gastroenteritis coronavirus indicates approximately 28% sequence identity between the two proteins over a 61 amino acid overlap, as calculated by FASTA (FIG. **15**). PFAM analysis of the protein indicates that the small envelope protein E is a member of the NS3_EnvE protein family. InterProScan (R. Apweiler et al., *Nucleic Acids Res* 29, 37-40, Jan. 1, 2001; Zdobnov, E. M. and R. Apweiler, *Bioinformatics* 17, 847-8, September, 2001) analysis indicates that the protein is a component of the viral envelope, and homologs of it are found in other viruses, including gastroenteritis virus and murine hepatitis virus. SignalP analysis indicates the presence of a transmembrane anchor (probability 0.939). TMpred analysis indicates a similar transmembrane anchor at positions 17-34 (VLLFLAFVVFLLVTLAIL, SEQ ID NO: 80), which is consistent with the known association of homologous proteins with the viral envelope. TMHMM indicates a type II membrane protein with the majority of the 46 residue C terminus hydrophilic domain (TALRLCAYCCNIVNVSLVKPTVYVYSRVKNLNSSEGVPDLLV; SEQ ID NO: 187) located on the surface of the viral particle. The E protein may be important for viral replication.

The Matrix glycoprotein M (FIGS. **2** and **12**; nucleotides 26383-27045 of the 29,736-base genome and nucleotides 26,398-27,063, ORF 6, of the 29,751-genome) encodes a protein of 221 amino acids (FIG. **6**; SEQ ID NO: 34). BLAST and FASTA analysis of the protein, while novel, reveals homologies to coronaviral matrix glycoproteins (FIG. **9**). The association of the spike glycoprotein (S) with the matrix glycoprotein (M) may be an essential step in the formation of the viral envelope and in the accumulation of both proteins at the site of virus assembly. Analysis of the amino acid sequence with SignalP indicates a signal sequence (probability 0.932), located at approximately residues 1-39 (MADNGTITVEELKQLLEQWNLVIGFLFLAWIMLLQFAYS; SEQ ID NO: 188) that is unlikely to be cleaved. TMHMM and TMpred analysis both indicate the presence of three transmembrane helices, located at approximately residues 15-37 (LLEQWNLVIGFLFLAWIMLLQFA; SEQ ID NO: 81), 50-72 (LVFLWLLWPVTLACFVLAAVYRI; SEQ ID NO: 82) and 77-99 (GGIAIAMACIVGLMWLSYFVASF; SEQ ID NO: 83), with the 121 amino acid hydrophilic domain on the inside of the virus particle, where it may interact with nucleocapsid. The hydrophilic domain may run from approximately amino acids PLRGTIVTRPLMESELVIGAVIIRGHLRMAGHSLGRCDIKDLPKEITVATSRTLS YYKLGASQRVGTDSGFAAYNRYRIGNYKLNTDHAGSNDNIALLVQ (SEQ ID NO: 189) i.e. approximately amino acids 95 or 99 to 221 of SEQ ID NO: 34. PFAM analysis reveals a match to PFAM domain PF01635, and alignments to 85 other sequences in the PFAM database bearing this domain, which is indicative of the coronavirus matrix glycoprotein.

ORF6 (FIG. **2**; nucleotides 27059-27247 of the 29,736-base genome sequence) or ORF 7 (FIG. **12**; nucleotides 27,074-27,265 of the 29,751-base genome sequence) encodes a protein of 63 amino acids (FIG. **20**; SEQ ID NO: 68). TMpred analysis indicates a trans-membrane helix located between residues 3 or 4 and 22 (HLVDFQVTIAEILIIIMRTF; SEQ ID NO: 84), with the N-terminus located outside the viral particle.

Similarly, the gene encoding ORF7 (FIG. **2**; nucleotides 27258-27623 of the 29,736-base genome sequence) or ORF 8 (FIG. **12**; nucleotides 27,273-27,641 of the 29,751-base genome sequence), encoding a protein of 122 amino acids (FIG. **21**; SEQ ID NO: 69), has no significant BLAST or FASTA matches to known proteins. Analysis of this sequence with SignalP indicates a cleaved signal sequence (MKIILFLTLIVFTSC; SEQ ID NO: 85) (probability 0.995), with the cleavage site located between residues 15 and 16. TMpred and TMHMM analysis also indicates a trans-membrane helix located approximately at residues 99-117 (SPLFLIVAALVFLILCFTI; SEQ ID NO: 86). Together these data indicate that this protein is a type I membrane protein with the major hydrophilic domain of the protein (residues 16-98; ELYHYQECVRGTTVLLKEPCP SGTYEGNSPFHPLADNKFALTCTSTHFAFACADGTRHTYQLRARSVSPKLFIRQ EEVQQELY; SEQ ID NO: 87) and the amino-terminus is oriented inside the lumen of the ER/Golgi, or on the surface of the cell membrane or virus particle,depending on the membrane localization of the protein.

ORF8 (FIG. **2**; nucleotides 27623-27754 of the 29,736-base genome sequence) or ORF9 (FIG. **12**; nucleotides 27,638-27,772 of the 29,751-base genome sequence), encodes a protein of 44 amino acids (FIG. **22**; SEQ ID NO: 70). FASTA analysis of this sequence revealed some weak similarities (37% identity over a 35 amino acid overlap) to Swiss-Prot accession Q9M883, annotated as a putative sterol-C5 desaturase. A similarly weak match to a hypothetical *Clostridium perfringens* protein (Swiss-Prot accession CPE2366) was also detected. TMpred indicated a single strong trans-membrane helix FYLCFLAFLLFLVLIMLIIFWFS, SEQ ID NO: 190, with little preference for alternate models in which the N-terminus was located inside or outside the particle.

Similarly ORF9 (FIG. **2**; nucleotides 27764-27880 of the 29,736-base genome sequence) or ORF10 (FIG. **12**; nucleotides 27,779-27,898 of the 29,751-base genome sequence) encoding a protein of 39 amino acids (FIG. **23**; SEQ ID NO: 71), exhibited no significant matches in BLAST and FASTA searches but encodes a trans-membrane helix LLIVLTCISLCSCICTVVQ (SEQ ID NO: 191) by TMPred, with the N-terminus located within the viral particle. The region immediately upstream of this protein exhibits a strong match to the TRS consensus (Table 2), indicating that a transcript initiates from this site. The large number of cysteine residues (6) may result in cross linking of the amino acids. Amino acids ICTVVQRCASNKPHVLEDPCKVQH (SEQ ID NO: 192) of this protein may be secreted. The secreted amino acids exhibit homology to toxin proteins, for example, to the conotoxin of *Conus ventricosus* (FIG. **27**). Antigenic peptides from the hydrophilic (secreted) region, for example, CICTVVQRCASNKPHVLEDPCK (SEQ ID NO: 193), were used to generate monoclonal antibodies using standard techniques. Furthermore, the C terminal amino acids form a sequence that shares homology to farnesylation sites (CKQH), which generally require C terminal location to be functional. This protein may act as a virulence factor and/or may facilitate transmission to humans.

ORF10 (FIG. **2**; nucleotides 27849-28100 of the 29,736-base genome sequence) or ORF11 (FIG. **12**; nucleotides 27,864-28118 of the 29,751-base genome sequence) encoding a protein of 84 amino acids (FIG. **24**; SEQ ID NO: 72) exhibited only very short (9-10 residues) matches to a region of the human coronavirus E2 glycoprotein precursor (starting at residue 801). Analysis by SignalP and TMHMM predict a soluble protein. A detectable alignment to the TRS consensus sequence was also found (Table 2).

The protein (422 amino acids; FIG. **8**; SEQ ID NO: 36) encoded by the Nucleocapsid gene (FIG. **2**; nucleotides 28105-29370 of the 29,736-base genome sequence; FIG. **12**, nucleotides 28,120-29,388 of the 29,751-base genome sequence) aligns well with nucleocapsid proteins from other representative coronaviruses (FIGS. **10**A-B), although a short lysine rich region (KTFPPTEPKKDKKKKTDEAQ; SEQ ID NO: 14) is unique to SARS. This region is suggestive of a nuclear localization signal Since some coronaviruses are able to replicate in enucleated cells, the SARS virus nucleocapsid protein may have evolved a novel nuclear function, which may play a role in pathogenesis. In addition, the basic nature of this peptide suggests it may assist in RNA binding. The SARS nucleocapsid protein is also a good candidate for diagnostic tests.

ORF13 (FIG. **12**; nucleotides 28,130-28,426 of the 29,751-base genome sequence) encodes a novel protein of 98 amino acids (FIG. **25**; SEQ ID NO: 73). ORF 14 (FIG. **12**; nucleotides 28,583-28,795 of the 29,751-base genome sequence) encodes a novel protein of 70 amino acids (FIG. **26**; SEQ ID NO: 74). TMPred predicts a single transmembrane helix VVAVIQEIQLLAAVGEILLLEW (SEQ ID NO: 194).

Various features of the SARS virus genome are summarised in Table 3. While Table 3 refers to the 29,751-base genome sequence, the features are also applicable to the 29,736-base genome sequence (SEQ ID NOs: 1 and 2).

TABLE 3

Features of the SARS virus 29,751-base genome sequence.

Feature	Start-End[1]	No. amino acids	No. bases	Frame	TRS
Orf 1a	265-13,398	4,382	13,149	+1	N/A
Orf 1b	13,398-21,485	2,628	7,887	+3	N/A
S protein	21,492-25,259	1,255	3,768	+3	Strong
Orf 3	25,268-26,092	274	825	+2	Strong
Orf 4	25,689-26,153	154	465	+3	Absent[2]
E protein	26,117-26,347	76	231	+2	Weak
M protein	26,398-27,063	221	666	+1	Strong
Orf 7	27,074-27,265	63	192	+2	Weak
Orf 8	27,273-27,641	122	369	+3	Strong
Orf 9	27,638-27,772	44	135	+2	Weak
Orf 10	27,779-27,898	39	120	+2	Strong
Orf 11	27,864-28,118	84	255	+3	Weak
N protein	28,120-29,388	422	1,269	+1	Strong
Orf 13[3]	28,130-28,426	98	297	+2	Absent[2]
Orf 14[3]	28,583-28,795	70	213	+2	Absent
s2m motif	29,590-29,621	N/A	30	N/A	N/A

[1]End coordinates include the stop codon, except for ORF 1a and s2m.
[2]These ORFs overlap substantially or completely with other and may share TRSs.
N/A indicates not applicable.

Various polymorphisms may exist in the SARS virus. In the SARS 29,736-base genome sequences (SEQ ID NO: 1 or 2), for example, nucleotides 7904, 16607, 19168, 24857, or 26842 may be C or T; or nucleotides 19049, 23205, or 25283 may be G or A, and in the SARS 29,751-base genome sequence (SEQ ID NO: 15), for example, nucleotides 7919, 16622, 19183, 24872, or 26857 may be C or T; or nucleotides 19064, 23220, or 25298 may be G or A. In some embodiments, the nucleotide changes may result in no change in the encoded amino acid, or in a conservative or non-conservative change in the encoded amino acid. In some embodiments, a nucleotide change, as described herein, at position 7904 or 7919, may result in a A to V amino acid substitution, in the Replicase 1A protein coding region; a change at position 19168 or 19183 may result in a V to A amino acid substitution, in the Replicase IB protein coding region; a change at position 23205 or 23220 may result in a A to S amino acid substitution (non-conservative change), affecting the Spike glycoprotein coding region; a change at position 25283 or 25298 may result in a R to G amino acid substitution (non-conservadve change), affecting ORF3; or a change at position 26842 or 26857 may result in a S to P amino acid substitution (non-conservative change), affecting the Nucleocapsid protein coding region, in the SARS 29,736-base (SEQ ID NO: 1 or 2) and 29,751-base genome (SEQ ID NO: 15) sequences, respectively. In various embodiments, a nucleotide or amino acid sequence including a particular polymorphism may be selected, for example, for use in the methods of the invention, or may be excluded, for example, from a particular use according to the invention.

Various alternative embodiments of the invention are described below. These embodiments include, without limitation, identification and use of SARS virus nucleic acid and amino acid sequences for diagnostic or therapeutic uses.

Diagnosis of SARS Virus-Related Disorders

A SARS virus-related disorder is any disorder that is mediated by the SARS virus, or by a nucleic acid molecule or polypeptide derived from the SARS virus. Accordingly, SARS virus nucleic acid molecules and polypeptides may be used to diagnose and identify a SARS virus-related disorder in a mammal, for example, a human or a domestic, farm, wild, or experimental animal. In some embodiments, SARS virus nucleic acid molecules and polypeptides may be used to screen such animals, e.g., civet cats, for the presence of SARS virus. A SARS virus-related disorder may be a hepatic, enteric, respiratory, or neurological disorder, and may be accompanied by one or more symptoms or indications including, but not limited to, fever, cough, shortness of breath, headache, low blood oxygen concentration, liver damage, or reduced lymphocyte numbers. Accordingly, samples for diagnosis may be obtained from cells, blood, serum, plasma, urine, stool, conjunctiva, sputum, asopharyngeal or oropharyngeal swabs, tracheal aspirates, bronchalveolar lavage, pleural fluid, amniotic fluid, or any other specimen, or any extract thereof, or by tissue biopsy of for example lungs or major organs, obtained from a patient (human or animal), test subject, or experimental animal.

A SARS virus-related disorder may be diagnosed by amplifying a SARS nucleic acid molecule or fragment thereof from a sample. Probes or primers for use in amplification may be prepared using standard techniques. In some embodiments, probes or primers are selected from regions of a SARS virus genome as described herein that show limited sequence homology or identity (e.g., less than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% identity) to other viruses or pathogens, or to host sequences.

Nucleic acid sequences can be amplified as needed by methods known in the art. For example, this can be accomplished by e.g., polymerase chain reaction "PCR" of DNA or of RNA by reverse transcriptase-PCR or "RT-PCR" (See generally PCR Technology: Principles and Applications for

DNA Amplification (ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. No. 4,683,202 issued Jul. 28, 1987 to Mullis) Variations of standard PCR techniques, such as for example real time RT-PCR using internal as well as amplification primers, resulting in increased sensitivity and speed, and reduction of risk of sample contamination (see for example Higuchi, R., et al., "Kinetic PCR Analysis: Real-time Monitoring of DNA Amplification Reactions," Bio/Technology, vol. 11, pp. 1026-1030 (1993); Heid et al, "Real Time Quantitative PCT", Genome Research, 1996, pp. 986-994; Gibson U E et al., "A novel method for real time quantitative RT-PCR," Genome Res. 1996 October; 6(10):995-1001), or the "Tacman" approach to PCR, described by for example Holland et al, Proc. Natl. Acad. Sci., 88: 7276-7280 (1991), may be performed.

Other suitable amplification and analytical methods include the single base primer extension (see for example U.S. Pat. No. 6,004,744), mini-sequencing, ligase chain reaction (LCR) (see for example Wu and Wallace, Genomics 4, 560 (1989), Landegren et al., Science 241, 1077 (1988), transcription amplification (Kwoh et al., Proc. Natl. Acad. Sci. USA 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., Proc. Nat. Acad. Sci. USA, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

A SARS virus-related disorder may also be diagnosed using an antibody directed against a SARS virus nucleic acid or amino acid sequence that specifically binds a nucleic acid molecule or polypeptide. In an alternative embodiment, the antibody may be directed against a SARS polypeptide, for example, the S polypeptide or fragment thereof that is located on the surface of the SARS virion. Methods for preparation of antibodies or for assaying antibody binding are well known in the art.

Serological diagnosis may included detection of antibodies against a SARS virus polypeptide or nucleic acid molecule, e.g., the Nucleocapsid protein, produced in response to infection using techniques such as indirect fluorescent antibody testing or enzyme-linked immunosorbent assays (ELISA). A SARS virus-related disorder may also be diagnosed by for example performing in situ probe hybridization studies on tissue specimens.

In some aspects, diagnostic tests as described herein or known to those of skill in the art may be performed for SARS virus variants that exhibit increased pathogenicity, such as strains having redundant sequences.

In some embodiments, reagents for diagnosis (e.g, probes, primers, antibodies, etc.) may be provided in kits which may optionally include instructions for using the reagent or may include other reagents for performing the appropriate assay e.g., controls, standards, buffers, etc.

Therapy or Prophylaxis for SARS Virus-Related Disorders

Compounds according to the invention may also be used to provide therapeutics or prophylactics for SARS virus-related disorders. Accordingly, such compounds may be used to treat a mammal, for example, a human or a domestic, farm, wild, or experimental animal that has or is at risk for a SARS virus-related disorder. Such compounds may include, without limitation, compounds that interfere with SARS virus replication, expression of SARS virus proteins, or the ability of the SARS virus to infect a host cell. Accordingly, in some embodiments, compounds that act as antagonists to SARS virus polypeptides may be used as therapeutics or prophylactics for SARS virus related disorders. In some embodiments, purified SARS virus polypeptides may be used as for example competitive inhibitors to disrupt viral function. For example, a Spike protein lacking a functional domain, or having some other modification that maintains binding but reduces or eliminates pathogenicity, may be used to disrupt viral function. In some embodiments, antibodies that bind SARS virus polypeptides or nucleic acid molecules, for example, humanized antibodies, may be used as therapeutics or prophylactics.

In some embodiments, the SARS-virus compounds may be used as vaccines, or may be used to develop vaccines. For example, peptides derived from portions of SARS-virus proteins or polypeptides located on the outside of the virion or cell surface may be useful for vaccines or for generation of therapeutic or prophylactic antibodies.

A "vaccine" is a composition that includes materials that elicit a desired immune response. A vaccine may select, activate or expand memory B and T cells of the immune system to, for example, enable the elimination of infectious agents, such as a SARS virus, or a component thereof. In some embodiments, a vaccine includes a suitable carrier, such as an adjuvant, which is an agent that acts in a non-specific manner to increase the immune response to a specific antigen, or to a group of antigens, enabling the reduction of the quantity of antigen in any given vaccine dose, or the reduction of the frequency of dosage required to generate the desired immune response.

Vaccines according to the invention may include SARS virus polypeptides and nucleic acid molecules described herein, or immunogenic fragments thereof. In some embodiments, a SARS virus Spike polypeptide, Envelope polypeptide, or membrane glycoprotein or fragments thereof may be suitable for vaccine applications. In some embodiments, the vaccines may be multivalent and include one or more epitopes from a SARS virus polypeptide or fragment thereof.

In some embodiments of the invention, a vaccine may include a live or killed microorganism e.g., a SARS virus or a component thereof. If a live SARS virus is used, which may be administered in the form of an oral vaccine, is may contain non-revertible genetic alterations (for example, large deletions or insertions in the genomic sequence) that reduce or eliminate the virulence of the virus ("attenuated virus"), but not its induction of an immune response. In some embodiments, a live vaccine may include an attenuated non-SARS microorganism (e.g, bacteria or virus such as vaccinia virus) that is capable of expressing a SARS virus polypeptide or immunogenic fragment thereof as described herein. In some embodiments, a vaccine may include SARS virus polypeptides or nucleic acid molecules having modifications that facilitate ease of administration. For example, an indigestible SARS virus polypeptide or nucleic acid molecule may be used for oral administration, and a modification that is suitable for inhalation may be used for administration to the lung.

A "nucleic acid vaccine" or "DNA vaccine" as used herein, is a nucleic acid construct comprising a polynucleotide encoding a polypeptide antigen, particularly an antigenic amino acid subsequence identified by methods described herein or known in the art. The nucleic acid construct can also include transcriptional promoter elements, enhancer elements, splicing signals, termination and polyadenylation signals, and other nucleic acid sequences. Thus, a nucleic acid vaccine is generally introduced into a subject animal using for example one or more DNA plasmids including one or more antigen-coding sequences (for example, a SARS virus Envelope polypeptide or membrane glycoprotein sequence) that are capable of transfecting cells in vivo and inducing an immune response (see for example Whalen RG et al. DNA-mediated immunization and the energetic immune response to hepatitis B surface antigen. Clin Immunol Immunopathol 1995; 75:1-12; Wolff J A et al. Direct gene transfer into mouse muscle in vivo. Science 1990; 247:1465-8; Fynan E F et al. DNA vaccines: protective immunizations by parental, mucosal, and genegun inoculations. Proc Natl Acad Sci USA 1993; 90:11478-82). In some embodiments, a library of nucleic acid fragments may be prepared by cloning SARS virus genomic DNA into a plasmid expression vector using known techniques and the library then used as a nucleic acid vaccine (see for example Barry M A, et al. Protection against mycoplasma infection using expression-library immunization. Nature 1995; 377:632-5).

The subject is administered the nucleic acid vaccine using standard methods. The vertebrate can be administered parenterally, subcutaneously, intravenously, intraperitoneally, intradermally, intramuscularly, topically, orally, rectally, nasally, buccally, vaginally, by inhalation spray, or via an implanted reservoir in dosage formulations containing conventional non-toxic, physiologically acceptable carriers or vehicles. Alternatively, the subject is administered the nucleic acid vaccine through the use of a particle acceleration or bombardment instrument (a "gene gun"). The form in which it is administered (e.g., capsule, tablet, solution, emulsion) will depend in part on the route by which it is administered. For example, for mucosal administration, nose drops, inhalants or suppositories can be used. The nucleic acid vaccine can be administered in conjunction with known adjuvants. The adjuvant is administered in a sufficient amount, which is that amount that is sufficient to generate an enhanced immune response to the nucleic acid vaccine. The adjuvant can be administered prior to (e.g., 1 or more days before) inoculation with the nucleic acid vaccine; concurrently with (e.g., within 24 hours of) inoculation with the nucleic acid vaccine; contemporaneously (simultaneously) with the nucleic acid vaccine (e.g., the adjuvant is mixed with the nucleic acid vaccine, and the mixture is administered to the vertebrate); or after (e.g., 1 or more days after) inoculation with the nucleic acid vaccine. The adjuvant can also be administered at more than one time (e.g., prior to inoculation with the nucleic acid vaccine and also after inoculation with the nucleic acid vaccine). As used herein, the term "in conjunction with" encompasses any time period, including those specifically described herein and combinations of the time periods specifically described herein, during which the adjuvant can be administered so as to generate an enhanced immune response to the nucleic acid vaccine (e.g., an increased antibody titer to the antigen encoded by the nucleic acid vaccine, or an increased antibody titer to the pathogenic agent). The adjuvant and the nucleic acid vaccine can be administered at approximately the same location on the vertebrate; for example, both the adjuvant and the nucleic acid vaccine are administered at a marked site on a limb of the subject.

In some embodiments, expression of a SARS virus gene or coding or non-coding region of interest may be inhibited or prevented using RNA interference (RNAi) technology, a type of post-transcriptional gene silencing. RNAi may be used to create a functional "knockout", i.e. a system in which the expression of a gene or coding or non-coding region of interest is reduced, resulting in an overall reduction of the encoded product. As such, RNAi may be performed to target a nucleic acid of interest or fragment or variant thereof, to in turn reduce its expression and the level of activity of the product which it encodes. Such a system may be used for therapy or prophylaxis, as well as for functional studies. RNAi is described in for example published US patent applications 20020173478 (Gewirtz; published Nov. 21, 2002) and 20020132788 (Lewis et al.; published Nov. 7, 2002). Reagents and kits for performing RNAi are available commercially from for example Ambion Inc. (Austin, Tex., USA) and New England Biolabs Inc. (Beverly, Mass., USA).

The initial agent for RNAi in some systems is thought to be dsRNA molecule corresponding to a target nucleic acid. The dsRNA is then thought to be cleaved into short interfering RNAs (siRNAs) which are 21-23 nucleotides in length (19-21 bp duplexes, each with 2 nucleotide 3' overhangs). The enzyme thought to effect this first cleavage step has been referred to as "Dicer" and is categorized as a member of the Rnase III family of dsRNA-specific ribonucleases. Alternatively, RNAi may be effected via directly introducing into the cell, or generating within the cell by introducing into the cell a suitable precursor (e.g. vector, etc.) of such an siRNA or siRNA-like molecule. An siRNA may then associate with other intracellular components to form an RNA-induced silencing complex (RISC). The RISC thus formed may subsequently target a transcript of interest via base-pairing interactions between its siRNA component and the target transcript by virtue of homology, resulting in the cleavage of the target transcript approximately 12 nucleotides from the 3' end of the siRNA. Thus the target mRNA is cleaved and the level of protein product it encodes is reduced.

RNAi may be effected by the introduction of suitable in vitro synthesized siRNA or siRNA-like molecules into cells. RNAi may for example be performed using chemically-synthesized RNA, for which suitable RNA molecules may chemically synthesized using known methods. Alternatively, suitable expression vectors may be used to transcribe such RNA either in vitro or in vivo. In vitro transcription of sense and antisense strands (encoded by sequences present on the same vector or on separate vectors) may be effected using for example T7 RNA polymerase, in which case the vector may comprise a suitable coding sequence operably-linked to a T7 promoter. The in vitro-transcribed RNA may in embodiments be processed (e.g. using *E. coli* RNase III) in vitro to a size conducive to RNAi. The sense and antisense transcripts combined to form an RNA duplex which is introduced into a target cell of interest. Other vectors may be used, which express small hairpin RNAs (shRNAs) which can be processed into siRNA-like molecules. Various vector-based methods are known in the art. Various methods for introducing such vectors into cells, either in vitro or in vivo (e.g. gene therapy) are known in the art.

Accordingly, in an embodiment, expression of a polypeptide including an amino acid sequence substantially identical to a SARS virus sequence may be inhibited by introducing into or generating within a cell an siRNA or siRNA-like molecule corresponding to a nucleic acid molecule encoding the polypeptide or fragment thereof, or to an nucleic acid homologous thereto. In various embodiments such a method may entail the direct administration of the siRNA or siRNA-like molecule into a cell, or use of the vector-based methods described above. In an embodiment, the siRNA or siRNA-like molecule is less than about 30 nucleotides in length. In a further embodiment, the siRNA or siRNA-like molecules are about 21-23 nucleotides in length. In an embodiment, siRNA or siRNA-like molecules comprise and 19-21 bp duplex portion, each strand having a 2 nucleotide 3' overhang. In embodiments, the siRNA or siRNA-like molecule is substantially identical to a nucleic acid encoding the polypeptide or a fragment or variant (or a fragment of a variant) thereof. Such a variant is capable of encoding a protein having the activity of a SARS virus polypeptide. In embodiments, the sense strand of the siRNA or siRNA-like molecule is substantially identical to a SARS virus nucleic acid molecule or a fragment thereof (RNA having U in place of T residues of the DNA sequence).

SARS Virus Protein Expression

In general, SARS virus polypeptides according to the invention, may be produced by transformation of a suitable host cell with all or part of a SARS virus polypeptide-encoding genomic or cDNA molecule or fragment thereof (e.g., the genomic DNA or cDNAs described herein) in a suitable expression vehicle. Those skilled in the field of molecular biology will understand that any of a wide variety of expression systems may be used to provide the recombinant protein. The precise host cell used is not critical to the invention. The SARS virus polypeptide may be produced in a prokaryotic host (e.g., *E. coli* or a virus, for example, a coronovirus such as human OC43 or 229E, a bovine coronavirus, or a virus used for gene therapy, such as an adenovirus) or in a eukaryotic host (e.g., *Saccharomyces cerevisiae*, insect cells, e.g., Sf21 cells, or mammalian cells, e.g., COS 1, NIH 3T3, VeroE6, or HeLa cells). Such cells are available from a wide range of sources (e.g., the American Type Culture Collection, Rockland, Md.; also, see, e.g., Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1994). The method of transformation or transfection and the choice of expression vehicle will depend on the host system selected. Transformation and transfection methods are described, e.g., in Ausubel et al. (supra); expression vehicles may be chosen from those provided, e.g., in Cloning Vectors: A Laboratory Manual, P. H. Pouwels et al, 1985, Supp. 1987), or from commercially available sources. Suitable animal models, e.g. a ferret animal model, or any other animal model suitable for analysis of SARS virus infection or expression of SARS virus nucleic acid molecules may be used.

In an alternative embodiment, the baculovirus expression system (using, for example, the vector pBacPAK9) available from Clontech (Pal Alto, Calif.) may be used. If desired, this system may be used in conjunction with other protein expression techniques, for example, the myc tag approach described by Evan et al. (Mol. Cell Biol. 5:3610-3616, 1985). In an alternative embodiment, a SARS virus polypeptide may be produced by a stably-transfected mammalian cell line. A number of vectors suitable for stable transfection of mammalian cells are available to the public, e.g., see Pouwels et al (supra); methods for constructing such cell lines are also publicly available, e.g., in Ausubel et al. (supra). In one example, cDNA encoding the SARS virus polypeptide is cloned into an expression vector which includes the dihydrofolate reductase (DHFR) gene. Integration of the plasmid and, therefore, the SARS virus polypeptide-encoding gene into the host cell chromosome is selected for by inclusion of 0.01-300 μM methotrexate in the cell culture medium (as described in Ausubel et al., supra). This dominant selection can be accomplished in most cell types. Recombinant protein expression can be increased by DHFR-mediated amplification of the transfected gene. Methods for selecting cell lines bearing gene amplifications are described in Ausubel et al. (supra); such methods generally involve extended culture in medium containing gradually increasing levels of methotrexate. DHFR-containing expression vectors commonly used for this purpose include pCVSEII-DHFR and pAdD26SV(A) (described in Ausubel et al., supra). Any of the host cells described above or, preferably, a DHFR-deficient CHO cell line (e.g., CHO DHFR.sup.—cells, ATCC Accession No. CRL 9096) are among the host cells preferred for DHFR selection of a stably-transfected cell line or DHFR-mediated gene amplification.

Once the recombinant SARS virus polypeptide is expressed, it is isolated, e.g., using affinity chromatography. In one example, an anti-SARS virus polypeptide antibody (e.g., produced as described herein) may be attached to a column and used to isolate the SARS virus polypeptide. Lysis and fractionation of SARS virus polypeptde-harboring cells prior to affinity chromatography may be performed by standard methods (see, e.g., Ausubel et al., supra). In another example, SARS virus polypeptides may be purified or substantially purified from a mixture of compounds such as an extract or supernatant obtained from cells (Ausubel et al., supra). Standard purification techniques can be used to progressively eliminate undesirable compounds from the mixture until a single compound or minimal number of effective compounds has been isolated.

Once isolated, the recombinant protein can, if desired, be further purified, e.g., by high performance liquid chromatography (see, e.g., Fisher, Laboratory Techniques In Biochemistry And Molecular Biology, eds., Work and Burdon, Elsevier, 1980).

Polypeptides of the invention, particularly short SARS virus peptide fragments, can also be produced by chemical synthesis (e.g., by the methods described in Solid Phase Peptide Synthesis, 2nd ed., 1984 The Pierce Chemical Co., Rockford, Ill.).

These general techniques of polypeptide expression and purification can also be used to produce and isolate useful SARS virus protein fragments or analogs (described herein).

In certain alternative embodiments, the SARS polypeptide might have attached any one of a variety of tags. Tags can be amino acid tags or chemical tags and can be added for the purpose of purification (for example a 6-histidine tag for purification over a nickel column). In other preferred embodiments, various labels can be used as means for detecting binding of a SARS polypeptide to another polypeptide, for example to a cell surface receptor. Alternatively, SARS DNA or RNA may be labeled for detection, for example in a hybridization assay. SARS virus nucleic acids or proteins, or derivatives thereof, may be directly or indirectly labeled, for example, with a radioscope, a fluorescent compound, a bioluminescent compound, a chemiluminescent compound, a metal chelator or an enzyme. Those of ordinary skill in the art will know of other suitable labels or will be able to ascertain such, using routine experimentation. In yet another embodiment of the invention, the polypeptides disclosed herein, or derivatives thereof, are linked to toxins.

Isolation and Identification of Additional SARS Virus Molecules

Based on the SARS virus sequences described herein, the isolation and identification of additional SARS virus-related sequences such as SARS virus genes and of additional SARS virus strains or isolates is made possible using standard techniques. In addition, the SARS virus sequences provided herein also provide the basis for identification of homologous sequences from other species and genera from both prokaryotes and eukaryotes such as viruses, bacteria, fungi, parasites, yeast, and/or mammals. In some embodiments, the nucleic acid sequences described herein may be used to design probes or primers, including degenerate oligonucleotide probes or primers, based upon the sequence of either DNA strand. The probes or primers may then be used to screen genomic or cDNA libraries for sequences from for example naturally occurring variants or isolates of SARS viruses, using standard amplification or hybridization techniques.

In some embodiments, binding partners may be identified by tagging the polypeptides of the invention (e.g., those substantially identical to SARS virus polypeptides described herein) with an epitope sequence (e.g., FLAG or 2HA), and delivering it into host cells, either by transfection with a suitable vector containing a nucleic acid sequence encoding a polypeptide of the invention, followed by immunoprecipitation and identification of the binding partner. Cells may be infected with strains expressing the FLAG or 2HA fusions, followed by lysis and immunoprecipitation with anti-FLAG or anti-2HA antibodies. Binding partners may be identified by mass spectroscopy. If the polypeptide of the invention is not produced in sufficient quantities, such a method may not deliver enough tagged protein to identify its partner. As part of a complementary approach, each polypeptide of the invention may be cloned into a mammalian transfection vector fused to, for example, 2HA, GFP and/or FLAG. Following transfection, HeLa cells may be lysed and the tagged polypeptide immunoprecipitated. The binding partner may be identified by SDS PAGE followed by mass spectroscopy.

In some embodiments, polypeptides or antibodies of the invention may be tagged, produced, and used for example on affinity columns and/or in immunological assays to identify and/or confirm identified target compounds. FLAG, HA, and/or His tagged proteins can be used for such affinity columns to pull out host cell factors from cell extracts, and any hits may be validated by standard binding assays, saturation curves, and other methods as described herein or known to those of skill in the art.

In some embodiments, a two hybrid system may be used to study protein-protein interactions. The nucleic acid sequences described herein, or sequences substantially identical thereto, can be cloned into the pBT bait plasmid of the two hybrid system, and a commercially available murine spleen library of 5×10^6 independent clones, may be used as the target library for the baits. Potential hits may be further characterized by recovering the plasmids and retransforming to reduce false positives resulting from clonal bait variants and library target clones which activate the reporter genes independent of the cloned bait. Reproducible hits may be studied further as described herein.

Virulence may be assayed as described herein or as known to those of skill in the art. Once coding sequences have been identified, they may be isolated using standard cloning techniques, and inserted into any suitable vector or replicon for, for example, production of polypeptides. Such vectors and replicons include, without limitation, bacteriophage X (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1 106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5 (*Saccharomyces*), YCp19 (*Saccharomyces*) or bovine papilloma virus (mammalian cells). In general, the polypeptides of the invention may be produced in any suitable host cell transformed or transfected with a suitable vector. The method of transformation or transfection and the choice of expression vehicle will depend on the host system selected. A wide variety of expression systems may be used, and the precise host cell used is not critical to the invention. For example, a polypeptide according to the invention may be produced in a prokaryotic host (e.g., *E. coli*) or in a eukaryotic host (e.g., *Saccharoinyces cerevisiae*, insect cells, e.g., Sf21 cells, or mammalian cells, e.g., NIH 3T3, HeLa, or COS cells). Such cells are available from a wide range of sources (e.g., the American Type Culture Collection, Manassus, Va.). Bacterial expression systems for polypeptide production include the *E. coli* pET expression system (Novagen, Inc., Madison, Wis.), and the pGEX expression system (Pharmacia).

Compounds

In one aspect, compounds according to the invention include SARS virus nucleic acid molecules and polypeptides, such as the sequences disclosed in the Figures and Tables herein, and throughout the specification, and fragments thereof. In alternative embodiments, compounds according to the invention may be nucleic acid molecules that are at least 10 nucleotides in length, and that are derived from the sequences described herein. In alternative embodiments, compounds according to the invention may be peptides that are at least 5 amino acids in length, and that are derived from the sequences described herein.

In alternative embodiments, a compound according to the invention can be a non-peptide molecule as well as a peptide or peptide analogue. A peptide or peptide analogue will generally be as small as feasible while retaining full biological activity. A non-peptide molecule can be any molecule that exhibits biological activity as described herein or known in the art. Biological activity can, for example, be measured in terms of ability to elicit a cytotoxic response, to mediate DNA replication, or any other function of a SARS virus molecule.

Compounds can be prepared by, for example, replacing, deleting, or inserting an amino acid residue of SARS peptide or peptide analogue, as described herein, with other conservative amino acid residues, i.e., residues having similar physical, biological, or chemical properties, and screening for biological function.

It is well known in the art that some modifications and changes can be made in the structure of a polypeptide without substantially altering the biological function of that peptide, to obtain a biologically equivalent polypeptide. Such modifications may be made for the purpose of modifying function, or for facilitating administration or enhancing stability or inhibiting breakdown for, for example, therapeutic uses. For example, an indigestible SARS virus compound according to the invention may be used for oral administration; a modification that is suitable for inhalation may be used for administration to the lung; or addition of a leader sequence may increase protein expression levels.

In one aspect of the invention, SARS virus-derived peptides or epitopes may include peptides that differ from a portion of a native leader, protein or SARS virus sequence by conservative amino acid substitutions. The peptides and epitopes of the present invention also extend to biologically equivalent peptides that differ from a portion of the sequence of novel peptides of the present invention by conservative amino acid substitutions. As used herein, the term "conserved amino acid substitutions" refers to the substitution of one amino acid for another at a given location in the peptide, where the substitution can be made without substantial loss of the relevant function. In making such changes, substitutions of like amino acid residues can be made on the basis of relative similarity of side-chain substituents, for example, their size, charge, hydrophobicity, hydrophilicity, and the like, and such substitutions may be assayed for their effect on the function of the peptide by routine testing.

In some embodiments, conserved amino acid substitutions may be made where an amino acid residue is substituted for another having a similar hydrophilicity value (e.g., within a value of plus or minus 2.0), where the following may-be an amino acid having a hydropathic index of about −1.6 such as Tyr (−1.3) or Pro (−1.6)s are assigned to amino acid residues (as detailed in U.S. Pat. No. 4,554,101, incorporated herein by reference): Arg (+3.0); Lys (+3.0); Asp (+3.0); Glu (+3.0); Ser (+0.3); Asn (+0.2); Gln (+0.2); Gly (0); Pro (−0.5); Thr (−0.4); Ala (−0.5); His (−0.5); Cys (−1.0); Met (−1.3); Val (−1.5); Leu (−1.8); Ile (−1.8); Tyr (−2.3); Phe (−2.5); and Trp (−3.4).

In alternative embodiments, conserved amino acid substitutions may be made where an amino acid residue is substituted for another having a similar hydropathic index (e.g., within a value of plus or minus 2.0). In such embodiments, each amino acid residue may be assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics, as follows: Ile (+4.5); Val (+4.2); Leu (+3.8); Phe (+2.8); Cys (+2.5); Met (+1.9); Ala (+1.8); Gly (−0.4); Thr (−0.7); Ser (−0.8); Trp (−0.9); Tyr (−1.3); Pro (−1.6); His (−3.2); Glu (−3.5); Gln (−3.5); Asp (−3.5); Asn (−3.5); Lys (−3.9); and Arg (−4.5).

In alternative embodiments, conserved amino acid substitutions may be made where an amino acid residue is substituted for another in the same class, where the amino acids are divided into non-polar, acidic, basic and neutral classes, as follows: non-polar: Ala, Val, Leu, Ile, Phe, Trp, Pro, Met; acidic: Asp, Glu; basic: Lys, Arg, His; neutral: Gly, Ser, Thr, Cys, Asn, Gln, Tyr.

Conservative amino acid changes can include the substitution of an L-amino acid by the corresponding D-amino acid, by a conservative D-amino acid, or by a naturally-occurring, non-genetically encoded form of amino acid, as well as a conservative substitution of an L-amino acid. Naturally-occurring non-genetically encoded amino acids include beta-alanine, 3-amino-propionic acid, 2,3-diamino propionic acid, alpha-aminoisobutyric acid, 4-amino-butyric acid, N-methylglycine (sarcosine), hydroxyproline, ornithine, citrulline, t-butylalanine, t-butylglycine, N-methylisoleucine, phenylglycine, cyclohexylalanine, norleucine, norvaline, 2-napthylalanine, pyridylalanine, 3-benzothienyl alanine, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, penicillamine, 1,2,3,4-tetrahydroisoquinoline-3-carboxylix acid, beta-2-thienylalanine, methionine sulfoxide, homoarginine, N-acetyl lysine, 2-amino butyric acid, 2-amino butyric acid, 2,4,-diamino butyric acid, p-aminophenylalanine, N-methylvaline, homocysteine, homoserine, cysteic acid, epsilon-amino hexanoic acid, delta-amino valeric acid, or 2,3-diaminobutyric acid.

In alternative embodiments, conservative amino acid changes include changes based on considerations of hydrophilicity or hydrophobicity, size or volume, or charge. Amino acids can be generally characterized as hydrophobic or hydrophilic, depending primarily on the properties of the amino acid side chain. A hydrophobic amino acid exhibits a hydrophobicity of greater than zero, and a hydrophilic amino acid exhibits a hydrophilicity of less than zero, based on the normalized consensus hydrophobicity scale of Eisenberg et aL (*J. Mol. Bio.* 179:125-142, 184). Genetically encoded hydrophobic amino acids include Gly, Ala, Phe, Val, Leu, Ile, Pro, Met and Trp, and genetically encoded hydrophilic amino acids include Thr, His, Glu, Gln, Asp, Arg, Ser, and Lys. Non-genetically encoded hydrophobic amino acids include t-butylalanine, while non-genetically encoded hydrophilic amino acids include citrulline and homocysteine.

Hydrophobic or hydrophilic amino acids can be further subdivided based on the characteristics of their side chains. For example, an aromatic amino acid is a hydrophobic amino acid with a side chain containing at least one aromatic or heteroaromatic ring, which may contain one or more substituents such as —OH, —SH, —CN, —F, —Cl, —Br, —I, $—NO_2$, —NO, $—NH_2$, —NHR, —NRR, —C(O)R, —C(O)OH, —C(O)OR, $—C(O)NH_2$, —C(O)NHR, —C(O)NRR, etc., where R is independently (C_1-C_6) alkyl, substituted (C_1-C_6) alkyl, (C_1-C_6) alkenyl, substituted (C_1-C_6) alkenyl, (C_1-C_6) alkynyl, substituted (C_1-C_6) alkynyl, (C_5-C_{20}) aryl, substituted (C_5-C_{20}) aryl, (C_6-C_{26}) alkaryl, substituted (C_6-C_{26}) alkaryl, 5-20 membered heteroaryl, substituted 5-20 membered heteroaryl, 6-26 membered alkheteroaryl or substituted 6-26 membered alkheteroaryl. Genetically encoded aromatic amino acids include Phe, Tyr, and Tryp, while non-genetically encoded aromatic amino acids include phenylglycine, 2-napthylalanine, beta-2-thienylalanine, 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluoropbenylalanine3-fluorophenylalanine, and 4-fluorophenylalanine.

An apolar amino acid is a hydrophobic amino acid with a side chain that is uncharged at physiological pH and which has bonds in which a pair of electrons shared in common by two atoms is generally held equally by each of the two atoms (i.e., the side chain is not polar). Genetically encoded apolar amino acids include Gly, Leu, Val, Ile, Ala, and Met, while non-genetically encoded apolar amino acids include cyclohexylalanine. Apolar amino acids can be further subdivided to include aliphatic amino acids, which is a hydrophobic amino acid having an aliphatic hydrocarbon side chain. Genetically encoded aliphatic amino acids include Ala, Leu, Val, and Ile, while non-genetically encoded aliphatic amino acids include norleucine.

A polar amino acid is a hydrophilic amino acid with a side chain that is uncharged at physiological pH, but which has one bond in which the pair of electrons shared in common by two atoms is held more closely by one of the atoms. Genetically encoded polar amino acids include Ser, Thr, Asn, and Gln, while non-genetically encoded polar amino acids include citrulline, N-acetyl lysine, and methionine sulfoxide.

An acidic amino acid is a hydrophilic amino acid with a side chain pKa value of less than 7. Acidic amino acids typically have negatively charged side chains at physiological pH due to loss of a hydrogen ion. Genetically encoded acidic amino acids include Asp and Glu. A basic amino acid is a hydrophilic amino acid with a side chain pKa value of greater than 7. Basic amino acids typically have positively charged side chains at physiological pH due to association with hydronium ion. Genetically encoded basic amino acids include Arg, Lys, and His, while non-genetically encoded basic amino acids include the non-cyclic amino acids ornithine, 2,3,-diaminopropionic acid, 2,4-diaminobutyric acid, and homoarginine.

It will be appreciated by one skilled in the art that the above classifications are not absolute and that an amino acid may be classified in more than one category. In addition, amino acids can be classified based on known behaviour and or characteristic chemical, physical, or biological properties based on specified assays or as compared with previously identified amino acids. Amino acids can also include bifunctional moieties having amino acid-like side chains.

Conservative changes can also include the substitution of a chemically derivatised moiety for a non-derivatised residue, by for example, reaction of a functional side group of an amino acid. Thus, these substitutions can include compounds whose free amino groups have been derivatised to amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Similarly, free carboxyl groups can be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides, and side chains can be derivatized to form O-acyl or O-alkyl derivatives for free hydroxyl groups or N-im-benzylhistidine for the imidazole nitrogen of histidine. Peptide analogues also include amino acids that have been chemically altered, for example, by methylation, by amidation of the C-terminal amino acid by an alkylamine such as ethylamine, ethanolamine, or ethylene diamine, or acylation or methylation of an amino acid side chain (such as acylation of the epsilon amino group of lysine). Peptide analogues can also include replacement of the amide linkage in the peptide with a substituted amide (for example, groups of the formula —C(O)—NR, where R is (C_1-C_6) alkyl, (C_1-C_6) alkenyl, (C_1-C_6) alkynyl, substituted (C_1-C_6) alkyl, substituted (C_1-C_6) alkenyl, or substituted (C_1-C_6) alkynyl) or isostere of an amide linkage (for example, —CH_2NH—, —CH_2S, —CH_2CH_2—, —CH═CH— (cis and trans), —C(O)CH_2—, —CH(OH)CH_2—, or —CH_2SO—).

The compound can be covalently linked, for example, by polymerisation or conjugation, to form homopolymers or heteropolymers. Spacers and linkers, typically composed of small neutral molecules, such as amino acids that are uncharged under physiological conditions, can be used. Linkages can be achieved in a number of ways. For example, cysteine residues can be added at the peptide termini, and multiple peptides can be covalently bonded by controlled oxidation. Alternatively, heterobifunctional agents, such as disulfide/amide forming agents or thioether/amide forming agents can be used. The compound can also be constrained, for example, by having cyclic portions.

In some embodiments, three dimensional molecular modeling techniques may be used to identify or generate compounds that may be useful as therapeutics or diagnostics. Standard molecular modeling tools may be used, for example, those described in L-H Hung and R. Samudrala, PROTINFO: secondary and tertiary protein structure prediction, Nucleic Acids Research, 2003, Vol. 31, No. 13 3296-3299; A. Yamaguchi, et al. , Enlarged FAMSBASE: protein 3D structure models of genome sequences for 41 species, Nucleic Acids Research, 2003, Vol. 31, No. 1 463-468; J. Chen, et al., MMDB: Entrez's 3D-structure database, Nucleic Acids Research, 2003, Vol. 31, No. 1 474-477; R. A. Chiang, et al., The Structure Superposition Database, Nucleic Acids Research, 2003, Vol. 31, No. 1 505-510.

Peptides or peptide analogues can be synthesized by standard chemical techniques, for example, by automated synthesis using solution or solid phase synthesis methodology. Automated peptide synthesizers are commercially available and use techniques well known in the art. Peptides and peptide analogues can also be prepared using recombinant DNA technology using standard methods such as those described in, for example, Sambrook, et aL (Molecular Cloning: A Laboratory Manual. 2.sup.nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) or Ausubel et al. (Current Protocols in Molecular Biology, John Wiley & Sons, 1994).

Compounds, such as peptides (or analogues thereof) can be identified by routine experimentation by, for example, modifying residues within SARS peptides; introducing single or multiple amino acid substitutions, deletions, or insertions, and identifying those compounds that retain biological activity, e.g., those compounds that have cytotoxic ability.

In general, candidate compounds for prevention or treatment of SARS virus-mediated disorders are identified from large libraries of both natural product or synthetic (or semi-synthetic) extracts or chemical libraries according to methods known in the art. Candidate or test compounds may include, without limitation, peptides, polypeptides, synthesised organic molecules, naturally occurring organic molecules, and nucleic acid molecules. In some embodiments, such compounds screen for the ability to inhibit SARS virus replication or pathogenicity, while maintaining the infected cell's ability to grow or survive.

Those skilled in the field of drug discovery and development will understand that the precise source of test extracts or compounds is not critical to the method(s) of the invention. Accordingly, virtually any number of chemical extracts or compounds can be screened using the exemplary methods described herein or using standard methods. Examples of such extracts or compounds include, but are not limited to, plant-, fungal-, prokaryotic- or animal-based extracts, fermentation broths, and synthetic compounds, as well as modification of existing compounds. Numerous methods are also available for generating random or directed synthesis (e.g., semi-synthesis or total synthesis) of any number of chemical compounds, including, but not limited to, saccharide-, lipid-, peptide-, and nucleic acid-based compounds. Synthetic compound libraries are commercially available. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant, and animal extracts are commercially available from a number of sources, including Biotics (Sussex, UK), Xenova (Slough, UK), Harbor Branch Oceanographic Institute (Ft. Pierce, Fla.), and PharmaMar, U.S.A. (Cambridge, Mass.). In addition, natural and synthetically produced libraries of, for example, SARS virus polypeptides containing leader sequences, are produced, if desired, according to methods known in the art, e.g., by standard extraction and fractionation methods. Furthermore, if desired, any library or compound is readily modified using standard chemical, physical, or biochemical methods.

When a crude extract is found to modulate cytotoxicity or viral infection, further fractionation of the positive lead extract is necessary to isolate chemical constituents responsible for the observed effect. Thus, the goal of the extraction, fractionation, and purification process is the careful characterization and identification of a chemical entity within the crude extract having, for example, anti-cytotoxicity or anti-viral properties. The same assays described herein for the detection of activities in mixtures of compounds can be used to purify the active component and to test derivatives thereof. Methods of fractionation and purification of such heterogenous extracts are known in the art. If desired, compounds shown to be useful agents for treatment are chemically modified according to methods known in the art. Compounds identified as being of therapeutic, prophylactic, diagnostic, or other value in for example cell culture systems, such as a Vero E6 culture system, may be subsequently analyzed using a ferret animal model, or any other animal model suitable for analysis of SARS.

Antibodies

The compounds of the invention can be used to prepare antibodies to SARS virus peptides, protein, polyproteins, or analogs thereof, or to SARS virus nucleic acid molecules or analogs thereof using standard techniques of preparation as, for example, described in Harlow and Lane (Antibodies; A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1988), or known to those skilled in the art. Antibodies may include polyclonal antibodies, monoclonal antibodies, hybrid antibodies (e.g., divalent antibodies having different pairs of heavy and light chains), chimeric antibodies (e.g., antibodies having constant and variable domains from different species and/or class), modified antibodies (e.g, antibodies in which the naturally occurring sequence has been altered by for example recombinant techniques), Fab antibodies, anti-idiotype antibodies, etc. Antibodies can be tailored to minimise adverse host immune response by, for example, using chimeric antibodies containing an antigen binding domain from one species and the Fc portion from another species, or by using antibodies made from hybridomas of the appropriate species. For example, "humanized" antibodies may be used for administration to humans.

To generate SARS virus polypeptide-specific antibodies, a SARS virus polypeptide coding sequence may be expressed, for example, as a C-terminal fusion with glutathione S-transferase (GST) (Smith et al., Gene 67:31-40, 1988). The fusion polypeptide may then be purified on glutathione-Sepharose beads, eluted with glutathione cleaved with thrombin (at the engineered cleavage site), and purified to the degree necessary for immunization of rabbits. Primary immunizations are carried out with Freud's complete adjuvant and subsequent immunizations with Freud's incomplete adjuvant. Antibody titres are monitored by Western blot and immunoprecipitation analyzes using the thrombin-cleaved SARS virus polypeptide fragment of the GST-SARS virus fusion polypeptide. Immune sera are affinity purified using CNBr-Sepharose-coupled SARS virus polypeptide. Antiserum specificity is determined using a panel of unrelated GST polypeptides.

As an alternate or adjunct immunogen to GST fusion polypeptides, peptides corresponding to relatively unique hydrophilic SARS virus polypeptides may be generated and coupled to keyhole limpet hemocyanin (KLH) through an introduced C-terminal lysine. Antiserum to each of these peptides is similarly affinity purified on peptides conjugated to BSA, and specificity tested in ELISA and Western blots using peptide conjugates, and by Western blot and immunoprecipitation using SARS virus polypeptide expressed as a GST fusion polypeptide.

Alternatively, monoclonal antibodies may be prepared using the SARS virus polypeptides described above and standard hybridoma technology (see, e.g., Kohler et al., Nature, 256:495, 1975; Kohler et al., Eur. J Immunol. 6:511, 1976; Kohler et al., Eur. J. Immunol. 6:292, 1976; Hammerling et al., In Monoclonal Antibodies and T Cell Hybridomas, Elsevier, NY, 1981; Ausubel et al., supra). Once produced, monoclonal antibodies are also tested for specific SARS virus polypeptide recognition by Western blot or immunoprecipitation analysis (by the methods described in Ausubel et al., supra). Antibodies which specifically recognize SARS virus polypeptides are considered to be useful in the invention; such antibodies may be used, e.g., in an immunoassay to monitor the level of SARS virus polypeptides produced by a mammal (for example, to determine the amount or location of a SARS virus polypeptide).

In an alternative embodiment, antibodies of the invention are not only produced using the whole SARS virus polypeptide, but using fragments of the SARS virus polypeptide which are unique or which lie outside highly conserved regions and appear likely to be antigenic, by criteria such as high frequency of charged residues may also be used. In one specific example, such fragments are generated by standard techniques of PCR and cloned into the pGEX expression vector (Ausubel et al., supra). Fusion polypeptides are expressed in *E. coli* and purified using a glutathione agarose affinity matrix as described in Ausubel et al. (supra). To attempt to minimize the potential problems of low affinity or specificity of antisera, two or three such fusions are generated for each polypeptide, and each fusion is injected into at least two rabbits. Antisera are raised by injections in a series, preferably including at least three booster injections. SARS virus antibodies may also be prepared against SARS virus nucleic acid molecules.

Antibodies may be used as diagnostics, therapeutics, or prophylactics for SARS virus-related disorders. Antibodies may also be used to isolate SARS virus and compounds by for example affinity chromatography, or to identify SARS virus compounds isolated or generated by other techniques.

Arrays and Libraries

In some aspects, biological assays, such as diagnostic or other assays, using high density nucleic acid, polypeptide, or antibody arrays, for example high density miniaturized arrays or "microarrays," of SARS virus nucleic acid molecules or polypeptides, or antibodies capable of specifically binding such nucleic acid molecules or polypeptides, may be performed. Macroarrays, performed for example by manual spotting techniques, may also be used. Arrays generally require a solid support (for example, nylon, glass, ceramic, plastic, silicon, nitrocellulose or PVDF membranes, microwells, microbeads, e.g., magnetic microbeads, etc.) to which the nucleic acid molecules or polypeptides or antibodies are attached in a specified two-dimensional arrangement, such that the pattern of hybridization is easily determinable. Suspension arrays (particles in suspension) that are coded to facilitate identification may also be used. SARS virus nucleic acid molecules or polypeptide probes or targets may be compounds as described herein.

In some embodiments, high density nucleic acid arrays may for example be used to monitor the presence or level of expression of a large number of SARS virus nucleic acid molecules or genes or for detecting or identifying SARS virus nucleic acid sequence variations, mutations or polymorphisms. For the purpose of such arrays, "nucleic acids" may include any polymer or oligomer of nucleosides or nucleotides (polynucleotides or oligonucleotides), which include pyrimidine and purine bases, preferably cytosine, thymine, and uracil, and adenine and guanine, respectively, or may include peptide nucleic acids (PNA). In an alternative aspect, the invention provides nucleic acid microarrays including a number of distinct nucleic acid sequence arrays of the invention, thus providing specific "sets" of sequences. The number of distinct sequences may for example be any integer between 2 and 1×10^5, such as at least 10^2, 10^3, 10^4, or 10^5.

The invention also provides gene knockout and expression libraries. Thus, nucleic acid molecules encoding SARS virus polypeptides or proteins (e.g., PCR products of ORF's or total mRNA) may for example be attached to a solid support, hybridized with single stranded detectably-labeled cDNAs (corresponding to an "antisense" orientation), and quantified using an appropriate method such that a signal is detected at each location at which hybridization has taken place. The intensity of the signal would then reflect the level of gene expression. Comparison of results from viruses, for example, of different strains or from different samples or subjects, would elucidate differing levels of expression of specified genes. Using similar techniques, homologous nucleic acids may be identified from different viruses if SARS virus nucleic acids are used in the microarray, and probed with nucleic acid molecules from different viruses or subjects. In some embodiments, this approach may involve constructing his-tagged ORP expression libraries of viral genomes in a bacterial host, similar to an expression library in yeast (Martzen M. R. et al., 1999. Science, 286:1153). ORF-encoded protein activities may for example be detected in purified his-tagged protein pools in cases where activities cannot be detected in extracts or cells. In one aspect of the invention, arrayed libraries may be constructed of viral strains each of which bears a plasmid expressing a different SARS virus ORF under control of an inducible promoter. ORFs are amplified using PCR and cloned into a vector that enables their expression as N-terminal his-tagged polypeptides. These amplicons are also used to construct hybridization microarrays and enable targeted gene disruption, reducing expenses. A suitable expression host is selected, and genes encoding particular biochemical activities are identified by screening arrayed pools of his-tagged proteins as described previously (Martzen M. R., McCraith S. M., Spinelli S. L., Torres F. M., Fields S., Grayhack E. J., and Phizicky E. M., 1999. Science, 286: 1153).

In some embodiments, protein arrays (including antibody or antigen arrays) may be used for the analysis and identification of SARS virus polypeptides or host responses to such polypeptides. Thus, protein arrays may be used to detect SARS virus polypeptides in a patient; distinguish a SARS virus polypeptide from a host polypeptide; detect interactions between SARS virus polypeptides and for example host proteins; determine the efficacy of potential therapeutics, such as small molecules or ligands that may bind SARS virus polypeptides; determine protein-antibody interactions; and/or detect the interaction of enzyme-substrate interactions. Protein arrays may also be used to detect SARS virus antigens and antibodies in samples; to profile expression of SARS virus polypeptides; to identify suitable antibodies or map epitopes; or for a variety of protein function analyses.

A variety of methods are known for making and using microarrays, as for example disclosed in Cheung V. G., et al., 1999. Nature Genetics Supplement, 21:15-19; Lipshutz R. J., et al., 1999. Nature Genetics Supplement, 21:20-24; Bowtell D. D. L., 1999. Nature Genetics Supplement, 21:25-32; Singh-Gasson S., et al., 1999. Nature Biotechnol., 17:974-978; and Schweitzer B., et al., 2002. Nature Biotechnol., 20:359-365. Thus, for example, microarrays may be designed by synthesizing oligonucleotides with sequence variations based on a reference sequences, such as any SARS virus sequences described herein. Methods for storing, querying and analyzing microarray data have for example been disclosed in, for example, U.S. Pat. No. 6,484,183; U.S. Pat. No. 6,188,783; and Holloway A. J., et al., 2002. Nature Genetics Supplement, 32:481-489. Protein arrays may be constructed, detected, and analysed using methods known in the art for example mass spectrometric techniques, immunoassays such as ELISA and western (dot) blotting combined with for example fluorescence detection techniques, and adapted for high throughput analysis, as described in for example MacBeath, G. and Schreiber, S. L. Science 2000, 289, 1760-1763; Levit-Binnun N, et al. (2003) Quantitative detection of protein arrays. Anal Chem 75:1436-41; Kukar T, et al. (2002) Protein microarrays to detect protein-protein interactions using red and green fluorescent proteins. Anal Biochem 306: 50-4; Borrebaeck C A, et al. (2001) Protein chips based on -recombinant antibody fragments: a highly sensitive approach as detected by mass spectrometry. Biotechniques 30:1126-1132; Huang R P (2001) Detection of multiple proteins in an antibody-based protein microarray system. J Immunol Methods 255:1-13; Emili A Q and Cagney G (2000) Large-scale functional analysis using peptide or protein arrays. Nature Biotechnol 18:393-397; Zhu H, et al. (2000) Analysis of yeast protein kinases using protein chips. Nature Genet 26:283-9; Lueking A, et al. (1999) Protein Microarrays for Gene Expression and Antibody Screening. Anal. Biochem. 270:103-111; or Templin M F, et al. (2002) Protein microarray technology. Drug Discov Today 7:815-822. Tools for microarray techniques are available commercially from for example Affymetrix, Santa Clara, Calif.; Nanogen, San Diego, Calif.; or Sequenom, San Diego, Calif.

Computer Readable Records

Nucleic acid and polypeptide sequences, as described herein, or a fragment thereof, may be provided in a variety of media to facilitate access to these sequences and enable the use thereof. According, SARS virus nucleic acid and polypeptide sequences of the invention may be recorded or stored on computer readable media, using any technique and format that is appropriate for the particular medium.

In alternative embodiments, the invention provides computer readable media encoded with a number of distinct nucleic acid or amino acid data sequences of the invention. The number of distinct sequences may for example be any integer between 2 and 1×10^5, such as at least 10^2, 10^3, 10^4 or 10^5. In one embodiment, the invention features a computer medium having a plurality of digitally encoded data records. Each data record may include a value representing a nucleic acid or amino acid sequence of the invention. In some embodiments, the data record may further include values representing the level of expression, level or activity of a nucleic acid or amino acid sequence of the invention. The data record can be structured as a table, for example, a table that is part of a database such as a relational database (for example, a SQL database of the Oracle or Sybase database environments). The invention also includes a method of communicating information about a sample, for example by transmitting information, for example transmitting a computer readable record as described herein, for example over a computer network. The polypeptide and nucleic acid sequences of the invention, and sequence information pertaining thereto, may be routinely accessed by one of ordinary skill in the art for a variety of purposes, including for the purposes of comparing substantially identical sequences, etc. Such access may be facilitated using publicly available software as described herein. By "computer readable media" is meant any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

Pharmaceutical and Veterinary Compositions, Dosages, and Administration

Compounds of the invention can be provided alone or in combination with other compounds (for example, small molecules, peptides, or peptide analogues), in the presence of a liposome, an adjuvant, or any pharmaceutically acceptable carrier, in a form suitable for administration to humans or to animals.

Conventional pharmaceutical practice may be employed to provide suitable formulations or compositions to administer the compounds to patients suffering from or presymptomatic for SARS. Any appropriate route of administration may be employed, for example, parenteral, intravenous, subcutaneous, intramuscular, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraspinal, intracisternal, intraperitoneal, intranasal, aerosol, or oral administration. In some embodiments, compounds are delivered directly to the lung, by for example, formulations suitable for inhalation. In some embodiments, gene therapy techniques may be used for administration of SARS virus nucleic acid molecules, for example, as DNA vaccines.Formulations may be in the form of liquid solutions or suspensions; for oral administration, formulations may be in the form of tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols.

Methods well known in the art for making formulations are found in, for example, "Remington's Pharmaceutical Sciences" (18th edition), ed. A. Gennaro, 1990, Mack Publishing Company, Easton, Pa. Formulations for parenteral administration may, for example, contain excipients, sterile water, or saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated napthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Other potentially useful parenteral delivery systems for modulatory compounds include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation may contain excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or may be oily solutions for administration in the form of nasal drops, or as a gel.

If desired, treatment with a compound according to the invention may be combined with more traditional therapies for the disease.

For therapeutic or prophylactic compositions, the compounds are administered to an individual in an amount sufficient to stop or slow the replication of the SARS virus, or to confer protective immunity against future SARS virus infection. Amounts considered sufficient will vary according to the specific compound used, the mode of administration, the stage and severity of the disease, the age, sex, and health of the individual being treated, and concurrent treatments. As a general rule, however, dosages can range from about 1 μg to about 100 mg per kg body weight of a patient for an initial dosage, with subsequent adjustments depending on the patient's response, which can be measured, for example by determining the presence of SARS nucleic acid molecules, polypeptides, or virions in the patient's peripheral blood.

In the case of vaccine formulations, an inmunogenically effective amount of a compound of the invention can be provided, alone or in combination with other compounds, with an adjuvant, for example, Freund's incomplete adjuvant or aluminum hydroxide. The compound may also be linked with a carrier molecule, such as bovine serum albumin or keyhole limpet hemocyanin to enhance immunogenicity. In general, compounds of the invention should be used without causing substantial toxicity. Toxicity of the compounds of the invention can be determined using standard techniques, for example, by testing in cell cultures or experimental animals and determining the therapeutic index, i.e., the ratio between the LD50 (the dose lethal to 50% of the population) and the LD100 (the dose lethal to 100% of the population). In some circumstances however, such as in severe disease conditions, it may be necessary to administer substantial excesses of the compositions.

Virus Isolation

Virus isolation was performed on a bronchoaveolar lavage specimen of a fatal SARS case belonging to the original case cluster from Toronto, Canada. All work with the infectious agent was performed in a biosafety level 3 (BSL3) laboratory using a N100 mask for personal protection. Samples were removed from BSL3 after addition of the RNA extraction buffer. The virus isolate, named the "Tor2 isolate" was grown in African Green Monkey Kidney (Vero E6) cells, the viral particles were purified, and the genetic material (RNA) was extracted from the Tor2 isolate (Poutanen, S. M. et al., N Engl J Med, Apr. 10, 2003). More specifically, one hundred microlitre specimens were used to inoculate Vero E6 cells (ATCC CRL 1586) on Dulbecco's Modified Eagle Medium supplemented with penicillin/streptomycin, glutamine and 2% fetal calf serum. The culture was incubated at 37° C. Cytopathogenic effect was observed 5 days post inoculation. The virus was passaged into newly seeded Vero E6 cells which showed a cytopathogenic effect as early as 2 days post infection (multiplicity of infection 10^{-2}). A virus stock was prepared from passage 2 of these cells and preserved in liquid nitrogen. The titer of the virus stock was determined to be 1×10^7 plaque forming units (p.f.u.) by plaque assay and 5×10^6 by tissue culture infectious dose (TCID) 50.

For virus propagation, 10×T-162 flasks of Vero E6 cells were infected with a multiplicity of infection of 10^{-2}. When infected cells showed a cytopathognic effect of '4+' (48 hours post infection), the cultures were then frozen and thawed to lyse the cells, and the supernatants were clarified from cell debris by centrifugation at 10,000 rpm in a Beckman high-speed centrifuge. The supernatants were treated with DNAse and RNAse for 3 hours at 37° C. to remove any cellular genomic nucleic acids and subsequently extracted with an equal volume of 1,1,2-trichloro-trifluoroethane. The top fraction was ultra-centrifuged through a 5%/40% glycerol step gradient at 151,000×g for 1 hour at 4° C. The virus pellet was resuspended in PBS. RNA was isolated using a commercial kit from QIAGEN and stored at −80° C. for further use.

cDNA Library Construction

The RNA and subsequent products were handled under biosafety level 2 (BSL2) conditions. The RNA sample was converted to a cDNA library, using a combined random-priming and oligo-dT priming strategy, and resultant subgenomic clones were processed under level 1 biosafety conditions. More specifically, purified viral RNA (55 ng) was used in the construction of a random primed and oligo-dT primed cDNA library, using the SuperScript Choice System for cDNA synthesis (Invitrogen). Linkers 5'-AATTCGCGGCCGCGTCGAC-3', SEQ ID NO: 195, and 5'-pGTCGACGCGGCCGCG-3', SEQ ID NO: 196, were ligated following cDNA synthesis. The cDNA synthesis products were visualized on agarose gels, revealing the anticipated low-yield smear. To produce sufficient cDNA for cloning, the cDNA product was size fractionated on a low-melting point preparative agarose gel, followed by PCR amplification using a single PCR primer 5'AATTCGCGGCCGCGTCGAC-3', SEQ ID NO: 197, specific to the linkers. This yielded sufficient material for cloning.

Size-selected cDNA products were cloned and single sequence reads were generated from each end of the insert from randomly picked clones. A list of the SARS virus clones is provided in the accompanying sequence listing, which is incorporated by reference herein (SEQ ID NOs: 92-159, 208 and 209).

More specifically, size-selected cDNAs were ligated into the pCR4-TOPO TA cloning vector (Invitrogen, CA), or after digestion with the restriction nuclease Not I into the pBR194c vector (The Institute for Genomic Research, Rockville, Md., USA). Ligated clones were then transformed by electroporation into DH10B T1 cells (Invitrogen), plated on 22 cm agar plates with the appropriate antibiotic and grown for 16 hours at 37° C. Colonies were picked into 384-well Axygen culture blocks containing 2×YT media and grown in a shaking incubator for 18 hours at 37° C. Cells were lysed and DNA purified using standard laboratory procedures. Sequencing primers for the 194c clones were 5'-GGCCTCTTCGCTAT-

TACGC-3' (forward primer) (SEQ ID NO: 159) and 5' TGCAGGTCGACTCTAGAGGAT-3' (reverse primer) (SEQ ID NO: 198).

DNA Sequencing and Assembly of Reads

Sequences were assembled and the assembly edited to produce the genomic sequence of the SARS virus. More specifically, DNA sequencing of both ends of the plasmid templates was achieved using Applied Biosystems BigDye terminator reagent (version 3), with electrophoresis and data collection on AB 3700 and 3730 XL instruments DNA sequence reads were screened for non-viral contaminating sequences, trimmed for quality using PHRED (Ewing, B, and P. Green, *Genome Res* 8, 186-94, March, 1998) and assembled using PHRAP (Gordon, D. et al. *Genome Res* 8, 195-202, March, 1998). Simultaneously, sequences were used in BLAST searches of viral nucleotide and non-redundant protein datasets (NCBI, National Library of Medicine) to search for similarities. Sequence assemblies were visualized using CONSED (Gordon, D. et al. *Genome Res* 8, 195-202, March, 1998). Sequence mis-assemblies and contig joins were identified using Miropeats (Parsons, J. D., *Comput Appl Biosci* 11, 615-9 (December, 1995). As sequence data accrued, the additional sequences were assembled until it became apparent that the additional depth of sampling was increasing depth of coverage but not extending the length of the contig. At this point, 3,080 sequencing reads were generated, 2,634 of which were assembled into a single large contig.

The sequence information was imported into an ACEDB database (Durbin, J. Thierry-Mieg. 1991. A C. elegans Database. Documentation, code and data available from anonymous FTP servers at lirmm "dot" lirmm "dot" fr; cele "dot" mrc-1mb "dot" cam "dot" ac "dot" uk; and ncbi "dot" n1m "dot" nih "dot" gov) and subjected to biological analysis including the identification of open reading frames, detection of similar sequences by BLAST and searching for apparent frameshifts. When frameshifts were identified by this analysis, the sequence assembly was consulted for evidence of sequencing errors and if found, they were corrected. The sequences were also searched for any that could extend the 5' end of the sequence and these were incorporated when found. High quality sequence discrepancies between different sequence reads were identified and resolved. Sequence reads classified as deleted or chimeric were identified through manual inspection and removed from the assembly. The resulting sequence has an average PHRED consensus quality score of 89.96. The lowest quality bases in the assembly are in the immediate vicinity of the 5' and 3' ends of the viral genome, with the lowest quality base having a PHRED score of 35. Most (29,694 of the 29,736 (99.86%)) of the bases have a consensus score of 90. Almost all regions of the genome are represented by reads derived from both strands of the plasmid sequencing templates, the exceptions being 50 bases at the 5' end represented by a single sequencing read, and 5 bases at the 3' end represented by a single read. The average base in the assembly is represented by 30 reads in the forward direction and 30 reads in the reverse direction, as determined by PHRED. RT-PCR products predicted from the sequence and spanning the entire genome yield PCR products of the anticipated size on agarose gels. To confirm the 5' end of the viral genome RACE was performed using the RLM-RACE kit from Ambion, and primers 5'-CAGGAAACAGCTATGACACCAAGAACAAGGCTCTCCA-3' (SEQ ID NO: 90) and 5'-CAGGAAACAGCTATGACGATAGGGCCTCTTCCACAGA-3' (SEQ ID NO: 91). Fourteen clones were recovered and sequenced. Analysis of these sequences confirmed the 5' end of the coronavirus genome. The SARS genomic sequences have been deposited into Genbank (Accession Nos. AY274119.1, AY274119.2, and AY274119.3).

While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure that come within known or customary practice within the art to which the invention pertains, and may be applied to the essential features set forth herein and in the scope of the appended claims.

All patents, patent applications, and publications referred to herein are hereby incorporated by reference in their entirety to the same extent as if each individual patent, patent application, or publication was specifically and individually indicated to be incorporated by reference in its entirety.

SEQUENCE LISTING

```
<160> NUMBER OF SEQ ID NOS: 206

<210> SEQ ID NO 1
<211> LENGTH: 29736
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 1

ctacccagga aaagccaacc aacctcgatc tcttgtagat ctgttctcta aacgaacttt      60

aaaatctgtg tagctgtcgc tcggctgcat gcctagtgca cctacgcagt ataaacaata     120

ataaatttta ctgtcgttga caagaaacga gtaactcgtc cctcttctgc agactgctta     180

cggtttcgtc cgtgttgcag tcgatcatca gcatacctag gtttcgtccg ggtgtgaccg     240

aaaggtaaga tggagagcct tgttcttggt gtcaacgaga aaacacacgt ccaactcagt     300

ttgcctgtcc ttcaggttag agacgtgcta gtgcgtggct tcggggactc tgtggaagag     360

gccctatcgg aggcacgtga acacctcaaa aatggcactt gtggtctagt agagctggaa     420
```

-continued

```
aaaggcgtac tgccccagct tgaacagccc tatgtgttca ttaaacgttc tgatgcctta    480
agcaccaatc acggccacaa ggtcgttgag ctggttgcag aaatggacgg cattcagtac    540
ggtcgtagcg gtataacact gggagtactc gtgccacatg tgggcgaaac cccaattgca    600
taccgcaatg ttcttcttcg taagaacggt aataagggag ccggtggtca tagctatggc    660
atcgatctaa agtcttatga cttaggtgac gagcttggca ctgatcccat tgaagattat    720
gaacaaaact ggaacactaa gcatggcagt ggtgcactcc gtgaactcac tcgtgagctc    780
aatggaggtg cagtcactcg ctatgtcgac aacaatttct gtggcccaga tgggtaccct    840
cttgattgca tcaaagattt tctcgcacgc gcgggcaagt caatgtgcac tctttccgaa    900
caacttgatt acatcgagtc gaagagaggt gtctactgct gccgtgacca tgagcatgaa    960
attgcctggt tcactgagcg ctctgataag agctacgagc accagacacc cttcgaaatt   1020
aagagtgcca agaaatttga cactttcaaa ggggaatgcc caaagtttgt gtttcctctt   1080
aactcaaaag tcaaagtcat tcaaccacgt gttgaaaaga aaaagactga gggtttcatg   1140
gggcgtatac gctctgtgta ccctgttgca tctccacagg agtgtaacaa tatgcacttg   1200
tctaccttga tgaaatgtaa tcattgcgat gaagtttcat ggcagacgtg cgactttctg   1260
aaagccactt gtgaacattg tggcactgaa aatttagtta ttgaaggacc tactacatgt   1320
gggtacctac ctactaatgc tgtagtgaaa atgccatgtc ctgcctgtca agacccagag   1380
attggacctg agcatagtgt tgcagattat cacaaccact caaacattga aactcgactc   1440
cgcaagggag gtaggactag atgttttgga ggctgtgtgt ttgcctatgt tggctgctat   1500
aataagcgtg cctactgggt tcctcgtgct agtgctgata ttggctcagg ccatactggc   1560
attactggtg acaatgtgga gaccttgaat gaggatctcc ttgagatact gagtcgtgaa   1620
cgtgttaaca ttaacattgt tggcgatttt catttgaatg aagaggttgc catcattttg   1680
gcatctttct ctgcttctac aagtgccttt attgacacta taaagagtct tgattacaag   1740
tctttcaaaa ccattgttga gtcctgcggt aactataaag ttaccaaggg aaagcccgta   1800
aaaggtgctt ggaacattgg acaacagaga tcagttttaa caccactgtg tggttttccc   1860
tcacaggctg ctggtgttat cagatcaatt tttgcgcgca cacttgatgc agcaaaccac   1920
tcaattcctg atttgcaaag agcagctgtc accatacttg atggtatttc tgaacagtca   1980
ttacgtcttg tcgacgccat ggtttatact tcagacctgc tcaccaacag tgtcattatt   2040
atggcatatg taactggtgg tcttgtacaa cagacttctc agtggttgtc taatcttttg   2100
ggcactactg ttgaaaaact caggcctatc tttgaatgga ttgaggcgaa acttagtgca   2160
ggagttgaat ttctcaagga tgcttgggag attctcaaat ttctcattac aggtgttttt   2220
gacatcgtca agggtcaaat acaggttgct tcagataaca tcaaggattg tgtaaaatgc   2280
ttcattgatg ttgttaacaa ggcactcgaa atgtgcattg atcaagtcac tatcgctggc   2340
gcaaagttgc gatcactcaa cttaggtgaa gtcttcatcg ctcaaagcaa gggactttac   2400
cgtcagtgta tacgtggcaa ggagcagctg caactactca tgcctcttaa ggcaccaaaa   2460
gaagtaacct ttcttgaagg tgattcacat gacacagtac ttacctctga ggaggttgtt   2520
ctcaagaacg gtgaactcga agcactcgag acgcccgttg atagcttcac aaatggagct   2580
atcgtcggca caccagtctg tgtaaatggc ctcatgctct tagagattaa ggacaaagaa   2640
caatactgcg cattgtctcc tggtttactg gctacaaaca atgtctttcg cttaaaaggg   2700
ggtgcaccaa ttaaaggtgt aacctttgga gaagatactg tttgggaagt tcaaggttac   2760
```

-continued

```
aagaatgtga gaatcacatt tgagcttgat gaacgtgttg acaaagtgct taatgaaaag   2820
tgctctgtct acactgttga atccggtacc gaagttactg agtttgcatg tgttgtagca   2880
gaggctgttg tgaagacttt acaaccagtt tctgatctcc ttaccaacat gggtattgat   2940
cttgatgagt ggagtgtagc tacattctac ttatttgatg atgctggtga agaaaacttt   3000
tcatcacgta tgtattgttc cttttaccct ccagatgagg aagaagagga cgatgcagag   3060
tgtgaggaag aagaaattga tgaaacctgt gaacatgagt acggtacaga ggatgattat   3120
caaggtctcc ctctggaatt tggtgcctca gctgaaacag ttcgagttga ggaagaagaa   3180
gaggaagact ggctggatga tactactgag caatcagaga ttgagccaga accagaacct   3240
acacctgaag aaccagttaa tcagtttact ggttatttaa aacttactga caatgttgcc   3300
attaaatgtg ttgacatcgt taaggaggca caaagtgcta atcctatggt gattgtaaat   3360
gctgctaaca tacacctgaa acatggtggt ggtgtagcag gtgcactcaa caaggcaacc   3420
aatggtgcca tgcaaaagga gagtgatgat tacattaagc taaatggccc tcttacagta   3480
ggagggtctt gtttgctttc tggacataat cttgctaaga agtgtctgca tgttgttgga   3540
cctaacctaa atgcaggtga ggacatccag cttcttaagg cagcatatga aaatttcaat   3600
tcacaggaca tcttacttgc accattgttg tcagcaggca tatttggtgc taaaccactt   3660
cagtctttac aagtgtgcgt gcagacggtt cgtacacagg tttatattgc agtcaatgac   3720
aaagctcttt atgagcaggt tgtcatggat tatcttgata acctgaagcc tagagtggaa   3780
gcacctaaac aagaggagcc accaaacaca gaagattcca aaactgagga gaaatctgtc   3840
gtacagaagc ctgtcgatgt gaagccaaaa attaaggcct gcattgatga ggttaccaca   3900
acactggaag aaactaagtt tcttaccaat aagttactct tgtttgctga tatcaatggt   3960
aagctttacc atgattctca gaacatgctt agaggtgaag atatgtcttt ccttgagaag   4020
gatgcacctt acatggtagg tgatgttatc actagtggtg atatcacttg tgttgtaata   4080
ccctccaaaa aggctggtgg cactactgag atgctctcaa gagctttgaa gaaagtgcca   4140
gttgatgagt atataaccac gtaccctgga caaggatgtg ctggttatac acttgaggaa   4200
gctaagactg ctcttaagaa atgcaaatct gcattttatg tactaccttc agaagcacct   4260
aatgctaagg aagagattct aggaactgta tcctggaatt tgagagaaat gcttgctcat   4320
gctgaagaga caagaaaatt aatgcctata tgcatggatg ttagagccat aatggcaacc   4380
atccaacgta agtataaagg aattaaaatt caagagggca tcgttgacta tggtgtccga   4440
ttcttctttt atactagtaa agagcctgta gcttctatta ttacgaagct gaactctcta   4500
aatgagccgc ttgtcacaat gccaattggt tatgtgacac atggttttaa tcttgaagag   4560
gctgcgcgct gtatgcgttc tcttaaagct cctgccgtag tgtcagtatc atcaccagat   4620
gctgttacta catataatgg atacctcact tcgtcatcaa agacatctga ggagcacttt   4680
gtagaaacag tttctttggc tggctcttac agagattggt cctattcagg acagcgtaca   4740
gagttaggtg ttgaatttct taagcgtggt gacaaaattg tgtaccacac tctggagagc   4800
cccgtcgagt ttcatcttga cggtgaggtt ctttcacttg acaaactaaa gagtctctta   4860
tccctgcggg aggttaagac tataaaagtg ttcacaactg tggacaacac taatctccac   4920
acacagcttg tggatatgtc tatgacatat ggacagcagt ttggtccaac atacttggat   4980
ggtgctgatg ttacaaaaat taaacctcat gtaaatcatg agggtaagac tttctttgta   5040
ctacctagtg atgacacact acgtagtgaa gctttcgagt actaccatac tcttgatgag   5100
agttttcttg gtaggtacat gtctgcttta aaccacacaa agaaatggaa atttcctcaa   5160
```

-continued

```
gttggtggtt taacttcaat taaatgggct gataacaatt gttatttgtc tagtgtttta   5220
ttagcacttc aacagcttga agtcaaattc aatgcaccag cacttcaaga ggcttattat   5280
agagcccgtg ctggtgatgc tgctaacttt tgtgcactca tactcgctta cagtaataaa   5340
actgttggcg agcttggtga tgtcagagaa actatgaccc atcttctaca gcatgctaat   5400
ttggaatctg caaagcgagt tcttaatgtg gtgtgtaaac attgtggtca gaaaactact   5460
accttaacgg gtgtagaagc tgtgatgtat atgggtactc tatcttatga taatcttaag   5520
acaggtgttt ccattccatg tgtgtgtggt cgtgatgcta cacaatatct agtacaacaa   5580
gagtcttctt ttgttatgat gtctgcacca cctgctgagt ataaattaca gcaaggtaca   5640
ttcttatgtg cgaatgagta cactggtaac tatcagtgtg gtcattacac tcatataact   5700
gctaaggaga ccctctatcg tattgacgga gctcacctta caaagatgtc agagtacaaa   5760
ggaccagtga ctgatgtttt ctacaaggaa acatcttaca ctacaaccat caagcctgtg   5820
tcgtataaac tcgatggagt tacttacaca gagattgaac caaaattgga tgggtattat   5880
aaaaaggata atgcttacta tacagagcag cctatagacc ttgtaccaac tcaaccatta   5940
ccaaatgcga gttttgataa tttcaaactc acatgttcta acacaaaatt tgctgatgat   6000
ttaaatcaaa tgacaggctt cacaaagcca gcttcacgag agctatctgt cacattcttc   6060
ccagacttga atggcgatgt agtggctatt gactatagac actattcagc gagtttcaag   6120
aaaggtgcta aattactgca taagccaatt gtttggcaca ttaaccaggc tacaaccaag   6180
acaacgttca aaccaaacac ttggtgttta cgttgtcttt ggagtacaaa gccagtagat   6240
acttcaaatt catttgaagt tctggcagta gaagacacac aaggaatgga caatcttgct   6300
tgtgaaagtc aacaacccac ctctgaagaa gtagtggaaa atcctaccat acagaaggaa   6360
gtcatagagt gtgacgtgaa aactaccgaa gttgtaggca atgtcatact taaaccatca   6420
gatgaaggtg ttaaagtaac acaagagtta ggtcatgagg atcttatggc tgcttatgtg   6480
gaaaacacaa gcattaccat taagaaacct aatgagcttt cactagcctt aggtttaaaa   6540
acaattgcca ctcatggtat tgctgcaatt aatagtgttc cttggagtaa aattttggct   6600
tatgtcaaac cattcttagg acaagcagca attacaacat caaattgcgc taagagatta   6660
gcacaacgtg tgtttaacaa ttatatgcct tatgtgttta cattattgtt ccaattgtgt   6720
acttttacta aaagtaccaa ttctagaatt agagcttcac tacctacaac tattgctaaa   6780
aatagtgtta agagtgttgc taaattatgt ttggatgccg gcattaatta tgtgaagtca   6840
cccaaatttt ctaaattgtt cacaatcgct atgtggctat tgttgttaag tatttgctta   6900
ggttctctaa tctgtgtaac tgctgctttt ggtgtactct tatctaattt tggtgctcct   6960
tcttattgta atggcgttag agaattgtat cttaattcgt ctaacgttac tactatggat   7020
ttctgtgaag gttcttttcc ttgcagcatt tgtttaagtg gattagactc ccttgattct   7080
tatccagctc ttgaaaccat tcaggtgacg atttcatcgt acaagctaga cttgacaatt   7140
ttaggtctgg ccgctgagtg ggttttggca tatatgttgt tcacaaaatt cttttattta   7200
ttaggtcttt cagctataat gcaggtgttc tttggctatt ttgctagtca tttcatcagc   7260
aattcttggc tcatgtggtt tatcattagt attgtacaaa tggcacccgt ttctgcaatg   7320
gttaggatgt acatcttctt tgcttctttc tactacatat ggaagagcta tgttcatatc   7380
atggatggtt gcacctcttc gacttgcatg atgtgctata agcgcaatcg tgccacacgc   7440
gttgagtgta caactattgt taatggcatg aagagatctt tctatgtcta tgcaaatgga   7500
```

-continued

```
ggccgtggct tctgcaagac tcacaattgg aattgtctca attgtgacac attttgcact   7560
ggtagtacat tcattagtga tgaagttgct cgtgatttgt cactccagtt taaaagacca   7620
atcaacccta ctgaccagtc atcgtatatt gttgatagtg ttgctgtgaa aaatggcgcg   7680
cttcacctct actttgacaa ggctggtcaa aagacctatg agagacatcc gctctcccat   7740
tttgtcaatt tagacaattt gagagctaac aacactaaag gttcactgcc tattaatgtc   7800
atagtttttg atggcaagtc caaatgcgac gagtctgctt ctaagtctgc ttctgtgtac   7860
tacagtcagc tgatgtgcca acctattctg ttgcttgacc aagctcttgt atcagacgtt   7920
ggagatagta ctgaagtttc cgttaagatg tttgatgctt atgtcgacac cttttcagca   7980
acttttagtg ttcctatgga aaaacttaag gcacttgttg ctacagctca cagcgagtta   8040
gcaaagggtg tagctttaga tggtgtcctt tctacattcg tgtcagctgc ccgacaaggt   8100
gttgttgata ccgatgttga cacaaaggat gttattgaat gtctcaaact ttcacatcac   8160
tctgacttag aagtgacagg tgacagttgt aacaatttca tgctcaccta taataaggtt   8220
gaaaacatga cgcccagaga tcttggcgca tgtattgact gtaatgcaag gcatatcaat   8280
gcccaagtag caaaaagtca caatgtttca ctcatctgga atgtaaaaga ctacatgtct   8340
ttatctgaac agctgcgtaa acaaattcgt agtgctgcca agaagaacaa catacctttt   8400
agactaactt gtgctacaac tagacaggtt gtcaatgtca taactactaa aatctcactc   8460
aagggtggta agattgttag tacttgtttt aaacttatgc ttaaggccac attattgtgc   8520
gttcttgctg cattggtttg ttatatcgtt atgccagtac atacattgtc aatccatgat   8580
ggttacacaa atgaaatcat tggttacaaa gccattcagg atggtgtcac tcgtgacatc   8640
atttctactg atgattgttt tgcaaataaa catgctggtt ttgacgcatg gtttagccag   8700
cgtggtggtt catacaaaaa tgacaaaagc tgccctgtag tagctgctat cattacaaga   8760
gagattggtt tcatagtgcc tggcttaccg ggtactgtgc tgagagcaat caatggtgac   8820
ttcttgcatt ttctacctcg tgtttttagt gctgttggca acatttgcta cacaccttcc   8880
aaactcattg agtatagtga ttttgctacc tctgcttgcg ttcttgctgc tgagtgtaca   8940
atttttaagg atgctatggg caaacctgtg ccatattgtt atgacactaa tttgctagag   9000
ggttctattt cttatagtga gcttcgtcca gacactcgtt atgtgcttat ggatggttcc   9060
atcatacagt ttcctaacac ttacctggag ggttctgtta gagtagtaac aacttttgat   9120
gctgagtact gtagacatgg tacatgcgaa aggtcagaag taggtatttg cctatctacc   9180
agtggtagat gggttcttaa taatgagcat tacagagctc tatcaggagt tttctgtggt   9240
gttgatgcga tgaatctcat agctaacatc tttactcctc ttgtgcaacc tgtgggtgct   9300
ttagatgtgt ctgcttcagt agtggctggt ggtattattg ccatattggt gacttgtgct   9360
gcctactact ttatgaaatt cagacgtgtt tttggtgagt acaaccatgt tgttgctgct   9420
aatgcacttt tgtttttgat gtctttcact atactctgtc tggtaccagc ttacagcttt   9480
ctgccgggag tctactcagt cttttacttg tacttgacat tctatttcac caatgatgtt   9540
tcattcttgg ctcaccttca atggtttgcc atgttttctc ctattgtgcc tttttggata   9600
acagcaatct atgtattctg tatttctctg aagcactgcc attggttctt taacaactat   9660
cttaggaaaa gagtcatgtt taatggagtt acatttagta ccttcgagga ggctgctttg   9720
tgtacctttt tgctcaacaa ggaaatgtac ctaaaattgc gtagcgagac actgttgcca   9780
cttacacagt ataacaggta tcttgctcta tataacaagt acaagtattt cagtggagcc   9840
ttagatacta ccagctatcg tgaagcagct tgctgccact tagcaaaggc tctaaatgac   9900
```

-continued

```
tttagcaact caggtgctga tgttctctac caaccaccac agacatcaat cacttctgct   9960
gttctgcaga gtggttttag gaaaatggca ttcccgtcag gcaaagttga agggtgcatg  10020
gtacaagtaa cctgtggaac tacaactctt aatggattgt ggttggatga cacagtatac  10080
tgtccaagac atgtcatttg cacagcagaa gacatgctta atcctaacta tgaagatctg  10140
ctcattcgca aatccaacca tagctttctt gttcaggctg gcaatgttca acttcgtgtt  10200
attggccatt ctatgcaaaa ttgtctgctt aggcttaaag ttgatacttc taaccctaag  10260
acacccaagt ataaatttgt ccgtatccaa cctggtcaaa cattttcagt tctagcatgc  10320
tacaatggtt caccatctgg tgtttatcag tgtgccatga gacctaatca taccattaaa  10380
ggttctttcc ttaatggatc atgtggtagt gttggtttta acattgatta tgattgcgtg  10440
tctttctgct atatgcatca tatggagctt ccaacaggag tacacgctgg tactgactta  10500
gaaggtaaat tctatggtcc atttgttgac agacaaactg cacaggctgc aggtacagac  10560
acaaccataa cattaaatgt tttggcatgg ctgtatgctg ctgttatcaa tggtgatagg  10620
tggtttctta atagattcac cactactttg aatgacttta accttgtggc aatgaagtac  10680
aactatgaac ctttgacaca agatcatgtt gacatattgg gacctctttc tgctcaaaca  10740
ggaattgccg tcttagatat gtgtgctgct ttgaaagagc tgctgcagaa tggtatgaat  10800
ggtcgtacta tccttggtag cactatttta gaagatgagt ttacaccatt tgatgttgtt  10860
agacaatgct ctggtgttac cttccaaggt aagttcaaga aaattgttaa gggcactcat  10920
cattggatgc ttttaacttt cttgacatca ctattgattc ttgttcaaag tacacagtgg  10980
tcactgtttt tctttgttta cgagaatgct ttcttgccat ttactcttgg tattatggca  11040
attgctgcat gtgctatgct gcttgttaag cataagcacg cattcttgtg cttgtttctg  11100
ttaccttctc ttgcaacagt tgcttacttt aatatggtct acatgcctgc tagctgggtg  11160
atgcgtatca tgacatggct tgaattggct gacactagct tgtctggtta taggcttaag  11220
gattgtgtta tgtatgcttc agctttagtt ttgcttattc tcatgacagc tcgcactgtt  11280
tatgatgatg ctgctagacg tgtttggaca ctgatgaatg tcattacact tgtttacaaa  11340
gtctactatg gtaatgcttt agatcaagct atttccatgt gggccttagt tatttctgta  11400
acctctaact attctggtgt cgttacgact atcatgtttt tagctagagc tatagtgttt  11460
gtgtgtgttg agtattaccc attgttattt attactggca acaccttaca gtgtatcatg  11520
cttgtttatt gtttcttagg ctattgttgc tgctgctact ttggcctttt ctgtttactc  11580
aaccgttact tcaggcttac tcttggtgtt tatgactact tggtctctac acaagaattt  11640
aggtatatga actcccaggg gcttttgcct cctaagagta gtattgatgc tttcaagctt  11700
aacattaagt tgttgggtat tggaggtaaa ccatgtatca aggttgctac tgtacagtct  11760
aaaatgtctg acgtaaagtg cacatctgtg gtactgctct cggttcttca acaacttaga  11820
gtagagtcat cttctaaatt gtgggcacaa tgtgtacaac tccacaatga tattcttctt  11880
gcaaaagaca caactgaagc tttcgagaag atggtttctc ttttgtctgt tttgctatcc  11940
atgcagggtg ctgtagacat taataggttg tgcgaggaaa tgctcgataa ccgtgctact  12000
cttcaggcta ttgcttcaga atttagttct ttaccatcat atgccgctta tgccactgcc  12060
caggaggcct atgagcaggc tgtagctaat ggtgattctg aagtcgttct caaaaagtta  12120
aagaaatctt tgaatgtggc taaatctgag tttgaccgtg atgctgccat gcaacgcaag  12180
ttggaaaaga tggcagatca ggctatgacc caaatgtaca aacaggcaag atctgaggac  12240
```

-continued

```
aagagggcaa aagtaactag tgctatgcaa acaatgctct tcactatgct taggaagctt  12300
gataatgatg cacttaacaa cattatcaac aatgcgcgtg atggttgtgt tccactcaac  12360
atcataccat tgactacagc agccaaactc atggttgttg tccctgatta tggtacctac  12420
aagaacactt gtgatggtaa cacctttaca tatgcatctg cactctggga aatccagcaa  12480
gttgttgatg cggatagcaa gattgttcaa cttagtgaaa ttaacatgga caattcacca  12540
aatttggctt ggcctcttat tgttacagct ctaagagcca actcagctgt taaactacag  12600
aataatgaac tgagtccagt agcactacga cagatgtcct gtgcggctgg taccacacaa  12660
acagcttgta ctgatgacaa tgcacttgcc tactataaca attcgaaggg aggtaggttt  12720
gtgctggcat tactatcaga ccaccaagat ctcaaatggg ctagattccc taagagtgat  12780
ggtacaggta caatttacac agaactggaa ccaccttgta ggtttgttac agacacacca  12840
aaagggccta aagtgaaata cttgtacttc atcaaaggct taaacaacct aaatagaggt  12900
atggtgctgg gcagtttagc tgctacagta cgtcttcagg ctggaaatgc tacagaagta  12960
cctgccaatt caactgtgct ttccttctgt gcttttgcag tagaccctgc taaagcatat  13020
aaggattacc tagcaagtgg aggacaacca atcaccaact gtgtgaagat gttgtgtaca  13080
cacactggta caggacaggc aattactgta acaccagaag ctaacatgga ccaagagtcc  13140
tttggtggtg cttcatgttg tctgtattgt agatgccaca ttgaccatcc aaatcctaaa  13200
ggattctgtg acttgaaagg taagtacgtc caaataccta ccacttgtgc taatgaccca  13260
gtgggtttta cacttagaaa cacagtctgt accgtctgcg gaatgtggaa aggttatggc  13320
tgtagttgtg accaactccg cgaacccttg atgcagtctg cggatgcatc aacgttttta  13380
aacgggtttg cggtgtaagt gcagcccgtc ttacaccgtg cggcacaggc actagtactg  13440
atgtcgtcta cagggctttt gatatttaca acgaaaaagt tgctggtttt gcaaagttcc  13500
taaaaactaa ttgctgtcgc ttccaggaga aggatgagga aggcaattta ttagactctt  13560
actttgtagt taagaggcat actatgtcta actaccaaca tgaagagact atttataact  13620
tggttaaaga ttgtccagcg gttgctgtcc atgacttttt caagtttaga gtagatggtg  13680
acatggtacc acatatatca cgtcagcgtc taactaaata cacaatggct gatttagtct  13740
atgctctacg tcattttgat gagggtaatt gtgatacatt aaaagaaata ctcgtcacat  13800
acaattgctg tgatgatgat tatttcaata agaaggattg gtatgacttc gtagagaatc  13860
ctgacatctt acgcgtatat gctaacttag gtgagcgtgt acgccaatca ttattaaaga  13920
ctgtacaatt ctgcgatgct atgcgtgatg caggcattgt aggcgtactg acattagata  13980
atcaggatct taatgggaac tggtacgatt tcggtgattt cgtacaagta gcaccaggct  14040
gcggagttcc tattgtggat tcatattact cattgctgat gcccatcctc actttgacta  14100
gggcattggc tgctgagtcc catatggatg ctgatctcgc aaaaccactt attaagtggg  14160
atttgctgaa atatgatttt acggaagaga gactttgtct cttcgaccgt tattttaaat  14220
attgggacca gacataccat cccaattgta ttaactgttt ggatgatagg tgtatccttc  14280
attgtgcaaa ctttaatgtg ttattttcta ctgtgtttcc acctacaagt tttggaccac  14340
tagtaagaaa aatatttgta gatggtgttc cttttgttgt ttcaactgga taccattttc  14400
gtgagttagg agtcgtacat aatcaggatg taaacttaca tagctcgcgt ctcagtttca  14460
aggaactttt agtgtatgct gctgatccag ctatgcatgc agcttctggc aatttattgc  14520
tagataaacg cactacatgc ttttcagtag ctgcactaac aaacaatgtt gcttttcaaa  14580
ctgtcaaacc cggtaatttt aataaagact tttatgactt tgctgtgtct aaaggtttct  14640
```

-continued

ttaaggaagg aagttctgtt gaactaaaac acttcttctt tgctcaggat ggcaacgctg 14700
ctatcagtga ttatgactat tatcgttata atctgccaac aatgtgtgat atcagacaac 14760
tcctattcgt agttgaagtt gttgataaat actttgattg ttacgatggt ggctgtatta 14820
atgccaacca agtaatcgtt aacaatctgg ataaatcagc tggtttccca tttaataaat 14880
ggggtaaggc tagactttat tatgactcaa tgagttatga ggatcaagat gcacttttcg 14940
cgtatactaa gcgtaatgtc atccctacta taactcaaat gaatcttaag tatgccatta 15000
gtgcaaagaa tagagctcgc accgtagctg gtgtctctat ctgtagtact atgacaaata 15060
gacagtttca tcagaaatta ttgaagtcaa tagccgccac tagaggagct actgtggtaa 15120
ttggaacaag caagttttac ggtggctggc ataatatgtt aaaaactgtt tacagtgatg 15180
tagaaactcc acaccttatg ggttgggatt atccaaaatg tgacagagcc atgcctaaca 15240
tgcttaggat aatggcctct cttgttcttg ctcgcaaaca taacacttgc tgtaacttat 15300
cacaccgttt ctacaggtta gctaacgagt gtgcgcaagt attaagtgag atggtcatgt 15360
gtggcggctc actatatgtt aaaccaggtg gaacatcatc cggtgatgct acaactgctt 15420
atgctaatag tgtctttaac atttgtcaag ctgttacagc caatgtaaat gcacttcttt 15480
caactgatgg taataagata gctgacaagt atgtccgcaa tctacaacac aggctctatg 15540
agtgtctcta tagaaatagg gatgttgatc atgaattcgt ggatgagttt tacgcttacc 15600
tgcgtaaaca tttctccatg atgattcttt ctgatgatgc cgttgtgtgc tataacagta 15660
actatgcggc tcaaggttta gtagctagca ttaagaactt taaggcagtt ctttattatc 15720
aaaataatgt gttcatgtct gaggcaaaat gttggactga gactgacctt actaaaggac 15780
ctcacgaatt ttgctcacag catacaatgc tagttaaaca aggagatgat tacgtgtacc 15840
tgccttaccc agatccatca agaatattag gcgcaggctg ttttgtcgat gatattgtca 15900
aaacagatgg tacacttatg attgaaaggt tcgtgtcact ggctattgat gcttacccac 15960
ttacaaaaca tcctaatcag gagtatgctg atgtctttca cttgtattta caatacatta 16020
gaaagttaca tgatgagctt actggccaca tgttggacat gtattccgta atgctaacta 16080
atgataacac ctcacggtac tgggaacctg agttttatga ggctatgtac acaccacata 16140
cagtcttgca ggctgtaggt gcttgtgtat tgtgcaattc acagacttca cttcgttgcg 16200
gtgcctgtat taggagacca ttcctatgtt gcaagtgctg ctatgaccat gtcatttcaa 16260
catcacacaa attagtgttg tctgttaatc cctatgtttg caatgcccca ggttgtgatg 16320
tcactgatgt gacacaactg tatctaggag gtatgagcta ttattgcaag tcacataagc 16380
ctcccattag ttttccatta tgtgctaatg gtcaggtttt tggtttatac aaaaacacat 16440
gtgtaggcag tgacaatgtc actgacttca atgcgatagc aacatgtgat tggactaatg 16500
ctggcgatta catacttgcc aacacttgta ctgagagact caagcttttc gcagcagaaa 16560
cgctcaaagc cactgaggaa acatttaagc tgtcatatgg tattgccact gtacgcgaag 16620
tactctctga cagagaattg catctttcat gggaggttgg aaaacctaga ccaccattga 16680
acagaaacta tgtctttact ggttaccgtg taactaaaaa tagtaaagta cagattggag 16740
agtacacctt tgaaaaaggt gactatggtg atgctgttgt gtacagaggt actacgacat 16800
acaagttgaa tgttggtgat tactttgtgt tgacatctca cactgtaatg ccacttagtg 16860
cacctactct agtgccacaa gagcactatg tgagaattac tggcttgtac ccaacactca 16920
acatctcaga tgagttttct agcaatgttg caaattatca aaaggtcggc atgcaaaagt 16980

-continued

```
actctacact ccaaggacca cctggtactg gtaagagtca ttttgccatc ggacttgctc  17040
tctattaccc atctgctcgc atagtgtata cggcatgctc tcatgcagct gttgatgccc  17100
tatgtgaaaa ggcattaaaa tatttgccca tagataaatg tagtagaatc atacctgcgc  17160
gtgcgcgcgt agagtgtttt gataaattca aagtgaattc aacactagaa cagtatgttt  17220
tctgcactgt aaatgcattg ccagaaacaa ctgctgacat tgtagtcttt gatgaaatct  17280
ctatggctac taattatgac ttgagtgttg tcaatgctag acttcgtgca aaacactacg  17340
tctatattgg cgatcctgct caattaccag ccccccgcac attgctgact aaaggcacac  17400
tagaaccaga atattttaat tcagtgtgca gacttatgaa aacaataggt ccagacatgt  17460
tccttggaac ttgtcgccgt tgtcctgctg aaattgttga cactgtgagt gctttagttt  17520
atgacaataa gctaaaagca cacaaggata agtcagctca atgcttcaaa atgttctaca  17580
aaggtgttat tacacatgat gtttcatctg caatcaacag acctcaaata ggcgttgtaa  17640
gagaatttct tacacgcaat cctgcttgga gaaaagctgt ttttatctca ccttataatt  17700
cacagaacgc tgtagcttca aaaatcttag gattgcctac gcagactgtt gattcatcac  17760
agggttctga atatgactat gtcatattca cacaaactac tgaaacagca cactcttgta  17820
atgtcaaccg cttcaatgtg gctatcacaa gggcaaaaat tggcattttg tgcataatgt  17880
ctgatagaga tctttatgac aaactgcaat ttacaagtct agaaatacca cgtcgcaatg  17940
tggctacatt acaagcagaa aatgtaactg gacttttaa ggactgtagt aagatcatta  18000
ctggtcttca tcctacacag gcacctacac acctcagcgt tgatataaag ttcaagactg  18060
aaggattatg tgttgacata ccaggcatac caaaggacat gacctaccgt agactcatct  18120
ctatgatggg tttcaaaatg aattaccaag tcaatggtta ccctaatatg tttatcaccc  18180
gcgaagaagc tattcgtcac gttcgtgcgt ggattggctt tgatgtagag ggctgtcatg  18240
caactagaga tgctgtgggt actaacctac ctctccagct aggattttct acaggtgtta  18300
acttagtagc tgtaccgact ggttatgttg acactgaaaa taacacagaa ttcaccagag  18360
ttaatgcaaa acctccacca ggtgaccagt ttaaacatct tataccactc atgtataaag  18420
gcttgccctg gaatgtagtg cgtattaaga tagtacaaat gctcagtgat acactgaaag  18480
gattgtcaga cagagtcgtg ttcgtccttt gggcgcatgg ctttgagctt acatcaatga  18540
agtactttgt caagattgga cctgaaagaa cgtgttgtct gtgtgacaaa cgtgcaactt  18600
gcttttctac ttcatcagat acttatgcct gctggaatca ttctgtgggt tttgactatg  18660
tctataaccc atttatgatt gatgttcagc agtggggctt tacgggtaac cttcagagta  18720
accatgacca acattgccag gtacatggaa atgcacatgt ggctagttgt gatgctatca  18780
tgactagatg tttagcagtc catgagtgct ttgttaagcg cgttgattgg tctgttgaat  18840
accctattat aggagatgaa ctgagggtta attctgcttg cagaaaagta caacacatgg  18900
ttgtgaagtc tgcattgctt gctgataagt ttccagttct tcatgacatt ggaaatccaa  18960
aggctatcaa gtgtgtgcct caggctgaag tagaatggaa gttctacgat gctcagccat  19020
gtagtgacaa agcttacaaa atagaggaac tcttctattc ttatgctaca catcacgata  19080
aattcactga tggtgtttgt ttgttttgga attgtaacgt tgatcgttac ccagccaatg  19140
caattgtgtg taggtttgac acaagagtct tgtcaaactt gaacttacca ggctgtgatg  19200
gtggtagttt gtatgtgaat aagcatgcat tccacactcc agctttcgat aaaagtgcat  19260
ttactaattt aaagcaattg cctttctttt actattctga tagtccttgt gagtctcatg  19320
gcaaacaagt agtgtcggat attgattatg ttccactcaa atctgctacg tgtattacac  19380
```

-continued

```
gatgcaattt aggtggtgct gtttgcagac accatgcaaa tgagtaccga cagtacttgg  19440
atgcatataa tatgatgatt tctgctggat ttagcctatg gatttacaaa caatttgata  19500
cttataacct gtggaataca tttaccaggt tacagagttt agaaaatgtg gcttataatg  19560
ttgttaataa aggacacttt gatggacacg ccggcgaagc acctgtttcc atcattaata  19620
atgctgttta cacaaaggta gatggtattg atgtggagat ctttgaaaat aagacaacac  19680
ttcctgttaa tgttgcattt gagctttggg ctaagcgtaa cattaaacca gtgccagaga  19740
ttaagatact caataatttg ggtgttgata tcgctgctaa tactgtaatc tgggactaca  19800
aaagagaagc cccagcacat gtatctacaa taggtgtctg cacaatgact gacattgcca  19860
agaaacctac tgagagtgct tgttcttcac ttactgtctt gtttgatggt agagtggaag  19920
gacaggtaga cctttttaga aacgcccgta atggtgtttt aataacagaa ggttcagtca  19980
aaggtctaac accttcaaag ggaccagcac aagctagcgt caatggagtc acattaattg  20040
gagaatcagt aaaaacacag tttaactact ttaagaaagt agacggcatt attcaacagt  20100
tgcctgaaac ctactttact cagagcagag acttagagga ttttaagccc agatcacaaa  20160
tggaaactga ctttctcgag ctcgctatgg atgaattcat acagcgatat aagctcgagg  20220
gctatgcctt cgaacacatc gtttatggag atttcagtca tggacaactt ggcggtcttc  20280
atttaatgat aggcttagcc aagcgctcac aagattcacc acttaaatta gaggatttta  20340
tccctatgga cagcacagtg aaaaattact tcataacaga tgcgcaaaca ggttcatcaa  20400
aatgtgtgtg ttctgtgatt gatcttttac ttgatgactt tgtcgagata ataaagtcac  20460
aagatttgtc agtgatttca aaagtggtca aggttacaat tgactatgct gaaatttcat  20520
tcatgctttg gtgtaaggat ggacatgttg aaaccttcta cccaaaacta caagcaagtc  20580
gagcgtggca accaggtgtt gcgatgccta acttgtacaa gatgcaaaga atgcttcttg  20640
aaaagtgtga ccttcagaat tatggtgaaa atgctgttat accaaaagga ataatgatga  20700
atgtcgcaaa gtatactcaa ctgtgtcaat acttaaatac acttacttta gctgtaccct  20760
acaacatgag agttattcac tttggtgctg gctctgataa aggagttgca ccaggtacag  20820
ctgtgctcag acaatggttg ccaactggca cactacttgt cgattcagat cttaatgact  20880
tcgtctccga cgcatattct actttaattg gagactgtgc aacagtacat acggctaata  20940
aatgggacct tattattagc gatatgtatg accctaggac caaacatgtg acaaaagaga  21000
atgactctaa agaagggttt ttcacttatc tgtgtggatt tataaagcaa aaactagccc  21060
tgggtggttc tatagctgta aagataacag agcattcttg gaatgctgac ctttacaagc  21120
ttatgggcca tttctcatgg tggacagctt ttgttacaaa tgtaaatgca tcatcatcgg  21180
aagcattttt aattggggct aactatcttg gcaagccgaa ggaacaaatt gatggctata  21240
ccatgcatgc taactacatt ttctggagga acacaaatcc tatccagttg tcttcctatt  21300
cactctttga catgagcaaa tttcctctta aattaagagg aactgctgta atgtctctta  21360
aggagaatca aatcaatgat atgatttatt ctcttctgga aaaaggtagg cttatcatta  21420
gagaaaacaa cagagttgtg gtttcaagtg atattcttgt taacaactaa acgaacatgt  21480
ttattttctt attatttctt actctcacta gtggtagtga ccttgaccgg tgcaccactt  21540
ttgatgatgt tcaagctcct aattacactc aacatacttc atctatgagg ggggtttact  21600
atcctgatga aatttttaga tcagacactc tttatttaac tcaggattta tttcttccat  21660
tttattctaa tgttacaggg tttcatacta ttaatcatac gtttggcaac cctgtcatac  21720
```

-continued

```
cttttaagga tggtatttat tttgctgcca cagagaaatc aaatgttgtc cgtggttggg  21780
tttttggttc taccatgaac aacaagtcac agtcggtgat tattattaac aattctacta  21840
atgttgttat acgagcatgt aactttgaat tgtgtgacaa ccctttcttt gctgtttcta  21900
aacccatggg tacacagaca catactatga tattcgataa tgcatttaat tgcactttcg  21960
agtacatatc tgatgccttt tcgcttgatg tttcagaaaa gtcaggtaat tttaaacact  22020
tacgagagtt tgtgtttaaa aataaagatg ggtttctcta tgtttataag ggctatcaac  22080
ctatagatgt agttcgtgat ctaccttctg gttttaacac tttgaaacct atttttaagt  22140
tgcctcttgg tattaacatt acaaatttta gagccattct tacagccttt tcacctgctc  22200
aagacatttg gggcacgtca gctgcagcct attttgttgg ctatttaaag ccaactacat  22260
ttatgctcaa gtatgatgaa aatggtacaa tcacagatgc tgttgattgt tctcaaaatc  22320
cacttgctga actcaaatgc tctgttaaga gctttgagat tgacaaagga atttaccaga  22380
cctctaattt cagggttgtt ccctcaggag atgttgtgag attccctaat attacaaact  22440
tgtgtccttt tggagaggtt tttaatgcta ctaaattccc ttctgtctat gcatgggaga  22500
gaaaaaaaat ttctaattgt gttgctgatt actctgtgct ctacaactca acatttttt  22560
caacctttaa gtgctatggc gtttctgcca ctaagttgaa tgatctttgc ttctccaatg  22620
tctatgcaga ttcttttgta gtcaagggag atgatgtaag acaaatagcg ccaggacaaa  22680
ctggtgttat tgctgattat aattataaat tgccagatga tttcatgggt tgtgtccttg  22740
cttggaatac taggaacatt gatgctactt caactggtaa ttataattat aaatataggt  22800
atcttagaca tggcaagctt aggccctttg agagagacat atctaatgtg cctttctccc  22860
ctgatggcaa accttgcacc ccacctgctc ttaattgtta ttggccatta aatgattatg  22920
gtttttacac cactactggc attggctacc aaccttacag agttgtagta ctttcttttg  22980
aacttttaaa tgcaccggcc acggtttgtg gaccaaaatt atccactgac cttattaaga  23040
accagtgtgt caattttaat tttaatggac tcactggtac tggtgtgtta actccttctt  23100
caaagagatt tcaaccattt caacaatttg gccgtgatgt ttctgatttc actgattccg  23160
ttcgagatcc taaaacatct gaaatattag acatttcacc ttgcgctttt gggggtgtaa  23220
gtgtaattac acctggaaca aatgcttcat ctgaagttgc tgttctatat caagatgtta  23280
actgcactga tgtttctaca gcaattcatg cagatcaact cacaccagct tggcgcatat  23340
attctactgg aaacaatgta ttccagactc aagcaggctg tcttatagga gctgagcatg  23400
tcgacacttc ttatgagtgc gacattccta ttggagctgg catttgtgct agttaccata  23460
cagtttcttt attacgtagt actagccaaa aatctattgt ggcttatact atgtctttag  23520
gtgctgatag ttcaattgct tactctaata acaccattgc tatacctact aacttttcaa  23580
ttagcattac tacagaagta atgcctgttt ctatggctaa aacctccgta gattgtaata  23640
tgtacatctg cggagattct actgaatgtg ctaatttgct tctccaatat ggtagctttt  23700
gcacacaact aaatcgtgca ctctcaggta ttgctgctga acaggatcgc aacacacgtg  23760
aagtgttcgc tcaagtcaaa caaatgtaca aaaccccaac tttgaaatat tttggtggtt  23820
ttaatttttc acaaatatta cctgaccctc taaagccaac taagaggtct tttattgagg  23880
acttgctctt taataaggtg acactcgctg atgctggctt catgaagcaa tatggcgaat  23940
gcctaggtga tattaatgct agagatctca tttgtgcgca gaagttcaat ggacttacag  24000
tgttgccacc tctgctcact gatgatatga ttgctgccta cactgctgct ctagttagtg  24060
gtactgccac tgctggatgg acatttggtg ctggcgctgc tcttcaaata ccttttgcta  24120
```

-continued

```
tgcaaatggc atataggttc aatggcattg gagttaccca aaatgttctc tatgagaacc  24180
aaaaacaaat cgccaaccaa tttaacaagg cgattagtca aattcaagaa tcacttacaa  24240
caacatcaac tgcattgggc aagctgcaag acgttgttaa ccagaatgct caagcattaa  24300
acacacttgt taaacaactt agctctaatt ttggtgcaat ttcaagtgtg ctaaatgata  24360
tcctttcgcg acttgataaa gtcgaggcgg aggtacaaat tgacaggtta attacaggca  24420
gacttcaaag ccttcaaacc tatgtaacac aacaactaat cagggctgct gaaatcaggg  24480
cttctgctaa tcttgctgct actaaaatgt ctgagtgtgt tcttggacaa tcaaaaagag  24540
ttgacttttg tggaaagggc taccacctta tgtccttccc acaagcagcc ccgcatggtg  24600
ttgtcttcct acatgtcacg tatgtgccat cccaggagag gaacttcacc acagcgccag  24660
caatttgtca tgaaggcaaa gcatacttcc ctcgtgaagg tgtttttgtg tttaatggca  24720
cttcttggtt tattacacag aggaacttct tttctccaca aataattact acagacaata  24780
catttgtctc aggaaattgt gatgtcgtta ttggcatcat taacaacaca gtttatgatc  24840
ctctgcaacc tgagcttgac tcattcaaag aagagctgga caagtacttc aaaaatcata  24900
catcaccaga tgttgatctt ggcgacattt caggcattaa cgcttctgtc gtcaacattc  24960
aaaaagaaat tgaccgcctc aatgaggtcg ctaaaaattt aaatgaatca ctcattgacc  25020
ttcaagaatt gggaaaatat gagcaatata ttaaatggcc ttggtatgtt tggctcggct  25080
tcattgctgg actaattgcc atcgtcatgg ttacaatctt gctttgttgc atgactagtt  25140
gttgcagttg cctcaagggt gcatgctctt gtggttcttg ctgcaagttt gatgaggatg  25200
actctgagcc agttctcaag ggtgtcaaat tacattacac ataaacgaac ttatggattt  25260
gtttatgaga tttttactc ttggatcaat tactgcacag ccagtaaaaa ttgacaatgc  25320
ttctcctgca agtactgttc atgctacagc aacgataccg ctacaagcct cactcccttt  25380
cggatggctt gttattggcg ttgcatttct tgctgttttt cagagcgcta ccaaaataat  25440
tgcgctcaat aaaagatggc agctagccct ttataagggc ttccagttca tttgcaattt  25500
actgctgcta tttgttacca tctattcaca tcttttgctt gtcgctgcag gtatggaggc  25560
gcaatttttg tacctctatg ccttgatata ttttctacaa tgcatcaacg catgtagaat  25620
tattatgaga tgttggcttt gttggaagtg caaatccaag aacccattac tttatgatgc  25680
caactacttt gtttgctggc acacacataa ctatgactac tgtataccat ataacagtgt  25740
cacagataca attgtcgtta ctgaaggtga cggcatttca acaccaaaac tcaaagaaga  25800
ctaccaaatt ggtggttatt ctgaggatag gcactcaggt gttaaagact atgtcgttgt  25860
acatggctat ttcaccgaag tttactacca gcttgagtct acacaaatta ctacagacac  25920
tggtattgaa aatgctacat tcttcatctt taacaagctt gttaaagacc caccgaatgt  25980
gcaaatacac acaatcgacg gctcttcagg agttgctaat ccagcaatgg atccaattta  26040
tgatgagccg acgacgacta ctagcgtgcc tttgtaagca caagaaagtg agtacgaact  26100
tatgtactca ttcgtttcgg aagaaacagg tacgttaata gttaatagcg tacttctttt  26160
tcttgctttc gtggtattct tgctagtcac actagccatc cttactgcgc ttcgattgtg  26220
tgcgtactgc tgcaatattg ttaacgtgag tttagtaaaa ccaacggttt acgtctactc  26280
gcgtgttaaa aatctgaact cttctgaagg agttcctgat cttctggtct aaacgaacta  26340
actattatta ttattctgtt tggaacttta acattgctta tcatggcaga caacggtact  26400
attaccgttg aggagcttaa acaactcctg gaacaatgga acctagtaat aggtttccta  26460
```

-continued

```
ttcctagcct ggattatgtt actacaattt gcctattcta atcggaacag gtttttgtac  26520
ataataaagc ttgttttcct ctggctcttg tggccagtaa cacttgcttg ttttgtgctt  26580
gctgctgtct acagaattaa ttgggtgact ggcgggattg cgattgcaat ggcttgtatt  26640
gtaggcttga tgtggcttag ctacttcgtt gcttccttca ggctgtttgc tcgtacccgc  26700
tcaatgtggt cattcaaccc agaaacaaac attcttctca atgtgcctct ccgggggaca  26760
attgtgacca gaccgctcat ggaaagtgaa cttgtcattg gtgctgtgat cattcgtggt  26820
cacttgcgaa tggccggaca ctccctaggg cgctgtgaca ttaaggacct gccaaaagag  26880
atcactgtgg ctacatcacg aacgctttct tattacaaat taggagcgtc gcagcgtgta  26940
ggcactgatt caggttttgc tgcatacaac cgctaccgta ttggaaacta taaattaaat  27000
acagaccacg ccggtagcaa cgacaatatt gctttgctag tacagtaagt gacaacagat  27060
gtttcatctt gttgacttcc aggttacaat agcagagata ttgattatca ttatgaggac  27120
tttcaggatt gctatttgga atcttgacgt tataataagt tcaatagtga gacaattatt  27180
taagcctcta actaagaaga attattcgga gttagatgat gaagaaccta tggagttaga  27240
ttatccataa aacgaacatg aaaattattc tcttcctgac attgattgta tttacatctt  27300
gcgagctata tcactatcag gagtgtgtta gaggtacgac tgtactacta aaagaacctt  27360
gcccatcagg aacatacgag ggcaattcac catttcaccc tcttgctgac aataaatttg  27420
cactaacttg cactagcaca cactttgctt ttgcttgtgc tgacggtact cgacatacct  27480
atcagctgcg tgcaagatca gtttcaccaa aacttttcat cagacaagag gaggttcaac  27540
aagagctcta ctcgccactt tttctcattg ttgctgctct agtatttta atactttgct  27600
tcaccattaa gagaaagaca gaatgaatga gctcacttta attgacttct atttgtgctt  27660
tttagccttt ctgctattcc ttgttttaat aatgcttatt atattttggt tttcactcga  27720
aatccaggat ctagaagaac cttgtaccaa agtctaaacg aacatgaaac ttctcattgt  27780
tttgacttgt atttctctat gcagttgcat atgcactgta gtacagcgct gtgcatctaa  27840
taaacctcat gtgcttgaag atccttgtaa ggtacaacac taggggtaat acttatagca  27900
ctgcttggct ttgtgctcta ggaaaggttt taccttttca tagatggcac actatggttc  27960
aaacatgcac acctaatgtt actatcaact gtcaagatcc agctggtggt gcgcttatag  28020
ctaggtgttg gtaccttcat gaaggtcacc aaactgctgc atttagagac gtacttgttg  28080
ttttaaataa acgaacaaat taaaatgtct gataatggac cccaatcaaa ccaacgtagt  28140
gccccccgca ttacatttgg tggacccaca gattcaactg acaataacca gaatggagga  28200
cgcaatgggg caaggccaaa acagcgccga ccccaaggtt tacccaataa tactgcgtct  28260
tggttcacag ctctcactca gcatggcaag gaggaactta gattccctcg aggccagggc  28320
gttccaatca acaccaatag tggtccagat gaccaaattg gctactaccg aagagctacc  28380
cgacgagttc gtggtggtga cggcaaaatg aaagagctca gccccagatg gtacttctat  28440
tacctaggaa ctggcccaga agcttcactt ccctacggcg ctaacaaaga aggcatcgta  28500
tgggttgcaa ctgagggagc cttgaataca cccaaagacc acattggcac ccgcaatcct  28560
aataacaatg ctgccaccgt gctacaactt cctcaaggaa caacattgcc aaaaggcttc  28620
tacgcagagg gaagcagagg cggcagtcaa gcctcttctc gctcctcatc acgtagtcgc  28680
ggtaattcaa gaaattcaac tcctggcagc agtaggggaa attctcctgc tcgaatggct  28740
agcggaggtg gtgaaactgc cctcgcgcta ttgctgctag acagattgaa ccagcttgag  28800
agcaaagttt ctggtaaagg ccaacaacaa caaggccaaa ctgtcactaa gaaatctgct  28860
```

```
gctgaggcat ctaaaaagcc tcgccaaaaa cgtactgcca caaaacagta caacgtcact  28920

caagcatttg ggagacgtgg tccagaacaa acccaaggaa atttcgggga ccaagaccta  28980

atcagacaag gaactgatta caaacattgg ccgcaaattg cacaatttgc tccaagtgcc  29040

tctgcattct ttggaatgtc acgcattggc atggaagtca caccttcggg aacatggctg  29100

acttatcatg gagccattaa attggatgac aaagatccac aattcaaaga caacgtcata  29160

ctgctgaaca agcacattga cgcatacaaa acattcccac caacagagcc taaaaaggac  29220

aaaaagaaaa agactgatga agctcagcct ttgccgcaga gacaaaagaa gcagcccact  29280

gtgactcttc ttcctgcggc tgacatggat gatttctcca gacaacttca aaattccatg  29340

agtggagctt ctgctgattc aactcaggca taaacactca tgatgaccac acaaggcaga  29400

tgggctatgt aaacgttttc gcaattccgt ttacgataca tagtctactc ttgtgcagaa  29460

tgaattctcg taactaaaca gcacaagtag gtttagttaa ctttaatctc acatagcaat  29520

ctttaatcaa tgtgtaacat tagggaggac ttgaaagagc caccacattt tcatcgaggc  29580

cacgcggagt acgatcgagg gtacagtgaa taatgctagg gagagctgcc tatatggaag  29640

agccctaatg tgtaaaatta attttagtag tgctatcccc atgtgatttt aatagcttct  29700

taggagaatg acaaaaaaaa aaaaaaaaaa aaaaaa                            29736
```

<210> SEQ ID NO 2
<211> LENGTH: 29736
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 2

```
ctacccagga aaagccaacc aacctcgatc tcttgtagat ctgttctcta aacgaacttt     60

aaaatctgtg tagctgtcgc tcggctgcat gcctagtgca cctacgcagt ataaacaata    120

ataaatttta ctgtcgttga caagaaacga gtaactcgtc cctcttctgc agactgctta    180

cggtttcgtc cgtgttgcag tcgatcatca gcatacctag gtttcgtccg ggtgtgaccg    240

aaaggtaaga tggagagcct tgttcttggt gtcaacgaga aaacacacgt ccaactcagt    300

ttgcctgtcc ttcaggttag agacgtgcta gtgcgtggct tcggggactc tgtggaagag    360

gccctatcgg aggcacgtga acacctcaaa aatggcactt gtggtctagt agagctggaa    420

aaaggcgtac tgccccagct tgaacagccc tatgtgttca ttaaacgttc tgatgcctta    480

agcaccaatc acggccacaa ggtcgttgag ctggttgcag aaatggacgg cattcagtac    540

ggtcgtagcg gtataacact gggagtactc gtgccacatg tgggcgaaac cccaattgca    600

taccgcaatg ttcttcttcg taagaacggt aataagggag ccggtggtca tagctatggc    660

atcgatctaa agtcttatga cttaggtgac gagcttggca ctgatcccat tgaagattat    720

gaacaaaact ggaacactaa gcatggcagt ggtgcactcc gtgaactcac tcgtgagctc    780

aatggaggtg cagtcactcg ctatgtcgac aacaatttct gtggcccaga tgggtaccct    840

cttgattgca tcaaagattt tctcgcacgc gcgggcaagt caatgtgcac tctttccgaa    900

caacttgatt acatcgagtc gaagagaggt gtctactgct gccgtgacca tgagcatgaa    960

attgcctggt tcactgagcg ctctgataag agctacgagc accagacacc cttcgaaatt   1020

aagagtgcca agaaatttga cactttcaaa ggggaatgcc caaagtttgt gtttcctctt   1080

aactcaaaag tcaaagtcat tcaaccacgt gttgaaaaga aaaagactga gggtttcatg   1140

gggcgtatac gctctgtgta ccctgttgca tctccacagg agtgtaacaa tatgcacttg   1200
```

-continued

```
tctaccttga tgaaatgtaa tcattgcgat gaagtttcat ggcagacgtg cgactttctg   1260
aaagccactt gtgaacattg tggcactgaa aatttagtta ttgaaggacc tactacatgt   1320
gggtacctac ctactaatgc tgtagtgaaa atgccatgtc ctgcctgtca agacccagag   1380
attggacctg agcatagtgt tgcagattat cacaaccact caaacattga aactcgactc   1440
cgcaagggag gtaggactag atgttttgga ggctgtgtgt ttgcctatgt tggctgctat   1500
aataagcgtg cctactgggt tcctcgtgct agtgctgata ttggctcagg ccatactggc   1560
attactggtg acaatgtgga gaccttgaat gaggatctcc ttgagatact gagtcgtgaa   1620
cgtgttaaca ttaacattgt tggcgatttt catttgaatg aagaggttgc catcattttg   1680
gcatctttct ctgcttctac aagtgccttt attgacacta taaagagtct tgattacaag   1740
tctttcaaaa ccattgttga gtcctgcggt aactataaag ttaccaaggg aaagcccgta   1800
aaaggtgctt ggaacattgg acaacagaga tcagttttaa caccactgtg tggttttccc   1860
tcacaggctg ctggtgttat cagatcaatt tttgcgcgca cacttgatgc agcaaaccac   1920
tcaattcctg atttgcaaag agcagctgtc accatacttg atggtatttc tgaacagtca   1980
ttacgtcttg tcgacgccat ggtttatact tcagacctgc tcaccaacag tgtcattatt   2040
atggcatatg taactggtgg tcttgtacaa cagacttctc agtggttgtc taatcttttg   2100
ggcactactg ttgaaaaact caggcctatc tttgaatgga ttgaggcgaa acttagtgca   2160
ggagttgaat ttctcaagga tgcttgggag attctcaaat ttctcattac aggtgttttt   2220
gacatcgtca agggtcaaat acaggttgct tcagataaca tcaaggattg tgtaaaatgc   2280
ttcattgatg ttgttaacaa ggcactcgaa atgtgcattg atcaagtcac tatcgctggc   2340
gcaaagttgc gatcactcaa cttaggtgaa gtcttcatcg ctcaaagcaa gggactttac   2400
cgtcagtgta tacgtggcaa ggagcagctg caactactca tgcctcttaa ggcaccaaaa   2460
gaagtaacct ttcttgaagg tgattcacat gacacagtac ttacctctga ggaggttgtt   2520
ctcaagaacg gtgaactcga agcactcgag acgcccgttg atagcttcac aaatggagct   2580
atcgttggca caccagtctg tgtaaatggc ctcatgctct tagagattaa ggacaaagaa   2640
caatactgcg cattgtctcc tggtttactg gctacaaaca atgtctttcg cttaaaaggg   2700
ggtgcaccaa ttaaaggtgt aacctttgga gaagatactg tttgggaagt tcaaggttac   2760
aagaatgtga gaatcacatt tgagcttgat gaacgtgttg acaaagtgct taatgaaaag   2820
tgctctgtct acactgttga atccggtacc gaagttactg agtttgcatg tgttgtagca   2880
gaggctgttg tgaagacttt acaaccagtt tctgatctcc ttaccaacat gggtattgat   2940
cttgatgagt ggagtgtagc tacattctac ttatttgatg atgctggtga agaaaacttt   3000
tcatcacgta tgtattgttc cttttaccct ccagatgagg aagaagagga cgatgcagag   3060
tgtgaggaag aagaaattga tgaaacctgt gaacatgagt acggtacaga ggatgattat   3120
caaggtctcc ctctggaatt tggtgcctca gctgaaacag ttcgagttga ggaagaagaa   3180
gaggaagact ggctggatga tactactgag caatcagaga ttgagccaga accagaacct   3240
acacctgaag aaccagttaa tcagtttact ggttatttaa aacttactga caatgttgcc   3300
attaaatgtg ttgacatcgt taaggaggca caaagtgcta atcctatggt gattgtaaat   3360
gctgctaaca tacacctgaa acatggtggt ggtgtagcag gtgcactcaa caaggcaacc   3420
aatggtgcca tgcaaaagga gagtgatgat tacattaagc taaatggccc tcttacagta   3480
ggagggtctt gtttgctttc tggacataat cttgctaaga agtgtctgca tgttgttgga   3540
cctaacctaa atgcaggtga ggacatccag cttcttaagg cagcatatga aaatttcaat   3600
```

-continued

```
tcacaggaca tcttacttgc accattgttg tcagcaggca tatttggtgc taaaccactt   3660
cagtctttac aagtgtgcgt gcagacggtt cgtacacagg tttatattgc agtcaatgac   3720
aaagctcttt atgagcaggt tgtcatggat tatcttgata acctgaagcc tagagtggaa   3780
gcacctaaac aagaggagcc accaaacaca gaagattcca aaactgagga gaaatctgtc   3840
gtacagaagc ctgtcgatgt gaagccaaaa attaaggcct gcattgatga ggttaccaca   3900
acactggaag aaactaagtt tcttaccaat aagttactct tgtttgctga tatcaatggt   3960
aagctttacc atgattctca gaacatgctt agaggtgaag atatgtcttt ccttgagaag   4020
gatgcacctt acatggtagg tgatgttatc actagtggtg atatcacttg tgttgtaata   4080
ccctccaaaa aggctggtgg cactactgag atgctctcaa gagctttgaa gaaagtgcca   4140
gttgatgagt atataaccac gtaccctgga caaggatgtg ctggttatac acttgaggaa   4200
gctaagactg ctcttaagaa atgcaaatct gcattttatg tactaccttc agaagcacct   4260
aatgctaagg aagagattct aggaactgta tcctggaatt tgagagaaat gcttgctcat   4320
gctgaagaga caagaaaatt aatgcctata tgcatggatg ttagagccat aatggcaacc   4380
atccaacgta agtataaagg aattaaaatt caagagggca tcgttgacta tggtgtccga   4440
ttcttctttt atactagtaa agagcctgta gcttctatta ttacgaagct gaactctcta   4500
aatgagccgc ttgtcacaat gccaattggt tatgtgacac atggttttaa tcttgaagag   4560
gctgcgcgct gtatgcgttc tcttaaagct cctgccgtag tgtcagtatc atcaccagat   4620
gctgttacta catataatgg atacctcact tcgtcatcaa agacatctga ggagcacttt   4680
gtagaaacag tttctttggc tggctcttac agagattggt cctattcagg acagcgtaca   4740
gagttaggtg ttgaatttct taagcgtggt gacaaaattg tgtaccacac tctggagagc   4800
cccgtcgagt ttcatcttga cggtgaggtt ctttcacttg acaaactaaa gagtctctta   4860
tccctgcggg aggttaagac tataaaagtg ttcacaactg tggacaacac taatctccac   4920
acacagcttg tggatatgtc tatgacatat ggacagcagt ttggtccaac atacttggat   4980
ggtgctgatg ttacaaaaat taaacctcat gtaaatcatg agggtaagac tttctttgta   5040
ctacctagtg atgacacact acgtagtgaa gctttcgagt actaccatac tcttgatgag   5100
agttttcttg gtaggtacat gtctgcttta aaccacacaa agaaatggaa atttcctcaa   5160
gttggtggtt taacttcaat taaatgggct gataacaatt gttatttgtc tagtgtttta   5220
ttagcacttc aacagcttga agtcaaattc aatgcaccag cacttcaaga ggcttattat   5280
agagcccgtg ctggtgatgc tgctaacttt tgtgcactca tactcgctta cagtaataaa   5340
actgttggcg agcttggtga tgtcagagaa actatgaccc atcttctaca gcatgctaat   5400
ttggaatctg caaagcgagt tcttaatgtg gtgtgtaaac attgtggtca gaaaactact   5460
accttaacgg gtgtagaagc tgtgatgtat atgggtactc tatcttatga taatcttaag   5520
acaggtgttt ccattccatg tgtgtgtggt cgtgatgcta cacaatatct agtacaacaa   5580
gagtcttctt ttgttatgat gtctgcacca cctgctgagt ataaattaca gcaaggtaca   5640
ttcttatgtg cgaatgagta cactggtaac tatcagtgtg gtcattacac tcatataact   5700
gctaaggaga ccctctatcg tattgacgga gctcacctta caaagatgtc agagtacaaa   5760
ggaccagtga ctgatgtttt ctacaaggaa acatcttaca ctacaaccat caagcctgtg   5820
tcgtataaac tcgatggagt tacttacaca gagattgaac caaaattgga tgggtattat   5880
aaaaaggata atgcttacta tacagagcag cctatagacc ttgtaccaac tcaaccatta   5940
```

-continued

```
ccaaatgcga gttttgataa tttcaaactc acatgttcta acacaaaatt tgctgatgat   6000
ttaaatcaaa tgacaggctt cacaaagcca gcttcacgag agctatctgt cacattcttc   6060
ccagacttga atggcgatgt agtggctatt gactatagac actattcagc gagtttcaag   6120
aaaggtgcta aattactgca taagccaatt gtttggcaca ttaaccaggc tacaaccaag   6180
acaacgttca aaccaaacac ttggtgttta cgttgtcttt ggagtacaaa gccagtagat   6240
acttcaaatt catttgaagt tctggcagta gaagacacac aaggaatgga caatcttgct   6300
tgtgaaagtc aacaacccac ctctgaagaa gtagtggaaa atcctaccat acagaaggaa   6360
gtcatagagt gtgacgtgaa aactaccgaa gttgtaggca atgtcatact taaaccatca   6420
gatgaaggtg ttaaagtaac acaagagtta ggtcatgagg atcttatggc tgcttatgtg   6480
gaaaacacaa gcattaccat taagaaacct aatgagcttt cactagcctt aggtttaaaa   6540
acaattgcca ctcatggtat tgctgcaatt aatagtgttc cttggagtaa aattttggct   6600
tatgtcaaac cattcttagg acaagcagca attacaacat caaattgcgc taagagatta   6660
gcacaacgtg tgtttaacaa ttatatgcct tatgtgttta cattattgtt ccaattgtgt   6720
acttttacta aaagtaccaa ttctagaatt agagcttcac tacctacaac tattgctaaa   6780
aatagtgtta agagtgttgc taaattatgt ttggatgccg gcattaatta tgtgaagtca   6840
cccaaatttt ctaaattgtt cacaatcgct atgtggctat tgttgttaag tatttgctta   6900
ggttctctaa tctgtgtaac tgctgctttt ggtgtactct tatctaattt tggtgctcct   6960
tcttattgta atggcgttag agaattgtat cttaattcgt ctaacgttac tactatggat   7020
ttctgtgaag gttcttttcc ttgcagcatt tgtttaagtg gattagactc ccttgattct   7080
tatccagctc ttgaaaccat tcaggtgacg atttcatcgt acaagctaga cttgacaatt   7140
ttaggtctgg ccgctgagtg ggttttggca tatatgttgt tcacaaaatt cttttattta   7200
ttaggtcttt cagctataat gcaggtgttc tttggctatt ttgctagtca tttcatcagc   7260
aattcttggc tcatgtggtt tatcattagt attgtacaaa tggcacccgt ttctgcaatg   7320
gttaggatgt acatcttctt tgcttctttc tactacatat ggaagagcta tgttcatatc   7380
atggatggtt gcacctcttc gacttgcatg atgtgctata agcgcaatcg tgccacacgc   7440
gttgagtgta caactattgt taatggcatg aagagatctt tctatgtcta tgcaaatgga   7500
ggccgtggct tctgcaagac tcacaattgg aattgtctca attgtgacac attttgcact   7560
ggtagtacat tcattagtga tgaagttgct cgtgatttgt cactccagtt taaaagacca   7620
atcaacccta ctgaccagtc atcgtatatt gttgatagtg ttgctgtgaa aaatggcgcg   7680
cttcacctct actttgacaa ggctggtcaa aagacctatg agagacatcc gctctcccat   7740
tttgtcaatt tagacaattt gagagctaac aacactaaag gttcactgcc tattaatgtc   7800
atagtttttg atggcaagtc caaatgcgac gagtctgctt ctaagtctgc ttctgtgtac   7860
tacagtcagc tgatgtgcca acctattctg ttgcttgacc aagctcttgt atcagacgtt   7920
ggagatagta ctgaagtttc cgttaagatg tttgatgctt atgtcgacac cttttcagca   7980
acttttagtg ttcctatgga aaaacttaag gcacttgttg ctacagctca cagcgagtta   8040
gcaaagggtg tagctttaga tggtgtcctt tctacattcg tgtcagctgc ccgacaaggt   8100
gttgttgata ccgatgttga cacaaaggat gttattgaat gtctcaaact ttcacatcac   8160
tctgacttag aagtgacagg tgacagttgt aacaatttca tgctcaccta taataaggtt   8220
gaaaacatga cgcccagaga tcttggcgca tgtattgact gtaatgcaag gcatatcaat   8280
gcccaagtag caaaaagtca caatgtttca ctcatctgga atgtaaaaga ctacatgtct   8340
```

-continued

```
ttatctgaac agctgcgtaa acaaattcgt agtgctgcca agaagaacaa catacctttt   8400
agactaactt gtgctacaac tagacaggtt gtcaatgtca taactactaa aatctcactc   8460
aagggtggta agattgttag tacttgtttt aaacttatgc ttaaggccac attattgtgc   8520
gttcttgctg cattggtttg ttatatcgtt atgccagtac atacattgtc aatccatgat   8580
ggttacacaa atgaaatcat tggttacaaa gccattcagg atggtgtcac tcgtgacatc   8640
atttctactg atgattgttt tgcaaataaa catgctggtt ttgacgcatg gtttagccag   8700
cgtggtggtt catacaaaaa tgacaaaagc tgccctgtag tagctgctat cattacaaga   8760
gagattggtt tcatagtgcc tggcttaccg ggtactgtgc tgagagcaat caatggtgac   8820
ttcttgcatt ttctacctcg tgtttttagt gctgttggca acatttgcta cacaccttcc   8880
aaactcattg agtatagtga ttttgctacc tctgcttgcg ttcttgctgc tgagtgtaca   8940
atttttaagg atgctatggg caaacctgtg ccatattgtt atgacactaa tttgctagag   9000
ggttctattt cttatagtga gcttcgtcca gacactcgtt atgtgcttat ggatggttcc   9060
atcatacagt ttcctaacac ttacctggag ggttctgtta gagtagtaac aacttttgat   9120
gctgagtact gtagacatgg tacatgcgaa aggtcagaag taggtatttg cctatctacc   9180
agtggtagat gggttcttaa taatgagcat tacagagctc tatcaggagt ttctgtggt   9240
gttgatgcga tgaatctcat agctaacatc tttactcctc ttgtgcaacc tgtgggtgct   9300
ttagatgtgt ctgcttcagt agtggctggt ggtattattg ccatattggt gacttgtgct   9360
gcctactact ttatgaaatt cagacgtgtt tttggtgagt acaaccatgt tgttgctgct   9420
aatgcacttt tgtttttgat gtctttcact atactctgtc tggtaccagc ttacagcttt   9480
ctgccgggag tctactcagt cttttacttg tacttgacat tctatttcac caatgatgtt   9540
tcattcttgg ctcaccttca atggtttgcc atgttttctc ctattgtgcc tttttggata   9600
acagcaatct atgtattctg tatttctctg aagcactgcc attggttctt taacaactat   9660
cttaggaaaa gagtcatgtt taatggagtt acatttagta ccttcgagga ggctgctttg   9720
tgtacctttt tgctcaacaa ggaaatgtac ctaaaattgc gtagcgagac actgttgcca   9780
cttacacagt ataacaggta tcttgctcta tataacaagt acaagtattt cagtggagcc   9840
ttagatacta ccagctatcg tgaagcagct tgctgccact tagcaaaggc tctaaatgac   9900
tttagcaact caggtgctga tgttctctac caaccaccac agacatcaat cacttctgct   9960
gttctgcaga gtggttttag gaaaatggca ttcccgtcag gcaaagttga agggtgcatg  10020
gtacaagtaa cctgtggaac tacaactctt aatggattgt ggttggatga cacagtatac  10080
tgtccaagac atgtcatttg cacagcagaa gacatgctta atcctaacta tgaagatctg  10140
ctcattcgca aatccaacca tagctttctt gttcaggctg gcaatgttca acttcgtgtt  10200
attggccatt ctatgcaaaa ttgtctgctt aggcttaaag ttgatacttc taaccctaag  10260
acacccaagt ataaatttgt ccgtatccaa cctggtcaaa cattttcagt tctagcatgc  10320
tacaatggtt caccatctgg tgtttatcag tgtgccatga gacctaatca taccattaaa  10380
ggttctttcc ttaatggatc atgtggtagt gttggtttta acattgatta tgattgcgtg  10440
tctttctgct atatgcatca tatggagctt ccaacaggag tacacgctgg tactgactta  10500
gaaggtaaat tctatggtcc atttgttgac agacaaactg cacaggctgc aggtacagac  10560
acaaccataa cattaaatgt tttggcatgg ctgtatgctg ctgttatcaa tggtgatagg  10620
tggtttctta atagattcac cactactttg aatgacttta accttgtggc aatgaagtac  10680
```

-continued

```
aactatgaac ctttgacaca agatcatgtt gacatattgg gacctctttc tgctcaaaca  10740
ggaattgccg tcttagatat gtgtgctgct ttgaaagagc tgctgcagaa tggtatgaat  10800
ggtcgtacta tccttggtag cactatttta gaagatgagt ttacaccatt tgatgttgtt  10860
agacaatgct ctggtgttac cttccaaggt aagttcaaga aaattgttaa gggcactcat  10920
cattggatgc ttttaacttt cttgacatca ctattgattc ttgttcaaag tacacagtgg  10980
tcactgtttt tctttgttta cgagaatgct ttcttgccat ttactcttgg tattatggca  11040
attgctgcat gtgctatgct gcttgttaag cataagcacg cattcttgtg cttgtttctg  11100
ttaccttctc ttgcaacagt tgcttacttt aatatggtct acatgcctgc tagctgggtg  11160
atgcgtatca tgacatggct tgaattggct gacactagct tgtctggtta taggcttaag  11220
gattgtgtta tgtatgcttc agctttagtt ttgcttattc tcatgacagc tcgcactgtt  11280
tatgatgatg ctgctagacg tgtttggaca ctgatgaatg tcattacact tgtttacaaa  11340
gtctactatg gtaatgcttt agatcaagct atttccatgt gggccttagt tatttctgta  11400
acctctaact attctggtgt cgttacgact atcatgtttt tagctagagc tatagtgttt  11460
gtgtgtgttg agtattaccc attgttattt attactggca acaccttaca gtgtatcatg  11520
cttgtttatt gtttcttagg ctattgttgc tgctgctact ttggcctttt ctgtttactc  11580
aaccgttact tcaggcttac tcttggtgtt tatgactact tggtctctac acaagaattt  11640
aggtatatga actcccaggg gcttttgcct cctaagagta gtattgatgc tttcaagctt  11700
aacattaagt tgttgggtat tggaggtaaa ccatgtatca aggttgctac tgtacagtct  11760
aaaatgtctg acgtaaagtg cacatctgtg gtactgctct cggttcttca acaacttaga  11820
gtagagtcat cttctaaatt gtgggcacaa tgtgtacaac tccacaatga tattcttctt  11880
gcaaaagaca caactgaagc tttcgagaag atggtttctc ttttgtctgt tttgctatcc  11940
atgcagggtg ctgtagacat taataggttg tgcgaggaaa tgctcgataa ccgtgctact  12000
cttcaggcta ttgcttcaga atttagttct ttaccatcat atgccgctta tgccactgcc  12060
caggaggcct atgagcaggc tgtagctaat ggtgattctg aagtcgttct caaaaagtta  12120
aagaaatctt tgaatgtggc taaatctgag tttgaccgtg atgctgccat gcaacgcaag  12180
ttggaaaaga tggcagatca ggctatgacc caaatgtaca aacaggcaag atctgaggac  12240
aagagggcaa aagtaactag tgctatgcaa acaatgctct tcactatgct taggaagctt  12300
gataatgatg cacttaacaa cattatcaac aatgcgcgtg atggttgtgt tccactcaac  12360
atcataccat tgactacagc agccaaactc atggttgttg tccctgatta tggtacctac  12420
aagaacactt gtgatggtaa cacctttaca tatgcatctg cactctggga aatccagcaa  12480
gttgttgatg cggatagcaa gattgttcaa cttagtgaaa ttaacatgga caattcacca  12540
aatttggctt ggcctcttat tgttacagct ctaagagcca actcagctgt taaactacag  12600
aataatgaac tgagtccagt agcactacga cagatgtcct gtgcggctgg taccacacaa  12660
acagcttgta ctgatgacaa tgcacttgcc tactataaca attcgaaggg aggtaggttt  12720
gtgctggcat tactatcaga ccaccaagat ctcaaatggg ctagattccc taagagtgat  12780
ggtacaggta caatttacac agaactggaa ccaccttgta ggtttgttac agacacacca  12840
aaagggccta aagtgaaata cttgtacttc atcaaaggct taaacaacct aaatagaggt  12900
atggtgctgg gcagtttagc tgctacagta cgtcttcagg ctggaaatgc tacagaagta  12960
cctgccaatt caactgtgct ttccttctgt gcttttgcag tagaccctgc taaagcatat  13020
aaggattacc tagcaagtgg aggacaacca atcaccaact gtgtgaagat gttgtgtaca  13080
```

-continued

```
cacactggta caggacaggc aattactgta acaccagaag ctaacatgga ccaagagtcc  13140
tttggtggtg cttcatgttg tctgtattgt agatgccaca ttgaccatcc aaatcctaaa  13200
ggattctgtg acttgaaagg taagtacgtc caaataccta ccacttgtgc taatgaccca  13260
gtgggtttta cacttagaaa cacagtctgt accgtctgcg gaatgtggaa aggttatggc  13320
tgtagttgtg accaactccg cgaacccttg atgcagtctg cggatgcatc aacgttttta  13380
aacgggtttg cggtgtaagt gcagcccgtc ttacaccgtg cggcacaggc actagtactg  13440
atgtcgtcta cagggctttt gatatttaca acgaaaaagt tgctggtttt gcaaagttcc  13500
taaaaactaa ttgctgtcgc ttccaggaga aggatgagga aggcaattta ttagactctt  13560
actttgtagt taagaggcat actatgtcta actaccaaca tgaagagact atttataact  13620
tggttaaaga ttgtccagcg gttgctgtcc atgacttttt caagtttaga gtagatggtg  13680
acatggtacc acatatatca cgtcagcgtc taactaaata cacaatggct gatttagtct  13740
atgctctacg tcattttgat gagggtaatt gtgatacatt aaaagaaata ctcgtcacat  13800
acaattgctg tgatgatgat tatttcaata agaaggattg gtatgacttc gtagagaatc  13860
ctgacatctt acgcgtatat gctaacttag gtgagcgtgt acgccaatca ttattaaaga  13920
ctgtacaatt ctgcgatgct atgcgtgatg caggcattgt aggcgtactg acattagata  13980
atcaggatct taatgggaac tggtacgatt tcggtgattt cgtacaagta gcaccaggct  14040
gcggagttcc tattgtggat tcatattact cattgctgat gcccatcctc actttgacta  14100
gggcattggc tgctgagtcc catatggatg ctgatctcgc aaaaccactt attaagtggg  14160
atttgctgaa atatgatttt acggaagaga gactttgtct cttcgaccgt tattttaaat  14220
attgggacca gacataccat cccaattgta ttaactgttt ggatgatagg tgtatccttc  14280
attgtgcaaa ctttaatgtg ttatttttcta ctgtgtttcc acctacaagt tttggaccac  14340
tagtaagaaa aatatttgta gatggtgttc cttttgttgt ttcaactgga taccattttc  14400
gtgagttagg agtcgtacat aatcaggatg taaacttaca tagctcgcgt ctcagtttca  14460
aggaactttt agtgtatgct gctgatccag ctatgcatgc agcttctggc aatttattgc  14520
tagataaacg cactacatgc ttttcagtag ctgcactaac aaacaatgtt gcttttcaaa  14580
ctgtcaaacc cggtaatttt aataaagact tttatgactt tgctgtgtct aaaggtttct  14640
ttaaggaagg aagttctgtt gaactaaaac acttcttctt tgctcaggat ggcaacgctg  14700
ctatcagtga ttatgactat tatcgttata atctgccaac aatgtgtgat atcagacaac  14760
tcctattcgt agttgaagtt gttgataaat actttgattg ttacgatggt ggctgtatta  14820
atgccaacca agtaatcgtt aacaatctgg ataaatcagc tggtttccca tttaataaat  14880
ggggtaaggc tagactttat tatgactcaa tgagttatga ggatcaagat gcacttttcg  14940
cgtatactaa gcgtaatgtc atccctacta taactcaaat gaatcttaag tatgccatta  15000
gtgcaaagaa tagagctcgc accgtagctg gtgtctctat ctgtagtact atgacaaata  15060
gacagtttca tcagaaatta ttgaagtcaa tagccgccac tagaggagct actgtggtaa  15120
ttggaacaag caagttttac ggtggctggc ataatatgtt aaaaactgtt tacagtgatg  15180
tagaaactcc acaccttatg ggttgggatt atccaaaatg tgacagagcc atgcctaaca  15240
tgcttaggat aatggcctct cttgttcttg ctcgcaaaca taacacttgc tgtaacttat  15300
cacaccgttt ctacaggtta gctaacgagt gtgcgcaagt attaagtgag atggtcatgt  15360
gtggcggctc actatatgtt aaaccaggtg gaacatcatc cggtgatgct acaactgctt  15420
```

-continued

```
atgctaatag tgtctttaac atttgtcaag ctgttacagc caatgtaaat gcacttcttt  15480
caactgatgg taataagata gctgacaagt atgtccgcaa tctacaacac aggctctatg  15540
agtgtctcta tagaaatagg gatgttgatc atgaattcgt ggatgagttt tacgcttacc  15600
tgcgtaaaca tttctccatg atgattcttt ctgatgatgc cgttgtgtgc tataacagta  15660
actatgcggc tcaaggttta gtagctagca ttaagaactt taaggcagtt ctttattatc  15720
aaaataatgt gttcatgtct gaggcaaaat gttggactga gactgacctt actaaaggac  15780
ctcacgaatt ttgctcacag catacaatgc tagttaaaca aggagatgat tacgtgtacc  15840
tgccttaccc agatccatca agaatattag gcgcaggctg ttttgtcgat gatattgtca  15900
aaacagatgg tacacttatg attgaaaggt tcgtgtcact ggctattgat gcttacccac  15960
ttacaaaaca tcctaatcag gagtatgctg atgtctttca cttgtattta caatacatta  16020
gaaagttaca tgatgagctt actggccaca tgttggacat gtattccgta atgctaacta  16080
atgataacac ctcacggtac tgggaacctg agttttatga ggctatgtac acaccacata  16140
cagtcttgca ggctgtaggt gcttgtgtat tgtgcaattc acagacttca cttcgttgcg  16200
gtgcctgtat taggagacca ttcctatgtt gcaagtgctg ctatgaccat gtcatttcaa  16260
catcacacaa attagtgttg tctgttaatc cctatgtttg caatgcccca ggttgtgatg  16320
tcactgatgt gacacaactg tatctaggag gtatgagcta ttattgcaag tcacataagc  16380
ctcccattag ttttccatta tgtgctaatg gtcaggtttt tggtttatac aaaaacacat  16440
gtgtaggcag tgacaatgtc actgacttca atgcgatagc aacatgtgat tggactaatg  16500
ctggcgatta catacttgcc aacacttgta ctgagagact caagcttttc gcagcagaaa  16560
cgctcaaagc cactgaggaa acatttaagc tgtcatatgg tattgccact gtacgcgaag  16620
tactctctga cagagaattg catctttcat gggaggttgg aaaacctaga ccaccattga  16680
acagaaacta tgtctttact ggttaccgtg taactaaaaa tagtaaagta cagattggag  16740
agtacacctt tgaaaaaggt gactatggtg atgctgttgt gtacagaggt actacgacat  16800
acaagttgaa tgttggtgat tactttgtgt tgacatctca cactgtaatg ccacttagtg  16860
cacctactct agtgccacaa gagcactatg tgagaattac tggcttgtac ccaacactca  16920
acatctcaga tgagttttct agcaatgttg caaattatca aaaggtcggc atgcaaaagt  16980
actctacact ccaaggacca cctggtactg gtaagagtca ttttgccatc ggacttgctc  17040
tctattaccc atctgctcgc atagtgtata cggcatgctc tcatgcagct gttgatgccc  17100
tatgtgaaaa ggcattaaaa tatttgccca tagataaatg tagtagaatc atacctgcgc  17160
gtgcgcgcgt agagtgtttt gataaattca aagtgaattc aacactagaa cagtatgttt  17220
tctgcactgt aaatgcattg ccagaaacaa ctgctgacat tgtagtcttt gatgaaatct  17280
ctatggctac taattatgac ttgagtgttg tcaatgctag acttcgtgca aaacactacg  17340
tctatattgg cgatcctgct caattaccag ccccccgcac attgctgact aaaggcacac  17400
tagaaccaga atattttaat tcagtgtgca gacttatgaa aacaataggt ccagacatgt  17460
tccttggaac ttgtcgccgt tgtcctgctg aaattgttga cactgtgagt gctttagttt  17520
atgacaataa gctaaaagca cacaaggata agtcagctca atgcttcaaa atgttctaca  17580
aaggtgttat tacacatgat gtttcatctg caatcaacag acctcaaata ggcgttgtaa  17640
gagaatttct tacacgcaat cctgcttgga gaaaagctgt ttttatctca ccttataatt  17700
cacagaacgc tgtagcttca aaaatcttag gattgcctac gcagactgtt gattcatcac  17760
agggttctga atatgactat gtcatattca cacaaactac tgaaacagca cactcttgta  17820
```

-continued

```
atgtcaaccg cttcaatgtg gctatcacaa gggcaaaaat tggcattttg tgcataatgt  17880
ctgatagaga tctttatgac aaactgcaat ttacaagtct agaaatacca cgtcgcaatg  17940
tggctacatt acaagcagaa aatgtaactg gactttttaa ggactgtagt aagatcatta  18000
ctggtcttca tcctacacag gcacctacac acctcagcgt tgatataaag ttcaagactg  18060
aaggattatg tgttgacata ccaggcatac caaaggacat gacctaccgt agactcatct  18120
ctatgatggg tttcaaaatg aattaccaag tcaatggtta ccctaatatg tttatcaccc  18180
gcgaagaagc tattcgtcac gttcgtgcgt ggattggctt tgatgtagag ggctgtcatg  18240
caactagaga tgctgtgggt actaacctac ctctccagct aggattttct acaggtgtta  18300
acttagtagc tgtaccgact ggttatgttg acactgaaaa taacacagaa ttcaccagag  18360
ttaatgcaaa acctccacca ggtgaccagt ttaaacatct tataccactc atgtataaag  18420
gcttgccctg gaatgtagtg cgtattaaga tagtacaaat gctcagtgat acactgaaag  18480
gattgtcaga cagagtcgtg ttcgtccttt gggcgcatgg ctttgagctt acatcaatga  18540
agtactttgt caagattgga cctgaaagaa cgtgttgtct gtgtgacaaa cgtgcaactt  18600
gcttttctac ttcatcagat acttatgcct gctggaatca ttctgtgggt tttgactatg  18660
tctataaccc atttatgatt gatgttcagc agtggggctt tacgggtaac cttcagagta  18720
accatgacca acattgccag gtacatggaa atgcacatgt ggctagttgt gatgctatca  18780
tgactagatg tttagcagtc catgagtgct ttgttaagcg cgttgattgg tctgttgaat  18840
accctattat aggagatgaa ctgagggtta attctgcttg cagaaaagta caacacatgg  18900
ttgtgaagtc tgcattgctt gctgataagt ttccagttct tcatgacatt ggaaatccaa  18960
aggctatcaa gtgtgtgcct caggctgaag tagaatggaa gttctacgat gctcagccat  19020
gtagtgacaa agcttacaaa atagaggaac tcttctattc ttatgctaca catcacgata  19080
aattcactga tggtgtttgt ttgttttgga attgtaacgt tgatcgttac ccagccaatg  19140
caattgtgtg taggtttgac acaagagtct tgtcaaactt gaacttacca ggctgtgatg  19200
gtggtagttt gtatgtgaat aagcatgcat tccacactcc agctttcgat aaaagtgcat  19260
ttactaattt aaagcaattg cctttctttt actattctga tagtccttgt gagtctcatg  19320
gcaaacaagt agtgtcggat attgattatg ttccactcaa atctgctacg tgtattacac  19380
gatgcaattt aggtggtgct gtttgcagac accatgcaaa tgagtaccga cagtacttgg  19440
atgcatataa tatgatgatt tctgctggat ttagcctatg gatttacaaa caatttgata  19500
cttataacct gtggaataca tttaccaggt tacagagttt agaaaatgtg gcttataatg  19560
ttgttaataa aggacacttt gatggacacg ccggcgaagc acctgtttcc atcattaata  19620
atgctgttta cacaaaggta gatggtattg atgtggagat ctttgaaaat aagacaacac  19680
ttcctgttaa tgttgcattt gagctttggg ctaagcgtaa cattaaacca gtgccagaga  19740
ttaagatact caataatttg ggtgttgata tcgctgctaa tactgtaatc tgggactaca  19800
aaagagaagc cccagcacat gtatctacaa taggtgtctg cacaatgact gacattgcca  19860
agaaacctac tgagagtgct tgttcttcac ttactgtctt gtttgatggt agagtggaag  19920
gacaggtaga cctttttaga aacgcccgta atggtgtttt aataacagaa ggttcagtca  19980
aaggtctaac accttcaaag ggaccagcac aagctagcgt caatggagtc acattaattg  20040
gagaatcagt aaaaacacag tttaactact ttaagaaagt agacggcatt attcaacagt  20100
tgcctgaaac ctactttact cagagcagag acttagagga ttttaagccc agatcacaaa  20160
```

-continued

```
tggaaactga ctttctcgag ctcgctatgg atgaattcat acagcgatat aagctcgagg  20220
gctatgcctt cgaacacatc gtttatggag atttcagtca tggacaactt ggcggtcttc  20280
atttaatgat aggcttagcc aagcgctcac aagattcacc acttaaatta gaggatttta  20340
tccctatgga cagcacagtg aaaaattact tcataacaga tgcgcaaaca ggttcatcaa  20400
aatgtgtgtg ttctgtgatt gatcttttac ttgatgactt tgtcgagata ataaagtcac  20460
aagatttgtc agtgatttca aaagtggtca aggttacaat tgactatgct gaaatttcat  20520
tcatgctttg gtgtaaggat ggacatgttg aaaccttcta cccaaaacta caagcaagtc  20580
aagcgtggca accaggtgtt gcgatgccta acttgtacaa gatgcaaaga atgcttcttg  20640
aaaagtgtga ccttcagaat tatggtgaaa atgctgttat accaaaagga ataatgatga  20700
atgtcgcaaa gtatactcaa ctgtgtcaat acttaaatac acttacttta gctgtaccct  20760
acaacatgag agttattcac tttggtgctg gctctgataa aggagttgca ccaggtacag  20820
ctgtgctcag acaatggttg ccaactggca cactacttgt cgattcagat cttaatgact  20880
tcgtctccga cgcagattct actttaattg gagactgtgc aacagtacat acggctaata  20940
aatgggacct tattattagc gatatgtatg accctaggac caaacatgtg acaaaagaga  21000
atgactctaa agaagggttt ttcacttatc tgtgtggatt tataaagcaa aaactagccc  21060
tgggtggttc tatagctgta aagataacag agcattcttg gaatgctgac ctttacaagc  21120
ttatgggcca tttctcatgg tggacagctt ttgttacaaa tgtaaatgca tcatcatcgg  21180
aagcattttt aattggggct aactatcttg gcaagccgaa ggaacaaatt gatggctata  21240
ccatgcatgc taactacatt ttctggagga acacaaatcc tatccagttg tcttcctatt  21300
cactctttga catgagcaaa tttcctctta aattaagagg aactgctgta atgtctctta  21360
aggagaatca aatcaatgat atgatttatt ctcttctgga aaaaggtagg cttatcatta  21420
gagaaaacaa cagagttgtg gtttcaagtg atattcttgt taacaactaa acgaacatgt  21480
ttattttctt attatttctt actctcacta gtggtagtga ccttgaccgg tgcaccactt  21540
ttgatgatgt tcaagctcct aattacactc aacatacttc atctatgagg ggggtttact  21600
atcctgatga aatttttaga tcagacactc tttatttaac tcaggattta tttcttccat  21660
tttattctaa tgttacaggg tttcatacta ttaatcatac gtttggcaac cctgtcatac  21720
cttttaagga tggtatttat tttgctgcca cagagaaatc aaatgttgtc cgtggttggg  21780
tttttggttc taccatgaac aacaagtcac agtcggtgat tattattaac aattctacta  21840
atgttgttat acgagcatgt aactttgaat tgtgtgacaa ccctttcttt gctgtttcta  21900
aacccatggg tacacagaca catactatga tattcgataa tgcatttaat tgcactttcg  21960
agtacatatc tgatgccttt tcgcttgatg tttcagaaaa gtcaggtaat tttaaacact  22020
tacgagagtt tgtgtttaaa aataaagatg ggtttctcta tgtttataag ggctatcaac  22080
ctatagatgt agttcgtgat ctaccttctg gttttaacac tttgaaacct atttttaagt  22140
tgcctcttgg tattaacatt acaaatttta gagccattct tacagccttt tcacctgctc  22200
aagacatttg ggcacgtca gctgcagcct attttgttgg ctatttaaag ccaactacat  22260
ttatgctcaa gtatgatgaa aatggtacaa tcacagatgc tgttgattgt tctcaaaatc  22320
cacttgctga actcaaatgc tctgttaaga gctttgagat tgacaaagga atttaccaga  22380
cctctaattt cagggttgtt ccctcaggag atgttgtgag attccctaat attacaaact  22440
tgtgtccttt tggagaggtt tttaatgcta ctaaattccc ttctgtctat gcatgggaga  22500
gaaaaaaaat ttctaattgt gttgctgatt actctgtgct ctacaactca acattttttt  22560
```

-continued

```
caacctttaa gtgctatggc gtttctgcca ctaagttgaa tgatctttgc ttctccaatg  22620
tctatgcaga ttcttttgta gtcaagggag atgatgtaag acaaatagcg ccaggacaaa  22680
ctggtgttat tgctgattat aattataaat tgccagatga tttcatgggt tgtgtccttg  22740
cttggaatac taggaacatt gatgctactt caactggtaa ttataattat aaatataggt  22800
atcttagaca tggcaagctt aggccctttg agagagacat atctaatgtg cctttctccc  22860
ctgatggcaa accttgcacc ccacctgctc ttaattgtta ttggccatta aatgattatg  22920
gtttttacac cactactggc attggctacc aaccttacag agttgtagta ctttcttttg  22980
aacttttaaa tgcaccggcc acggtttgtg gaccaaaatt atccactgac cttattaaga  23040
accagtgtgt caattttaat tttaatggac tcactggtac tggtgtgtta actccttctt  23100
caaagagatt tcaaccattt caacaatttg gccgtgatgt ttctgatttc actgattccg  23160
ttcgagatcc taaaacatct gaaatattag acatttcacc ttgcgctttt gggggtgtaa  23220
gtgtaattac acctggaaca aatgcttcat ctgaagttgc tgttctatat caagatgtta  23280
actgcactga tgtttctaca gcaattcatg cagatcaact cacaccagct tggcgcatat  23340
attctactgg aaacaatgta ttccagactc aagcaggctg tcttatagga gctgagcatg  23400
tcgacacttc ttatgagtgc gacattccta ttggagctgg catttgtgct agttaccata  23460
cagtttcttt attacgtagt actagccaaa aatctattgt ggcttatact atgtctttag  23520
gtgctgatag ttcaattgct tactctaata acaccattgc tatacctact aacttttcaa  23580
ttagcattac tacagaagta atgcctgttt ctatggctaa aacctccgta gattgtaata  23640
tgtacatctg cggagattct actgaatgtg ctaatttgct tctccaatat ggtagctttt  23700
gcacacaact aaatcgtgca ctctcaggta ttgctgctga acaggatcgc aacacacgtg  23760
aagtgttcgc tcaagtcaaa caaatgtaca aaaccccaac tttgaaatat tttggtggtt  23820
ttaatttttc acaaatatta cctgaccctc taaagccaac taagaggtct tttattgagg  23880
acttgctctt taataaggtg acactcgctg atgctggctt catgaagcaa tatggcgaat  23940
gcctaggtga tattaatgct agagatctca tttgtgcgca gaagttcaat ggacttacag  24000
tgttgccacc tctgctcact gatgatatga ttgctgccta cactgctgct ctagttagtg  24060
gtactgccac tgctggatgg acatttggtg ctggcgctgc tcttcaaata ccttttgcta  24120
tgcaaatggc atataggttc aatggcattg gagttaccca aaatgttctc tatgagaacc  24180
aaaaacaaat cgccaaccaa tttaacaagg cgattagtca aattcaagaa tcacttacaa  24240
caacatcaac tgcattgggc aagctgcaag acgttgttaa ccagaatgct caagcattaa  24300
acacacttgt taaacaactt agctctaatt ttggtgcaat ttcaagtgtg ctaaatgata  24360
tcctttcgcg acttgataaa gtcgaggcgg aggtacaaat tgacaggtta attacaggca  24420
gacttcaaag ccttcaaacc tatgtaacac aacaactaat cagggctgct gaaatcaggg  24480
cttctgctaa tcttgctgct actaaaatgt ctgagtgtgt tcttggacaa tcaaaaagag  24540
ttgacttttg tggaaagggc taccacctta tgtccttccc acaagcagcc ccgcatggtg  24600
ttgtcttcct acatgtcacg tatgtgccat cccaggagag gaacttcacc acagcgccag  24660
caatttgtca tgaaggcaaa gcatacttcc ctcgtgaagg tgtttttgtg tttaatggca  24720
cttcttggtt tattacacag aggaacttct tttctccaca aataattact acagacaata  24780
catttgtctc aggaaattgt gatgtcgtta ttggcatcat taacaacaca gtttatgatc  24840
ctctgcaacc tgagcttgac tcattcaaag aagagctgga caagtacttc aaaaatcata  24900
```

-continued

```
catcaccaga tgttgatctt ggcgacattt caggcattaa cgcttctgtc gtcaacattc  24960
aaaaagaaat tgaccgcctc aatgaggtcg ctaaaaattt aaatgaatca ctcattgacc  25020
ttcaagaatt gggaaaatat gagcaatata ttaaatggcc ttggtatgtt tggctcggct  25080
tcattgctgg actaattgcc atcgtcatgg ttacaatctt gctttgttgc atgactagtt  25140
gttgcagttg cctcaagggt gcatgctctt gtggttcttg ctgcaagttt gatgaggatg  25200
actctgagcc agttctcaag ggtgtcaaat tacattacac ataaacgaac ttatggattt  25260
gtttatgaga tttttactc ttagatcaat tactgcacag ccagtaaaaa ttgacaatgc  25320
ttctcctgca agtactgttc atgctacagc aacgataccg ctacaagcct cactcccttt  25380
cggatggctt gttattggcg ttgcatttct tgctgttttt cagagcgcta ccaaaataat  25440
tgcgctcaat aaaagatggc agctagccct ttataagggc ttccagttca tttgcaattt  25500
actgctgcta tttgttacca tctattcaca tcttttgctt gtcgctgcag gtatggaggc  25560
gcaattttg tacctctatg ccttgatata ttttctacaa tgcatcaacg catgtagaat  25620
tattatgaga tgttggcttt gttggaagtg caaatccaag aacccattac tttatgatgc  25680
caactacttt gtttgctggc acacacataa ctatgactac tgtataccat ataacagtgt  25740
cacagataca attgtcgtta ctgaaggtga cggcatttca acaccaaaac tcaaagaaga  25800
ctaccaaatt ggtggttatt ctgaggatag gcactcaggt gttaaagact atgtcgttgt  25860
acatggctat ttcaccgaag tttactacca gcttgagtct acacaaatta ctacagacac  25920
tggtattgaa aatgctacat tcttcatctt taacaagctt gttaaagacc caccgaatgt  25980
gcaaatacac acaatcgacg gctcttcagg agttgctaat ccagcaatgg atccaattta  26040
tgatgagccg acgacgacta ctagcgtgcc tttgtaagca caagaaagtg agtacgaact  26100
tatgtactca ttcgtttcgg aagaaacagg tacgttaata gttaatagcg tacttctttt  26160
tcttgctttc gtggtattct tgctagtcac actagccatc cttactgcgc ttcgattgtg  26220
tgcgtactgc tgcaatattg ttaacgtgag tttagtaaaa ccaacggttt acgtctactc  26280
gcgtgttaaa aatctgaact cttctgaagg agttcctgat cttctggtct aaacgaacta  26340
actattatta ttattctgtt tggaacttta acattgctta tcatggcaga caacggtact  26400
attaccgttg aggagcttaa acaactcctg gaacaatgga acctagtaat aggtttccta  26460
ttcctagcct ggattatgtt actacaattt gcctattcta atcggaacag gtttttgtac  26520
ataataaagc ttgttttcct ctggctcttg tggccagtaa cacttgcttg ttttgtgctt  26580
gctgctgtct acagaattaa ttgggtgact ggcgggattg cgattgcaat ggcttgtatt  26640
gtaggcttga tgtggcttag ctacttcgtt gcttccttca ggctgtttgc tcgtacccgc  26700
tcaatgtggt cattcaaccc agaaacaaac attcttctca atgtgcctct ccgggggaca  26760
attgtgacca gaccgctcat ggaaagtgaa cttgtcattg gtgctgtgat cattcgtggt  26820
cacttgcgaa tggccggaca ctccctaggg cgctgtgaca ttaaggacct gccaaaagag  26880
atcactgtgg ctacatcacg aacgctttct tattacaaat taggagcgtc gcagcgtgta  26940
ggcactgatt caggttttgc tgcatacaac cgctaccgta ttggaaacta taaattaaat  27000
acagaccacg ccggtagcaa cgacaatatt gctttgctag tacagtaagt gacaacagat  27060
gtttcatctt gttgacttcc aggttacaat agcagagata ttgattatca ttatgaggac  27120
tttcaggatt gctatttgga atcttgacgt tataataagt tcaatagtga gacaattatt  27180
taagcctcta actaagaaga attattcgga gttagatgat gaagaaccta tggagttaga  27240
ttatccataa aacgaacatg aaaattattc tcttcctgac attgattgta tttacatctt  27300
```

-continued

```
gcgagctata tcactatcag gagtgtgtta gaggtacgac tgtactacta aaagaacctt  27360
gcccatcagg aacatacgag ggcaattcac catttcaccc tcttgctgac aataaatttg  27420
cactaacttg cactagcaca cactttgctt ttgcttgtgc tgacggtact cgacatacct  27480
atcagctgcg tgcaagatca gtttcaccaa aacttttcat cagacaagag gaggttcaac  27540
aagagctcta ctcgccactt tttctcattg ttgctgctct agtatttta atactttgct  27600
tcaccattaa gagaaagaca gaatgaatga gctcacttta attgacttct atttgtgctt  27660
tttagccttt ctgctattcc ttgttttaat aatgcttatt atattttggt tttcactcga  27720
aatccaggat ctagaagaac cttgtaccaa agtctaaacg aacatgaaac ttctcattgt  27780
tttgacttgt atttctctat gcagttgcat atgcactgta gtacagcgct gtgcatctaa  27840
taaacctcat gtgcttgaag atccttgtaa ggtacaacac taggggtaat acttatagca  27900
ctgcttggct ttgtgctcta ggaaaggttt tacctttca tagatggcac actatggttc  27960
aaacatgcac acctaatgtt actatcaact gtcaagatcc agctggtggt gcgcttatag  28020
ctaggtgttg gtaccttcat gaaggtcacc aaactgctgc atttagagac gtacttgttg  28080
ttttaaataa acgaacaaat taaaatgtct gataatggac cccaatcaaa ccaacgtagt  28140
gccccccgca ttacatttgg tggacccaca gattcaactg acaataacca gaatggagga  28200
cgcaatgggg caaggccaaa acagcgccga ccccaaggtt tacccaataa tactgcgtct  28260
tggttcacag ctctcactca gcatggcaag gaggaactta gattccctcg aggccagggc  28320
gttccaatca acaccaatag tggtccagat gaccaaattg gctactaccg aagagctacc  28380
cgacgagttc gtggtggtga cggcaaaatg aaagagctca gccccagatg gtacttctat  28440
tacctaggaa ctggcccaga agcttcactt ccctacggcg ctaacaaaga aggcatcgta  28500
tgggttgcaa ctgagggagc cttgaataca cccaaagacc acattggcac ccgcaatcct  28560
aataacaatg ctgccaccgt gctacaactt cctcaaggaa caacattgcc aaaaggcttc  28620
tacgcagagg gaagcagagg cggcagtcaa gcctcttctc gctcctcatc acgtagtcgc  28680
ggtaattcaa gaaattcaac tcctggcagc agtaggggaa attctcctgc tcgaatggct  28740
agcggaggtg gtgaaactgc cctcgcgcta ttgctgctag acagattgaa ccagcttgag  28800
agcaaagttt ctggtaaagg ccaacaacaa caaggccaaa ctgtcactaa gaaatctgct  28860
gctgaggcat ctaaaaagcc tcgccaaaaa cgtactgcca caaaacagta caacgtcact  28920
caagcatttg ggagacgtgg tccagaacaa acccaaggaa atttcgggga ccaagaccta  28980
atcagacaag gaactgatta caaacattgg ccgcaaattg cacaatttgc tccaagtgcc  29040
tctgcattct ttggaatgtc acgcattggc atggaagtca caccttcggg aacatggctg  29100
acttatcatg gagccattaa attggatgac aaagatccac aattcaaaga caacgtcata  29160
ctgctgaaca agcacattga cgcatacaaa acattcccac caacagagcc taaaaaggac  29220
aaaaagaaaa agactgatga agctcagcct ttgccgcaga gacaaaagaa gcagcccact  29280
gtgactcttc ttcctgcggc tgacatggat gatttctcca gacaacttca aaattccatg  29340
agtggagctt ctgctgattc aactcaggca taaacactca tgatgaccac acaaggcaga  29400
tgggctatgt aaacgttttc gcaattccgt ttacgataca tagtctactc ttgtgcagaa  29460
tgaattctcg taactaaaca gcacaagtag gtttagttaa ctttaatctc acatagcaat  29520
ctttaatcaa tgtgtaacat tagggaggac ttgaaagagc caccacattt tcatcgaggc  29580
cacgcggagt acgatcgagg gtacagtgaa taatgctagg gagagctgcc tatatggaag  29640
```

-continued

agccctaatg tgtaaaatta attttagtag tgctatcccc atgtgatttt aatagcttct 29700

taggagaatg acaaaaaaaa aaaaaaaaaa aaaaaa 29736

<210> SEQ ID NO 3
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 3

tctctaaacg aactttaaaa tctgtg 26

<210> SEQ ID NO 4
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 4

caactaaacg aacatg 16

<210> SEQ ID NO 5
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 5

cacataaacg aacttatg 18

<210> SEQ ID NO 6
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 6

tgagtacgaa cttatg 16

<210> SEQ ID NO 7
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 7

ggtctaaacg aactaact 18

<210> SEQ ID NO 8
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 8

aactataaat t 11

<210> SEQ ID NO 9
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 9

tccataaaac gaacatg 17

<210> SEQ ID NO 10
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

-continued

<400> SEQUENCE: 10

tgctctagta tttttaatac tttg 24

<210> SEQ ID NO 11
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 11

agtctaaacg aacatg 16

<210> SEQ ID NO 12
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 12

ctaataaacc tcatg 15

<210> SEQ ID NO 13
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 13

taaataaacg aacaaattaa aatg 24

<210> SEQ ID NO 14
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 14

Lys Thr Phe Pro Pro Thr Glu Pro Lys Lys Asp Lys Lys Lys Lys Thr
1 5 10 15

Asp Glu Ala Gln
20

<210> SEQ ID NO 15
<211> LENGTH: 29751
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 15

atattaggtt tttacctacc caggaaaagc caaccaacct cgatctcttg tagatctgtt 60

ctctaaacga actttaaaat ctgtgtagct gtcgctcggc tgcatgccta gtgcacctac 120

gcagtataaa caataataaa ttttactgtc gttgacaaga aacgagtaac tcgtccctct 180

tctgcagact gcttacggtt tcgtccgtgt tgcagtcgat catcagcata cctaggtttc 240

gtccgggtgt gaccgaaagg taagatggag agccttgttc ttggtgtcaa cgagaaaaca 300

cacgtccaac tcagtttgcc tgtccttcag gttagagacg tgctagtgcg tggcttcggg 360

gactctgtgg aagaggccct atcggaggca cgtgaacacc tcaaaaatgg cacttgtggt 420

ctagtagagc tggaaaaagg cgtactgccc cagcttgaac agccctatgt gttcattaaa 480

cgttctgatg ccttaagcac caatcacggc cacaaggtcg ttgagctggt tgcagaaatg 540

gacggcattc agtacggtcg tagcggtata acactgggag tactcgtgcc acatgtgggc 600

gaaaccccaa ttgcataccg caatgttctt cttcgtaaga acggtaataa gggagccggt 660

-continued

```
ggtcatagct atggcatcga tctaaagtct tatgacttag gtgacgagct tggcactgat    720
cccattgaag attatgaaca aaactggaac actaagcatg gcagtggtgc actccgtgaa    780
ctcactcgtg agctcaatgg aggtgcagtc actcgctatg tcgacaacaa tttctgtggc    840
ccagatgggt accctcttga ttgcatcaaa gattttctcg cacgcgcggg caagtcaatg    900
tgcactcttt ccgaacaact tgattacatc gagtcgaaga gaggtgtcta ctgctgccgt    960
gaccatgagc atgaaattgc ctggttcact gagcgctctg ataagagcta cgagcaccag   1020
acacccttcg aaattaagag tgccaagaaa tttgacactt tcaaagggga atgcccaaag   1080
tttgtgtttc ctcttaactc aaaagtcaaa gtcattcaac cacgtgttga aaagaaaaag   1140
actgagggtt tcatggggcg tatacgctct gtgtaccctg ttgcatctcc acaggagtgt   1200
aacaatatgc acttgtctac cttgatgaaa tgtaatcatt gcgatgaagt ttcatggcag   1260
acgtgcgact ttctgaaagc cacttgtgaa cattgtggca ctgaaaattt agttattgaa   1320
ggacctacta catgtgggta cctacctact aatgctgtag tgaaaatgcc atgtcctgcc   1380
tgtcaagacc cagagattgg acctgagcat agtgttgcag attatcacaa ccactcaaac   1440
attgaaactc gactccgcaa gggaggtagg actagatgtt ttggaggctg tgtgtttgcc   1500
tatgttggct gctataataa gcgtgcctac tgggttcctc gtgctagtgc tgatattggc   1560
tcaggccata ctggcattac tggtgacaat gtggagacct tgaatgagga tctccttgag   1620
atactgagtc gtgaacgtgt taacattaac attgttggcg attttcattt gaatgaagag   1680
gttgccatca ttttggcatc tttctctgct tctacaagtg cctttattga cactataaag   1740
agtcttgatt acaagtcttt caaaaccatt gttgagtcct gcggtaacta taaagttacc   1800
aagggaaagc ccgtaaaagg tgcttggaac attggacaac agagatcagt tttaacacca   1860
ctgtgtggtt ttccctcaca ggctgctggt gttatcagat caatttttgc gcgcacactt   1920
gatgcagcaa accactcaat tcctgatttg caaagagcag ctgtcaccat acttgatggt   1980
atttctgaac agtcattacg tcttgtcgac gccatggttt atacttcaga cctgctcacc   2040
aacagtgtca ttattatggc atatgtaact ggtggtcttg tacaacagac ttctcagtgg   2100
ttgtctaatc ttttgggcac tactgttgaa aaactcaggc ctatctttga atggattgag   2160
gcgaaactta gtgcaggagt tgaatttctc aaggatgctt gggagattct caaatttctc   2220
attacaggtg tttttgacat cgtcaagggt caaatacagg ttgcttcaga taacatcaag   2280
gattgtgtaa aatgcttcat tgatgttgtt aacaaggcac tcgaaatgtg cattgatcaa   2340
gtcactatcg ctggcgcaaa gttgcgatca ctcaacttag gtgaagtctt catcgctcaa   2400
agcaagggac tttaccgtca gtgtatacgt ggcaaggagc agctgcaact actcatgcct   2460
cttaaggcac caaaagaagt aacctttctt gaaggtgatt cacatgacac agtacttacc   2520
tctgaggagg ttgttctcaa gaacggtgaa ctcgaagcac tcgagacgcc cgttgatagc   2580
ttcacaaatg gagctatcgt tggcacacca gtctgtgtaa atggcctcat gctcttagag   2640
attaaggaca aagaacaata ctgcgcattg tctcctggtt tactggctac aaacaatgtc   2700
tttcgcttaa aagggggtgc accaattaaa ggtgtaacct ttggagaaga tactgtttgg   2760
gaagttcaag gttacaagaa tgtgagaatc acatttgagc ttgatgaacg tgttgacaaa   2820
gtgcttaatg aaaagtgctc tgtctacact gttgaatccg gtaccgaagt tactgagttt   2880
gcatgtgttg tagcagaggc tgttgtgaag actttacaac cagtttctga tctccttacc   2940
aacatgggta ttgatcttga tgagtggagt gtagctacat tctacttatt tgatgatgct   3000
ggtgaagaaa acttttcatc acgtatgtat tgttcctttt accctccaga tgaggaagaa   3060
```

-continued

```
gaggacgatg cagagtgtga ggaagaagaa attgatgaaa cctgtgaaca tgagtacggt   3120
acagaggatg attatcaagg tctccctctg gaatttggtg cctcagctga aacagttcga   3180
gttgaggaag aagaagagga agactggctg gatgatacta ctgagcaatc agagattgag   3240
ccagaaccag aacctacacc tgaagaacca gttaatcagt ttactggtta tttaaaactt   3300
actgacaatg ttgccattaa atgtgttgac atcgttaagg aggcacaaag tgctaatcct   3360
atggtgattg taaatgctgc taacatacac ctgaaacatg gtggtggtgt agcaggtgca   3420
ctcaacaagg caaccaatgg tgccatgcaa aaggagagtg atgattacat taagctaaat   3480
ggccctctta cagtaggagg gtcttgtttg ctttctggac ataatcttgc taagaagtgt   3540
ctgcatgttg ttggacctaa cctaaatgca ggtgaggaca tccagcttct taaggcagca   3600
tatgaaaatt tcaattcaca ggacatctta cttgcaccat tgttgtcagc aggcatattt   3660
ggtgctaaac cacttcagtc tttacaagtg tgcgtgcaga cggttcgtac acaggtttat   3720
attgcagtca atgacaaagc tctttatgag caggttgtca tggattatct tgataacctg   3780
aagcctagag tggaagcacc taaacaagag gagccaccaa acacagaaga ttccaaaact   3840
gaggagaaat ctgtcgtaca gaagcctgtc gatgtgaagc caaaaattaa ggcctgcatt   3900
gatgaggtta ccacaacact ggaagaaact aagtttctta ccaataagtt actcttgttt   3960
gctgatatca atggtaagct ttaccatgat tctcagaaca tgcttagagg tgaagatatg   4020
tctttccttg agaaggatgc accttacatg gtaggtgatg ttatcactag tggtgatatc   4080
acttgtgttg taataccctc caaaaaggct ggtggcacta ctgagatgct ctcaagagct   4140
ttgaagaaag tgccagttga tgagtatata accacgtacc ctggacaagg atgtgctggt   4200
tatacacttg aggaagctaa gactgctctt aagaaatgca aatctgcatt ttatgtacta   4260
ccttcagaag cacctaatgc taaggaagag attctaggaa ctgtatcctg gaatttgaga   4320
gaaatgcttg ctcatgctga agagacaaga aaattaatgc ctatatgcat ggatgttaga   4380
gccataatgg caaccatcca acgtaagtat aaaggaatta aaattcaaga gggcatcgtt   4440
gactatggtg tccgattctt cttttatact agtaaagagc ctgtagcttc tattattacg   4500
aagctgaact ctctaaatga gccgcttgtc acaatgccaa ttggttatgt gacacatggt   4560
tttaatcttg aagaggctgc gcgctgtatg cgttctctta aagctcctgc cgtagtgtca   4620
gtatcatcac cagatgctgt tactacatat aatggatacc tcacttcgtc atcaaagaca   4680
tctgaggagc actttgtaga aacagtttct ttggctggct cttacagaga ttggtcctat   4740
tcaggacagc gtacagagtt aggtgttgaa tttcttaagc gtggtgacaa aattgtgtac   4800
cacactctgg agagccccgt cgagtttcat cttgacggtg aggttctttc acttgacaaa   4860
ctaaagagtc tcttatccct gcgggaggtt aagactataa aagtgttcac aactgtggac   4920
aacactaatc tccacacaca gcttgtggat atgtctatga catatggaca gcagtttggt   4980
ccaacatact tggatggtgc tgatgttaca aaaattaaac ctcatgtaaa tcatgagggt   5040
aagactttct ttgtactacc tagtgatgac acactacgta gtgaagcttt cgagtactac   5100
catactcttg atgagagttt tcttggtagg tacatgtctg ctttaaacca cacaaagaaa   5160
tggaaatttc ctcaagttgg tggtttaact tcaattaaat gggctgataa caattgttat   5220
ttgtctagtg ttttattagc acttcaacag cttgaagtca aattcaatgc accagcactt   5280
caagaggctt attatagagc ccgtgctggt gatgctgcta acttttgtgc actcatactc   5340
gcttacagta ataaaactgt tggcgagctt ggtgatgtca gagaaactat gacccatctt   5400
```

-continued

```
ctacagcatg ctaatttgga atctgcaaag cgagttctta atgtggtgtg taaacattgt   5460
ggtcagaaaa ctactacctt aacgggtgta gaagctgtga tgtatatggg tactctatct   5520
tatgataatc ttaagacagg tgtttccatt ccatgtgtgt gtggtcgtga tgctacacaa   5580
tatctagtac aacaagagtc ttcttttgtt atgatgtctg caccacctgc tgagtataaa   5640
ttacagcaag gtacattctt atgtgcgaat gagtacactg gtaactatca gtgtggtcat   5700
tacactcata taactgctaa ggagaccctc tatcgtattg acggagctca ccttacaaag   5760
atgtcagagt acaaaggacc agtgactgat gttttctaca aggaaacatc ttacactaca   5820
accatcaagc ctgtgtcgta taaactcgat ggagttactt acacagagat tgaaccaaaa   5880
ttggatgggt attataaaaa ggataatgct tactatacag agcagcctat agaccttgta   5940
ccaactcaac cattaccaaa tgcgagtttt gataatttca aactcacatg ttctaacaca   6000
aaatttgctg atgatttaaa tcaaatgaca ggcttcacaa agccagcttc acgagagcta   6060
tctgtcacat tcttcccaga cttgaatggc gatgtagtgg ctattgacta tagacactat   6120
tcagcgagtt tcaagaaagg tgctaaatta ctgcataagc caattgtttg gcacattaac   6180
caggctacaa ccaagacaac gttcaaacca aacacttggt gtttacgttg tctttggagt   6240
acaaagccag tagatacttc aaattcattt gaagttctgg cagtagaaga cacacaagga   6300
atggacaatc ttgcttgtga aagtcaacaa cccacctctg aagaagtagt ggaaaatcct   6360
accatacaga aggaagtcat agagtgtgac gtgaaaacta ccgaagttgt aggcaatgtc   6420
atacttaaac catcagatga aggtgttaaa gtaacacaag agttaggtca tgaggatctt   6480
atggctgctt atgtggaaaa cacaagcatt accattaaga aacctaatga gctttcacta   6540
gccttaggtt taaaaacaat tgccactcat ggtattgctg caattaatag tgttccttgg   6600
agtaaaattt tggcttatgt caaaccattc ttaggacaag cagcaattac aacatcaaat   6660
tgcgctaaga gattagcaca acgtgtgttt aacaattata tgccttatgt gtttacatta   6720
ttgttccaat tgtgtacttt tactaaaagt accaattcta gaattagagc ttcactacct   6780
acaactattg ctaaaaatag tgttaagagt gttgctaaat tatgtttgga tgccggcatt   6840
aattatgtga agtcacccaa attttctaaa ttgttcacaa tcgctatgtg gctattgttg   6900
ttaagtattt gcttaggttc tctaatctgt gtaactgctg cttttggtgt actcttatct   6960
aattttggtg ctccttctta ttgtaatggc gttagagaat tgtatcttaa ttcgtctaac   7020
gttactacta tggatttctg tgaaggttct tttccttgca gcatttgttt aagtggatta   7080
gactcccttg attcttatcc agctcttgaa accattcagg tgacgatttc atcgtacaag   7140
ctagacttga caattttagg tctggccgct gagtgggttt tggcatatat gttgttcaca   7200
aaattctttt atttattagg tctttcagct ataatgcagg tgttctttgg ctattttgct   7260
agtcatttca tcagcaattc ttggctcatg tggtttatca ttagtattgt acaaatggca   7320
cccgtttctg caatggttag gatgtacatc ttctttgctt ctttctacta catatggaag   7380
agctatgttc atatcatgga tggttgcacc tcttcgactt gcatgatgtg ctataagcgc   7440
aatcgtgcca cacgcgttga gtgtacaact attgttaatg gcatgaagag atctttctat   7500
gtctatgcaa atggaggccg tggcttctgc aagactcaca attggaattg tctcaattgt   7560
gacacatttt gcactggtag tacattcatt agtgatgaag ttgctcgtga tttgtcactc   7620
cagtttaaaa gaccaatcaa ccctactgac cagtcatcgt atattgttga tagtgttgct   7680
gtgaaaaatg gcgcgcttca cctctacttt gacaaggctg gtcaaaagac ctatgagaga   7740
catccgctct cccattttgt caatttagac aatttgagag ctaacaacac taaaggttca   7800
```

-continued

```
ctgcctatta atgtcatagt ttttgatggc aagtccaaat gcgacgagtc tgcttctaag   7860
tctgcttctg tgtactacag tcagctgatg tgccaaccta ttctgttgct tgaccaagct   7920
cttgtatcag acgttggaga tagtactgaa gtttccgtta agatgtttga tgcttatgtc   7980
gacacctttt cagcaacttt tagtgttcct atggaaaaac ttaaggcact tgttgctaca   8040
gctcacagcg agttagcaaa gggtgtagct ttagatggtg tcctttctac attcgtgtca   8100
gctgcccgac aaggtgttgt tgataccgat gttgacacaa aggatgttat tgaatgtctc   8160
aaactttcac atcactctga cttagaagtg acaggtgaca gttgtaacaa tttcatgctc   8220
acctataata aggttgaaaa catgacgccc agagatcttg gcgcatgtat tgactgtaat   8280
gcaaggcata tcaatgccca agtagcaaaa agtcacaatg tttcactcat ctggaatgta   8340
aaagactaca tgtctttatc tgaacagctg cgtaaacaaa ttcgtagtgc tgccaagaag   8400
aacaacatac cttttagact aacttgtgct acaactagac aggttgtcaa tgtcataact   8460
actaaaatct cactcaaggg tggtaagatt gttagtactt gttttaaact tatgcttaag   8520
gccacattat tgtgcgttct tgctgcattg gtttgttata tcgttatgcc agtacataca   8580
ttgtcaatcc atgatggtta cacaaatgaa atcattggtt acaaagccat tcaggatggt   8640
gtcactcgtg acatcatttc tactgatgat tgttttgcaa ataaacatgc tggttttgac   8700
gcatggttta gccagcgtgg tggttcatac aaaaatgaca aaagctgccc tgtagtagct   8760
gctatcatta caagagagat tggtttcata gtgcctggct taccgggtac tgtgctgaga   8820
gcaatcaatg gtgacttctt gcattttcta cctcgtgttt ttagtgctgt tggcaacatt   8880
tgctacacac cttccaaact cattgagtat agtgattttg ctacctctgc ttgcgttctt   8940
gctgctgagt gtacaatttt taaggatgct atgggcaaac ctgtgccata ttgttatgac   9000
actaatttgc tagagggttc tatttcttat agtgagcttc gtccagacac tcgttatgtg   9060
cttatggatg gttccatcat acagtttcct aacacttacc tggagggttc tgttagagta   9120
gtaacaactt ttgatgctga gtactgtaga catggtacat gcgaaaggtc agaagtaggt   9180
atttgcctat ctaccagtgg tagatgggtt cttaataatg agcattacag agctctatca   9240
ggagttttct gtggtgttga tgcgatgaat ctcatagcta acatctttac tcctcttgtg   9300
caacctgtgg gtgctttaga tgtgtctgct tcagtagtgg ctggtggtat tattgccata   9360
ttggtgactt gtgctgccta ctactttatg aaattcagac gtgtttttgg tgagtacaac   9420
catgttgttg ctgctaatgc acttttgttt ttgatgtctt tcactatact ctgtctggta   9480
ccagcttaca gctttctgcc gggagtctac tcagtctttt acttgtactt gacattctat   9540
ttcaccaatg atgtttcatt cttggctcac cttcaatggt ttgccatgtt ttctcctatt   9600
gtgccttttt ggataacagc aatctatgta ttctgtattt ctctgaagca ctgccattgg   9660
ttctttaaca actatcttag gaaaagagtc atgtttaatg gagttacatt tagtaccttc   9720
gaggaggctg ctttgtgtac ctttttgctc aacaaggaaa tgtacctaaa attgcgtagc   9780
gagacactgt tgccacttac acagtataac aggtatcttg ctctatataa caagtacaag   9840
tatttcagtg gagccttaga tactaccagc tatcgtgaag cagcttgctg ccacttagca   9900
aaggctctaa atgactttag caactcaggt gctgatgttc tctaccaacc accacagaca   9960
tcaatcactt ctgctgttct gcagagtggt tttaggaaaa tggcattccc gtcaggcaaa  10020
gttgaagggt gcatggtaca agtaacctgt ggaactacaa ctcttaatgg attgtggttg  10080
gatgacacag tatactgtcc aagacatgtc atttgcacag cagaagacat gcttaatcct  10140
```

-continued

```
aactatgaag atctgctcat tcgcaaatcc aaccatagct ttcttgttca ggctggcaat  10200
gttcaacttc gtgttattgg ccattctatg caaaattgtc tgcttaggct taaagttgat  10260
acttctaacc ctaagacacc caagtataaa tttgtccgta tccaacctgg tcaaacattt  10320
tcagttctag catgctacaa tggttcacca tctggtgttt atcagtgtgc catgagacct  10380
aatcatacca ttaaaggttc tttccttaat ggatcatgtg gtagtgttgg ttttaacatt  10440
gattatgatt gcgtgtcttt ctgctatatg catcatatgg agcttccaac aggagtacac  10500
gctggtactg acttagaagg taaattctat ggtccatttg ttgacagaca aactgcacag  10560
gctgcaggta cagacacaac cataacatta aatgttttgg catggctgta tgctgctgtt  10620
atcaatggtg ataggtggtt tcttaataga ttcaccacta ctttgaatga ctttaacctt  10680
gtggcaatga agtacaacta tgaacctttg acacaagatc atgttgacat attgggacct  10740
ctttctgctc aaacaggaat tgccgtctta gatatgtgtg ctgctttgaa agagctgctg  10800
cagaatggta tgaatggtcg tactatcctt ggtagcacta ttttagaaga tgagtttaca  10860
ccatttgatg ttgttagaca atgctctggt gttaccttcc aaggtaagtt caagaaaatt  10920
gttaagggca ctcatcattg gatgctttta actttcttga catcactatt gattcttgtt  10980
caaagtacac agtggtcact gtttttcttt gtttacgaga atgctttctt gccatttact  11040
cttggtatta tggcaattgc tgcatgtgct atgctgcttg ttaagcataa gcacgcattc  11100
ttgtgcttgt ttctgttacc ttctcttgca acagttgctt actttaatat ggtctacatg  11160
cctgctagct gggtgatgcg tatcatgaca tggcttgaat tggctgacac tagcttgtct  11220
ggttataggc ttaaggattg tgttatgtat gcttcagctt tagttttgct tattctcatg  11280
acagctcgca ctgtttatga tgatgctgct agacgtgttt ggacactgat gaatgtcatt  11340
acacttgttt acaaagtcta ctatggtaat gctttagatc aagctatttc catgtgggcc  11400
ttagttattt ctgtaacctc taactattct ggtgtcgtta cgactatcat gtttttagct  11460
agagctatag tgtttgtgtg tgttgagtat tacccattgt tatttattac tggcaacacc  11520
ttacagtgta tcatgcttgt ttattgtttc ttaggctatt gttgctgctg ctactttggc  11580
cttttctgtt tactcaaccg ttacttcagg cttactcttg gtgtttatga ctacttggtc  11640
tctacacaag aatttaggta tatgaactcc caggggcttt tgcctcctaa gagtagtatt  11700
gatgctttca agcttaacat taagttgttg ggtattggag gtaaaccatg tatcaaggtt  11760
gctactgtac agtctaaaat gtctgacgta aagtgcacat ctgtggtact gctctcggtt  11820
cttcaacaac ttagagtaga gtcatcttct aaattgtggg cacaatgtgt acaactccac  11880
aatgatattc ttcttgcaaa agacacaact gaagctttcg agaagatggt ttctcttttg  11940
tctgttttgc tatccatgca gggtgctgta gacattaata ggttgtgcga ggaaatgctc  12000
gataaccgtg ctactcttca ggctattgct tcagaattta gttctttacc atcatatgcc  12060
gcttatgcca ctgcccagga ggcctatgag caggctgtag ctaatggtga ttctgaagtc  12120
gttctcaaaa agttaaagaa atctttgaat gtggctaaat ctgagtttga ccgtgatgct  12180
gccatgcaac gcaagttgga aaagatggca gatcaggcta tgacccaaat gtacaaacag  12240
gcaagatctg aggacaagag ggcaaaagta actagtgcta tgcaaacaat gctcttcact  12300
atgcttagga agcttgataa tgatgcactt aacaacatta tcaacaatgc gcgtgatggt  12360
tgtgttccac tcaacatcat accattgact acagcagcca aactcatggt tgttgtccct  12420
gattatggta cctacaagaa cacttgtgat ggtaacacct ttacatatgc atctgcactc  12480
tgggaaatcc agcaagttgt tgatgcggat agcaagattg ttcaacttag tgaaattaac  12540
```

-continued

```
atggacaatt caccaaattt ggcttggcct cttattgtta cagctctaag agccaactca  12600
gctgttaaac tacagaataa tgaactgagt ccagtagcac tacgacagat gtcctgtgcg  12660
gctggtacca cacaaacagc ttgtactgat gacaatgcac ttgcctacta taacaattcg  12720
aagggaggta ggtttgtgct ggcattacta tcagaccacc aagatctcaa atgggctaga  12780
ttccctaaga gtgatggtac aggtacaatt tacacagaac tggaaccacc ttgtaggttt  12840
gttacagaca caccaaaagg gcctaaagtg aaatacttgt acttcatcaa aggcttaaac  12900
aacctaaata gaggtatggt gctgggcagt ttagctgcta cagtacgtct tcaggctgga  12960
aatgctacag aagtacctgc caattcaact gtgctttcct tctgtgcttt tgcagtagac  13020
cctgctaaag catataagga ttacctagca agtggaggac aaccaatcac caactgtgtg  13080
aagatgttgt gtacacacac tggtacagga caggcaatta ctgtaacacc agaagctaac  13140
atggaccaag agtcctttgg tggtgcttca tgttgtctgt attgtagatg ccacattgac  13200
catccaaatc ctaaaggatt ctgtgacttg aaaggtaagt acgtccaaat acctaccact  13260
tgtgctaatg acccagtggg ttttacactt agaaacacag tctgtaccgt ctgcggaatg  13320
tggaaaggtt atggctgtag ttgtgaccaa ctccgcgaac ccttgatgca gtctgcggat  13380
gcatcaacgt ttttaaacgg gtttgcggtg taagtgcagc ccgtcttaca ccgtgcggca  13440
caggcactag tactgatgtc gtctacaggg cttttgatat ttacaacgaa aaagttgctg  13500
gttttgcaaa gttcctaaaa actaattgct gtcgcttcca ggagaaggat gaggaaggca  13560
atttattaga ctcttacttt gtagttaaga ggcatactat gtctaactac caacatgaag  13620
agactattta taacttggtt aaagattgtc cagcggttgc tgtccatgac tttttcaagt  13680
ttagagtaga tggtgacatg gtaccacata tatcacgtca gcgtctaact aaatacacaa  13740
tggctgattt agtctatgct ctacgtcatt ttgatgaggg taattgtgat acattaaaag  13800
aaatactcgt cacatacaat tgctgtgatg atgattattt caataagaag gattggtatg  13860
acttcgtaga gaatcctgac atcttacgcg tatatgctaa cttaggtgag cgtgtacgcc  13920
aatcattatt aaagactgta caattctgcg atgctatgcg tgatgcaggc attgtaggcg  13980
tactgacatt agataatcag gatcttaatg ggaactggta cgatttcggt gatttcgtac  14040
aagtagcacc aggctgcgga gttcctattg tggattcata ttactcattg ctgatgccca  14100
tcctcacttt gactagggca ttggctgctg agtcccatat ggatgctgat ctcgcaaaac  14160
cacttattaa gtgggatttg ctgaaatatg attttacgga agagagactt tgtctcttcg  14220
accgttattt taaatattgg gaccagacat accatcccaa ttgtattaac tgtttggatg  14280
ataggtgtat ccttcattgt gcaaacttta atgtgttatt ttctactgtg tttccaccta  14340
caagttttgg accactagta agaaaaatat ttgtagatgg tgttcctttt gttgtttcaa  14400
ctggatacca ttttcgtgag ttaggagtcg tacataatca ggatgtaaac ttacatagct  14460
cgcgtctcag tttcaaggaa cttttagtgt atgctgctga tccagctatg catgcagctt  14520
ctggcaattt attgctagat aaacgcacta catgcttttc agtagctgca ctaacaaaca  14580
atgttgcttt tcaaactgtc aaacccggta attttaataa agacttttat gactttgctg  14640
tgtctaaagg tttctttaag gaaggaagtt ctgttgaact aaaacacttc ttctttgctc  14700
aggatggcaa cgctgctatc agtgattatg actattatcg ttataatctg ccaacaatgt  14760
gtgatatcag acaactccta ttcgtagttg aagttgttga taaatacttt gattgttacg  14820
atggtggctg tattaatgcc aaccaagtaa tcgttaacaa tctggataaa tcagctggtt  14880
```

-continued

```
tcccatttaa taaatggggt aaggctagac tttattatga ctcaatgagt tatgaggatc  14940
aagatgcact tttcgcgtat actaagcgta atgtcatccc tactataact caaatgaatc  15000
ttaagtatgc cattagtgca aagaatagag ctcgcaccgt agctggtgtc tctatctgta  15060
gtactatgac aaatagacag tttcatcaga aattattgaa gtcaatagcc gccactagag  15120
gagctactgt ggtaattgga acaagcaagt tttacggtgg ctggcataat atgttaaaaa  15180
ctgtttacag tgatgtagaa actccacacc ttatgggttg ggattatcca aaatgtgaca  15240
gagccatgcc taacatgctt aggataatgg cctctcttgt tcttgctcgc aaacataaca  15300
cttgctgtaa cttatcacac cgtttctaca ggttagctaa cgagtgtgcg caagtattaa  15360
gtgagatggt catgtgtggc ggctcactat atgttaaacc aggtggaaca tcatccggtg  15420
atgctacaac tgcttatgct aatagtgtct ttaacatttg tcaagctgtt acagccaatg  15480
taaatgcact tctttcaact gatggtaata agatagctga caagtatgtc cgcaatctac  15540
aacacaggct ctatgagtgt ctctatagaa atagggatgt tgatcatgaa ttcgtggatg  15600
agttttacgc ttacctgcgt aaacatttct ccatgatgat tctttctgat gatgccgttg  15660
tgtgctataa cagtaactat gcggctcaag gtttagtagc tagcattaag aactttaagg  15720
cagttcttta ttatcaaaat aatgtgttca tgtctgaggc aaaatgttgg actgagactg  15780
accttactaa aggacctcac gaattttgct cacagcatac aatgctagtt aaacaaggag  15840
atgattacgt gtacctgcct tacccagatc catcaagaat attaggcgca ggctgttttg  15900
tcgatgatat tgtcaaaaca gatggtacac ttatgattga aaggttcgtg tcactggcta  15960
ttgatgctta cccacttaca aaacatccta atcaggagta tgctgatgtc tttcacttgt  16020
atttacaata cattagaaag ttacatgatg agcttactgg ccacatgttg gacatgtatt  16080
ccgtaatgct aactaatgat aacacctcac ggtactggga acctgagttt tatgaggcta  16140
tgtacacacc acatacagtc ttgcaggctg taggtgcttg tgtattgtgc aattcacaga  16200
cttcacttcg ttgcggtgcc tgtattagga gaccattcct atgttgcaag tgctgctatg  16260
accatgtcat ttcaacatca cacaaattag tgttgtctgt taatccctat gtttgcaatg  16320
ccccaggttg tgatgtcact gatgtgacac aactgtatct aggaggtatg agctattatt  16380
gcaagtcaca taagcctccc attagttttc cattatgtgc taatggtcag gtttttggtt  16440
tatacaaaaa cacatgtgta ggcagtgaca atgtcactga cttcaatgcg atagcaacat  16500
gtgattggac taatgctggc gattacatac ttgccaacac ttgtactgag agactcaagc  16560
ttttcgcagc agaaacgctc aaagccactg aggaaacatt taagctgtca tatggtattg  16620
ccactgtacg cgaagtactc tctgacagag aattgcatct ttcatgggag gttggaaaac  16680
ctagaccacc attgaacaga aactatgtct ttactggtta ccgtgtaact aaaaatagta  16740
aagtacagat tggagagtac acctttgaaa aaggtgacta tggtgatgct gttgtgtaca  16800
gaggtactac gacatacaag ttgaatgttg gtgattactt tgtgttgaca tctcacactg  16860
taatgccact tagtgcacct actctagtgc cacaagagca ctatgtgaga attactggct  16920
tgtacccaac actcaacatc tcagatgagt tttctagcaa tgttgcaaat tatcaaaagg  16980
tcggcatgca aaagtactct acactccaag gaccacctgg tactggtaag agtcattttg  17040
ccatcggact tgctctctat tacccatctg ctcgcatagt gtatacggca tgctctcatg  17100
cagctgttga tgccctatgt gaaaaggcat taaaatattt gcccatagat aaatgtagta  17160
gaatcatacc tgcgcgtgcg cgcgtagagt gttttgataa attcaaagtg aattcaacac  17220
tagaacagta tgttttctgc actgtaaatg cattgccaga aacaactgct gacattgtag  17280
```

-continued

```
tctttgatga aatctctatg gctactaatt atgacttgag tgttgtcaat gctagacttc  17340
gtgcaaaaca ctacgtctat attggcgatc ctgctcaatt accagccccc cgcacattgc  17400
tgactaaagg cacactagaa ccagaatatt ttaattcagt gtgcagactt atgaaaacaa  17460
taggtccaga catgttcctt ggaacttgtc gccgttgtcc tgctgaaatt gttgacactg  17520
tgagtgcttt agtttatgac aataagctaa aagcacacaa ggataagtca gctcaatgct  17580
tcaaaatgtt ctacaaaggt gttattacac atgatgtttc atctgcaatc aacagacctc  17640
aaataggcgt tgtaagagaa tttcttacac gcaatcctgc ttggagaaaa gctgttttta  17700
tctcacctta taattcacag aacgctgtag cttcaaaaat cttaggattg cctacgcaga  17760
ctgttgattc atcacagggt tctgaatatg actatgtcat attcacacaa actactgaaa  17820
cagcacactc ttgtaatgtc aaccgcttca atgtggctat cacaagggca aaaattggca  17880
ttttgtgcat aatgtctgat agagatcttt atgacaaact gcaatttaca agtctagaaa  17940
taccacgtcg caatgtggct acattacaag cagaaaatgt aactggactt tttaaggact  18000
gtagtaagat cattactggt cttcatccta cacaggcacc tacacacctc agcgttgata  18060
taaagttcaa gactgaagga ttatgtgttg acataccagg cataccaaag gacatgacct  18120
accgtagact catctctatg atgggtttca aaatgaatta ccaagtcaat ggttacccta  18180
atatgtttat cacccgcgaa gaagctattc gtcacgttcg tgcgtggatt ggctttgatg  18240
tagagggctg tcatgcaact agagatgctg tgggtactaa cctacctctc cagctaggat  18300
tttctacagg tgttaactta gtagctgtac cgactggtta tgttgacact gaaaataaca  18360
cagaattcac cagagttaat gcaaaacctc caccaggtga ccagtttaaa catcttatac  18420
cactcatgta taaaggcttg ccctggaatg tagtgcgtat taagatagta caaatgctca  18480
gtgatacact gaaaggattg tcagacagag tcgtgttcgt cctttgggcg catggctttg  18540
agcttacatc aatgaagtac tttgtcaaga ttggacctga aagaacgtgt tgtctgtgtg  18600
acaaacgtgc aacttgcttt tctacttcat cagatactta tgcctgctgg aatcattctg  18660
tgggttttga ctatgtctat aacccattta tgattgatgt tcagcagtgg ggctttacgg  18720
gtaaccttca gagtaaccat gaccaacatt gccaggtaca tggaaatgca catgtggcta  18780
gttgtgatgc tatcatgact agatgtttag cagtccatga gtgctttgtt aagcgcgttg  18840
attggtctgt tgaatacccct attataggag atgaactgag ggttaattct gcttgcagaa  18900
aagtacaaca catggttgtg aagtctgcat tgcttgctga taagtttcca gttcttcatg  18960
acattggaaa tccaaaggct atcaagtgtg tgcctcaggc tgaagtagaa tggaagttct  19020
acgatgctca gccatgtagt gacaaagctt acaaaataga ggaactcttc tattcttatg  19080
ctacacatca cgataaattc actgatggtg tttgtttgtt ttggaattgt aacgttgatc  19140
gttacccagc caatgcaatt gtgtgtaggt ttgacacaag agtcttgtca aacttgaact  19200
taccaggctg tgatggtggt agtttgtatg tgaataagca tgcattccac actccagctt  19260
tcgataaaag tgcatttact aatttaaagc aattgccttt cttttactat tctgatagtc  19320
cttgtgagtc tcatggcaaa caagtagtgt cggatattga ttatgttcca ctcaaatctg  19380
ctacgtgtat tacacgatgc aatttaggtg gtgctgtttg cagacaccat gcaaatgagt  19440
accgacagta cttggatgca tataatatga tgatttctgc tggatttagc ctatggattt  19500
acaaacaatt tgatacttat aacctgtgga atacatttac caggttacag agtttagaaa  19560
atgtggctta taatgttgtt aataaaggac actttgatgg acacgccggc gaagcacctg  19620
```

-continued

```
tttccatcat taataatgct gtttacacaa aggtagatgg tattgatgtg gagatctttg  19680
aaaataagac aacacttcct gttaatgttg catttgagct ttgggctaag cgtaacatta  19740
aaccagtgcc agagattaag atactcaata atttgggtgt tgatatcgct gctaatactg  19800
taatctggga ctacaaaaga gaagccccag cacatgtatc tacaataggt gtctgcacaa  19860
tgactgacat tgccaagaaa cctactgaga gtgcttgttc ttcacttact gtcttgtttg  19920
atggtagagt ggaaggacag gtagaccttt ttagaaacgc ccgtaatggt gttttaataa  19980
cagaaggttc agtcaaaggt ctaacacctt caaagggacc agcacaagct agcgtcaatg  20040
gagtcacatt aattggagaa tcagtaaaaa cacagtttaa ctactttaag aaagtagacg  20100
gcattattca acagttgcct gaaacctact ttactcagag cagagactta gaggatttta  20160
agcccagatc acaaatggaa actgactttc tcgagctcgc tatggatgaa ttcatacagc  20220
gatataagct cgagggctat gccttcgaac acatcgttta tggagatttc agtcatggac  20280
aacttggcgg tcttcattta atgataggct tagccaagcg ctcacaagat tcaccactta  20340
aattagagga ttttatccct atggacagca cagtgaaaaa ttacttcata acagatgcgc  20400
aaacaggttc atcaaaatgt gtgtgttctg tgattgatct tttacttgat gactttgtcg  20460
agataataaa gtcacaagat ttgtcagtga tttcaaaagt ggtcaaggtt acaattgact  20520
atgctgaaat ttcattcatg ctttggtgta aggatggaca tgttgaaacc ttctacccaa  20580
aactacaagc aagtcaagcg tggcaaccag gtgttgcgat gcctaacttg tacaagatgc  20640
aaagaatgct tcttgaaaag tgtgaccttc agaattatgg tgaaaatgct gttataccaa  20700
aaggaataat gatgaatgtc gcaaagtata ctcaactgtg tcaatactta aatacactta  20760
ctttagctgt accctacaac atgagagtta ttcactttgg tgctggctct gataaaggag  20820
ttgcaccagg tacagctgtg ctcagacaat ggttgccaac tggcacacta cttgtcgatt  20880
cagatcttaa tgacttcgtc tccgacgcag attctacttt aattggagac tgtgcaacag  20940
tacatacggc taataaatgg gaccttatta ttagcgatat gtatgaccct aggaccaaac  21000
atgtgacaaa agagaatgac tctaaagaag ggtttttcac ttatctgtgt ggatttataa  21060
agcaaaaact agccctgggt ggttctatag ctgtaaagat aacagagcat tcttggaatg  21120
ctgaccttta caagcttatg ggccatttct catggtggac agcttttgtt acaaatgtaa  21180
atgcatcatc atcggaagca tttttaattg ggctaacta tcttggcaag ccgaaggaac  21240
aaattgatgg ctataccatg catgctaact acattttctg gaggaacaca aatcctatcc  21300
agttgtcttc ctattcactc tttgacatga gcaaatttcc tcttaaatta agaggaactg  21360
ctgtaatgtc tcttaaggag aatcaaatca atgatatgat ttattctctt ctggaaaaag  21420
gtaggcttat cattagagaa aacaacagag ttgtggtttc aagtgatatt cttgttaaca  21480
actaaacgaa catgtttatt ttcttattat ttcttactct cactagtggt agtgaccttg  21540
accggtgcac cacttttgat gatgttcaag ctcctaatta cactcaacat acttcatcta  21600
tgagggggt ttactatcct gatgaaattt ttagatcaga cactctttat ttaactcagg  21660
atttatttct tccattttat tctaatgtta cagggtttca tactattaat catacgtttg  21720
gcaaccctgt catacctttt aaggatggta tttattttgc tgccacagag aaatcaaatg  21780
ttgtccgtgg ttgggttttt ggttctacca tgaacaacaa gtcacagtcg gtgattatta  21840
ttaacaattc tactaatgtt gttatacgag catgtaactt tgaattgtgt gacaaccctt  21900
tctttgctgt ttctaaaccc atgggtacac agacacatac tatgatattc gataatgcat  21960
ttaattgcac tttcgagtac atatctgatg ccttttcgct tgatgtttca gaaaagtcag  22020
```

-continued

```
gtaattttaa acacttacga gagtttgtgt ttaaaaataa agatgggttt ctctatgttt  22080
ataagggcta tcaacctata gatgtagttc gtgatctacc ttctggtttt aacactttga  22140
aacctatttt taagttgcct cttggtatta acattacaaa ttttagagcc attcttacag  22200
ccttttcacc tgctcaagac atttggggca cgtcagctgc agcctatttt gttggctatt  22260
taaagccaac tacatttatg ctcaagtatg atgaaaatgg tacaatcaca gatgctgttg  22320
attgttctca aaatccactt gctgaactca aatgctctgt taagagcttt gagattgaca  22380
aaggaattta ccagacctct aatttcaggg ttgttccctc aggagatgtt gtgagattcc  22440
ctaatattac aaacttgtgt ccttttggag aggtttttaa tgctactaaa ttcccttctg  22500
tctatgcatg ggagagaaaa aaaatttcta attgtgttgc tgattactct gtgctctaca  22560
actcaacatt tttttcaacc tttaagtgct atggcgtttc tgccactaag ttgaatgatc  22620
tttgcttctc caatgtctat gcagattctt ttgtagtcaa gggagatgat gtaagacaaa  22680
tagcgccagg acaaactggt gttattgctg attataatta taaattgcca gatgatttca  22740
tgggttgtgt ccttgcttgg aatactagga acattgatgc tacttcaact ggtaattata  22800
attataaata taggtatctt agacatggca agcttaggcc ctttgagaga gacatatcta  22860
atgtgccttt ctcccctgat ggcaaacctt gcaccccacc tgctcttaat tgttattggc  22920
cattaaatga ttatggtttt tacaccacta ctggcattgg ctaccaacct tacagagttg  22980
tagtactttc ttttgaactt ttaaatgcac cggccacggt ttgtggacca aaattatcca  23040
ctgaccttat taagaaccag tgtgtcaatt ttaattttaa tggactcact ggtactggtg  23100
tgttaactcc ttcttcaaag agatttcaac catttcaaca atttggccgt gatgtttctg  23160
atttcactga ttccgttcga gatcctaaaa catctgaaat attagacatt tcaccttgcg  23220
cttttggggg tgtaagtgta attacacctg gaacaaatgc ttcatctgaa gttgctgttc  23280
tatatcaaga tgttaactgc actgatgttt ctacagcaat tcatgcagat caactcacac  23340
cagcttggcg catatattct actggaaaca atgtattcca gactcaagca ggctgtctta  23400
taggagctga gcatgtcgac acttcttatg agtgcgacat tcctattgga gctggcattt  23460
gtgctagtta ccatacagtt tctttattac gtagtactag ccaaaaatct attgtggctt  23520
atactatgtc tttaggtgct gatagttcaa ttgcttactc taataacacc attgctatac  23580
ctactaactt ttcaattagc attactacag aagtaatgcc tgtttctatg gctaaaacct  23640
ccgtagattg taatatgtac atctgcggag attctactga atgtgctaat ttgcttctcc  23700
aatatggtag cttttgcaca caactaaatc gtgcactctc aggtattgct gctgaacagg  23760
atcgcaacac acgtgaagtg ttcgctcaag tcaaacaaat gtacaaaacc ccaactttga  23820
aatattttgg tggttttaat ttttcacaaa tattacctga ccctctaaag ccaactaaga  23880
ggtcttttat tgaggacttg ctctttaata aggtgacact cgctgatgct ggcttcatga  23940
agcaatatgg cgaatgccta ggtgatatta atgctagaga tctcatttgt gcgcagaagt  24000
tcaatggact tacagtgttg ccacctctgc tcactgatga tatgattgct gcctacactg  24060
ctgctctagt tagtggtact gccactgctg gatggacatt tggtgctggc gctgctcttc  24120
aaataccttt tgctatgcaa atggcatata ggttcaatgg cattggagtt acccaaaatg  24180
ttctctatga gaaccaaaaa caaatcgcca accaatttaa caaggcgatt agtcaaattc  24240
aagaatcact tacaacaaca tcaactgcat tgggcaagct gcaagacgtt gttaaccaga  24300
atgctcaagc attaaacaca cttgttaaac aacttagctc taattttggt gcaatttcaa  24360
```

-continued

```
gtgtgctaaa tgatatcctt tcgcgacttg ataaagtcga ggcggaggta caaattgaca  24420
ggttaattac aggcagactt caaagccttc aaacctatgt aacacaacaa ctaatcaggg  24480
ctgctgaaat cagggcttct gctaatcttg ctgctactaa aatgtctgag tgtgttcttg  24540
gacaatcaaa aagagttgac ttttgtggaa agggctacca ccttatgtcc ttcccacaag  24600
cagccccgca tggtgttgtc ttcctacatg tcacgtatgt gccatcccag gagaggaact  24660
tcaccacagc gccagcaatt tgtcatgaag gcaaagcata cttccctcgt gaaggtgttt  24720
ttgtgtttaa tggcacttct tggtttatta cacagaggaa cttcttttct ccacaaataa  24780
ttactacaga caatacattt gtctcaggaa attgtgatgt cgttattggc atcattaaca  24840
acacagttta tgatcctctg caacctgagc ttgactcatt caaagaagag ctggacaagt  24900
acttcaaaaa tcatacatca ccagatgttg atcttggcga catttcaggc attaacgctt  24960
ctgtcgtcaa cattcaaaaa gaaattgacc gcctcaatga ggtcgctaaa aatttaaatg  25020
aatcactcat tgaccttcaa gaattgggaa aatatgagca atatattaaa tggccttggt  25080
atgtttggct cggcttcatt gctggactaa ttgccatcgt catggttaca atcttgcttt  25140
gttgcatgac tagttgttgc agttgcctca agggtgcatg ctcttgtggt tcttgctgca  25200
agtttgatga ggatgactct gagccagttc tcaagggtgt caaattacat tacacataaa  25260
cgaacttatg gatttgttta tgagattttt tactcttaga tcaattactg cacagccagt  25320
aaaaattgac aatgcttctc ctgcaagtac tgttcatgct acagcaacga taccgctaca  25380
agcctcactc cctttcggat ggcttgttat tggcgttgca tttcttgctg tttttcagag  25440
cgctaccaaa ataattgcgc tcaataaaag atggcagcta gccctttata agggcttcca  25500
gttcatttgc aatttactgc tgctatttgt taccatctat tcacatcttt tgcttgtcgc  25560
tgcaggtatg gaggcgcaat ttttgtacct ctatgccttg atatattttc tacaatgcat  25620
caacgcatgt agaattatta tgagatgttg gctttgttgg aagtgcaaat ccaagaaccc  25680
attactttat gatgccaact actttgtttg ctggcacaca cataactatg actactgtat  25740
accatataac agtgtcacag atacaattgt cgttactgaa ggtgacggca tttcaacacc  25800
aaaactcaaa gaagactacc aaattggtgg ttattctgag gataggcact caggtgttaa  25860
agactatgtc gttgtacatg gctatttcac cgaagtttac taccagcttg agtctacaca  25920
aattactaca gacactggta ttgaaaatgc tacattcttc atctttaaca agcttgttaa  25980
agacccaccg aatgtgcaaa tacacacaat cgacggctct tcaggagttg ctaatccagc  26040
aatggatcca atttatgatg agccgacgac gactactagc gtgcctttgt aagcacaaga  26100
aagtgagtac gaacttatgt actcattcgt ttcggaagaa acaggtacgt taatagttaa  26160
tagcgtactt ctttttcttg ctttcgtggt attcttgcta gtcacactag ccatccttac  26220
tgcgcttcga ttgtgtgcgt actgctgcaa tattgttaac gtgagtttag taaaaccaac  26280
ggtttacgtc tactcgcgtg ttaaaaatct gaactcttct gaaggagttc ctgatcttct  26340
ggtctaaacg aactaactat tattattatt ctgtttggaa ctttaacatt gcttatcatg  26400
gcagacaacg gtactattac cgttgaggag cttaaacaac tcctggaaca atggaaccta  26460
gtaataggtt tcctattcct agcctggatt atgttactac aatttgccta ttctaatcgg  26520
aacaggtttt tgtacataat aaagcttgtt ttcctctggc tcttgtggcc agtaacactt  26580
gcttgttttg tgcttgctgc tgtctacaga attaattggg tgactggcgg gattgcgatt  26640
gcaatggctt gtattgtagg cttgatgtgg cttagctact tcgttgcttc cttcaggctg  26700
tttgctcgta cccgctcaat gtggtcattc aacccagaaa caaacattct tctcaatgtg  26760
```

-continued

```
cctctccggg ggacaattgt gaccagaccg ctcatggaaa gtgaacttgt cattggtgct  26820
gtgatcattc gtggtcactt gcgaatggcc ggacactccc tagggcgctg tgacattaag  26880
gacctgccaa aagagatcac tgtggctaca tcacgaacgc tttcttatta caaattagga  26940
gcgtcgcagc gtgtaggcac tgattcaggt tttgctgcat acaaccgcta ccgtattgga  27000
aactataaat taaatacaga ccacgccggt agcaacgaca atattgcttt gctagtacag  27060
taagtgacaa cagatgtttc atcttgttga cttccaggtt acaatagcag agatattgat  27120
tatcattatg aggactttca ggattgctat ttggaatctt gacgttataa taagttcaat  27180
agtgagacaa ttatttaagc ctctaactaa gaagaattat tcggagttag atgatgaaga  27240
acctatggag ttagattatc cataaaacga acatgaaaat tattctcttc ctgacattga  27300
ttgtatttac atcttgcgag ctatatcact atcaggagtg tgttagaggt acgactgtac  27360
tactaaaaga accttgccca tcaggaacat acgagggcaa ttcaccattt caccctcttg  27420
ctgacaataa atttgcacta acttgcacta gcacacactt tgcttttgct tgtgctgacg  27480
gtactcgaca tacctatcag ctgcgtgcaa gatcagtttc accaaaactt ttcatcagac  27540
aagaggaggt tcaacaagag ctctactcgc cactttttct cattgttgct gctctagtat  27600
ttttaatact ttgcttcacc attaagagaa agacagaatg aatgagctca ctttaattga  27660
cttctatttg tgctttttag cctttctgct attccttgtt ttaataatgc ttattatatt  27720
ttggttttca ctcgaaatcc aggatctaga agaaccttgt accaaagtct aaacgaacat  27780
gaaacttctc attgttttga cttgtatttc tctatgcagt tgcatatgca ctgtagtaca  27840
gcgctgtgca tctaataaac ctcatgtgct tgaagatcct tgtaaggtac aacactaggg  27900
gtaatactta tagcactgct tggctttgtg ctctaggaaa ggttttacct tttcatagat  27960
ggcacactat ggttcaaaca tgcacaccta atgttactat caactgtcaa gatccagctg  28020
gtggtgcgct tatagctagg tgttggtacc ttcatgaagg tcaccaaact gctgcattta  28080
gagacgtact tgttgtttta aataaacgaa caaattaaaa tgtctgataa tggaccccaa  28140
tcaaaccaac gtagtgcccc ccgcattaca tttggtggac ccacagattc aactgacaat  28200
aaccagaatg gaggacgcaa tggggcaagg ccaaaacagc gccgacccca aggtttaccc  28260
aataatactg cgtcttggtt cacagctctc actcagcatg gcaaggagga acttagattc  28320
cctcgaggcc agggcgttcc aatcaacacc aatagtggtc cagatgacca aattggctac  28380
taccgaagag ctacccgacg agttcgtggt ggtgacggca aaatgaaaga gctcagcccc  28440
agatggtact tctattacct aggaactggc ccagaagctt cacttcccta cggcgctaac  28500
aaagaaggca tcgtatgggt tgcaactgag ggagccttga atacacccaa agaccacatt  28560
ggcacccgca atcctaataa caatgctgcc accgtgctac aacttcctca aggaacaaca  28620
ttgccaaaag gcttctacgc agagggaagc agaggcggca gtcaagcctc ttctcgctcc  28680
tcatcacgta gtcgcggtaa ttcaagaaat tcaactcctg gcagcagtag gggaaattct  28740
cctgctcgaa tggctagcgg aggtggtgaa actgccctcg cgctattgct gctagacaga  28800
ttgaaccagc ttgagagcaa agtttctggt aaaggccaac aacaacaagg ccaaactgtc  28860
actaagaaat ctgctgctga ggcatctaaa aagcctcgcc aaaaacgtac tgccacaaaa  28920
cagtacaacg tcactcaagc atttgggaga cgtggtccag aacaaaccca aggaaatttc  28980
ggggaccaag acctaatcag acaaggaact gattacaaac attggccgca aattgcacaa  29040
tttgctccaa gtgcctctgc attctttgga atgtcacgca ttggcatgga agtcacacct  29100
```

-continued

```
tcgggaacat ggctgactta tcatggagcc attaaattgg atgacaaaga tccacaattc  29160

aaagacaacg tcatactgct gaacaagcac attgacgcat acaaaacatt cccaccaaca  29220

gagcctaaaa aggacaaaaa gaaaaagact gatgaagctc agcctttgcc gcagagacaa  29280

aagaagcagc ccactgtgac tcttcttcct gcggctgaca tggatgattt ctccagacaa  29340

cttcaaaatt ccatgagtgg agcttctgct gattcaactc aggcataaac actcatgatg  29400

accacacaag gcagatgggc tatgtaaacg ttttcgcaat tccgtttacg atacatagtc  29460

tactcttgtg cagaatgaat tctcgtaact aaacagcaca agtaggttta gttaacttta  29520

atctcacata gcaatcttta atcaatgtgt aacattaggg aggacttgaa agagccacca  29580

cattttcatc gaggccacgc ggagtacgat cgagggtaca gtgaataatg ctagggagag  29640

ctgcctatat ggaagagccc taatgtgtaa aattaatttt agtagtgcta tccccatgtg  29700

attttaatag cttcttagga gaatgacaaa aaaaaaaaaa aaaaaaaaaa a           29751
```

<210> SEQ ID NO 16
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 16

```
acattttcat cgaggccacg cggagtacga tcgagggtac agtgaat                   47
```

<210> SEQ ID NO 17
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 17

```
cgaggccacg cggagtacga tcgagggtac ag                                   32
```

<210> SEQ ID NO 18
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 18

```
acactcatga tgaccacaca aggcagatgg gctatgtaaa cgttttcgca attccgttta     60

cgatacatag tctactcttg tgcagaatga attctcgtaa ctaaacagca caagtaggtt    120

tagttaactt taatctcaca tagcaatctt taatcaatgt gtaacattag ggaggacttg    180

aaagagccac cacattttca tcgaggccac gcggagtacg atcgagggta cagtgaataa    240

tgctagggag agctgcctat atggaagagc cctaatgtgt aaaattaatt ttagtagtgc    300

tatccccatg tgattttaat agcttcttag gagaatgac                           339
```

<210> SEQ ID NO 19
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: s2m motif
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (23)..(23)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 19

gccgnggcca cgcsgagtas gancgagggt acags 35

<210> SEQ ID NO 20
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 20

ucucuaaacg aacuuuaaaa ucugug 26

<210> SEQ ID NO 21
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 21

caacuaaacg aacaug 16

<210> SEQ ID NO 22
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 22

cacauaaacg aacuuaug 18

<210> SEQ ID NO 23
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 23

ugaguacgaa cuuaug 16

<210> SEQ ID NO 24
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 24

ggucuaaacg aacuaacu 18

<210> SEQ ID NO 25
<211> LENGTH: 11
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 25

aacuauaaau u 11

<210> SEQ ID NO 26
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 26

uccauaaaac gaacaug 17

<210> SEQ ID NO 27
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 27

ugcucuagua uuuuuaauac uuug 24

<210> SEQ ID NO 28
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 28

agucuaaacg aacaug 16

<210> SEQ ID NO 29
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 29

cuaauaaacc ucaug 15

<210> SEQ ID NO 30
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 30

uaaauaaacg aacaaauuaa aaug 24

<210> SEQ ID NO 31
<211> LENGTH: 136
<212> TYPE: DNA
<213> ORGANISM: Equine rhinovirus

<400> SEQUENCE: 31

acccgttacc ctaaaattcc ctcccctttc tcttcactcg ccgaggccac gccgagtagg 60

accgagggta cagcgagtct tttagtttaa ggtgttagat gtaaggtacg tgggctttct 120

tttggtttac ttcttc 136

<210> SEQ ID NO 32
<211> LENGTH: 178
<212> TYPE: DNA
<213> ORGANISM: Avian infectious bronchitis

<400> SEQUENCE: 32

tagtttagtt taagttagtt tagagtaggt ataaagatgc cagtgccggg gccacgcgga 60

gtacgatcga gggtacagca ctaggacgcc cattagggga agagctaaat tttagtttaa 120

gttaagttta attggctaag tatagttaaa atttataggc tagtatagag ttagagca 178

<210> SEQ ID NO 33
<211> LENGTH: 1255
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 33

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1   5   10   15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
            20   25   30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
        35   40   45

-continued

```
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
    50                  55                  60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65                  70                  75                  80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
                85                  90                  95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
            100                 105                 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
        115                 120                 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
    130                 135                 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145                 150                 155                 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
                165                 170                 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
            180                 185                 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
        195                 200                 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
    210                 215                 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225                 230                 235                 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
                245                 250                 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
            260                 265                 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
        275                 280                 285

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

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305                 310                 315                 320

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

Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
            340                 345                 350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
        355                 360                 365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
    370                 375                 380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385                 390                 395                 400

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
                405                 410                 415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
            420                 425                 430

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
        435                 440                 445

Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
    450                 455                 460

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
```

-continued

```
465                 470                 475                 480

Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
                485                 490                 495

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
            500                 505                 510

Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
        515                 520                 525

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
    530                 535                 540

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545                 550                 555                 560

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
                565                 570                 575

Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
            580                 585                 590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
        595                 600                 605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
    610                 615                 620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625                 630                 635                 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
                645                 650                 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
            660                 665                 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
        675                 680                 685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
    690                 695                 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705                 710                 715                 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
                725                 730                 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740                 745                 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
        755                 760                 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
    770                 775                 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785                 790                 795                 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
                805                 810                 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
            820                 825                 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
        835                 840                 845

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
    850                 855                 860

Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865                 870                 875                 880

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
                885                 890                 895
```

-continued

```
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
            900                 905                 910

Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
        915                 920                 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
    930                 935                 940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945                 950                 955                 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
                965                 970                 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
            980                 985                 990

Gln Leu Ile Arg Ala Ala Glu Ile  Arg Ala Ser Ala Asn  Leu Ala Ala
        995                 1000                 1005

Thr Lys  Met Ser Glu Cys Val  Leu Gly Gln Ser Lys  Arg Val Asp
    1010                 1015                 1020

Phe Cys  Gly Lys Gly Tyr His  Leu Met Ser Phe Pro  Gln Ala Ala
    1025                 1030                 1035

Pro His  Gly Val Val Phe Leu  His Val Thr Tyr Val  Pro Ser Gln
    1040                 1045                 1050

Glu Arg  Asn Phe Thr Thr Ala  Pro Ala Ile Cys His  Glu Gly Lys
    1055                 1060                 1065

Ala Tyr  Phe Pro Arg Glu Gly  Val Phe Val Phe Asn  Gly Thr Ser
    1070                 1075                 1080

Trp Phe  Ile Thr Gln Arg Asn  Phe Phe Ser Pro Gln  Ile Ile Thr
    1085                 1090                 1095

Thr Asp  Asn Thr Phe Val Ser  Gly Asn Cys Asp Val  Val Ile Gly
    1100                 1105                 1110

Ile Ile  Asn Asn Thr Val Tyr  Asp Pro Leu Gln Pro  Glu Leu Asp
    1115                 1120                 1125

Ser Phe  Lys Glu Glu Leu Asp  Lys Tyr Phe Lys Asn  His Thr Ser
    1130                 1135                 1140

Pro Asp  Val Asp Leu Gly Asp  Ile Ser Gly Ile Asn  Ala Ser Val
    1145                 1150                 1155

Val Asn  Ile Gln Lys Glu Ile  Asp Arg Leu Asn Glu  Val Ala Lys
    1160                 1165                 1170

Asn Leu  Asn Glu Ser Leu Ile  Asp Leu Gln Glu Leu  Gly Lys Tyr
    1175                 1180                 1185

Glu Gln  Tyr Ile Lys Trp Pro  Trp Tyr Val Trp Leu  Gly Phe Ile
    1190                 1195                 1200

Ala Gly  Leu Ile Ala Ile Val  Met Val Thr Ile Leu  Leu Cys Cys
    1205                 1210                 1215

Met Thr  Ser Cys Cys Ser Cys  Leu Lys Gly Ala Cys  Ser Cys Gly
    1220                 1225                 1230

Ser Cys  Cys Lys Phe Asp Glu  Asp Asp Ser Glu Pro  Val Leu Lys
    1235                 1240                 1245

Gly Val  Lys Leu His Tyr Thr
    1250                 1255
```

<210> SEQ ID NO 34
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 34

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

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
20 25 30

Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
35 40 45

Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
50 55 60

Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
65 70 75 80

Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
85 90 95

Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
100 105 110

Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
115 120 125

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

Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
145 150 155 160

Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
165 170 175

Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
180 185 190

Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
195 200 205

His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val
210 215 220

<210> SEQ ID NO 35
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 35

Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
1 5 10 15

Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
20 25 30

Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
35 40 45

Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
50 55 60

Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
65 70 75

<210> SEQ ID NO 36
<211> LENGTH: 422
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 36

Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
1 5 10 15

Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly

-continued

```
            20                  25                  30

Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
        35                  40                  45

Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
    50                  55                  60

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65                  70                  75                  80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
                85                  90                  95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
            100                 105                 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
        115                 120                 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
    130                 135                 140

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

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
                165                 170                 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
            180                 185                 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
        195                 200                 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
    210                 215                 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
225                 230                 235                 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
                245                 250                 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
            260                 265                 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
        275                 280                 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
    290                 295                 300

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

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
                325                 330                 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
            340                 345                 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
        355                 360                 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
    370                 375                 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
385                 390                 395                 400

Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
                405                 410                 415

Ala Asp Ser Thr Gln Ala
            420

<210> SEQ ID NO 37
```

-continued

<211> LENGTH: 230
<212> TYPE: PRT
<213> ORGANISM: Bovine coronavirus

<400> SEQUENCE: 37

Met Ser Ser Val Thr Thr Pro Ala Pro Val Tyr Thr Trp Thr Ala Asp
1 5 10 15

Glu Ala Ile Lys Phe Leu Lys Glu Trp Asn Phe Ser Leu Gly Ile Ile
20 25 30

Leu Leu Phe Ile Thr Val Ile Leu Gln Phe Gly Tyr Thr Ser Arg Ser
35 40 45

Met Phe Val Tyr Val Ile Lys Met Val Ile Leu Trp Leu Met Trp Pro
50 55 60

Leu Thr Ile Ile Leu Thr Ile Phe Asn Cys Val Tyr Ala Leu Asn Asn
65 70 75 80

Val Tyr Leu Gly Phe Ser Ile Val Phe Thr Ile Val Ala Ile Ile Met
85 90 95

Trp Ile Val Tyr Phe Val Asn Ser Ile Arg Leu Phe Ile Arg Thr Gly
100 105 110

Ser Trp Trp Ser Phe Asn Pro Glu Thr Asn Asn Leu Met Cys Ile Asp
115 120 125

Met Lys Gly Arg Met Tyr Val Arg Pro Ile Ile Glu Asp Tyr His Thr
130 135 140

Leu Thr Val Thr Ile Ile Arg Gly His Leu Tyr Met Gln Gly Ile Lys
145 150 155 160

Leu Gly Thr Gly Tyr Ser Leu Ser Asp Leu Pro Ala Tyr Val Thr Val
165 170 175

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

Ile Gly Asp Thr Ser Gly Phe Ala Val Tyr Val Lys Ser Lys Val Gly
195 200 205

Asn Tyr Arg Leu Pro Ser Thr Gln Lys Gly Ser Gly Leu Asp Thr Ala
210 215 220

Leu Leu Arg Asn Asn Ile
225 230

<210> SEQ ID NO 38
<211> LENGTH: 226
<212> TYPE: PRT
<213> ORGANISM: Avian infectious bronchitis virus

<400> SEQUENCE: 38

Met Ser Asn Gly Thr Glu Asn Cys Thr Leu Ser Thr Gln Gln Ala Ala
1 5 10 15

Glu Leu Phe Lys Glu Tyr Asn Leu Phe Ile Thr Ala Phe Leu Leu Phe
20 25 30

Leu Thr Ile Leu Leu Gln Tyr Gly Tyr Ala Thr Arg Ser Arg Phe Ile
35 40 45

Tyr Ile Leu Lys Met Ile Val Leu Trp Cys Phe Trp Pro Leu Asn Ile
50 55 60

Ala Val Gly Ile Ile Ser Cys Ile Tyr Pro Pro Asn Thr Gly Gly Leu
65 70 75 80

Val Ala Ala Ile Ile Leu Thr Val Phe Ala Cys Leu Ser Phe Val Gly
85 90 95

Tyr Trp Ile Gln Ser Phe Arg Leu Phe Lys Arg Cys Arg Ser Trp Trp
100 105 110

```
Ser Phe Asn Pro Glu Ser Asn Ala Val Gly Ser Ile Leu Leu Thr Asn
        115                 120                 125

Gly Gln Gln Cys Asn Phe Ala Ile Glu Ser Val Pro Met Val Leu Ser
    130                 135                 140

Pro Ile Ile Lys Asn Gly Ala Leu Tyr Cys Glu Gly Gln Trp Leu Ala
145                 150                 155                 160

Lys Cys Glu Pro Asp His Leu Pro Lys Asp Ile Phe Val Cys Thr Pro
                165                 170                 175

Asp Arg Arg Asn Ile Tyr Arg Met Val Gln Lys Tyr Thr Gly Asp Gln
            180                 185                 190

Ser Gly Asn Lys Lys Arg Phe Ala Thr Phe Val Tyr Ala Lys Gln Ser
        195                 200                 205

Val Asp Thr Gly Glu Leu Gly Ser Val Ala Thr Gly Gly Ser Ser Leu
    210                 215                 220

Tyr Thr
225


<210> SEQ ID NO 39
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Transmissible gastroenteritis virus

<400> SEQUENCE: 39

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

Glu Arg Tyr Cys Ala Met Lys Ser Asp Thr Asp Leu Ser Cys Arg Asn
            20                  25                  30

Ser Thr Ala Ser Asp Cys Glu Ser Cys Phe Asn Gly Gly Asp Leu Ile
        35                  40                  45

Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Ile Ile Leu Ile Val
    50                  55                  60

Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln Phe Ser Trp Phe Val
65                  70                  75                  80

Tyr Gly Ile Lys Met Leu Ile Met Trp Leu Leu Trp Pro Val Val Leu
                85                  90                  95

Ala Leu Thr Ile Phe Asn Ala Tyr Ser Glu Tyr Gln Val Ser Arg Tyr
            100                 105                 110

Val Met Phe Gly Phe Ser Ile Ala Gly Ala Ile Val Thr Phe Val Leu
        115                 120                 125

Trp Ile Met Tyr Phe Val Arg Ser Ile Gln Leu Tyr Arg Arg Thr Lys
    130                 135                 140

Ser Trp Trp Ser Phe Asn Pro Glu Thr Lys Ala Ile Leu Cys Val Ser
145                 150                 155                 160

Ala Leu Gly Arg Ser Tyr Val Leu Pro Leu Glu Gly Val Pro Thr Gly
                165                 170                 175

Val Thr Leu Thr Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys
            180                 185                 190

Ile Ala Gly Gly Met Asn Ile Asp Asn Leu Pro Lys Tyr Val Met Val
        195                 200                 205

Ala Leu Pro Ser Arg Thr Ile Val Tyr Thr Leu Val Gly Lys Lys Leu
    210                 215                 220

Lys Ala Ser Ser Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala
225                 230                 235                 240

Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu Gln Glu
```

-continued

245 250 255

Lys Leu Leu His Met Val
260

<210> SEQ ID NO 40
<211> LENGTH: 263
<212> TYPE: PRT
<213> ORGANISM: feline coronavirus

<400> SEQUENCE: 40

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

Glu Gln Ile Arg Tyr Cys Ala Met Gln Glu Thr Gly Leu Ser Cys Arg
20 25 30

Asn Gly Thr Ala Ser Asp Cys Glu Ser Cys Phe Asn Gly Gly Asp Leu
35 40 45

Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Ile Ile Leu Ile
50 55 60

Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln Phe Ser Trp Phe
65 70 75 80

Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu Leu Trp Pro Ile Val
85 90 95

Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser Glu Tyr Glu Val Ser Arg
100 105 110

Tyr Val Met Phe Gly Phe Ser Val Ala Gly Ala Val Val Thr Phe Ala
115 120 125

Leu Trp Met Met Tyr Phe Val Arg Ser Ile Gln Leu Tyr Arg Arg Thr
130 135 140

Lys Ser Trp Trp Ser Phe Asn Pro Glu Thr Asn Ala Ile Leu Cys Val
145 150 155 160

Asn Ala Leu Gly Arg Ser Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr
165 170 175

Gly Val Thr Leu Thr Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe
180 185 190

Lys Met Ala Gly Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met
195 200 205

Ile Arg Thr Pro Asn Arg Thr Ile Val Tyr Thr Leu Val Gly Lys Gln
210 215 220

Leu Lys Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys
225 230 235 240

Ala Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His
245 250 255

Glu Lys Leu Leu His Met Val
260

<210> SEQ ID NO 41
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Human coronavirus OC43
MSSKTTPAPVYIWTADEAIKFLKEWNFSLGIILLFITIILQFGYTSRSMFVYVIKMIILWLMWPLT
IILTIFNCVYALNNVYLGLSIVFTIVAIIMWIVYFVNSIRLFIRTGSFWSFNPETNNLMCIDMKGT
MYVRPIIEDYHTLTVTIIRGHLYIQGIKLGTGYSWADLPAYMTVAKVTHLCTYKRGFLDRISDTSG
FAVYVKSKVGNYRLPSTQKGSGMDTALLRNNI
<SEQ ID NO:37;prt;Porcine hemagglutinating encephalomyelitis virus

<400> SEQUENCE: 41

Met Ser Ser Pro Thr Thr Pro Val Pro Val Ile Ser Trp Thr Ala Asp
1 5 10 15

-continued

```
Glu Ala Ile Lys Phe Leu Lys Glu Trp Asn Phe Ser Leu Gly Ile Ile
            20                  25                  30

Val Leu Phe Ile Thr Ile Ile Leu Gln Phe Gly Tyr Thr Ser Arg Ser
        35                  40                  45

Met Phe Val Tyr Val Ile Lys Met Val Ile Leu Trp Leu Met Trp Pro
    50                  55                  60

Leu Thr Ile Ile Leu Thr Ile Phe Asn Cys Val Tyr Ala Leu Asn Asn
65                  70                  75                  80

Val Tyr Leu Gly Phe Ser Ile Val Phe Thr Ile Val Ala Ile Ile Met
                85                  90                  95

Trp Val Val Tyr Phe Val Asn Ser Ile Arg Leu Phe Ile Arg Thr Gly
            100                 105                 110

Ser Trp Trp Ser Phe Asn Pro Glu Thr Asn Asn Leu Met Cys Ile Asp
        115                 120                 125

Met Lys Gly Arg Met Tyr Val Arg Pro Ile Ile Glu Asp Tyr His Thr
    130                 135                 140

Leu Thr Ala Thr Ile Ile Arg Gly His Leu Tyr Ile Gln Gly Ile Lys
145                 150                 155                 160

Leu Gly Thr Gly Tyr Ser Leu Ser Asp Leu Pro Ala Tyr Val Thr Val
                165                 170                 175

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

Ile Gly Asp Thr Ser Gly Phe Ala Val Tyr Val Lys Ser Lys Val Gly
        195                 200                 205

Asn Tyr Arg Leu Pro Ser Thr His Lys Gly Ser Gly Met Asp Thr Ala
    210                 215                 220

Leu Leu Arg Asn Asn Ile Met
225                 230


<210> SEQ ID NO 42
<211> LENGTH: 223
<212> TYPE: PRT
<213> ORGANISM: Avian infectious bronchitis virus

<400> SEQUENCE: 42

Met Met Glu Asn Cys Thr Leu Asn Leu Glu Gln Ala Thr Leu Leu Phe
1               5                   10                  15

Lys Glu Tyr Asn Leu Phe Ile Thr Ala Phe Leu Leu Phe Leu Thr Ile
            20                  25                  30

Leu Leu Gln Tyr Gly Tyr Ala Thr Arg Ser Arg Phe Ile Tyr Ile Leu
        35                  40                  45

Lys Met Ile Val Leu Trp Cys Phe Trp Pro Leu Asn Ile Ala Val Gly
    50                  55                  60

Val Ile Ser Cys Ile Tyr Pro Pro Asn Thr Gly Gly Leu Val Ala Ala
65                  70                  75                  80

Ile Ile Leu Thr Val Phe Ala Cys Leu Ser Phe Val Gly Tyr Trp Ile
                85                  90                  95

Gln Ser Cys Arg Leu Phe Lys Arg Cys Arg Ser Trp Trp Ser Phe Asn
            100                 105                 110

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

Cys Asn Phe Ala Ile Glu Ser Val Pro Met Val Leu Ala Pro Ile Ile
    130                 135                 140

Lys Asn Gly Val Leu Tyr Cys Glu Gly Gln Trp Leu Ala Lys Cys Glu
```

-continued

```
145                 150                 155                 160

Pro Asp His Leu Pro Lys Asp Ile Phe Val Cys Thr Pro Asp Arg Arg
                165                 170                 175

Asn Ile Tyr Arg Met Val Gln Lys Tyr Thr Gly Asp Gln Ser Gly Asn
            180                 185                 190

Lys Lys Arg Val Ala Thr Phe Val Tyr Ala Lys Gln Ser Val Asp Thr
        195                 200                 205

Gly Glu Leu Glu Ser Val Pro Thr Gly Gly Ser Ser Leu Tyr Thr
    210                 215                 220


<210> SEQ ID NO 43
<211> LENGTH: 455
<212> TYPE: PRT
<213> ORGANISM: Mouse Hepatitis Virus

<400> SEQUENCE: 43

Met Ser Phe Val Pro Gly Gln Glu Asn Ala Gly Ser Arg Ser Ser Ser
1               5                   10                  15

Val Asn Arg Ala Gly Asn Gly Ile Leu Lys Lys Thr Thr Trp Ala Asp
            20                  25                  30

Gln Thr Glu Arg Gly Pro Asn Asn Gln Asn Arg Gly Arg Arg Asn Gln
        35                  40                  45

Pro Lys Gln Thr Ala Thr Thr Gln Pro Asn Ser Gly Ser Val Val Pro
    50                  55                  60

His Tyr Ser Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu
65                  70                  75                  80

Phe Gln Phe Ala Gln Gly Gln Gly Val Pro Ile Ala Asn Gly Ile Pro
                85                  90                  95

Ala Ser Glu Gln Lys Gly Tyr Trp Tyr Arg His Asn Arg Arg Ser Phe
            100                 105                 110

Lys Thr Pro Asp Gly Gln Gln Lys Gln Leu Leu Pro Arg Trp Tyr Phe
        115                 120                 125

Tyr Tyr Leu Gly Thr Gly Pro His Ala Gly Ala Glu Tyr Gly Asp Asp
    130                 135                 140

Ile Asp Gly Val Val Trp Val Ala Ser Gln Gln Ala Asp Thr Lys Thr
145                 150                 155                 160

Thr Ala Asp Ile Val Glu Arg Asp Pro Ser Ser His Glu Ala Ile Pro
                165                 170                 175

Thr Arg Phe Ala Pro Gly Thr Val Leu Pro Gln Gly Phe Tyr Val Glu
            180                 185                 190

Gly Ser Gly Arg Ser Ala Pro Ala Ser Arg Ser Gly Ser Arg Ser Gln
        195                 200                 205

Ser Arg Gly Pro Asn Asn Arg Ala Arg Ser Ser Ser Asn Gln Arg Gln
    210                 215                 220

Pro Ala Ser Thr Val Lys Pro Asp Met Ala Glu Glu Ile Ala Ala Leu
225                 230                 235                 240

Val Leu Ala Lys Leu Gly Lys Asp Ala Gly Gln Pro Lys Gln Val Thr
                245                 250                 255

Lys Gln Ser Ala Lys Glu Val Arg Gln Lys Ile Leu Asn Lys Pro Arg
            260                 265                 270

Gln Lys Arg Thr Pro Asn Lys Gln Cys Pro Val Gln Gln Cys Phe Gly
        275                 280                 285

Lys Arg Gly Pro Asn Gln Asn Phe Gly Gly Ser Glu Met Leu Lys Leu
    290                 295                 300
```

-continued

```
Gly Thr Ser Asp Pro Gln Phe Pro Ile Leu Ala Glu Leu Ala Pro Thr
305                 310                 315                 320

Pro Ser Ala Phe Phe Phe Gly Ser Lys Leu Glu Leu Val Lys Lys Asn
                325                 330                 335

Ser Gly Gly Ala Asp Asp Pro Thr Lys Asp Val Tyr Glu Leu Gln Tyr
            340                 345                 350

Ser Gly Ala Ile Arg Phe Asp Ser Thr Leu Pro Gly Phe Glu Thr Ile
        355                 360                 365

Met Lys Val Leu Asn Glu Asn Leu Asp Ala Tyr Gln Asp Gln Ala Gly
    370                 375                 380

Gly Ala Asp Val Val Ser Pro Lys Pro Gln Arg Lys Arg Gly Thr Lys
385                 390                 395                 400

Gln Lys Ala Leu Lys Gly Glu Val Asp Asn Val Ser Val Ala Lys Pro
                405                 410                 415

Lys Ser Ser Val Gln Arg Asn Val Ser Arg Glu Leu Thr Pro Glu Asp
            420                 425                 430

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

Leu Glu Asp Asp Ser Asn Val
    450                 455


<210> SEQ ID NO 44
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Bovine coronavirus

<400> SEQUENCE: 44

Met Ser Phe Thr Pro Gly Lys Gln Ser Ser Ser Arg Ala Ser Ser Gly
1               5                   10                  15

Asn Arg Ser Gly Asn Gly Ile Leu Lys Trp Ala Asp Gln Ser Asp Gln
            20                  25                  30

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

Ala Thr Ser Gln Gln Pro Ser Gly Gly Asn Val Val Pro Tyr Tyr Ser
    50                  55                  60

Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu Phe Glu Phe
65                  70                  75                  80

Ala Glu Gly Gln Gly Val Pro Ile Ala Pro Gly Val Pro Ala Thr Glu
                85                  90                  95

Ala Lys Gly Tyr Trp Tyr Arg His Asn Arg Arg Ser Phe Lys Thr Ala
            100                 105                 110

Asp Gly Asn Gln Arg Gln Leu Leu Pro Arg Trp Tyr Phe Tyr Tyr Leu
        115                 120                 125

Gly Thr Gly Pro His Ala Lys Asp Gln Tyr Gly Thr Asp Ile Asp Gly
    130                 135                 140

Val Tyr Trp Val Ala Ser Asn Gln Ala Asp Val Asn Thr Pro Ala Asp
145                 150                 155                 160

Ile Leu Asp Arg Asp Pro Ser Ser Asp Glu Ala Ile Pro Thr Arg Phe
                165                 170                 175

Pro Pro Gly Thr Val Leu Pro Gln Gly Tyr Tyr Ile Glu Gly Ser Gly
            180                 185                 190

Arg Ser Ala Pro Asn Ser Arg Ser Thr Ser Arg Ala Ser Ser Arg Ala
        195                 200                 205

Ser Ser Ala Gly Ser Arg Ser Arg Ala Asn Ser Gly Asn Arg Thr Pro
    210                 215                 220
```

-continued

Thr Ser Gly Val Thr Pro Asp Met Ala Asp Gln Ile Ala Ser Leu Val
225 230 235 240

Leu Ala Lys Leu Gly Lys Asp Ala Ala Lys Pro Gln Gln Val Thr Lys
245 250 255

Gln Thr Ala Lys Glu Ile Arg Gln Lys Ile Leu Asn Lys Pro Arg Gln
260 265 270

Lys Arg Ser Pro Asn Lys Gln Cys Thr Val Gln Gln Cys Phe Gly Lys
275 280 285

Arg Gly Pro Asn Gln Asn Phe Gly Gly Gly Glu Met Leu Lys Leu Gly
290 295 300

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

Gly Ala Phe Phe Phe Gly Ser Arg Leu Glu Leu Ala Lys Val Gln Asn
325 330 335

Leu Ser Gly Asn Leu Asp Glu Pro Gln Lys Asp Val Tyr Glu Leu Arg
340 345 350

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

Ile Met Lys Val Leu Asn Glu Asn Leu Asn Ala Tyr Gln Gln Gln Asp
370 375 380

Gly Thr Met Asn Met Ser Pro Lys Pro Gln Arg Gln Arg Gly Gln Lys
385 390 395 400

Asn Gly Gln Gly Glu Asn Asp Asn Ile Ser Val Ala Ala Pro Lys Ser
405 410 415

Arg Val Gln Gln Asn Lys Ile Arg Glu Leu Thr Ala Glu Asp Ile Ser
420 425 430

Leu Leu Lys Lys Met Asp Glu Pro Phe Thr Glu Asp Thr Ser Glu Ile
435 440 445

<210> SEQ ID NO 45
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Avian infectious bronchitis virus

<400> SEQUENCE: 45

Met Ala Ser Gly Lys Ala Ala Gly Lys Thr Asp Ala Pro Ala Pro Val
1 5 10 15

Ile Lys Leu Gly Gly Pro Lys Pro Pro Lys Val Gly Ser Ser Gly Asn
20 25 30

Ala Ser Trp Phe Gln Ala Leu Lys Ala Lys Lys Leu Asn Ala Pro Ala
35 40 45

Pro Lys Phe Glu Gly Ser Gly Val Pro Asp Asn Glu Asn Leu Lys Ile
50 55 60

Ser Gln Gln His Gly Tyr Trp Arg Arg Gln Ala Arg Tyr Lys Pro Gly
65 70 75 80

Lys Gly Gly Arg Lys Pro Val Pro Asp Ala Trp Tyr Phe Tyr Tyr Thr
85 90 95

Gly Thr Gly Pro Ala Ala Asp Leu Asn Trp Gly Asp Ser Gln Asp Gly
100 105 110

Ile Val Trp Val Ala Ala Lys Gly Ala Asp Val Lys Ser Arg Ser Asn
115 120 125

Gln Gly Thr Arg Asp Pro Asp Lys Phe Asp Gln Tyr Pro Leu Arg Phe
130 135 140

Ser Asp Gly Gly Pro Asp Gly Asn Phe Arg Trp Asp Phe Ile Pro Leu

-continued

```
145                 150                 155                 160

Asn Arg Gly Arg Ser Gly Arg Ser Thr Ala Ala Ser Ser Ala Ala Ser
                165                 170                 175

Ser Arg Ala Pro Ser Arg Glu Gly Ser Arg Gly Arg Leu Asn Gly Ala
            180                 185                 190

Glu Asp Asp Leu Ile Ala Arg Ala Ala Lys Ile Ile Gln Asp Gln Gln
        195                 200                 205

Lys Lys Gly Ser Arg Ile Thr Lys Ala Lys Ala Glu Glu Met Ile His
    210                 215                 220

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

Val Phe Gly Pro Arg Thr Lys Gly Lys Glu Gly Asn Phe Gly Asp Asp
                245                 250                 255

Lys Met Asn Glu Glu Gly Ile Lys Asp Gly Arg Val Thr Ala Met Leu
            260                 265                 270

Asn Leu Val Pro Ser Ser His Ala Cys Leu Phe Gly Ser Gln Val Thr
        275                 280                 285

Pro Lys Leu Gln Pro Asp Gly Leu His Leu Thr Phe Arg Phe Thr Thr
    290                 295                 300

Val Val Ser Arg Asp Asp Pro Gln Phe Asp Asn Tyr Val Lys Ile Cys
305                 310                 315                 320

Asp Glu Cys Val Asp Gly Val Gly Thr Arg Pro Lys Asp Glu Val Val
                325                 330                 335

Arg Pro Lys Ser Arg Ser Ser Ser Arg Pro Ala Thr Arg Gly Thr Ser
            340                 345                 350

Pro Ala Pro Lys Gln Gln Arg Pro Lys Lys Glu Lys Lys Pro Lys Lys
        355                 360                 365

Gln Asp Asp Glu Val Asp Lys Ala Leu Thr Ser Asp Glu Glu Arg Asn
    370                 375                 380

Asn Ala Gln Leu Glu Phe Asp Asp Glu Pro Lys Val Ile Asn Trp Gly
385                 390                 395                 400

Asp Ser Ala Leu Gly Glu Asn Glu Leu
                405


<210> SEQ ID NO 46
<211> LENGTH: 376
<212> TYPE: PRT
<213> ORGANISM: Feline coronavirus

<400> SEQUENCE: 46

Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser Lys
1               5                   10                  15

Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp Ile Pro
            20                  25                  30

Leu Ser Tyr Phe Asn Pro Ile Thr Leu Asp Gln Gly Ser Lys Phe Trp
        35                  40                  45

Asn Leu Cys Pro Arg Asp Phe Val Pro Lys Gly Ile Gly Asn Lys Asp
    50                  55                  60

Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ala Arg Tyr Arg Ile Val Lys
65                  70                  75                  80

Gly Gln Arg Val Glu Leu Pro Glu Arg Trp Phe Phe Tyr Phe Leu Gly
                85                  90                  95

Thr Gly Pro His Ala Asp Ala Lys Phe Lys Ala Lys Ile Asp Gly Val
            100                 105                 110
```

-continued

```
Phe Trp Val Ala Arg Asp Gly Ala Met Asn Lys Pro Thr Ser Leu Gly
        115                 120                 125

Thr Arg Gly Thr Asn Asn Glu Ser Lys Pro Leu Lys Phe Asp Gly Lys
    130                 135                 140

Ile Pro Pro Gln Phe Gln Leu Glu Val Asn Arg Ser Arg Asn Asn Ser
145                 150                 155                 160

Arg Ser Gly Ser Gln Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser
                165                 170                 175

Arg Gly Arg Gln Gln Ser Asn Asn Gln Asn Thr Asn Val Glu Asp Thr
            180                 185                 190

Ile Val Ala Val Leu Gln Lys Leu Gly Val Thr Asp Lys Gln Arg Ser
        195                 200                 205

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

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

Asp Val Thr Asn Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe Gly
                245                 250                 255

Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr Pro Gln
            260                 265                 270

Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Leu Phe Gly Ser Gln
        275                 280                 285

Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val Thr Leu Thr His
    290                 295                 300

Asn Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr Ser Gln Phe Leu Glu
305                 310                 315                 320

Gln Ile Asp Ala Tyr Lys Arg Pro Ser Glu Val Ala Lys Asp Gln Arg
                325                 330                 335

Gln Arg Lys Ser Arg Ser Lys Ser Ala Asp Lys Lys Pro Glu Glu Leu
            340                 345                 350

Ser Val Thr Leu Glu Ala Tyr Thr Asp Val Phe Asp Asp Thr Gln Val
        355                 360                 365

Glu Met Ile Asp Glu Val Thr Asn
    370                 375


<210> SEQ ID NO 47
<211> LENGTH: 382
<212> TYPE: PRT
<213> ORGANISM: porcine transmissible gastroenteritis virus

<400> SEQUENCE: 47

Met Ala Asn Gln Gly Gln Arg Val Ser Trp Gly Asp Glu Ser Thr Lys
1               5                   10                  15

Thr Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asn Ile Pro
            20                  25                  30

Leu Ser Phe Phe Asn Pro Ile Thr Leu Gln Gln Gly Ser Lys Phe Trp
        35                  40                  45

Asn Leu Cys Pro Arg Asp Phe Val Pro Lys Gly Ile Gly Asn Arg Asp
    50                  55                  60

Gln Gln Ile Gly Tyr Trp Asn Arg Gln Thr Arg Tyr Arg Met Val Lys
65                  70                  75                  80

Gly Gln Arg Lys Glu Leu Pro Glu Arg Trp Phe Phe Tyr Tyr Leu Gly
                85                  90                  95

Thr Gly Pro His Ala Asp Ala Lys Phe Lys Asp Lys Leu Asp Gly Val
            100                 105                 110
```

-continued

```
Val Trp Val Ala Lys Asp Gly Ala Met Asn Lys Pro Thr Thr Leu Gly
        115                 120                 125

Ser Arg Gly Ala Asn Asn Glu Ser Lys Ala Leu Lys Phe Asp Gly Lys
    130                 135                 140

Val Pro Gly Glu Phe Gln Leu Glu Val Asn Gln Ser Arg Asp Asn Ser
145                 150                 155                 160

Arg Leu Arg Ser Gln Ser Arg Ser Arg Ser Arg Asn Arg Ser Gln Ser
                165                 170                 175

Arg Gly Arg Gln Gln Ser Asn Asn Lys Lys Asp Asp Ser Val Glu Gln
            180                 185                 190

Ala Val Leu Ala Ala Leu Lys Lys Leu Gly Val Tyr Thr Glu Lys Gln
        195                 200                 205

Gln Gln Arg Ser Arg Ser Lys Ser Lys Glu Arg Ser Asn Ser Lys Ile
    210                 215                 220

Arg Asp Thr Thr Pro Lys Asn Glu Asn Lys His Thr Trp Lys Arg Thr
225                 230                 235                 240

Ala Gly Lys Gly Asp Val Thr Arg Phe Tyr Gly Thr Arg Ser Asn Ser
                245                 250                 255

Ala Asn Phe Gly Asp Ser Asp Leu Val Ala Asn Gly Ser Ser Ala Lys
            260                 265                 270

His Tyr Pro Gln Leu Ala Glu Cys Val Pro Ser Val Ser Ser Ile Leu
        275                 280                 285

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

Thr Phe Thr His Lys Tyr His Leu Pro Lys Asp Asp Pro Lys Thr Gly
305                 310                 315                 320

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

Lys Glu Gln Arg Lys Arg Lys Ser Arg Ser Lys Ser Ala Glu Arg Ser
            340                 345                 350

Glu Gln Glu Val Val Pro Asp Ala Leu Ile Glu Asn Tyr Thr Asp Val
        355                 360                 365

Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val Thr Asn
    370                 375                 380


<210> SEQ ID NO 48
<211> LENGTH: 389
<212> TYPE: PRT
<213> ORGANISM: Human coronavirus 229E

<400> SEQUENCE: 48

Met Ala Thr Val Lys Trp Ala Asp Ala Ser Glu Pro Gln Arg Gly Arg
1               5                   10                  15

Gln Gly Arg Ile Pro Tyr Ser Leu Tyr Ser Pro Leu Leu Val Asp Ser
            20                  25                  30

Glu Gln Pro Trp Lys Val Ile Pro Arg Asn Leu Val Pro Ile Asn Lys
        35                  40                  45

Lys Asp Lys Asn Lys Leu Ile Gly Tyr Trp Asn Val Gln Lys Arg Phe
    50                  55                  60

Arg Thr Arg Lys Gly Lys Arg Val Asp Leu Ser Pro Lys Leu His Phe
65                  70                  75                  80

Tyr Tyr Leu Gly Thr Gly Pro His Lys Asp Ala Lys Phe Arg Glu Arg
                85                  90                  95

Val Glu Gly Val Val Trp Val Ala Val Asp Gly Ala Lys Thr Glu Pro
```

-continued

```
            100                 105                 110

Thr Gly Tyr Gly Val Arg Arg Lys Asn Ser Glu Pro Glu Ile Pro His
        115                 120                 125

Phe Asn Gln Lys Leu Pro Asn Gly Val Thr Val Val Glu Glu Pro Asp
    130                 135                 140

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

Gly Glu Ser Lys Pro Gln Ser Arg Asn Pro Ser Ser Asp Arg Asn His
                165                 170                 175

Asn Ser Gln Asp Asp Ile Met Lys Ala Val Ala Ala Ala Leu Lys Ser
            180                 185                 190

Leu Gly Phe Asp Lys Pro Gln Glu Lys Asp Lys Lys Ser Ala Lys Thr
        195                 200                 205

Gly Thr Pro Lys Pro Ser Arg Asn Gln Ser Pro Ala Ser Ser Gln Thr
    210                 215                 220

Ser Ala Lys Ser Leu Ala Arg Ser Gln Ser Ser Glu Thr Lys Glu Gln
225                 230                 235                 240

Lys His Glu Met Gln Lys Pro Arg Trp Lys Arg Gln Pro Asn Asp Asp
                245                 250                 255

Val Thr Ser Asn Val Thr Gln Cys Phe Gly Pro Arg Asp Leu Asp His
            260                 265                 270

Asn Phe Gly Ser Ala Gly Val Val Ala Asn Gly Val Lys Ala Lys Gly
        275                 280                 285

Tyr Pro Gln Phe Ala Glu Leu Val Pro Ser Thr Ala Ala Met Leu Phe
    290                 295                 300

Asp Ser His Ile Val Ser Lys Glu Ser Gly Asn Thr Val Val Leu Thr
305                 310                 315                 320

Phe Thr Thr Arg Val Thr Val Pro Lys Asp His Pro His Leu Gly Lys
                325                 330                 335

Phe Leu Glu Glu Leu Asn Ala Phe Thr Arg Glu Met Gln Gln His Pro
            340                 345                 350

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

Ala Thr Ala Glu Pro Val Arg Asp Glu Val Ser Ile Glu Thr Asp Ile
    370                 375                 380

Ile Asp Glu Val Asn
385


<210> SEQ ID NO 49
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Human coronavirus

<400> SEQUENCE: 49

Met Ser Phe Thr Pro Gly Lys Gln Ser Ser Ser Arg Ala Ser Ser Gly
1               5                   10                  15

Asn Arg Ser Gly Asn Gly Ile Leu Lys Trp Ala Asp Gln Ser Asp Gln
            20                  25                  30

Val Arg Asn Val Gln Thr Arg Gly Arg Arg Ala Gln Pro Lys Gln Thr
        35                  40                  45

Ala Thr Ser Gln Gln Pro Ser Gly Gly Asn Val Val Pro Tyr Tyr Ser
    50                  55                  60

Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu Phe Glu Phe
65                  70                  75                  80
```

-continued

```
Val Glu Gly Gln Gly Pro Pro Ile Ala Pro Gly Val Pro Ala Thr Glu
                85                  90                  95

Ala Lys Gly Tyr Trp Tyr Arg His Asn Arg Gly Ser Phe Lys Thr Ala
            100                 105                 110

Asp Gly Asn Gln Arg Gln Leu Leu Pro Arg Trp Tyr Phe Tyr Tyr Leu
        115                 120                 125

Gly Thr Gly Pro His Ala Lys Asp Gln Tyr Gly Thr Asp Ile Asp Gly
    130                 135                 140

Val Tyr Trp Val Ala Ser Asn Gln Ala Asp Val Asn Thr Pro Ala Asp
145                 150                 155                 160

Ile Val Asp Arg Asp Pro Ser Ser Asp Glu Ala Ile Pro Thr Arg Phe
                165                 170                 175

Pro Pro Gly Thr Val Leu Pro Gln Gly Tyr Tyr Ile Glu Gly Ser Gly
            180                 185                 190

Arg Ser Ala Pro Asn Ser Arg Ser Thr Ser Arg Thr Ser Ser Arg Ala
        195                 200                 205

Ser Ser Ala Gly Ser Arg Ser Arg Ala Asn Ser Gly Asn Arg Thr Pro
    210                 215                 220

Thr Ser Gly Val Thr Pro Asp Met Ala Asp Gln Ile Ala Ser Leu Val
225                 230                 235                 240

Leu Ala Lys Leu Gly Lys Asp Ala Thr Lys Pro Gln Gln Val Thr Lys
                245                 250                 255

His Thr Ala Lys Glu Val Arg Gln Lys Ile Leu Asn Lys Pro Arg Gln
            260                 265                 270

Lys Arg Ser Pro Asn Lys Gln Cys Thr Val Gln Gln Cys Phe Gly Lys
        275                 280                 285

Arg Gly Pro Asn Gln Asn Phe Gly Gly Gly Glu Met Leu Lys Leu Gly
    290                 295                 300

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

Gly Ala Phe Phe Phe Gly Ser Arg Leu Glu Leu Ala Lys Val Gln Asn
                325                 330                 335

Leu Ser Gly Asn Pro Asp Glu Pro Gln Lys Asp Val Tyr Glu Leu Arg
            340                 345                 350

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

Ile Met Lys Val Leu Asn Glu Asn Leu Asn Ala Tyr Gln Gln Gln Asp
    370                 375                 380

Gly Met Met Asn Met Ser Pro Lys Pro Gln Arg Gln Arg Gly His Lys
385                 390                 395                 400

Asn Gly Gln Gly Glu Asn Asp Asn Ile Ser Val Ala Val Pro Lys Ser
                405                 410                 415

Arg Val Gln Gln Asn Lys Ser Arg Glu Leu Thr Ala Glu Asp Ile Ser
            420                 425                 430

Leu Leu Lys Lys Met Asp Glu Pro Tyr Thr Glu Asp Thr Ser Glu Ile
        435                 440                 445
```

<210> SEQ ID NO 50
<211> LENGTH: 449
<212> TYPE: PRT
<213> ORGANISM: porcine hemagglutinating encephalomyelitis

<400> SEQUENCE: 50

```
Met Ser Phe Thr Pro Gly Lys Gln Ser Ser Ser Arg Ala Ser Ser Gly
1               5                   10                  15
```

-continued

```
Asn Arg Ser Gly Asn Gly Ile Leu Lys Trp Ala Asp Gln Ser Asp Gln
            20                  25                  30

Ser Arg Asn Val Gln Thr Arg Gly Arg Arg Val Gln Ser Lys Gln Thr
        35                  40                  45

Ala Thr Ser Gln Gln Pro Ser Gly Gly Thr Val Val Pro Tyr Tyr Ser
    50                  55                  60

Trp Phe Ser Gly Ile Thr Gln Phe Gln Lys Gly Lys Glu Phe Glu Phe
65                  70                  75                  80

Ala Glu Gly Gln Gly Val Pro Ile Ala Pro Gly Val Pro Ser Thr Glu
                85                  90                  95

Ala Lys Gly Tyr Trp Tyr Arg His Asn Arg Arg Ser Phe Lys Thr Ala
            100                 105                 110

Asp Gly Asn Gln Arg Gln Leu Leu Pro Arg Trp Tyr Phe Tyr Tyr Leu
        115                 120                 125

Gly Thr Gly Pro His Ala Lys Asp Gln Tyr Gly Thr Asp Ile Asp Gly
    130                 135                 140

Val Phe Trp Val Ala Ser Asn Gln Ala Asp Ile Asn Thr Pro Ala Asp
145                 150                 155                 160

Ile Val Asp Arg Asp Pro Ser Ser Asp Glu Ala Ile Pro Thr Arg Phe
                165                 170                 175

Pro Pro Gly Thr Val Leu Pro Gln Gly Tyr Tyr Ile Glu Gly Ser Gly
            180                 185                 190

Arg Ser Ala Pro Asn Ser Arg Ser Thr Ser Arg Ala Pro Asn Arg Ala
        195                 200                 205

Pro Ser Ala Gly Ser Arg Ser Arg Ala Asn Ser Gly Asn Arg Thr Ser
    210                 215                 220

Thr Pro Gly Val Thr Pro Asp Met Ala Asp Gln Ile Ala Ser Leu Val
225                 230                 235                 240

Leu Ala Lys Leu Gly Lys Asp Ala Thr Lys Pro Gln Gln Val Thr Lys
                245                 250                 255

Gln Thr Ala Lys Glu Val Arg Gln Lys Ile Leu Asn Lys Pro Arg Gln
            260                 265                 270

Lys Arg Ser Pro Asn Lys Gln Cys Thr Val Gln Gln Cys Phe Gly Lys
        275                 280                 285

Arg Gly Pro Asn Gln Asn Phe Gly Gly Gly Glu Met Leu Lys Leu Gly
    290                 295                 300

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

Gly Ala Phe Phe Phe Gly Ser Arg Leu Glu Leu Ala Lys Val Gln Asn
                325                 330                 335

Leu Ser Gly Asn Pro Asp Glu Pro Gln Lys Asp Val Tyr Glu Leu Arg
            340                 345                 350

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

Ile Met Lys Val Leu Asn Gln Asn Leu Asn Ala Tyr Gln His Gln Glu
    370                 375                 380

Asp Gly Met Met Asn Ile Ser Pro Lys Pro Gln Arg Gln Arg Gly Gln
385                 390                 395                 400

Lys Asn Gly Gln Val Glu Asn Asp Asn Val Ser Val Ala Ala Pro Lys
                405                 410                 415

Ser Arg Val Gln Gln Asn Lys Ser Arg Glu Leu Thr Ala Glu Asp Ile
            420                 425                 430
```

-continued

```
Ser Leu Leu Lys Lys Met Asp Glu Pro Tyr Thr Glu Asp Thr Ser Glu
        435                 440                 445

Ile


<210> SEQ ID NO 51
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: turkey coronavirus

<400> SEQUENCE: 51

Met Ala Ser Gly Lys Ala Thr Gly Lys Thr Asp Ala Pro Ala Pro Ile
1               5                   10                  15

Ile Lys Leu Gly Gly Pro Lys Pro Pro Lys Val Gly Ser Ser Gly Asn
            20                  25                  30

Ala Ser Trp Phe Gln Ser Ile Lys Ala Lys Lys Leu Asn Ser Pro Gln
        35                  40                  45

Pro Lys Phe Glu Gly Ser Gly Val Pro Asp Asn Glu Asn Ile Lys Thr
    50                  55                  60

Ser Gln Gln His Gly Tyr Trp Arg Arg Gln Ala Arg Phe Lys Pro Gly
65                  70                  75                  80

Lys Gly Gly Arg Lys Pro Val Pro Asp Ala Trp Tyr Phe Tyr Tyr Thr
                85                  90                  95

Gly Thr Gly Pro Ala Ala Asp Leu Asn Trp Gly Asp Thr Gln Asp Gly
            100                 105                 110

Ile Val Trp Val Ala Ala Lys Gly Ala Asp Val Lys Ser Arg Ser Asn
        115                 120                 125

Gln Gly Thr Arg Asp Pro Asp Lys Phe Asp Gln Tyr Pro Leu Arg Phe
    130                 135                 140

Ser Asp Gly Gly Pro Asp Ser Asn Phe Arg Trp Asp Phe Ile Pro Leu
145                 150                 155                 160

His Arg Gly Arg Ser Gly Arg Ser Thr Ala Ala Ser Ser Ala Ala Ser
                165                 170                 175

Ser Arg Ala Pro Ser Arg Asp Gly Ser Arg Gly Arg Arg Ser Gly Ser
            180                 185                 190

Glu Asp Asp Leu Ile Ala Arg Ala Ala Lys Ile Ile Gln Asp Gln Gln
        195                 200                 205

Lys Lys Gly Ser Arg Ile Thr Lys Ala Lys Ala Asp Glu Met Ala His
    210                 215                 220

Arg Arg Tyr Cys Lys Arg Thr Val Pro Pro Gly Tyr Lys Val Asp Gln
225                 230                 235                 240

Val Phe Gly Pro Arg Thr Lys Gly Lys Glu Gly Asn Phe Gly Asp Asp
                245                 250                 255

Lys Met Asn Glu Glu Gly Ile Lys Asp Gly Arg Val Thr Ala Met Leu
            260                 265                 270

Asn Leu Val Pro Ser Ser His Ala Cys Leu Phe Gly Ser Arg Val Thr
        275                 280                 285

Pro Lys Leu Gln Pro Asp Gly Leu His Leu Arg Phe Glu Phe Thr Thr
    290                 295                 300

Val Val Pro Arg Asp Asp Pro Gln Phe Asp Asn Tyr Val Thr Ile Cys
305                 310                 315                 320

Asp Gln Cys Val Asp Gly Ile Gly Thr Arg Pro Lys Asp Asn Glu Pro
                325                 330                 335

Arg Pro Lys Ser Arg Pro Ser Ser Arg Pro Ala Thr Arg Gly Asn Ser
            340                 345                 350
```

-continued

```
Pro Ala Pro Arg Gln Gln Arg Pro Lys Lys Glu Lys Lys Pro Lys Lys
        355                 360                 365

Gln Asp Asp Glu Val Asp Lys Ala Leu Thr Ser Asp Glu Glu Arg Asn
    370                 375                 380

Asn Ala Gln Leu Glu Phe Asp Asp Glu Pro Lys Val Ile Asn Trp Gly
385                 390                 395                 400

Asp Ser Ala Leu Gly Glu Asn His Leu
                405


&lt;210&gt; SEQ ID NO 52
&lt;211&gt; LENGTH: 1173
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Human coronavirus 229E

&lt;400&gt; SEQUENCE: 52

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

Gln Thr Thr Asn Gly Leu Asn Thr Ser Tyr Ser Val Cys Asn Gly Cys
            20                  25                  30

Val Gly Tyr Ser Glu Asn Val Phe Ala Val Glu Ser Gly Gly Tyr Ile
        35                  40                  45

Pro Ser Asp Phe Ala Phe Asn Asn Trp Phe Leu Leu Thr Asn Thr Ser
    50                  55                  60

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

Cys Leu Trp Ser Val Ser Gly Leu Arg Phe Thr Thr Gly Phe Val Tyr
                85                  90                  95

Phe Asn Gly Thr Gly Arg Gly Asp Cys Lys Gly Phe Ser Ser Asp Val
            100                 105                 110

Leu Ser Asp Val Ile Arg Tyr Asn Leu Asn Phe Glu Glu Asn Leu Arg
        115                 120                 125

Arg Gly Thr Ile Leu Phe Lys Thr Ser Tyr Gly Val Val Val Phe Tyr
    130                 135                 140

Cys Thr Asn Asn Thr Leu Val Ser Gly Asp Ala His Ile Pro Phe Gly
145                 150                 155                 160

Thr Val Leu Gly Asn Phe Tyr Cys Phe Val Asn Thr Thr Ile Gly Thr
                165                 170                 175

Glu Thr Thr Ser Ala Phe Val Gly Ala Leu Pro Lys Thr Val Arg Glu
            180                 185                 190

Phe Val Ile Ser Arg Thr Gly His Phe Tyr Ile Asn Gly Tyr Arg Tyr
        195                 200                 205

Phe Thr Leu Gly Asn Val Glu Ala Val Asn Phe Asn Val Thr Thr Ala
    210                 215                 220

Glu Thr Thr Asp Phe Phe Thr Val Ala Leu Ala Ser Tyr Ala Asp Val
225                 230                 235                 240

Leu Val Asn Val Ser Gln Thr Ser Ile Ala Asn Ile Ile Tyr Cys Asn
                245                 250                 255

Ser Val Ile Asn Arg Leu Arg Cys Asp Gln Leu Ser Phe Tyr Val Pro
            260                 265                 270

Asp Gly Phe Tyr Ser Thr Ser Pro Ile Gln Ser Val Glu Leu Pro Val
        275                 280                 285

Ser Ile Val Ser Leu Pro Val Tyr His Lys His Met Phe Ile Val Leu
    290                 295                 300

Tyr Val Asp Phe Lys Pro Gln Ser Gly Gly Gly Lys Cys Phe Asn Cys
305                 310                 315                 320
```

-continued

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

Gly Pro Leu Cys Val Asp Thr Ser His Phe Thr Thr Lys Tyr Val Ala
            340                 345                 350

Val Tyr Ala Asn Val Gly Arg Trp Ser Ala Ser Ile Asn Thr Gly Asn
        355                 360                 365

Cys Pro Phe Ser Phe Gly Lys Val Asn Asn Phe Val Lys Phe Gly Ser
    370                 375                 380

Val Cys Phe Ser Leu Lys Asp Ile Pro Gly Gly Cys Ala Met Pro Ile
385                 390                 395                 400

Val Ala Asn Trp Ala Tyr Ser Lys Tyr Tyr Thr Ile Gly Thr Leu Tyr
                405                 410                 415

Val Ser Trp Ser Asp Gly Asp Gly Ile Thr Gly Val Pro Gln Pro Val
            420                 425                 430

Glu Gly Val Ser Ser Phe Met Asn Val Thr Leu Asp Lys Cys Thr Lys
        435                 440                 445

Tyr Asn Ile Tyr Asp Val Ser Gly Val Gly Val Ile Arg Val Ser Asn
    450                 455                 460

Asp Thr Phe Leu Asn Gly Ile Thr Tyr Thr Ser Thr Ser Gly Asn Leu
465                 470                 475                 480

Leu Gly Phe Lys Asp Val Thr Lys Gly Thr Ile Tyr Ser Ile Thr Pro
                485                 490                 495

Cys Asn Pro Pro Asp Gln Leu Val Val Tyr Gln Gln Ala Val Val Gly
            500                 505                 510

Ala Met Leu Ser Glu Asn Phe Thr Ser Tyr Gly Phe Ser Asn Val Val
        515                 520                 525

Glu Leu Pro Lys Phe Phe Tyr Ala Ser Asn Gly Thr Tyr Asn Cys Thr
    530                 535                 540

Asp Ala Val Leu Thr Tyr Ser Ser Phe Gly Val Cys Ala Asp Gly Ser
545                 550                 555                 560

Ile Ile Ala Val Gln Pro Arg Asn Val Ser Tyr Asp Ser Val Ser Ala
                565                 570                 575

Ile Val Thr Ala Asn Leu Ser Ile Pro Ser Asn Trp Thr Ile Ser Val
            580                 585                 590

Gln Val Glu Tyr Leu Gln Ile Thr Ser Thr Pro Ile Val Val Asp Cys
        595                 600                 605

Ser Thr Tyr Val Cys Asn Gly Asn Val Arg Cys Val Glu Leu Leu Lys
    610                 615                 620

Gln Tyr Thr Ser Ala Cys Lys Thr Ile Glu Asp Ala Leu Arg Asn Ser
625                 630                 635                 640

Ala Arg Leu Glu Ser Ala Asp Val Ser Glu Met Leu Thr Phe Asp Lys
                645                 650                 655

Lys Ala Phe Thr Leu Ala Asn Val Ser Ser Phe Gly Asp Tyr Asn Leu
            660                 665                 670

Ser Ser Val Ile Pro Ser Leu Pro Thr Ser Gly Ser Arg Val Ala Gly
        675                 680                 685

Arg Ser Ala Ile Glu Asp Ile Leu Phe Ser Lys Ile Val Thr Ser Gly
    690                 695                 700

Leu Gly Thr Val Asp Ala Asp Tyr Lys Asn Cys Thr Lys Gly Leu Ser
705                 710                 715                 720

Ile Ala Asp Leu Ala Cys Ala Gln Tyr Tyr Asn Gly Ile Met Val Leu
                725                 730                 735
```

-continued

```
Pro Gly Val Ala Asp Ala Glu Arg Met Ala Met Tyr Thr Gly Ser Leu
            740                 745                 750

Ile Gly Gly Ile Ala Leu Gly Gly Leu Thr Ser Ala Val Ser Ile Pro
        755                 760                 765

Phe Ser Leu Ala Ile Gln Ala Arg Leu Asn Tyr Val Ala Leu Gln Thr
    770                 775                 780

Asp Val Leu Gln Glu Asn Gln Lys Ile Leu Ala Ala Ser Phe Asn Lys
785                 790                 795                 800

Ala Met Thr Asn Ile Val Asp Ala Phe Thr Gly Val Asn Asp Ala Ile
                805                 810                 815

Thr Gln Thr Ser Gln Ala Leu Gln Thr Val Ala Thr Ala Leu Asn Lys
            820                 825                 830

Ile Gln Asp Val Val Asn Gln Gln Gly Asn Ser Leu Asn His Leu Thr
        835                 840                 845

Ser Gln Leu Arg Gln Asn Phe Gln Ala Ile Ser Ser Ser Ile Gln Ala
    850                 855                 860

Ile Tyr Asp Arg Leu Asp Thr Ile Gln Ala Asp Gln Gln Val Asp Arg
865                 870                 875                 880

Leu Ile Thr Gly Arg Leu Ala Ala Leu Asn Val Phe Val Ser His Thr
                885                 890                 895

Leu Thr Lys Tyr Thr Glu Val Arg Ala Ser Arg Gln Leu Ala Gln Gln
            900                 905                 910

Lys Val Asn Glu Cys Val Lys Ser Gln Ser Lys Arg Tyr Gly Phe Cys
        915                 920                 925

Gly Asn Gly Thr His Ile Phe Ser Ile Val Asn Ala Ala Pro Glu Gly
    930                 935                 940

Leu Val Phe Leu His Thr Val Leu Leu Pro Thr Gln Tyr Lys Asp Val
945                 950                 955                 960

Glu Ala Trp Ser Gly Leu Cys Val Asp Gly Thr Asn Gly Tyr Val Leu
                965                 970                 975

Arg Gln Pro Asn Leu Ala Leu Tyr Lys Glu Gly Asn Tyr Tyr Arg Ile
            980                 985                 990

Thr Ser Arg Ile Met Phe Glu Pro  Arg Ile Pro Thr Met  Ala Asp Phe
        995                 1000                 1005

Val Gln  Ile Glu Asn Cys Asn  Val Thr Phe Val Asn  Ile Ser Arg
    1010                 1015                 1020

Ser Glu  Leu Gln Thr Ile Val  Pro Glu Tyr Ile Asp  Val Asn Lys
    1025                 1030                 1035

Thr Leu  Gln Glu Leu Ser Tyr  Lys Leu Pro Asn Tyr  Thr Val Pro
    1040                 1045                 1050

Asp Leu  Val Val Glu Gln Tyr  Asn Gln Thr Ile Leu  Asn Leu Thr
    1055                 1060                 1065

Ser Glu  Ile Ser Thr Leu Glu  Asn Lys Ser Ala Glu  Leu Asn Tyr
    1070                 1075                 1080

Thr Val  Gln Lys Leu Gln Thr  Leu Ile Asp Asn Ile  Asn Ser Thr
    1085                 1090                 1095

Leu Val  Asp Leu Lys Trp Leu  Asn Arg Val Glu Thr  Tyr Ile Lys
    1100                 1105                 1110

Trp Pro  Trp Trp Val Trp Leu  Cys Ile Ser Val Val  Leu Ile Phe
    1115                 1120                 1125

Val Val  Ser Met Leu Leu Leu  Cys Cys Cys Ser Thr  Gly Cys Cys
    1130                 1135                 1140

Gly Phe  Phe Ser Cys Phe Ala  Ser Ser Ile Arg Gly  Cys Cys Glu
```

-continued

```
    1145                1150                1155

Ser Thr  Lys Leu Pro Tyr Tyr  Asp Val Glu Lys Ile  His Ile Gln
    1160                1165                1170


<210> SEQ ID NO 53
<211> LENGTH: 1164
<212> TYPE: PRT
<213> ORGANISM: Avian infectious bronchitis virus

<400> SEQUENCE: 53

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

Ser Ala Asn Leu Phe Asp Pro Ala Asn Tyr Val Tyr Tyr Tyr Gln Ser
            20                  25                  30

Ala Phe Arg Pro Ser Asn Gly Trp His Leu Gln Gly Gly Ala Tyr Ala
        35                  40                  45

Val Val Asn Ser Ser Asn Tyr Ala Asn Asn Ala Gly Ser Ala Ser Glu
    50                  55                  60

Cys Thr Val Gly Val Ile Lys Asp Val Tyr Asn Gln Ser Ala Ala Ser
65                  70                  75                  80

Ile Ala Met Thr Ala Pro Leu Gln Gly Met Ala Trp Ser Lys Ser Gln
                85                  90                  95

Phe Cys Ser Ala His Cys Asp Phe Ser Glu Ile Thr Val Phe Val Thr
            100                 105                 110

His Cys Tyr Ser Ser Gly Ser Gly Ser Cys Pro Ile Thr Gly Met Ile
        115                 120                 125

Ala Arg Gly His Ile Arg Ile Ser Ala Met Lys Asn Gly Ser Leu Phe
    130                 135                 140

Tyr Asn Leu Thr Val Ser Val Ser Lys Tyr Pro Asn Phe Lys Ser Phe
145                 150                 155                 160

Gln Cys Val Asn Asn Phe Thr Ser Val Tyr Leu Asn Gly Asp Leu Val
                165                 170                 175

Phe Thr Ser Asn Lys Thr Thr Asp Val Thr Ser Ala Gly Val Tyr Phe
            180                 185                 190

Lys Ala Gly Gly Pro Val Asn Tyr Ser Ile Met Lys Glu Phe Lys Val
        195                 200                 205

Leu Ala Tyr Phe Val Asn Gly Thr Ala Gln Asp Val Ile Leu Cys Asp
    210                 215                 220

Asn Ser Pro Lys Gly Leu Leu Ala Cys Gln Tyr Asn Thr Gly Asn Phe
225                 230                 235                 240

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

Phe Ile Val Tyr Arg Glu Ser Ser Val Asn Thr Thr Leu Ala Leu Thr
            260                 265                 270

Asn Phe Thr Phe Thr Asn Val Ser Asn Ala Gln Pro Asn Ser Gly Gly
        275                 280                 285

Val His Thr Phe His Leu Tyr Gln Thr Gln Thr Ala Gln Ser Gly Tyr
    290                 295                 300

Tyr Asn Phe Asn Leu Ser Phe Leu Ser Gln Phe Val Tyr Lys Ala Ser
305                 310                 315                 320

Asp Tyr Met Tyr Gly Ser Tyr His Pro Ile Cys Ala Phe Arg Pro Glu
                325                 330                 335

Thr Ile Asn Ser Gly Leu Trp Phe Asn Ser Leu Ser Val Ser Leu Thr
            340                 345                 350
```

-continued

```
Tyr Gly Pro Leu Gln Gly Gly Tyr Lys Gln Ser Val Phe Ser Gly Lys
        355                 360                 365

Ala Thr Cys Cys Tyr Ala Tyr Ser Tyr Asn Gly Pro Arg Ala Cys Lys
    370                 375                 380

Gly Val Tyr Ser Gly Glu Leu Ser Arg Asp Phe Glu Cys Gly Leu Leu
385                 390                 395                 400

Val Tyr Val Thr Lys Ser Asp Gly Ser Arg Ile Gln Thr Arg Thr Glu
                405                 410                 415

Pro Leu Val Leu Thr Gln His Asn Tyr Asn Asn Ile Thr Leu Asp Lys
            420                 425                 430

Cys Val Ala Tyr Asn Ile Tyr Gly Arg Val Gly Gln Gly Phe Ile Thr
        435                 440                 445

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

Leu Ala Ile Leu Asp Thr Ser Gly Ala Ile Asp Val Phe Val Val Gln
465                 470                 475                 480

Gly Ser Tyr Gly Leu Asn Tyr Tyr Lys Val Asn Pro Cys Glu Asp Val
                485                 490                 495

Asn Gln Gln Phe Val Val Ser Gly Gly Asn Ile Val Gly Ile Leu Thr
            500                 505                 510

Ser Arg Asn Glu Thr Gly Ser Glu Gln Val Glu Asn Gln Phe Tyr Val
        515                 520                 525

Lys Leu Thr Asn Ser Ser His Arg Arg Arg Arg Ser Ile Gly Gln Asn
    530                 535                 540

Val Thr Ser Cys Pro Tyr Val Ser Tyr Gly Arg Phe Cys Ile Glu Pro
545                 550                 555                 560

Asp Gly Ser Leu Lys Met Ile Val Pro Glu Glu Leu Lys Gln Phe Val
                565                 570                 575

Ala Pro Leu Leu Asn Ile Thr Glu Ser Val Leu Ile Pro Asn Ser Phe
            580                 585                 590

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

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

Lys Leu Phe Gln Gln Tyr Gly Pro Val Cys Asp Asn Ile Leu Ser Val
625                 630                 635                 640

Val Asn Ser Val Ser Gln Lys Glu Asp Met Glu Leu Leu Ser Phe Tyr
                645                 650                 655

Ser Ser Thr Lys Pro Lys Gly Tyr Asp Thr Pro Val Leu Ser Asn Val
            660                 665                 670

Ser Thr Gly Glu Phe Asn Ile Ser Leu Leu Leu Thr Pro Pro Ser Ser
        675                 680                 685

Pro Ser Gly Arg Ser Phe Val Glu Asp Leu Leu Phe Thr Ser Val Glu
    690                 695                 700

Thr Val Gly Leu Pro Thr Asp Ala Glu Tyr Lys Lys Cys Thr Ala Gly
705                 710                 715                 720

Pro Leu Gly Thr Leu Lys Asp Leu Ile Cys Ala Arg Glu Tyr Asn Gly
                725                 730                 735

Leu Leu Val Leu Pro Pro Ile Ile Thr Ala Asp Met Gln Thr Met Tyr
            740                 745                 750

Thr Ala Ser Leu Val Gly Ala Met Ala Phe Gly Gly Ile Thr Ser Ala
        755                 760                 765

Ala Ala Ile Pro Phe Ala Thr Gln Ile Gln Ala Arg Ile Asn His Leu
```

-continued

```
    770                 775                 780

Gly Ile Ala Gln Ser Leu Leu Met Lys Asn Gln Glu Lys Ile Ala Ala
785                 790                 795                 800

Ser Phe Asn Lys Ala Ile Gly His Met Gln Glu Gly Phe Arg Ser Thr
                805                 810                 815

Ser Leu Ala Leu Gln Gln Val Gln Asp Val Val Asn Lys Gln Ser Ala
            820                 825                 830

Ile Leu Thr Glu Thr Met Asn Ser Leu Asn Lys Asn Phe Gly Ala Ile
        835                 840                 845

Ser Ser Val Ile Gln Asp Ile Tyr Ala Gln Leu Asp Ala Ile Gln Ala
    850                 855                 860

Asp Ala Gln Val Asp Arg Leu Ile Thr Gly Arg Leu Ser Ser Leu Ser
865                 870                 875                 880

Val Leu Ala Ser Ala Lys Gln Ser Glu Tyr Ile Arg Val Ser Gln Gln
                885                 890                 895

Arg Glu Leu Ala Thr Gln Lys Ile Asn Glu Cys Val Lys Ser Gln Ser
            900                 905                 910

Asn Arg Tyr Gly Phe Cys Gly Ser Gly Arg His Val Leu Ser Ile Pro
        915                 920                 925

Gln Asn Ala Pro Asn Gly Ile Val Phe Ile His Phe Thr Tyr Thr Pro
    930                 935                 940

Glu Thr Phe Val Asn Val Thr Ala Ile Val Gly Phe Cys Val Asn Pro
945                 950                 955                 960

Leu Asn Ala Ser Gln Tyr Ala Ile Val Pro Ala Asn Gly Arg Gly Ile
                965                 970                 975

Phe Ile Gln Val Asn Gly Thr Tyr Tyr Ile Thr Ser Arg Asp Met Tyr
            980                 985                 990

Met Pro Arg Asp Ile Thr Ala Gly  Asp Ile Val Thr Leu  Thr Ser Cys
        995                 1000                1005

Gln Ala  Asn Tyr Val Asn Val  Asn Lys Thr Val Ile  Thr Thr Phe
    1010                1015                1020

Val Glu  Asp Asp Asp Phe Asn  Phe Asp Asp Glu Leu  Ser Lys Trp
    1025                1030                1035

Trp Asn  Asp Thr Lys His Gly  Leu Pro Asp Phe Asp  Asp Phe Asn
    1040                1045                1050

Tyr Thr  Val Pro Ile Leu Asn  Ile Ser Gly Glu Ile  Asp Asn Ile
    1055                1060                1065

Gln Gly  Val Ile Gln Gly Leu  Asn Asp Ser Leu Ile  Asn Leu Glu
    1070                1075                1080

Glu Leu  Ser Ile Ile Lys Thr  Tyr Ile Lys Trp Pro  Trp Tyr Val
    1085                1090                1095

Trp Leu  Ala Ile Gly Phe Ala  Ile Ile Ile Phe Ile  Leu Ile Leu
    1100                1105                1110

Gly Trp  Val Phe Phe Met Thr  Gly Cys Cys Gly Cys  Cys Cys Gly
    1115                1120                1125

Cys Phe  Gly Ile Ile Pro Leu  Ile Ser Lys Cys Gly  Lys Lys Ser
    1130                1135                1140

Ser Tyr  Tyr Thr Thr Phe Asp  Asn Asp Val Val Thr  Glu Gln Tyr
    1145                1150                1155

Arg Pro  Lys Lys Ser Val
    1160
```

<210> SEQ ID NO 54

<211> LENGTH: 1363
<212> TYPE: PRT
<213> ORGANISM: Bovine coronoavirus

<400> SEQUENCE: 54

```
Met Phe Leu Ile Leu Leu Ile Ser Leu Pro Met Ala Phe Ala Val Ile
1               5                   10                  15

Gly Asp Leu Lys Cys Thr Thr Val Ser Ile Asn Asp Val Asp Thr Gly
            20                  25                  30

Ala Pro Ser Ile Ser Thr Asp Ile Val Asp Val Thr Asn Gly Leu Gly
        35                  40                  45

Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
    50                  55                  60

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

Lys Gly Thr Leu Leu Leu Ser Arg Leu Trp Phe Lys Pro Pro Phe Leu
                85                  90                  95

Ser Asp Phe Ile Asn Gly Ile Phe Ala Lys Val Lys Asn Thr Lys Val
            100                 105                 110

Ile Lys Lys Gly Val Met Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
        115                 120                 125

Ser Thr Phe Val Asn Thr Ser Tyr Ser Val Val Val Gln Pro His Thr
    130                 135                 140

Thr Asn Leu Asp Asn Lys Leu Gln Gly Leu Leu Glu Ile Ser Val Cys
145                 150                 155                 160

Gln Tyr Thr Met Cys Glu Tyr Pro His Thr Ile Cys His Pro Lys Leu
                165                 170                 175

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

Cys Leu Tyr Lys Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu
        195                 200                 205

Tyr Phe His Phe Tyr Gln Glu Gly Gly Thr Phe Tyr Ala Tyr Phe Thr
    210                 215                 220

Asp Thr Gly Val Val Thr Lys Phe Leu Phe Asn Val Tyr Leu Gly Thr
225                 230                 235                 240

Val Leu Ser His Tyr Tyr Val Leu Pro Leu Thr Cys Ser Ser Ala Met
                245                 250                 255

Thr Leu Glu Tyr Trp Val Thr Pro Leu Thr Ser Lys Gln Tyr Leu Leu
            260                 265                 270

Ala Phe Asn Gln Asp Gly Val Ile Phe Asn Ala Val Asp Cys Lys Ser
        275                 280                 285

Asp Phe Met Ser Glu Ile Lys Cys Lys Thr Leu Ser Ile Ala Pro Ser
    290                 295                 300

Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Ile Ala Asp
305                 310                 315                 320

Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asn Ile Glu Ala Trp
                325                 330                 335

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

Phe Ser Asn Cys Asn Phe Asn Met Ser Ser Leu Met Ser Phe Ile Gln
        355                 360                 365

Ala Asp Ser Phe Thr Cys Asn Asn Ile Asp Ala Ala Lys Ile Tyr Gly
    370                 375                 380

Met Cys Phe Ser Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Gly
```

-continued

```
385                 390                 395                 400

Arg Lys Val Asp Leu Gln Leu Gly Asn Leu Gly Tyr Leu Gln Ser Phe
                405                 410                 415

Asn Tyr Arg Ile Asp Thr Thr Ala Thr Ser Cys Gln Leu Tyr Tyr Asn
            420                 425                 430

Leu Pro Ala Ala Asn Val Ser Val Ser Arg Phe Asn Pro Ser Thr Trp
        435                 440                 445

Asn Arg Arg Phe Gly Phe Thr Glu Gln Phe Val Phe Lys Pro Gln Pro
    450                 455                 460

Val Gly Val Phe Thr His His Asp Val Val Tyr Ala Gln His Cys Phe
465                 470                 475                 480

Lys Ala Pro Lys Asn Phe Cys Pro Cys Lys Leu Asp Gly Ser Leu Cys
                485                 490                 495

Val Gly Asn Gly Pro Gly Ile Asp Ala Gly Tyr Lys Asn Ser Gly Ile
            500                 505                 510

Gly Thr Cys Pro Ala Gly Thr Asn Tyr Leu Thr Cys His Asn Ala Ala
        515                 520                 525

Gln Cys Asp Cys Leu Cys Thr Pro Asp Pro Ile Thr Ser Lys Ser Thr
    530                 535                 540

Gly Pro Tyr Lys Cys Pro Gln Thr Lys Tyr Leu Val Gly Ile Gly Glu
545                 550                 555                 560

His Cys Ser Gly Leu Ala Ile Lys Ser Asp Tyr Cys Gly Gly Asn Pro
                565                 570                 575

Cys Thr Cys Gln Pro Gln Ala Phe Leu Gly Trp Ser Val Asp Ser Cys
            580                 585                 590

Leu Gln Gly Asp Arg Cys Asn Ile Phe Ala Asn Phe Ile Phe His Asp
        595                 600                 605

Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Lys Ser Asn Thr
    610                 615                 620

Asp Ile Ile Leu Gly Val Cys Val Asn Tyr Asp Leu Tyr Gly Ile Thr
625                 630                 635                 640

Gly Gln Gly Ile Phe Val Glu Val Asn Ala Thr Tyr Tyr Asn Ser Trp
                645                 650                 655

Gln Asn Leu Leu Tyr Asp Ser Asn Gly Asn Leu Tyr Gly Phe Arg Asp
            660                 665                 670

Tyr Leu Thr Asn Arg Thr Phe Met Ile Arg Ser Cys Tyr Ser Gly Arg
        675                 680                 685

Val Ser Ala Ala Phe His Ala Asn Ser Ser Glu Pro Ala Leu Leu Phe
    690                 695                 700

Arg Asn Ile Lys Cys Asn Tyr Val Phe Asn Asn Thr Leu Ser Arg Gln
705                 710                 715                 720

Leu Gln Pro Ile Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val Val Asn
                725                 730                 735

Ala Asp Asn Ser Thr Ser Ser Val Val Gln Thr Cys Asp Leu Thr Val
            740                 745                 750

Gly Ser Gly Tyr Cys Val Asp Tyr Ser Thr Lys Arg Arg Ser Arg Arg
        755                 760                 765

Ala Ile Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe Thr Val
    770                 775                 780

Asn Ser Val Asn Asp Ser Leu Glu Pro Val Gly Gly Leu Tyr Glu Ile
785                 790                 795                 800

Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Met Glu Glu Phe Ile Gln
                805                 810                 815
```

-continued

```
Thr Ser Ser Pro Lys Val Thr Ile Asp Cys Ser Ala Phe Val Cys Gly
            820                 825                 830

Asp Tyr Ala Ala Cys Lys Ser Gln Leu Val Glu Tyr Gly Ser Phe Cys
        835                 840                 845

Asp Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu Asp Thr
    850                 855                 860

Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr Leu Ser
865                 870                 875                 880

Thr Lys Leu Lys Asp Gly Val Asn Phe Asn Val Asp Asp Ile Asn Phe
                885                 890                 895

Ser Pro Val Leu Gly Cys Leu Gly Ser Ala Cys Asn Lys Val Ser Ser
            900                 905                 910

Arg Ser Ala Ile Glu Asp Leu Leu Phe Ser Lys Val Lys Leu Ser Asp
        915                 920                 925

Val Gly Phe Val Glu Ala Tyr Asn Asn Cys Thr Gly Gly Ala Glu Ile
    930                 935                 940

Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val Leu Pro
945                 950                 955                 960

Pro Leu Leu Ser Val Asn Gln Ile Ser Gly Tyr Thr Leu Ala Ala Thr
                965                 970                 975

Ser Ala Ser Leu Phe Pro Pro Leu Ser Ala Ala Val Gly Val Pro Phe
            980                 985                 990

Tyr Leu Asn Val Gln Tyr Arg Ile  Asn Gly Ile Gly Val  Thr Met Asp
        995                 1000                 1005

Val Leu  Ser Gln Asn Gln Lys  Leu Ile Ala Asn Ala  Phe Asn Asn
    1010                 1015                 1020

Ala Leu  Asp Ala Ile Gln Glu  Gly Phe Asp Ala Thr  Asn Ser Ala
    1025                 1030                 1035

Leu Val  Lys Ile Gln Ala Val  Val Asn Ala Asn Ala  Glu Ala Leu
    1040                 1045                 1050

Asn Asn  Leu Leu Gln Gln Leu  Ser Asn Arg Phe Gly  Ala Ile Ser
    1055                 1060                 1065

Ser Ser  Leu Gln Glu Ile Leu  Ser Arg Leu Asp Ala  Leu Glu Ala
    1070                 1075                 1080

Gln Ala  Gln Ile Asp Arg Leu  Ile Asn Gly Arg Leu  Thr Ala Leu
    1085                 1090                 1095

Asn Val  Tyr Val Ser Gln Gln  Leu Ser Asp Ser Thr  Leu Val Lys
    1100                 1105                 1110

Phe Ser  Ala Ala Gln Ala Met  Glu Lys Val Asn Glu  Cys Val Lys
    1115                 1120                 1125

Ser Gln  Ser Ser Arg Ile Asn  Phe Cys Gly Asn Gly  Asn His Ile
    1130                 1135                 1140

Ile Ser  Leu Val Gln Asn Ala  Pro Tyr Gly Leu Tyr  Phe Ile His
    1145                 1150                 1155

Phe Ser  Tyr Val Pro Thr Lys  Tyr Val Thr Ala Lys  Val Ser Pro
    1160                 1165                 1170

Gly Leu  Cys Ile Ala Gly Asp  Arg Gly Ile Ala Pro  Lys Ser Gly
    1175                 1180                 1185

Tyr Phe  Val Asn Val Asn Asn  Thr Trp Met Phe Thr  Gly Ser Gly
    1190                 1195                 1200

Tyr Tyr  Tyr Pro Glu Pro Ile  Thr Gly Asn Asn Val  Val Val Met
    1205                 1210                 1215
```

-continued

Ser Thr Cys Ala Val Asn Tyr Thr Lys Ala Pro Asp Val Met Leu
1220 1225 1230

Asn Ile Ser Thr Pro Asn Leu His Asp Phe Lys Glu Glu Leu Asp
1235 1240 1245

Gln Trp Phe Lys Asn Gln Thr Ser Val Ala Pro Asp Leu Ser Leu
1250 1255 1260

Asp Tyr Ile Asn Val Thr Phe Leu Asp Leu Gln Asp Glu Met Asn
1265 1270 1275

Arg Leu Gln Glu Ala Ile Lys Val Leu Asn Gln Ser Tyr Ile Asn
1280 1285 1290

Leu Lys Asp Ile Gly Thr Tyr Glu Tyr Tyr Val Lys Trp Pro Trp
1295 1300 1305

Tyr Val Trp Leu Leu Ile Gly Phe Ala Gly Val Ala Met Leu Val
1310 1315 1320

Leu Leu Phe Phe Ile Cys Cys Cys Thr Gly Cys Gly Thr Ser Cys
1325 1330 1335

Phe Lys Ile Cys Gly Gly Cys Cys Asp Asp Tyr Thr Gly His Gln
1340 1345 1350

Glu Leu Val Ile Lys Thr Ser His Asp Asp
1355 1360

<210> SEQ ID NO 55
<211> LENGTH: 1453
<212> TYPE: PRT
<213> ORGANISM: canine coronavirus

<400> SEQUENCE: 55

Met Ile Val Leu Ile Leu Cys Leu Leu Leu Phe Ser Tyr Asn Ser Val
1 5 10 15

Ile Cys Thr Ser Asn Asn Asp Cys Val Gln Gly Asn Val Thr Gln Leu
20 25 30

Pro Gly Asn Glu Asn Ile Ile Lys Asp Phe Leu Phe His Thr Phe Lys
35 40 45

Glu Glu Pro Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val Trp
50 55 60

Tyr Asn Cys Ser Arg Ser Ala Thr Thr Thr Ala Tyr Lys Asp Phe Ser
65 70 75 80

Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser Thr
85 90 95

Gly Asn Ala Arg Gly Lys Pro Leu Leu Val His Val His Gly Asp Pro
100 105 110

Val Ser Ile Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Pro
115 120 125

Arg Pro Leu Leu Lys His Gly Leu Leu Cys Ile Thr Lys Asn Lys Ile
130 135 140

Ile Asp Tyr Asn Thr Phe Thr Ser Ala Gln Trp Ser Ala Ile Cys Leu
145 150 155 160

Gly Asp Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly
165 170 175

Thr Lys Ile Phe Gly Leu Glu Trp Asn Asp Asp Tyr Val Thr Ala Tyr
180 185 190

Ile Ser Asp Arg Ser His His Leu Asn Ile Asn Asn Asn Trp Phe Asn
195 200 205

Asn Val Thr Ile Leu Tyr Ser Arg Ser Ser Ser Ala Thr Trp Gln Lys
210 215 220

-continued

```
Ser Ala Ala Tyr Val Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr Lys
225                 230                 235                 240

Leu Asn Asn Thr Asn Gly Leu Lys Ser Tyr Glu Leu Cys Glu Asp Tyr
                245                 250                 255

Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val Gly
            260                 265                 270

Gly Tyr Ile Pro His Gly Phe Ser Phe Asn Asn Trp Phe Met Arg Thr
        275                 280                 285

Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro Leu
    290                 295                 300

Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala Gln
305                 310                 315                 320

Gln Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val Ser
                325                 330                 335

Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr Ala
            340                 345                 350

Leu Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr Thr
        355                 360                 365

Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Asn Asp Thr Val Ser Glu
    370                 375                 380

Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Ser Phe Gly Val Thr Asp Gly
385                 390                 395                 400

Pro Arg Tyr Cys Phe Ala Leu Tyr Asn Gly Thr Ala Leu Lys Tyr Leu
                405                 410                 415

Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp Gly
            420                 425                 430

His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile Asp
        435                 440                 445

Cys Ile Ser Phe Asn Leu Thr Thr Gly Asp Ser Gly Ala Phe Trp Thr
    450                 455                 460

Ile Ala Tyr Thr Ser Tyr Thr Asp Ala Leu Val Gln Val Glu Asn Thr
465                 470                 475                 480

Ala Ile Lys Lys Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile Lys
                485                 490                 495

Cys Ser Gln Leu Thr Ala Asn Leu Gln Asn Gly Phe Tyr Pro Val Ala
            500                 505                 510

Ser Ser Glu Val Gly Leu Val Asn Lys Ser Val Val Leu Leu Pro Ser
        515                 520                 525

Phe Tyr Ser His Thr Ser Val Asn Ile Thr Ile Asp Leu Gly Met Lys
    530                 535                 540

Arg Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile Thr
545                 550                 555                 560

Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser Asn
                565                 570                 575

Arg Phe Ser Val Tyr Phe His Ser Thr Cys Lys Ser Ser Leu Trp Asp
            580                 585                 590

Asp Val Phe Asn Ser Asp Cys Thr Asp Val Leu Tyr Ala Thr Ala Val
        595                 600                 605

Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn Tyr
    610                 615                 620

Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Asn Pro Val Gly Ala Asn
625                 630                 635                 640
```

-continued

```
Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val Val
                645                 650                 655

Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly Val
            660                 665                 670

Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu Asp
        675                 680                 685

Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Ile Thr Gly Val Gly Ile Ile
    690                 695                 700

Arg Gln Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser Leu
705                 710                 715                 720

Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile Tyr
                725                 730                 735

Ser Val Thr Pro Cys Asp Val Ser Ala His Ala Ala Val Ile Asp Gly
            740                 745                 750

Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly Leu
        755                 760                 765

Thr His Trp Thr Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr Asn
    770                 775                 780

Tyr Thr Asn Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp Val
785                 790                 795                 800

Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys Asn
                805                 810                 815

Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val Gln
            820                 825                 830

Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile Ser
        835                 840                 845

Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile Asp
    850                 855                 860

Cys Ser Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu Leu
865                 870                 875                 880

Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala Met
                885                 890                 895

Gly Ala Arg Leu Glu Asn Met Glu Ile Asp Ser Met Leu Phe Val Ser
            900                 905                 910

Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr Glu
        915                 920                 925

Thr Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser Trp
    930                 935                 940

Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg Lys
945                 950                 955                 960

Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr Ser
                965                 970                 975

Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly Tyr
            980                 985                 990

Asp Ile Ala Asp Leu Val Cys Ala  Gln Tyr Tyr Asn Gly  Ile Met Val
        995                 1000                1005

Leu Pro  Gly Val Ala Asn Asp  Asp Lys Met Ala Met  Tyr Thr Ala
    1010                1015                1020

Ser Leu  Ala Gly Gly Ile Thr  Leu Gly Ser Leu Gly  Gly Gly Ala
    1025                1030                1035

Val Ser  Ile Pro Phe Ala Ile  Ala Val Gln Ala Arg  Leu Asn Tyr
    1040                1045                1050

Val Ala  Leu Gln Thr Asp Val  Leu Asn Lys Asn Gln  Gln Ile Leu
```

-continued

```
    1055                1060                1065

Ala Asn  Ala Phe Asn Gln Ala  Ile Gly Asn Ile Thr  Gln Ala Phe
    1070                1075                1080

Gly Lys  Val Asn Asp Ala Ile  His Gln Thr Ser Gln  Gly Leu Ala
    1085                1090                1095

Thr Val  Ala Lys Val Leu Ala  Lys Val Gln Asp Val  Val Asn Thr
    1100                1105                1110

Gln Gly  Gln Ala Leu Ser His  Leu Thr Leu Gln Leu  Gln Asn Asn
    1115                1120                1125

Phe Gln  Ala Ile Ser Ser Ser  Ile Ser Asp Ile Tyr  Asn Arg Leu
    1130                1135                1140

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

Arg Leu  Thr Ala Leu Asn Ala  Phe Val Ser Gln Thr  Leu Thr Arg
    1160                1165                1170

Gln Ala  Glu Val Arg Ala Ser  Arg Gln Leu Ala Lys  Asp Lys Val
    1175                1180                1185

Asn Glu  Cys Val Arg Ser Gln  Ser Gln Arg Phe Gly  Phe Cys Gly
    1190                1195                1200

Asn Gly  Thr His Leu Phe Ser  Leu Ala Asn Ala Ala  Pro Asn Gly
    1205                1210                1215

Met Ile  Phe Phe His Thr Val  Leu Leu Pro Thr Ala  Tyr Glu Thr
    1220                1225                1230

Val Thr  Ala Trp Ser Gly Ile  Cys Ala Ser Asp Gly  Asp Arg Thr
    1235                1240                1245

Phe Gly  Leu Val Val Lys Asp  Val Gln Leu Thr Leu  Phe Arg Asn
    1250                1255                1260

Leu Asp  Asp Lys Phe Tyr Leu  Thr Pro Arg Thr Met  Tyr Gln Pro
    1265                1270                1275

Ile Val  Ala Thr Ser Ser Asp  Phe Val Gln Ile Glu  Gly Cys Asp
    1280                1285                1290

Val Leu  Phe Val Asn Ala Thr  Val Ile Asp Leu Pro  Ser Ile Ile
    1295                1300                1305

Pro Asp  Tyr Ile Asp Ile Asn  Gln Thr Val Gln Asp  Ile Leu Glu
    1310                1315                1320

Asn Phe  Arg Pro Asn Trp Thr  Val Pro Glu Leu Pro  Leu Asp Ile
    1325                1330                1335

Phe Asn  Ala Thr Tyr Leu Asn  Leu Thr Gly Glu Ile  Asn Asp Leu
    1340                1345                1350

Glu Phe  Arg Ser Glu Lys Leu  His Asn Thr Thr Val  Glu Leu Ala
    1355                1360                1365

Ile Leu  Ile Asp Asn Ile Asn  Asn Thr Leu Val Asn  Leu Glu Trp
    1370                1375                1380

Leu Asn  Arg Ile Glu Thr Tyr  Val Lys Trp Pro Trp  Tyr Val Trp
    1385                1390                1395

Leu Leu  Ile Gly Leu Val Val  Ile Phe Cys Ile Pro  Ile Leu Leu
    1400                1405                1410

Phe Cys  Cys Cys Ser Thr Gly  Cys Cys Gly Cys Ile  Gly Cys Leu
    1415                1420                1425

Gly Ser  Cys Cys His Ser Ile  Cys Ser Arg Arg Gln  Phe Glu Ser
    1430                1435                1440

Tyr Glu  Pro Ile Glu Lys Val  His Val His
    1445                1450
```

<210> SEQ ID NO 56
<211> LENGTH: 1464
<212> TYPE: PRT
<213> ORGANISM: Feline infectious peritonitis virus

<400> SEQUENCE: 56

```
Met Ile Phe Ile Ile Leu Thr Leu Leu Ser Val Ala Lys Ser Glu Asp
1               5                   10                  15

Ala Pro His Gly Val Thr Leu Pro Gln Phe Asn Thr Ser His Asn Asn
            20                  25                  30

Glu Arg Phe Glu Leu Asn Phe Tyr Asn Phe Leu Gln Thr Trp Asp Ile
        35                  40                  45

Pro Pro Asn Thr Glu Thr Ile Leu Gly Gly Tyr Leu Pro Tyr Cys Gly
    50                  55                  60

Ala Gly Val Asn Cys Gly Trp Tyr Asn Phe Ser Gln Ser Val Gly Gln
65                  70                  75                  80

Asn Gly Lys Tyr Ala Tyr Ile Asn Thr Gln Asn Leu Asn Ile Pro Asn
                85                  90                  95

Val His Gly Val Tyr Phe Asp Val Arg Glu His Asn Asn Asp Gly Glu
            100                 105                 110

Trp Asp Asp Arg Asp Lys Val Gly Leu Leu Ile Ala Ile His Gly Asn
        115                 120                 125

Ser Lys Tyr Ser Leu Leu Met Val Leu Gln Asp Ala Val Glu Ala Asn
    130                 135                 140

Gln Pro His Val Ala Val Lys Ile Cys His Trp Lys Pro Gly Asn Ile
145                 150                 155                 160

Ser Ser Tyr His Ala Phe Ser Val Asn Leu Gly Asp Gly Gly Gln Cys
                165                 170                 175

Val Phe Asn Gln Arg Phe Ser Leu Asp Thr Val Leu Thr Thr Asn Asp
            180                 185                 190

Phe Tyr Gly Phe Gln Trp Thr Asp Thr Tyr Val Asp Ile Tyr Leu Gly
        195                 200                 205

Gly Thr Ile Thr Lys Val Trp Val Asp Asn Asp Trp Ser Ile Val Glu
    210                 215                 220

Ala Ser Ile Ser Tyr His Trp Asn Arg Ile Asn Tyr Gly Tyr Tyr Met
225                 230                 235                 240

Gln Phe Val Asn Arg Thr Thr Tyr Tyr Ala Tyr Asn Asn Thr Gly Gly
                245                 250                 255

Ala Asn Tyr Thr Gln Leu Gln Leu Ser Glu Cys His Thr Asp Tyr Cys
            260                 265                 270

Ala Gly Tyr Ala Lys Asn Val Phe Val Pro Ile Asp Gly Lys Ile Pro
        275                 280                 285

Glu Asp Phe Ser Phe Ser Asn Trp Phe Leu Leu Ser Asp Lys Ser Thr
    290                 295                 300

Leu Val Gln Gly Arg Val Leu Ser Ser Gln Pro Val Phe Val Gln Cys
305                 310                 315                 320

Leu Arg Pro Val Pro Ser Trp Ser Asn Asn Thr Ala Val Val His Phe
                325                 330                 335

Lys Asn Asp Ala Phe Cys Pro Asn Val Thr Ala Asp Val Leu Arg Phe
            340                 345                 350

Asn Leu Asn Phe Ser Asp Thr Asp Val Tyr Thr Asp Ser Thr Asn Asp
        355                 360                 365

Glu Gln Leu Phe Phe Thr Phe Glu Asp Asn Thr Thr Ala Ser Ile Ala
```

```
    370                 375                 380

Cys Tyr Ser Ser Ala Asn Val Thr Asp Phe Gln Pro Ala Asn Asn Ser
385                 390                 395                 400

Val Ser His Ile Pro Phe Gly Lys Thr Ala His Phe Cys Phe Ala Asn
                405                 410                 415

Phe Ser His Ser Ile Val Ser Arg Gln Phe Leu Gly Ile Leu Pro Pro
            420                 425                 430

Thr Val Arg Glu Phe Ala Phe Gly Arg Asp Gly Ser Ile Phe Val Asn
        435                 440                 445

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

Ile Ser Ser Val Glu Glu Tyr Gly Phe Trp Thr Ile Ala Tyr Thr Asn
465                 470                 475                 480

Tyr Thr Asp Val Met Val Asp Val Asn Gly Thr Ala Ile Thr Arg Leu
                485                 490                 495

Phe Tyr Cys Asp Ser Pro Leu Asn Arg Ile Lys Cys Gln Gln Leu Lys
            500                 505                 510

His Glu Leu Pro Asp Gly Phe Tyr Ser Ala Ser Met Leu Val Lys Lys
        515                 520                 525

Asp Leu Pro Lys Thr Phe Val Thr Met Pro Gln Phe Tyr His Trp Met
    530                 535                 540

Asn Val Thr Leu His Val Val Leu Asn Asp Thr Glu Lys Lys Tyr Asp
545                 550                 555                 560

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

Phe Glu Ile Ala Gln Ala Asn Gly Ser Val Thr Asn Val Thr Ser Leu
            580                 585                 590

Cys Val Gln Ala Arg Gln Leu Ala Leu Phe Tyr Lys Tyr Thr Ser Leu
        595                 600                 605

Gln Gly Leu Tyr Thr Tyr Ser Asn Leu Val Glu Leu Gln Asn Tyr Asp
    610                 615                 620

Cys Pro Phe Ser Pro Gln Gln Phe Asn Asn Tyr Leu Gln Phe Glu Thr
625                 630                 635                 640

Leu Cys Phe Asp Val Asn Pro Ala Val Ala Gly Cys Lys Trp Ser Leu
                645                 650                 655

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

Tyr Lys His Gly Ser Met Ile Thr Thr His Ala Lys Gly His Ser Trp
        675                 680                 685

Gly Phe Gln Asp Thr Ser Val Leu Val Lys Asp Glu Cys Thr Asp Tyr
    690                 695                 700

Asn Ile Tyr Gly Phe Gln Gly Thr Gly Ile Ile Arg Asn Thr Thr Ser
705                 710                 715                 720

Arg Leu Val Ala Gly Leu Tyr Tyr Thr Ser Ile Ser Gly Asp Leu Leu
                725                 730                 735

Ala Phe Lys Asn Ser Thr Thr Gly Glu Ile Phe Thr Val Val Pro Cys
            740                 745                 750

Asp Leu Thr Ala Gln Val Ala Val Ile Asn Asp Glu Ile Val Gly Ala
        755                 760                 765

Ile Thr Ala Val Asn Gln Thr Asp Leu Phe Glu Phe Val Asn Asn Thr
    770                 775                 780

Gln Ala Arg Arg Ser Arg Ser Ser Thr Pro Asn Phe Val Thr Ser Tyr
785                 790                 795                 800
```

-continued

```
Thr Met Pro Gln Phe Tyr Tyr Ile Thr Lys Trp Asn Asn Asp Thr Ser
                805                 810                 815

Ser Asn Cys Thr Ser Ala Ile Thr Tyr Ser Ser Phe Ala Ile Cys Asn
            820                 825                 830

Thr Gly Glu Ile Lys Tyr Val Asn Val Thr His Val Glu Ile Val Asp
        835                 840                 845

Asp Ser Ile Gly Val Ile Lys Pro Val Ser Thr Gly Asn Ile Ser Ile
    850                 855                 860

Pro Lys Asn Phe Thr Val Ala Val Gln Ala Glu Tyr Ile Gln Ile Gln
865                 870                 875                 880

Val Lys Pro Val Val Val Asp Cys Ala Thr Tyr Val Cys Asn Gly Asn
                885                 890                 895

Thr His Cys Leu Lys Leu Leu Thr Gln Tyr Thr Ser Ala Cys Gln Thr
            900                 905                 910

Ile Glu Asn Ala Leu Asn Leu Gly Ala Arg Leu Glu Ser Leu Met Leu
        915                 920                 925

Asn Asp Met Ile Thr Val Ser Asp Arg Gly Leu Glu Leu Ala Thr Val
    930                 935                 940

Glu Arg Phe Asn Ala Thr Ala Leu Gly Gly Glu Lys Leu Gly Gly Leu
945                 950                 955                 960

Tyr Phe Asp Gly Leu Ser Ser Leu Leu Pro Pro Lys Ile Gly Lys Arg
                965                 970                 975

Ser Ala Val Glu Asp Leu Leu Phe Asn Lys Val Val Thr Ser Gly Leu
            980                 985                 990

Gly Thr Val Asp Asp Asp Tyr Lys  Lys Cys Ser Ser Gly  Thr Asp Val
        995                 1000                 1005

Ala Asp  Leu Val Cys Ala Gln  Tyr Tyr Asn Gly Ile  Met Val Leu
    1010                 1015                 1020

Pro Gly  Val Val Asp Gly Asn  Lys Met Ser Met Tyr  Thr Ala Ser
    1025                 1030                 1035

Leu Ile  Gly Gly Met Ala Leu  Gly Ser Ile Thr Ser  Ala Val Ala
    1040                 1045                 1050

Val Pro  Phe Ala Met Gln Val  Gln Ala Arg Leu Asn  Tyr Val Ala
    1055                 1060                 1065

Leu Gln  Thr Asp Val Leu Gln  Glu Asn Gln Lys Ile  Leu Ala Asn
    1070                 1075                 1080

Ala Phe  Asn Asn Ala Ile Gly  Asn Ile Thr Leu Ala  Leu Gly Lys
    1085                 1090                 1095

Val Ser  Asn Ala Ile Thr Thr  Thr Ser Asp Gly Phe  Asn Ser Met
    1100                 1105                 1110

Ala Ser  Ala Leu Thr Lys Ile  Gln Ser Val Val Asn  Gln Gln Gly
    1115                 1120                 1125

Glu Ala  Leu Ser Gln Leu Thr  Ser Gln Leu Gln Lys  Asn Phe Gln
    1130                 1135                 1140

Ala Ile  Ser Ser Ser Ile Ala  Glu Ile Tyr Asn Arg  Leu Glu Lys
    1145                 1150                 1155

Val Glu  Ala Asp Ala Gln Val  Asp Arg Leu Ile Thr  Gly Arg Leu
    1160                 1165                 1170

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

Glu Val  Lys Ala Ser Arg Gln  Ile Ala Leu Glu Lys  Val Asn Glu
    1190                 1195                 1200
```

-continued

```
Cys Val  Lys Ser Gln Ser Asn  Arg Tyr Gly Phe Cys  Gly Asn Gly
    1205                 1210                 1215

Thr His  Leu Phe Ser Leu Val  Asn Ser Ala Pro Glu  Gly Leu Leu
    1220                 1225                 1230

Phe Phe  His Thr Val Leu Leu  Pro Thr Glu Trp Glu  Glu Val Thr
    1235                 1240                 1245

Ala Trp  Ser Gly Ile Cys Val  Asn Asp Thr Tyr Ala  Tyr Val Leu
    1250                 1255                 1260

Lys Asp  Phe Asp His Ser Ile  Phe Ser Tyr Asn Gly  Thr Tyr Met
    1265                 1270                 1275

Val Thr  Pro Arg Asn Met Phe  Gln Pro Arg Lys Pro  Gln Met Ser
    1280                 1285                 1290

Asp Phe  Val Gln Ile Thr Ser  Cys Glu Val Thr Phe  Leu Asn Met
    1295                 1300                 1305

Thr Tyr  Thr Thr Phe Gln Glu  Ile Val Ile Asp Tyr  Ile Asp Ile
    1310                 1315                 1320

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

Thr Thr  Pro Glu Leu Asn Leu  Leu Leu Asp Ile Phe  Asn Gln Thr
    1340                 1345                 1350

Lys Leu  Asn Leu Thr Ala Glu  Ile Asp Gln Leu Glu  Gln Arg Ala
    1355                 1360                 1365

Asp Asn  Leu Thr Thr Ile Ala  His Glu Leu Gln Gln  Tyr Ile Asp
    1370                 1375                 1380

Asn Leu  Asn Lys Thr Leu Val  Asp Leu Asp Trp Leu  Asn Arg Ile
    1385                 1390                 1395

Glu Thr  Tyr Val Lys Trp Pro  Trp Tyr Val Trp Leu  Leu Ile Gly
    1400                 1405                 1410

Leu Val  Val Val Phe Cys Ile  Pro Leu Leu Leu Phe  Cys Cys Leu
    1415                 1420                 1425

Ser Thr  Gly Phe Cys Gly Cys  Phe Gly Cys Val Gly  Ser Cys Cys
    1430                 1435                 1440

His Ser  Leu Cys Ser Arg Arg  Gln Phe Glu Thr Tyr  Glu Pro Ile
    1445                 1450                 1455

Glu Lys  Val His Ile His
    1460


<210> SEQ ID NO 57
<211> LENGTH: 1235
<212> TYPE: PRT
<213> ORGANISM: Mouse hepatitis virus

<400> SEQUENCE: 57

Met Leu Phe Val Phe Ile Leu Leu Leu Pro Ser Cys Leu Gly Tyr Ile
1               5                   10                  15

Gly Asp Phe Arg Cys Ile Gln Thr Val Asn Tyr Asn Gly Asn Asn Ala
            20                  25                  30

Ser Ala Pro Ser Ile Ser Thr Glu Ala Val Asp Val Ser Lys Gly Arg
        35                  40                  45

Gly Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Ala Thr Leu Leu
    50                  55                  60

Leu Thr Gly Tyr Tyr Pro Val Asp Gly Ser Asn Tyr Arg Asn Leu Ala
65                  70                  75                  80

Leu Thr Gly Thr Asn Thr Leu Ser Leu Thr Trp Phe Lys Pro Pro Phe
                85                  90                  95
```

-continued

```
Leu Ser Glu Phe Asn Asp Gly Ile Phe Ala Lys Val Gln Asn Leu Lys
                100                 105                 110

Thr Asn Thr Pro Thr Gly Ala Thr Ser Tyr Phe Pro Thr Ile Val Ile
            115                 120                 125

Gly Ser Leu Phe Gly Asn Thr Ser Tyr Thr Val Val Leu Glu Pro Tyr
    130                 135                 140

Asn Asn Ile Ile Met Ala Ser Val Cys Thr Tyr Thr Ile Cys Gln Leu
145                 150                 155                 160

Pro Tyr Thr Pro Cys Lys Pro Asn Thr Asn Gly Asn Arg Val Ile Gly
                165                 170                 175

Phe Trp His Thr Asp Val Lys Pro Pro Ile Cys Leu Leu Lys Arg Asn
                180                 185                 190

Phe Thr Phe Asn Val Asn Ala Pro Trp Leu Tyr Phe His Phe Tyr Gln
            195                 200                 205

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

Thr Phe Leu Phe Ser Val Tyr Ile Gly Asp Ile Leu Thr Gln Tyr Phe
225                 230                 235                 240

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

Leu Tyr Trp Val Thr Pro Leu Leu Lys Arg Gln Tyr Leu Phe Asn Phe
            260                 265                 270

Asn Glu Lys Gly Val Ile Thr Ser Ala Val Asp Cys Ala Ser Ser Tyr
        275                 280                 285

Ile Ser Glu Ile Lys Cys Lys Thr Gln Ser Leu Leu Pro Ser Thr Gly
    290                 295                 300

Val Tyr Asp Leu Ser Gly Tyr Thr Val Gln Pro Val Gly Val Val Tyr
305                 310                 315                 320

Arg Arg Val Pro Asn Leu Pro Asp Cys Lys Ile Glu Glu Trp Leu Thr
                325                 330                 335

Ala Lys Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Arg Thr Phe Gln
            340                 345                 350

Asn Cys Asn Phe Asn Leu Ser Ser Leu Leu Arg Tyr Val Gln Ala Glu
        355                 360                 365

Ser Leu Ser Cys Asn Asn Ile Asp Ala Ser Lys Val Tyr Gly Met Cys
    370                 375                 380

Phe Gly Ser Val Ser Val Asp Lys Phe Ala Ile Pro Arg Ser Arg Gln
385                 390                 395                 400

Ile Asp Leu Gln Ile Gly Asn Ser Gly Phe Leu Gln Thr Ala Asn Tyr
                405                 410                 415

Lys Ile Asp Thr Ala Ala Thr Ser Cys Gln Leu Tyr Tyr Ser Leu Pro
            420                 425                 430

Lys Asn Asn Val Thr Ile Asn Asn Tyr Asn Pro Ser Ser Trp Asn Arg
        435                 440                 445

Arg Tyr Gly Phe Lys Val Asn Asp Arg Cys Gln Ile Phe Ala Asn Ile
    450                 455                 460

Leu Leu Asn Gly Ile Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln
465                 470                 475                 480

Leu Pro Asn Thr Glu Val Ala Thr Gly Val Cys Val Arg Tyr Asp Leu
                485                 490                 495

Tyr Gly Ile Thr Gly Gln Gly Val Phe Lys Glu Val Lys Ala Asp Tyr
            500                 505                 510
```

-continued

```
Tyr Asn Ser Trp Gln Ala Leu Leu Tyr Asp Val Asn Gly Asn Leu Asn
        515                 520                 525

Gly Phe Arg Asp Leu Thr Thr Asn Lys Thr Tyr Thr Ile Arg Ser Cys
    530                 535                 540

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

Ala Leu Leu Tyr Arg Asn Ile Asn Cys Ser Tyr Val Phe Thr Asn Asn
                565                 570                 575

Ile Ser Arg Glu Glu Asn Pro Leu Asn Tyr Phe Asp Ser Tyr Leu Gly
            580                 585                 590

Cys Val Val Asn Ala Asp Asn Arg Thr Asp Glu Ala Leu Pro Asn Cys
        595                 600                 605

Asn Leu Arg Met Gly Ala Gly Leu Cys Val Asp Tyr Ser Lys Ser Arg
    610                 615                 620

Arg Ala Arg Arg Ser Val Ser Thr Gly Tyr Arg Leu Thr Thr Phe Glu
625                 630                 635                 640

Pro Tyr Met Pro Met Leu Val Asn Asp Ser Val Gln Ser Val Gly Gly
                645                 650                 655

Leu Tyr Glu Met Gln Ile Pro Thr Asn Phe Thr Ile Gly His His Glu
            660                 665                 670

Glu Phe Ile Gln Ile Arg Ala Pro Lys Val Thr Ile Asp Cys Ala Ala
        675                 680                 685

Phe Val Cys Gly Asp Asn Ala Ala Cys Arg Gln Gln Leu Val Glu Tyr
    690                 695                 700

Gly Ser Phe Cys Asp Asn Val Asn Ala Ile Leu Asn Glu Val Asn Asn
705                 710                 715                 720

Leu Leu Asp Asn Met Gln Leu Gln Val Ala Ser Ala Leu Met Gln Gly
                725                 730                 735

Val Thr Ile Ser Ser Arg Leu Pro Asp Gly Ile Ser Gly Pro Ile Asp
            740                 745                 750

Asp Ile Asn Phe Ser Pro Leu Leu Gly Cys Ile Gly Ser Thr Cys Ala
        755                 760                 765

Glu Asp Gly Asn Gly Pro Ser Ala Ile Arg Gly Arg Ser Ala Ile Glu
    770                 775                 780

Asp Leu Leu Phe Asp Lys Val Lys Leu Ser Asp Val Gly Phe Val Glu
785                 790                 795                 800

Ala Tyr Asn Asn Cys Thr Gly Gly Gln Glu Val Arg Asp Leu Leu Cys
                805                 810                 815

Val Gln Ser Phe Asn Gly Ile Lys Val Leu Pro Pro Val Leu Ser Glu
            820                 825                 830

Ser Gln Ile Ser Gly Tyr Thr Ala Gly Ala Thr Ala Ala Ala Met Phe
        835                 840                 845

Pro Pro Trp Thr Ala Ala Ala Gly Val Pro Phe Ser Leu Asn Val Gln
    850                 855                 860

Tyr Arg Ile Asn Gly Leu Gly Val Thr Met Asn Val Leu Ser Glu Asn
865                 870                 875                 880

Gln Lys Met Ile Ala Ser Ala Phe Asn Asn Ala Leu Gly Ala Ile Gln
                885                 890                 895

Glu Gly Phe Asp Ala Thr Asn Ser Ala Leu Gly Lys Ile Gln Ser Val
            900                 905                 910

Val Asn Ala Asn Ala Glu Ala Leu Asn Asn Leu Leu Asn Gln Leu Ser
        915                 920                 925

Asn Arg Phe Gly Ala Ile Ser Ala Ser Leu Gln Glu Ile Leu Thr Arg
```

-continued

```
    930                 935                 940

Leu Asp Ala Val Glu Ala Lys Ala Gln Ile Asp Arg Leu Ile Asn Gly
945                 950                 955                 960

Arg Leu Thr Ala Leu Asn Ala Tyr Ile Ser Lys Gln Leu Ser Asp Ser
                965                 970                 975

Thr Leu Ile Lys Phe Ser Ala Ala Gln Ala Ile Glu Lys Val Asn Glu
            980                 985                 990

Cys Val Lys Ser Gln Thr Thr Arg  Ile Asn Phe Cys Gly  Asn Gly Asn
        995                 1000                1005

His Ile  Leu Ser Leu Val Gln  Asn Ala Pro Tyr Gly  Leu Cys Phe
    1010                 1015                1020

Ile His  Phe Ser Tyr Val Pro  Thr Ser Phe Lys Thr  Ala Asn Val
    1025                 1030                1035

Ser Pro  Gly Leu Cys Ile Ser  Gly Asp Arg Gly Leu  Ala Pro Lys
    1040                 1045                1050

Ala Gly  Tyr Phe Val Gln Asp  Asn Gly Glu Trp Lys  Phe Thr Gly
    1055                 1060                1065

Ser Asn  Tyr Tyr Tyr Pro Glu  Pro Ile Thr Asp Lys  Asn Ser Val
    1070                 1075                1080

Ala Met  Ile Ser Cys Ala Val  Asn Tyr Thr Lys Ala  Pro Glu Val
    1085                 1090                1095

Phe Leu  Asn Asn Ser Ile Pro  Asn Leu Pro Asp Phe  Lys Glu Glu
    1100                 1105                1110

Leu Asp  Lys Trp Phe Lys Asn  Gln Thr Ser Ile Ala  Pro Asp Leu
    1115                 1120                1125

Ser Leu  Asp Phe Glu Lys Leu  Asn Val Thr Phe Leu  Asp Leu Thr
    1130                 1135                1140

Tyr Glu  Met Asn Arg Ile Gln  Asp Ala Ile Lys Lys  Leu Asn Glu
    1145                 1150                1155

Ser Tyr  Ile Asn Leu Lys Glu  Val Gly Thr Tyr Glu  Met Tyr Val
    1160                 1165                1170

Lys Trp  Pro Trp Tyr Val Trp  Leu Leu Ile Gly Leu  Ala Gly Val
    1175                 1180                1185

Ala Val  Cys Val Leu Leu Phe  Phe Ile Cys Cys Cys  Thr Gly Cys
    1190                 1195                1200

Gly Ser  Cys Cys Phe Arg Lys  Cys Gly Ser Cys Cys  Asp Glu Tyr
    1205                 1210                1215

Gly Gly  His Gln Asp Ser Ile  Val Ile His Asn Ile  Ser Ala His
    1220                 1225                1230

Glu Asp
    1235


<210> SEQ ID NO 58
<211> LENGTH: 1363
<212> TYPE: PRT
<213> ORGANISM: human coronavirus

<400> SEQUENCE: 58

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

Gly Asp Leu Lys Cys Thr Thr Val Ala Ile Asn Asp Val Asp Thr Gly
            20                  25                  30

Val Pro Ser Thr Ser Thr Asp Ile Val Asp Val Thr Asn Gly Leu Gly
        35                  40                  45
```

-continued

```
Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
    50                  55                  60

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

Lys Gly Thr Leu Leu Leu Ser Arg Leu Trp Phe Lys Pro Pro Phe Leu
                85                  90                  95

Ser Asp Phe Ile Asn Gly Ile Phe Ala Lys Val Lys Asn Thr Lys Val
            100                 105                 110

Ile Lys His Gly Val Met Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
        115                 120                 125

Ser Thr Phe Val Asn Thr Ser Tyr Ser Val Val Val Gln Pro His Thr
    130                 135                 140

Thr Asn Leu Asp Asn Lys Leu Gln Gly Leu Leu Glu Ile Ser Val Cys
145                 150                 155                 160

Gln Tyr Thr Met Cys Glu Tyr Pro Asn Thr Ile Cys His Pro Asn Leu
                165                 170                 175

Gly Asn Arg Arg Val Glu Leu Trp His Trp Asp Thr Gly Val Val Ser
            180                 185                 190

Cys Leu Tyr Lys Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu
        195                 200                 205

Tyr Phe His Phe Tyr Gln Glu Gly Gly Ile Phe Tyr Ala Tyr Phe Thr
    210                 215                 220

Asp Thr Gly Val Val Thr Lys Phe Leu Phe Asn Val Tyr Leu Gly Thr
225                 230                 235                 240

Val Leu Ser Tyr Tyr Tyr Val Met Pro Leu Thr Cys Asn Ser Ala Met
                245                 250                 255

Thr Leu Glu Tyr Trp Val Thr Pro Leu Thr Ser Lys Gln Tyr Leu Leu
            260                 265                 270

Ala Phe Asn Gln Asp Gly Val Ile Phe Asn Ala Val Asp Cys Lys Ser
        275                 280                 285

Asp Phe Met Ser Glu Ile Lys Cys Lys Thr Leu Ser Ile Ala Pro Ser
    290                 295                 300

Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Ile Ala Asp
305                 310                 315                 320

Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asn Ile Glu Ala Trp
                325                 330                 335

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

Phe Ser Asn Cys Asn Phe Asn Met Ser Ser Leu Met Ser Phe Ile Gln
        355                 360                 365

Ala Asp Ser Phe Thr Cys Asn Asn Ile Asp Ala Ala Lys Ile Tyr Gly
    370                 375                 380

Met Cys Phe Ser Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Gly
385                 390                 395                 400

Arg Lys Val Asp Leu Gln Leu Gly Asn Leu Gly Tyr Leu Gln Ser Phe
                405                 410                 415

Asn Tyr Arg Ile Asp Thr Thr Ala Thr Ser Cys Gln Leu Tyr Tyr Asn
            420                 425                 430

Leu Pro Ala Ala Asn Val Ser Val Ser Arg Phe Asn Pro Ser Ile Trp
        435                 440                 445

Asn Arg Arg Phe Gly Phe Thr Glu Gln Ser Val Phe Lys Pro Gln Pro
    450                 455                 460

Ala Gly Val Phe Thr Asp His Asp Val Val Tyr Ala Gln His Cys Phe
```

-continued

```
465                 470                 475                 480

Lys Ala Pro Thr Asn Phe Cys Pro Cys Lys Leu Asp Gly Ser Leu Cys
                485                 490                 495

Val Gly Asn Gly Pro Gly Ile Asp Ala Gly Tyr Lys Asn Ser Gly Ile
            500                 505                 510

Gly Thr Cys Pro Ala Gly Thr Asn Tyr Leu Thr Cys His Asn Ala Val
        515                 520                 525

Gln Cys Asn Cys Leu Cys Thr Pro Asp Pro Ile Thr Ser Lys Ser Thr
    530                 535                 540

Gly Pro Tyr Lys Cys Pro Gln Thr Lys Tyr Leu Val Gly Ile Gly Glu
545                 550                 555                 560

His Cys Ser Gly Leu Ala Ile Lys Ser Asp Tyr Cys Gly Gly Asn Pro
                565                 570                 575

Cys Thr Cys Gln Pro Gln Ala Phe Leu Gly Trp Ser Val Asp Ser Cys
            580                 585                 590

Leu Gln Gly Asp Arg Cys Asn Ile Phe Ala Asn Phe Ile Leu His Asp
        595                 600                 605

Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Lys Ser Asn Thr
    610                 615                 620

Asp Ile Ile Leu Gly Val Cys Val Asn Tyr Asp Leu Tyr Gly Ile Thr
625                 630                 635                 640

Gly Gln Gly Ile Phe Val Glu Val Asn Ala Pro Tyr Tyr Asn Ser Trp
                645                 650                 655

Gln Asn Leu Leu Tyr Asp Ser Asn Gly Asn Leu Tyr Gly Phe Arg Asp
            660                 665                 670

Tyr Leu Thr Asn Arg Thr Phe Met Ile Arg Ser Cys Tyr Ser Gly Arg
        675                 680                 685

Val Ser Ala Ala Phe His Ala Asn Ser Ser Glu Pro Ala Leu Leu Phe
    690                 695                 700

Arg Asn Ile Lys Cys Asn Tyr Val Phe Asn Asn Thr Leu Ser Arg Gln
705                 710                 715                 720

Leu Gln Pro Ile Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val Val Asn
                725                 730                 735

Ala Asp Asn Ser Thr Ala Ser Ala Val Gln Thr Cys Asp Leu Thr Val
            740                 745                 750

Gly Ser Gly Tyr Cys Val Asp Tyr Ser Thr Lys Arg Arg Ser Arg Arg
        755                 760                 765

Ala Ile Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe Thr Val
    770                 775                 780

Asn Ser Val Asn Asp Ser Leu Glu His Val Gly Gly Leu Tyr Glu Ile
785                 790                 795                 800

Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Met Glu Glu Phe Ile Gln
                805                 810                 815

Thr Ser Ser Pro Lys Val Thr Ile Asp Cys Ser Ala Phe Val Cys Gly
            820                 825                 830

Asp Cys Ala Ala Cys Lys Ser Gln Leu Val Glu Tyr Gly Ser Phe Cys
        835                 840                 845

Asp Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu Asp Thr
    850                 855                 860

Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr Leu Ser
865                 870                 875                 880

Thr Lys Leu Lys Asp Gly Val Asn Phe Asn Val Asp Asp Val Asn Phe
                885                 890                 895
```

-continued

```
Ser Pro Val Leu Gly Cys Leu Gly Ser Glu Cys Asn Lys Val Ser Ser
            900                 905                 910

Arg Ser Ala Ile Glu Asp Leu Leu Phe Ser Lys Val Arg Leu Ser Asp
        915                 920                 925

Val Gly Phe Val Glu Ala Tyr Asn Asn Cys Thr Gly Gly Ala Gly Ile
    930                 935                 940

Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val Leu Pro
945                 950                 955                 960

Pro Leu Leu Ser Asp Asn Gln Ile Ser Gly Tyr Thr Leu Ala Ala Thr
                965                 970                 975

Ser Ala Asn Leu Phe Pro Pro Trp Ser Ala Ala Ala Gly Val Pro Phe
            980                 985                 990

Tyr Leu Asn Val Gln Tyr Arg Ile  Asn Gly Ile Gly Val  Thr Met Asp
        995                 1000                 1005

Val Leu  Ser Gln Asn Gln Lys  Leu Ile Ala Asn Ala  Phe Asn Asn
    1010                 1015                 1020

Ala Leu  Asp Ala Ile Gln Glu  Gly Phe Asp Ala Thr  Asn Ser Ala
    1025                 1030                 1035

Leu Val  Lys Ile Gln Ala Val  Val Asn Ala Asp Ala  Glu Ala Leu
    1040                 1045                 1050

Asn Asn  Leu Leu Gln Gln Leu  Ser Asn Arg Phe Gly  Ala Ile Ser
    1055                 1060                 1065

Ser Ser  Leu Gln Glu Ile Leu  Ser Arg Leu Asp Ala  Leu Glu Ala
    1070                 1075                 1080

Gln Ala  Gln Ile Asp Arg Leu  Ile Asn Gly Arg Leu  Thr Ala Leu
    1085                 1090                 1095

Asp Ala  Tyr Val Ser Gln Gln  Leu Ser Asp Ser Thr  Leu Val Lys
    1100                 1105                 1110

Phe Ser  Ala Ala Gln Ala Met  Glu Lys Val Asn Glu  Cys Val Lys
    1115                 1120                 1125

Ser Gln  Ser Ser Arg Ile Asn  Phe Cys Gly Asn Gly  Asn His Ile
    1130                 1135                 1140

Ile Ser  Leu Val Gln Asn Ala  Pro Tyr Gly Leu Tyr  Phe Ile His
    1145                 1150                 1155

Phe Ser  Tyr Val Pro Thr Lys  Tyr Val Thr Ala Lys  Val Ser Pro
    1160                 1165                 1170

Gly Leu  Cys Ile Ala Gly Asp  Arg Gly Ile Ala Pro  Lys Ser Gly
    1175                 1180                 1185

Tyr Phe  Val Asn Val Asn Asn  Thr Trp Met Phe Thr  Gly Ser Arg
    1190                 1195                 1200

Tyr Tyr  Tyr Pro Glu Pro Ile  Thr Gly Asn Asn Val  Val Val Met
    1205                 1210                 1215

Ser Thr  Cys Ala Val Asn Tyr  Thr Lys Ala Pro Asp  Val Met Leu
    1220                 1225                 1230

Asn Ile  Ser Thr Pro Asn Leu  Pro Asp Phe Lys Glu  Glu Leu Asp
    1235                 1240                 1245

Gln Trp  Phe Lys Asn Gln Thr  Leu Val Ala Pro Asp  Leu Ser Leu
    1250                 1255                 1260

Asp Tyr  Ile Asn Val Thr Phe  Leu Asp Leu Gln Asp  Glu Met Asn
    1265                 1270                 1275

Arg Leu  Gln Glu Ala Ile Lys  Val Leu Asn Gln Ser  Tyr Ile Asn
    1280                 1285                 1290
```

-continued

```
Leu Lys  Asp Ile Gly Thr Tyr  Glu Tyr Tyr Val Lys  Trp Pro Trp
    1295                1300                1305

Tyr Val  Trp Leu Leu Ile Gly  Phe Ala Gly Val Ala  Met Leu Val
    1310                1315                1320

Leu Leu  Phe Phe Ile Cys Cys  Cys Thr Gly Cys Gly  Thr Ser Cys
    1325                1330                1335

Phe Lys  Lys Cys Gly Gly Cys  Cys Asp Asp Tyr Thr  Gly His Gln
    1340                1345                1350

Glu Leu  Val Ile Lys Thr Ser  His Glu Gly
    1355                1360


<210> SEQ ID NO 59
<211> LENGTH: 1383
<212> TYPE: PRT
<213> ORGANISM: Porcine epidemic diarrhea virus

<400> SEQUENCE: 59

Met Arg Ser Leu Ile Tyr Phe Trp Leu Leu Leu Pro Val Leu Pro Thr
1               5                   10                  15

Leu Ser Leu Pro Gln Asp Val Thr Arg Cys Gln Ser Thr Thr Asn Phe
            20                  25                  30

Arg Arg Phe Phe Ser Lys Phe Asn Val Gln Ala Pro Ala Val Val Val
        35                  40                  45

Leu Gly Gly Tyr Leu Pro Ser Met Asn Ser Ser Ser Trp Tyr Cys Gly
    50                  55                  60

Thr Gly Ile Glu Thr Ala Ser Gly Val His Gly Ile Phe Leu Ser Tyr
65                  70                  75                  80

Ile Asp Ser Gly Gln Gly Phe Glu Ile Gly Ile Ser Gln Glu Pro Phe
                85                  90                  95

Asp Pro Ser Gly Tyr Gln Leu Tyr Leu His Lys Ala Thr Asn Gly Asn
            100                 105                 110

Thr Asn Ala Thr Ala Arg Leu Arg Ile Cys Gln Phe Pro Asp Asn Lys
        115                 120                 125

Thr Leu Gly Pro Thr Val Asn Asp Val Thr Thr Gly Arg Asn Cys Leu
    130                 135                 140

Phe Asn Lys Ala Ile Pro Ala Tyr Met Arg Asp Gly Lys Asp Ile Val
145                 150                 155                 160

Val Gly Ile Thr Trp Asp Asn Asp Arg Val Thr Val Phe Ala Asp Lys
                165                 170                 175

Ile Tyr His Phe Tyr Leu Lys Asn Asp Trp Ser Arg Val Ala Thr Arg
            180                 185                 190

Cys Tyr Asn Arg Arg Ser Cys Ala Met Gln Tyr Val Tyr Thr Pro Thr
        195                 200                 205

Tyr Tyr Met Leu Asn Val Thr Ser Ala Gly Glu Asp Gly Ile Tyr Tyr
    210                 215                 220

Glu Pro Cys Thr Ala Asn Cys Thr Gly Tyr Ala Ala Asn Val Phe Ala
225                 230                 235                 240

Thr Asp Ser Asn Gly His Ile Pro Glu Gly Phe Ser Phe Asn Asn Trp
                245                 250                 255

Phe Leu Leu Ser Asn Asp Ser Thr Leu Leu His Gly Lys Val Val Ser
            260                 265                 270

Asn Gln Pro Leu Leu Val Asn Cys Leu Leu Ala Ile Pro Lys Ile Tyr
        275                 280                 285

Gly Leu Gly Gln Phe Phe Ser Phe Asn His Thr Met Asp Gly Val Cys
    290                 295                 300
```

-continued

```
Asn Gly Ala Ala Val Asp Arg Ala Pro Glu Ala Leu Arg Phe Asn Ile
305                 310                 315                 320

Asn Asp Thr Ser Val Ile Leu Ala Glu Gly Ser Ile Val Leu His Thr
                325                 330                 335

Ala Leu Gly Thr Asn Leu Ser Phe Val Cys Ser Asn Ser Ser Asp Pro
            340                 345                 350

His Leu Ala Ile Phe Ala Ile Pro Leu Gly Ala Thr Glu Val Pro Tyr
        355                 360                 365

Tyr Cys Phe Leu Lys Val Asp Thr Tyr Asn Ser Thr Val Tyr Lys Phe
    370                 375                 380

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

Gly Asp Val Tyr Val Asn Gly Phe Gly Tyr Leu His Leu Gly Leu Leu
                405                 410                 415

Asp Ala Val Thr Ile Tyr Phe Thr Gly His Gly Thr Asp Asp Asp Val
            420                 425                 430

Ser Gly Phe Trp Thr Ile Ala Ser Thr Asn Phe Val Asp Ala Leu Ile
        435                 440                 445

Glu Val Gln Gly Thr Ser Ile Gln Arg Ile Leu Tyr Cys Asp Asp Pro
    450                 455                 460

Val Ser Gln Leu Lys Cys Ser Gln Val Ala Phe Asp Leu Asp Asp Gly
465                 470                 475                 480

Phe Tyr Pro Ile Ser Ser Arg Asn Leu Leu Ser His Glu Gln Pro Ile
                485                 490                 495

Ser Phe Val Thr Leu Pro Ser Phe Asn Asp His Ser Phe Val Asn Ile
            500                 505                 510

Thr Val Ser Ala Ala Phe Gly Gly Leu Ser Ser Ala Asn Leu Val Ala
        515                 520                 525

Ser Asp Thr Thr Ile Asn Gly Phe Ser Ser Phe Cys Val Asp Thr Arg
    530                 535                 540

Gln Phe Thr Ile Thr Leu Phe Tyr Asn Val Thr Asn Ser Tyr Gly Tyr
545                 550                 555                 560

Val Ser Lys Ser Gln Asp Ser Asn Cys Pro Phe Thr Leu Gln Ser Val
                565                 570                 575

Asn Asp Tyr Leu Ser Phe Ser Lys Phe Cys Val Ser Thr Ser Leu Leu
            580                 585                 590

Ala Gly Ala Cys Thr Ile Asp Leu Phe Gly Tyr Pro Ala Phe Gly Ser
        595                 600                 605

Gly Val Lys Leu Thr Ser Leu Tyr Phe Gln Phe Thr Lys Gly Glu Leu
    610                 615                 620

Ile Thr Gly Thr Pro Lys Pro Leu Glu Gly Ile Thr Asp Val Ser Phe
625                 630                 635                 640

Met Thr Leu Asp Val Cys Thr Lys Tyr Thr Ile Tyr Gly Phe Lys Gly
                645                 650                 655

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

Tyr Thr Ser Asp Ser Gly Gln Leu Leu Ala Phe Lys Asn Val Thr Ser
        675                 680                 685

Gly Ala Val Tyr Ser Val Thr Pro Cys Ser Phe Ser Glu Gln Ala Ala
    690                 695                 700

Tyr Val Asn Asp Asp Ile Val Gly Val Ile Ser Ser Leu Ser Asn Ser
705                 710                 715                 720
```

-continued

```
Thr Phe Asn Asn Thr Arg Glu Leu Pro Gly Phe Phe Tyr His Ser Asn
            725                 730                 735

Asp Gly Ser Asn Cys Thr Glu Pro Val Leu Val Tyr Ser Asn Ile Gly
        740                 745                 750

Val Cys Lys Ser Gly Ser Ile Gly Tyr Val Pro Ser Gln Tyr Gly Gln
    755                 760                 765

Val Lys Ile Ala Pro Thr Val Thr Gly Asn Ile Ser Ile Pro Thr Asn
    770                 775                 780

Phe Ser Met Ser Ile Arg Thr Glu Tyr Leu Gln Leu Tyr Asn Thr Pro
785                 790                 795                 800

Val Ser Val Asp Cys Ala Thr Tyr Val Cys Asn Gly Asn Ser Arg Cys
            805                 810                 815

Lys Gln Leu Leu Thr Gln Tyr Thr Ala Ala Cys Lys Thr Ile Glu Ser
        820                 825                 830

Ala Leu Gln Leu Ser Ala Arg Leu Glu Ser Val Glu Val Asn Ser Met
    835                 840                 845

Leu Thr Ile Ser Glu Glu Ala Leu Gln Leu Ala Thr Ile Ser Ser Phe
    850                 855                 860

Asn Gly Asp Gly Tyr Asn Phe Thr Asn Val Leu Gly Ala Ser Val Tyr
865                 870                 875                 880

Asp Pro Ala Ser Gly Arg Val Val Gln Lys Arg Ser Val Ile Glu Asp
            885                 890                 895

Leu Leu Phe Asn Lys Val Val Thr Asn Gly Leu Gly Thr Val Asp Glu
        900                 905                 910

Asp Tyr Lys Arg Cys Ser Asn Gly Arg Ser Val Ala Asp Leu Val Cys
    915                 920                 925

Ala Gln Tyr Tyr Ser Gly Val Met Val Leu Pro Gly Val Val Asp Ala
    930                 935                 940

Glu Lys Leu His Met Tyr Ser Ala Ser Leu Ile Gly Gly Met Ala Leu
945                 950                 955                 960

Gly Gly Ile Thr Ala Ala Ala Ala Leu Pro Phe Ser Tyr Ala Val Gln
            965                 970                 975

Ala Arg Leu Asn Tyr Leu Ala Leu Gln Thr Asp Val Leu Gln Arg Asn
        980                 985                 990

Gln Gln Leu Leu Ala Glu Ser Phe  Asn Ser Ala Ile Gly  Asn Ile Thr
        995                 1000                1005

Ser Ala  Phe Glu Ser Val Lys  Glu Ala Ile Ser Gln  Thr Ser Lys
    1010                 1015                 1020

Gly Leu  Asn Thr Val Ala His  Ala Leu Thr Lys Val  Gln Glu Val
    1025                 1030                 1035

Val Asn  Ser Gln Gly Ser Ala  Leu Asn Gln Leu Thr  Val Gln Leu
    1040                 1045                 1050

Gln His  Asn Phe Gln Ala Ile  Ser Ser Ser Ile Asp  Asp Ile Tyr
    1055                 1060                 1065

Ser Arg  Leu Asp Ile Leu Leu  Ala Asp Val Gln Val  Asp Arg Leu
    1070                 1075                 1080

Ile Thr  Gly Arg Leu Ser Ala  Leu Asn Ala Phe Val  Ala Gln Thr
    1085                 1090                 1095

Leu Thr  Lys Tyr Thr Glu Val  Gln Ala Ser Arg Lys  Leu Ala Gln
    1100                 1105                 1110

Gln Lys  Val Asn Glu Cys Val  Lys Ser Gln Ser Gln  Arg Tyr Gly
    1115                 1120                 1125

Phe Cys  Gly Gly Asp Gly Glu  His Ile Phe Ser Leu  Val Gln Ala
```

-continued

1130 1135 1140

Ala Pro Gln Gly Leu Leu Phe Leu His Thr Val Leu Val Pro Gly
1145 1150 1155

Asp Phe Val Asn Val Leu Ala Ile Ala Gly Leu Cys Val Asn Gly
1160 1165 1170

Glu Ile Ala Leu Thr Leu Arg Glu Pro Gly Leu Val Leu Phe Thr
1175 1180 1185

His Glu Leu Gln Thr Tyr Thr Ala Thr Glu Tyr Phe Val Ser Ser
1190 1195 1200

Arg Arg Met Phe Glu Pro Arg Lys Pro Thr Val Ser Asp Phe Val
1205 1210 1215

Gln Ile Glu Ser Cys Val Val Thr Tyr Val Asn Leu Thr Ser Asp
1220 1225 1230

Gln Leu Pro Asp Val Ile Pro Asp Tyr Ile Asp Val Asn Lys Thr
1235 1240 1245

Leu Asp Glu Ile Leu Ala Ser Leu Pro Asn Arg Thr Gly Pro Ser
1250 1255 1260

Leu Pro Leu Asp Val Phe Asn Ala Thr Tyr Leu Asn Leu Thr Gly
1265 1270 1275

Glu Ile Ala Asp Leu Glu Gln Arg Ser Glu Ser Leu Arg Asn Thr
1280 1285 1290

Thr Glu Glu Leu Arg Ser Leu Ile Asn Asn Ile Asn Asn Thr Leu
1295 1300 1305

Val Asp Leu Glu Trp Leu Asn Arg Val Glu Thr Tyr Ile Lys Trp
1310 1315 1320

Pro Trp Trp Val Trp Leu Ile Ile Val Ile Val Leu Ile Phe Val
1325 1330 1335

Val Ser Leu Leu Val Phe Cys Cys Ile Ser Thr Gly Cys Cys Gly
1340 1345 1350

Cys Cys Gly Cys Cys Gly Ala Cys Phe Ser Gly Cys Cys Arg Gly
1355 1360 1365

Pro Arg Leu Gln Pro Tyr Glu Ala Phe Glu Lys Val His Val Gln
1370 1375 1380

<210> SEQ ID NO 60
<211> LENGTH: 1349
<212> TYPE: PRT
<213> ORGANISM: porcine hemagglutinating encephalomyelitis virus

<400> SEQUENCE: 60

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

Gly Asp Leu Lys Cys Thr Thr Ser Leu Ile Asn Asp Val Asp Thr Gly
20 25 30

Val Pro Ser Ile Ser Ser Glu Val Val Asp Val Thr Asn Gly Leu Gly
35 40 45

Thr Phe Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
50 55 60

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

Lys Gly Thr Arg Leu Leu Ser Thr Leu Trp Phe Lys Pro Pro Phe Leu
85 90 95

Ser Pro Phe Asn Asp Gly Ile Phe Ala Lys Val Lys Asn Ser Arg Phe
100 105 110

-continued

```
Ser Lys Asp Gly Val Ile Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
        115                 120                 125

Ser Thr Phe Val Asn Thr Ser Tyr Ser Ile Val Val Glu Pro His Thr
    130                 135                 140

Ser Leu Ile Asn Gly Asn Leu Gln Gly Leu Leu Gln Ile Ser Val Cys
145                 150                 155                 160

Gln Tyr Thr Met Cys Glu Tyr Pro His Thr Ile Cys His Pro Asn Leu
                165                 170                 175

Gly Asn Gln Arg Ile Glu Leu Trp His Tyr Asp Thr Asp Val Val Ser
            180                 185                 190

Cys Leu Tyr Arg Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu
        195                 200                 205

Tyr Phe His Phe Tyr Gln Glu Gly Gly Thr Phe Tyr Ala Tyr Phe Thr
    210                 215                 220

Asp Thr Gly Phe Val Thr Lys Phe Leu Phe Lys Leu Tyr Leu Gly Thr
225                 230                 235                 240

Val Leu Ser His Tyr Tyr Val Met Pro Leu Thr Cys Asn Ser Ala Leu
                245                 250                 255

Ser Leu Glu Tyr Trp Val Thr Pro Leu Thr Thr Arg Gln Phe Leu Leu
            260                 265                 270

Ala Phe Asp Gln Asp Gly Val Leu Tyr His Ala Val Asp Cys Ala Ser
        275                 280                 285

Asp Phe Met Ser Glu Ile Met Cys Lys Thr Ser Ser Ile Thr Pro Pro
    290                 295                 300

Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Val Ala Thr
305                 310                 315                 320

Val Tyr Arg Arg Ile Pro Asp Leu Pro Asn Cys Asp Ile Glu Ala Trp
                325                 330                 335

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

Phe Ser Asn Cys Asn Phe Asn Met Gly Arg Leu Met Ser Phe Ile Gln
        355                 360                 365

Ala Asp Ser Phe Gly Cys Asn Asn Ile Asp Ala Ser Arg Leu Tyr Gly
    370                 375                 380

Met Cys Phe Gly Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Ser
385                 390                 395                 400

Arg Lys Val Asp Leu Gln Val Gly Lys Ser Gly Tyr Leu Gln Ser Phe
                405                 410                 415

Asn Tyr Lys Ile Asp Thr Ala Val Ser Ser Cys Gln Leu Tyr Tyr Ser
            420                 425                 430

Leu Pro Ala Ala Asn Val Ser Val Thr His Tyr Asn Pro Ser Ser Trp
        435                 440                 445

Asn Arg Arg Tyr Gly Phe Asn Asn Gln Ser Phe Gly Ser Arg Gly Leu
    450                 455                 460

His Asp Ala Val Tyr Ser Gln Gln Cys Phe Asn Thr Pro Asn Thr Tyr
465                 470                 475                 480

Cys Pro Cys Arg Thr Ser Gln Cys Ile Gly Gly Ala Gly Thr Gly Thr
                485                 490                 495

Cys Pro Val Gly Thr Thr Val Arg Lys Cys Phe Ala Ala Val Thr Lys
            500                 505                 510

Ala Thr Lys Cys Thr Cys Trp Cys Gln Pro Asp Pro Ser Thr Tyr Lys
        515                 520                 525

Gly Val Asn Ala Trp Thr Cys Pro Gln Ser Lys Val Ser Ile Gln Pro
```

-continued

```
    530                 535                 540

Gly Gln His Cys Pro Gly Leu Gly Leu Val Glu Asp Asp Cys Ser Gly
545                 550                 555                 560

Asn Pro Cys Thr Cys Lys Pro Gln Ala Phe Ile Gly Trp Ser Ser Glu
                565                 570                 575

Thr Cys Leu Gln Asn Gly Arg Cys Asn Ile Phe Ala Asn Phe Ile Leu
            580                 585                 590

Asn Asp Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Gln Gly
        595                 600                 605

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

Ile Thr Gly Gln Gly Ile Leu Ile Glu Val Asn Ala Thr Tyr Tyr Asn
625                 630                 635                 640

Ser Trp Gln Asn Leu Leu Tyr Asp Ser Ser Gly Asn Leu Tyr Gly Phe
                645                 650                 655

Arg Asp Tyr Leu Ser Asn Arg Thr Phe Leu Ile Arg Ser Cys Tyr Ser
            660                 665                 670

Gly Arg Val Ser Ala Val Phe His Ala Asn Ser Ser Glu Pro Ala Leu
        675                 680                 685

Met Phe Arg Asn Leu Lys Cys Ser His Val Phe Asn Asn Thr Ile Leu
    690                 695                 700

Arg Gln Ile Gln Leu Val Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val
705                 710                 715                 720

Val Asn Ala Tyr Asn Asn Thr Ala Ser Ala Val Ser Thr Cys Asp Leu
                725                 730                 735

Thr Val Gly Ser Gly Tyr Cys Val Asp Tyr Val Thr Ala Leu Arg Ser
            740                 745                 750

Arg Arg Ser Phe Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe
        755                 760                 765

Ala Ala Asn Leu Val Asn Asp Ser Ile Glu Pro Val Gly Gly Leu Tyr
    770                 775                 780

Glu Ile Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Leu Glu Glu Phe
785                 790                 795                 800

Ile Gln Thr Arg Ser Pro Lys Val Thr Ile Asp Cys Ala Thr Phe Val
                805                 810                 815

Cys Gly Asp Tyr Ala Ala Cys Arg Gln Gln Leu Ala Glu Tyr Gly Ser
            820                 825                 830

Phe Cys Glu Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu
        835                 840                 845

Asp Thr Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr
    850                 855                 860

Leu Ser Thr Lys Ile Lys Asp Gly Ile Asn Phe Asn Val Asp Asp Ile
865                 870                 875                 880

Asn Phe Ser Pro Val Leu Gly Cys Leu Gly Ser Glu Cys Asn Arg Ala
                885                 890                 895

Ser Thr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Lys Leu
            900                 905                 910

Ser Asp Val Gly Phe Val Gln Ala Tyr Asn Asn Cys Thr Gly Gly Ala
        915                 920                 925

Glu Ile Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val
    930                 935                 940

Leu Pro Pro Leu Leu Ser Glu Asn Gln Ile Ser Gly Tyr Thr Leu Ala
945                 950                 955                 960
```

-continued

```
Ala Thr Ala Ala Ser Leu Phe Pro Pro Trp Thr Ala Ala Ala Gly Val
                965                 970                 975

Pro Phe Tyr Leu Asn Val Gln Tyr Arg Ile Asn Gly Leu Gly Val Thr
            980                 985                 990

Met Asp Val Leu Ser Gln Asn Gln  Lys Leu Ile Ala Ser  Ala Phe Asn
        995                 1000                 1005

Asn Ala  Leu Asp Ala Ile Gln  Glu Gly Phe Asp Ala  Thr Asn Ser
    1010                 1015                 1020

Ala Leu  Val Lys Ile Gln Ala  Val Val Asn Ala Asn  Ala Glu Ala
    1025                 1030                 1035

Leu Asn  Asn Leu Leu Gln Gln  Leu Ser Asn Arg Phe  Gly Ala Ile
    1040                 1045                 1050

Ser Ala  Ser Leu Gln Glu Ile  Leu Ser Arg Leu Asp  Ala Leu Glu
    1055                 1060                 1065

Ala Lys  Ala Gln Ile Asp Arg  Leu Ile Asn Gly Arg  Leu Thr Ala
    1070                 1075                 1080

Leu Asn  Ala Tyr Val Ser Gln  Gln Leu Ser Asp Ser  Thr Leu Val
    1085                 1090                 1095

Lys Phe  Ser Ala Ala Gln Ala  Ile Glu Lys Val Asn  Glu Cys Val
    1100                 1105                 1110

Lys Ser  Gln Ser Ser Arg Ile  Asn Phe Cys Gly Asn  Gly Asn His
    1115                 1120                 1125

Ile Ile  Ser Leu Val Gln Asn  Ala Pro Tyr Gly Leu  Tyr Phe Ile
    1130                 1135                 1140

His Phe  Ser Tyr Val Pro Thr  Lys Tyr Val Thr Ala  Lys Val Ser
    1145                 1150                 1155

Pro Gly  Leu Cys Ile Ala Gly  Asp Ile Gly Ile Ser  Pro Lys Ser
    1160                 1165                 1170

Gly Tyr  Phe Ile Asn Val Asn  Asn Ser Trp Met Phe  Thr Gly Ser
    1175                 1180                 1185

Ser Tyr  Tyr Tyr Pro Glu Pro  Ile Thr Gln Asn Asn  Val Val Val
    1190                 1195                 1200

Met Ser  Thr Cys Ala Val Asn  Tyr Thr Lys Ala Pro  Asp Leu Met
    1205                 1210                 1215

Leu Asn  Thr Ser Thr Pro Asn  Leu Pro Asp Phe Lys  Glu Glu Leu
    1220                 1225                 1230

Tyr Gln  Trp Phe Lys Asn Gln  Ser Ser Val Ala Pro  Asp Leu Ser
    1235                 1240                 1245

Leu Asp  Tyr Ile Asn Val Thr  Phe Leu Asp Leu Gln  Asp Glu Met
    1250                 1255                 1260

Asn Arg  Leu Gln Glu Ala Ile  Lys Val Leu Asn Gln  Ser Tyr Ile
    1265                 1270                 1275

Asn Leu  Lys Asp Ile Gly Thr  Tyr Glu Tyr Tyr Val  Lys Trp Pro
    1280                 1285                 1290

Trp Tyr  Val Trp Leu Leu Ile  Gly Leu Ala Gly Val  Ala Met Leu
    1295                 1300                 1305

Val Leu  Leu Phe Phe Ile Cys  Cys Cys Thr Gly Cys  Gly Thr Ser
    1310                 1315                 1320

Cys Phe  Lys Lys Cys Gly Gly  Cys Cys Asp Asp Tyr  Thr Gly His
    1325                 1330                 1335

Gln Glu  Phe Val Ile Lys Thr  Ser His Asp Asp
    1340                 1345
```

<210> SEQ ID NO 61
<211> LENGTH: 1225
<212> TYPE: PRT
<213> ORGANISM: Porcine respiratory coronavirus

<400> SEQUENCE: 61

```
Met Lys Lys Leu Phe Val Val Leu Val Val Met Pro Leu Ile Tyr Gly
1               5                   10                  15

Asp Lys Phe Pro Thr Ser Val Val Ser Asn Cys Thr Asp Gln Cys Ala
            20                  25                  30

Ser Tyr Val Ala Asn Val Phe Thr Thr Gln Pro Gly Gly Phe Ile Pro
        35                  40                  45

Ser Asp Phe Ser Phe Asn Asn Trp Phe Leu Leu Thr Asn Ser Ser Thr
    50                  55                  60

Leu Val Ser Gly Lys Leu Val Thr Lys Gln Pro Leu Leu Val Asn Cys
65                  70                  75                  80

Leu Trp Pro Val Pro Ser Phe Glu Glu Ala Ala Ser Thr Phe Cys Phe
                85                  90                  95

Glu Gly Ala Asp Phe Asp Gln Cys Asn Gly Ala Val Leu Asn Asn Thr
            100                 105                 110

Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr Thr Asn Val Gln Ser
        115                 120                 125

Gly Lys Gly Ala Thr Val Phe Ser Leu Asn Thr Thr Gly Gly Val Thr
    130                 135                 140

Leu Glu Ile Ser Cys Tyr Asn Asp Thr Val Ser Asp Ser Ser Phe Ser
145                 150                 155                 160

Ser Tyr Gly Glu Ile Pro Phe Gly Val Thr Asn Gly Pro Arg Tyr Cys
                165                 170                 175

Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr Leu Gly Thr Leu Pro
            180                 185                 190

Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp Gly His Phe Tyr Ile
        195                 200                 205

Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile Asp Cys Ile Ser Phe
    210                 215                 220

Asn Leu Thr Thr Gly Asp Ser Asp Val Phe Trp Thr Ile Ala Tyr Thr
225                 230                 235                 240

Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn Thr Ala Ile Thr Asn
                245                 250                 255

Val Thr Tyr Cys Asn Ser Tyr Val Asn Asn Ile Lys Cys Ser Gln Leu
            260                 265                 270

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

Gly Ser Val Asn Lys Ser Val Val Leu Leu Pro Ser Phe Leu Thr His
    290                 295                 300

Thr Ile Val Asn Ile Thr Ile Gly Leu Gly Met Lys Arg Ser Gly Tyr
305                 310                 315                 320

Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile Thr Leu Pro Met Gln
                325                 330                 335

Asp Asn Asn Thr Asp Val Tyr Cys Val Arg Ser Asp Gln Phe Ser Val
            340                 345                 350

Tyr Val His Ser Thr Cys Lys Ser Ala Leu Trp Asp Asn Val Phe Lys
        355                 360                 365

Arg Asn Cys Thr Asp Val Leu Asp Ala Thr Ala Val Ile Lys Thr Gly
    370                 375                 380
```

-continued

```
Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn Tyr Leu Thr Phe Asn
385                 390                 395                 400

Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala Asn Cys Lys Phe Asp
                405                 410                 415

Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val Val Arg Ser Leu Tyr
            420                 425                 430

Val Ile Tyr Glu Glu Gly Asp Ser Ile Val Gly Val Pro Ser Asp Asn
        435                 440                 445

Ser Gly Leu His Asp Leu Ser Val Leu His Leu Asp Ser Cys Thr Asp
    450                 455                 460

Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile Ile Arg Gln Thr Asn
465                 470                 475                 480

Arg Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser Leu Ser Gly Asp Leu
                485                 490                 495

Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile Tyr Ser Val Thr Pro
            500                 505                 510

Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp Gly Thr Ile Val Gly
        515                 520                 525

Ala Ile Thr Ser Ile Asn Ser Glu Leu Leu Gly Leu Thr His Trp Thr
    530                 535                 540

Ile Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr Asn Tyr Thr Asn Asp
545                 550                 555                 560

Lys Thr Arg Gly Thr Pro Ile Asp Ser Asn Asp Val Gly Cys Glu Pro
                565                 570                 575

Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys Asn Gly Ala Leu Val
            580                 585                 590

Phe Ile Asn Val Thr His Ser Asp Gly Asp Val Gln Pro Ile Ser Thr
        595                 600                 605

Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile Ser Val Gln Val Glu
    610                 615                 620

Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile Asp Cys Ser Arg Tyr
625                 630                 635                 640

Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu Leu Thr Gln Tyr Val
                645                 650                 655

Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala Met Gly Ala Arg Leu
            660                 665                 670

Glu Asn Met Glu Val Asp Ser Met Leu Phe Val Ser Glu Asn Ala Leu
        675                 680                 685

Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Ser Glu Thr Leu Asp Pro
    690                 695                 700

Ile Tyr Thr Gln Trp Pro Asn Ile Gly Gly Phe Trp Leu Glu Gly Leu
705                 710                 715                 720

Lys Tyr Ile Leu Pro Ser Asp Asn Ser Lys Arg Lys Tyr Arg Ser Ala
                725                 730                 735

Ile Glu Asp Leu Leu Phe Ser Lys Val Val Thr Ser Gly Leu Gly Thr
            740                 745                 750

Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly Tyr Asp Ile Ala Asp
        755                 760                 765

Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met Val Leu Pro Gly Val
    770                 775                 780

Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala Ser Leu Ala Gly Gly
785                 790                 795                 800
```

-continued

```
Ile Thr Leu Gly Ala Phe Gly Gly Gly Ala Val Ser Ile Pro Phe Ala
                805                 810                 815

Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala Leu Gln Thr Asp Val
            820                 825                 830

Leu Asn Lys Asn Gln Gln Ile Leu Ala Ser Ala Phe Asn Gln Ala Ile
        835                 840                 845

Gly Asn Ile Thr Gln Ser Phe Gly Lys Val Asn Asp Ala Ile His Gln
    850                 855                 860

Thr Ser Arg Gly Leu Thr Thr Val Ala Lys Ala Leu Ala Lys Val Gln
865                 870                 875                 880

Asp Val Val Asn Thr Gln Gly Gln Ala Leu Arg His Leu Thr Val Gln
                885                 890                 895

Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser Ile Ser Asp Ile Tyr
            900                 905                 910

Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln Val Asp Arg Leu Ile
        915                 920                 925

Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val Ser Gln Thr Leu Thr
    930                 935                 940

Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu Ala Lys Asp Lys Val
945                 950                 955                 960

Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe Gly Phe Cys Gly Asn
                965                 970                 975

Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala Pro Asn Gly Met Ile
            980                 985                 990

Phe Phe His Thr Val Leu Leu Pro  Thr Ala Tyr Glu Thr  Val Thr Ala
        995                 1000                1005

Trp Ser  Gly Ile Cys Ala Leu  Asp Gly Asp Arg Thr  Phe Gly Leu
    1010                1015                1020

Val Val  Lys Asp Val Gln Leu  Thr Leu Phe Arg Asn  Leu Asp Asp
    1025                1030                1035

Lys Phe  Tyr Leu Thr Pro Arg  Thr Met Tyr Gln Pro  Arg Val Ala
    1040                1045                1050

Thr Ser  Ser Asp Phe Val Gln  Ile Glu Gly Cys Asp  Val Leu Phe
    1055                1060                1065

Val Asn  Thr Thr Val Ser Asp  Leu Pro Ser Ile Ile  Pro Asp Tyr
    1070                1075                1080

Ile Asp  Ile Asn Gln Thr Val  Gln Asp Ile Leu Glu  Asn Phe Arg
    1085                1090                1095

Pro Asn  Trp Thr Val Pro Glu  Leu Thr Leu Asp Val  Phe Asn Ala
    1100                1105                1110

Thr Tyr  Leu Asn Leu Thr Gly  Glu Ile Asp Asp Leu  Glu Phe Arg
    1115                1120                1125

Ser Glu  Lys Leu His Asn Thr  Thr Val Glu Leu Ala  Ile Leu Ile
    1130                1135                1140

Asp Asn  Ile Asn Asn Thr Leu  Val Asn Leu Glu Trp  Leu Asn Arg
    1145                1150                1155

Ile Glu  Thr Tyr Val Lys Trp  Pro Trp Tyr Val Trp  Leu Leu Ile
    1160                1165                1170

Gly Leu  Val Val Ile Phe Cys  Ile Pro Leu Leu Leu  Phe Cys Cys
    1175                1180                1185

Cys Ser  Thr Gly Cys Cys Gly  Cys Ile Gly Cys Leu  Gly Ser Cys
    1190                1195                1200

Cys His  Ser Ile Phe Ser Arg  Arg Gln Phe Glu Asn  Tyr Glu Pro
```

-continued

```
    1205                1210                1215

Ile Glu  Lys Val His Val His
    1220                1225


<210> SEQ ID NO 62
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Porcine transmissible gastroenteritis coronoavirus

<400> SEQUENCE: 62

Met Thr Phe Pro Arg Ala Leu Thr Val Ile Asp Asp Asn Gly Met Val
1               5                   10                  15

Ile Asn Ile Ile Phe Trp Phe Leu Leu Ile Ile Ile Leu Ile Leu Leu
            20                  25                  30

Ser Ile Ala Leu Leu Asn Ile Ile Lys Leu Cys Met Val Cys Cys Asn
        35                  40                  45

Leu Gly Arg Thr Val Ile Ile Val Pro Ala Gln His Ala Tyr Asp Ala
    50                  55                  60

Tyr Lys Asn Phe Met Arg Ile Lys Ala Tyr Asn Pro Asp Gly Ala Leu
65                  70                  75                  80

Leu Ala


<210> SEQ ID NO 63
<211> LENGTH: 4376
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 63

Met Glu Ser Leu Val Leu Gly Val Asn Glu Lys Thr His Val Gln Leu
1               5                   10                  15

Ser Leu Pro Val Leu Gln Val Arg Asp Val Leu Val Arg Gly Phe Gly
            20                  25                  30

Asp Ser Val Glu Glu Ala Leu Ser Glu Ala Arg Glu His Leu Lys Asn
        35                  40                  45

Gly Thr Cys Gly Leu Val Glu Leu Glu Lys Gly Val Leu Pro Gln Leu
    50                  55                  60

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

His Gly His Lys Val Val Glu Leu Val Ala Glu Met Asp Gly Ile Gln
                85                  90                  95

Tyr Gly Arg Ser Gly Ile Thr Leu Gly Val Leu Val Pro His Val Gly
            100                 105                 110

Glu Thr Pro Ile Ala Tyr Arg Asn Val Leu Leu Arg Lys Asn Gly Asn
        115                 120                 125

Lys Gly Ala Gly Gly His Ser Tyr Gly Ile Asp Leu Lys Ser Tyr Asp
    130                 135                 140

Leu Gly Asp Glu Leu Gly Thr Asp Pro Ile Glu Asp Tyr Glu Gln Asn
145                 150                 155                 160

Trp Asn Thr Lys His Gly Ser Gly Ala Leu Arg Glu Leu Thr Arg Glu
                165                 170                 175

Leu Asn Gly Gly Ala Val Thr Arg Tyr Val Asp Asn Asn Phe Cys Gly
            180                 185                 190

Pro Asp Gly Tyr Pro Leu Asp Cys Ile Lys Asp Phe Leu Ala Arg Ala
        195                 200                 205

Gly Lys Ser Met Cys Thr Leu Ser Glu Gln Leu Asp Tyr Ile Glu Ser
    210                 215                 220
```

-continued

Lys Arg Gly Val Tyr Cys Cys Arg Asp His Glu His Glu Ile Ala Trp
225 230 235 240

Phe Thr Glu Arg Ser Asp Lys Ser Tyr Glu His Gln Thr Pro Phe Glu
245 250 255

Ile Lys Ser Ala Lys Lys Phe Asp Thr Phe Lys Gly Glu Cys Pro Lys
260 265 270

Phe Val Phe Pro Leu Asn Ser Lys Val Lys Val Ile Gln Pro Arg Val
275 280 285

Glu Lys Lys Lys Thr Glu Gly Phe Met Gly Arg Ile Arg Ser Val Tyr
290 295 300

Pro Val Ala Ser Pro Gln Glu Cys Asn Asn Met His Leu Ser Thr Leu
305 310 315 320

Met Lys Cys Asn His Cys Asp Glu Val Ser Trp Gln Thr Cys Asp Phe
325 330 335

Leu Lys Ala Thr Cys Glu His Cys Gly Thr Glu Asn Leu Val Ile Glu
340 345 350

Gly Pro Thr Thr Cys Gly Tyr Leu Pro Thr Asn Ala Val Val Lys Met
355 360 365

Pro Cys Pro Ala Cys Gln Asp Pro Glu Ile Gly Pro Glu His Ser Val
370 375 380

Ala Asp Tyr His Asn His Ser Asn Ile Glu Thr Arg Leu Arg Lys Gly
385 390 395 400

Gly Arg Thr Arg Cys Phe Gly Gly Cys Val Phe Ala Tyr Val Gly Cys
405 410 415

Tyr Asn Lys Arg Ala Tyr Trp Val Pro Arg Ala Ser Ala Asp Ile Gly
420 425 430

Ser Gly His Thr Gly Ile Thr Gly Asp Asn Val Glu Thr Leu Asn Glu
435 440 445

Asp Leu Leu Glu Ile Leu Ser Arg Glu Arg Val Asn Ile Asn Ile Val
450 455 460

Gly Asp Phe His Leu Asn Glu Glu Val Ala Ile Ile Leu Ala Ser Phe
465 470 475 480

Ser Ala Ser Thr Ser Ala Phe Ile Asp Thr Ile Lys Ser Leu Asp Tyr
485 490 495

Lys Ser Phe Lys Thr Ile Val Glu Ser Cys Gly Asn Tyr Lys Val Thr
500 505 510

Lys Gly Lys Pro Val Lys Gly Ala Trp Asn Ile Gly Gln Gln Arg Ser
515 520 525

Val Leu Thr Pro Leu Cys Gly Phe Pro Ser Gln Ala Ala Gly Val Ile
530 535 540

Arg Ser Ile Phe Ala Arg Thr Leu Asp Ala Ala Asn His Ser Ile Pro
545 550 555 560

Asp Leu Gln Arg Ala Ala Val Thr Ile Leu Asp Gly Ile Ser Glu Gln
565 570 575

Ser Leu Arg Leu Val Asp Ala Met Val Tyr Thr Ser Asp Leu Leu Thr
580 585 590

Asn Ser Val Ile Ile Met Ala Tyr Val Thr Gly Gly Leu Val Gln Gln
595 600 605

Thr Ser Gln Trp Leu Ser Asn Leu Leu Gly Thr Thr Val Glu Lys Leu
610 615 620

Arg Pro Ile Phe Glu Trp Ile Glu Ala Lys Leu Ser Ala Gly Val Glu
625 630 635 640

-continued

```
Phe Leu Lys Asp Ala Trp Glu Ile Leu Lys Phe Leu Ile Thr Gly Val
                645                 650                 655

Phe Asp Ile Val Lys Gly Gln Ile Gln Val Ala Ser Asp Asn Ile Lys
            660                 665                 670

Asp Cys Val Lys Cys Phe Ile Asp Val Val Asn Lys Ala Leu Glu Met
        675                 680                 685

Cys Ile Asp Gln Val Thr Ile Ala Gly Ala Lys Leu Arg Ser Leu Asn
    690                 695                 700

Leu Gly Glu Val Phe Ile Ala Gln Ser Lys Gly Leu Tyr Arg Gln Cys
705                 710                 715                 720

Ile Arg Gly Lys Glu Gln Leu Gln Leu Leu Met Pro Leu Lys Ala Pro
                725                 730                 735

Lys Glu Val Thr Phe Leu Glu Gly Asp Ser His Asp Thr Val Leu Thr
            740                 745                 750

Ser Glu Glu Val Val Leu Lys Asn Gly Glu Leu Glu Ala Leu Glu Thr
        755                 760                 765

Pro Val Asp Ser Phe Thr Asn Gly Ala Ile Val Gly Thr Pro Val Cys
    770                 775                 780

Val Asn Gly Leu Met Leu Leu Glu Ile Lys Asp Lys Glu Gln Tyr Cys
785                 790                 795                 800

Ala Leu Ser Pro Gly Leu Leu Ala Thr Asn Asn Val Phe Arg Leu Lys
                805                 810                 815

Gly Gly Ala Pro Ile Lys Gly Val Thr Phe Gly Glu Asp Thr Val Trp
            820                 825                 830

Glu Val Gln Gly Tyr Lys Asn Val Arg Ile Thr Phe Glu Leu Asp Glu
        835                 840                 845

Arg Val Asp Lys Val Leu Asn Glu Lys Cys Ser Val Tyr Thr Val Glu
    850                 855                 860

Ser Gly Thr Glu Val Thr Glu Phe Ala Cys Val Val Ala Glu Ala Val
865                 870                 875                 880

Val Lys Thr Leu Gln Pro Val Ser Asp Leu Leu Thr Asn Met Gly Ile
                885                 890                 895

Asp Leu Asp Glu Trp Ser Val Ala Thr Phe Tyr Leu Phe Asp Asp Ala
            900                 905                 910

Gly Glu Glu Asn Phe Ser Ser Arg Met Tyr Cys Ser Phe Tyr Pro Pro
        915                 920                 925

Asp Glu Glu Glu Glu Asp Asp Ala Glu Cys Glu Glu Glu Glu Ile Asp
    930                 935                 940

Glu Thr Cys Glu His Glu Tyr Gly Thr Glu Asp Asp Tyr Gln Gly Leu
945                 950                 955                 960

Pro Leu Glu Phe Gly Ala Ser Ala Glu Thr Val Arg Val Glu Glu Glu
                965                 970                 975

Glu Glu Glu Asp Trp Leu Asp Asp Thr Thr Glu Gln Ser Glu Ile Glu
            980                 985                 990

Pro Glu Pro Glu Pro Thr Pro Glu  Glu Pro Val Asn Gln  Phe Thr Gly
        995                 1000                 1005

Tyr Leu  Lys Leu Thr Asp Asn  Val Ala Ile Lys Cys  Val Asp Ile
    1010                 1015                 1020

Val Lys  Glu Ala Gln Ser Ala  Asn Pro Met Val Ile  Val Asn Ala
    1025                 1030                 1035

Ala Asn  Ile His Leu Lys His  Gly Gly Gly Val Ala  Gly Ala Leu
    1040                 1045                 1050

Asn Lys  Ala Thr Asn Gly Ala  Met Gln Lys Glu Ser  Asp Asp Tyr
```

-continued

```
    1055                1060                1065

Ile Lys  Leu Asn Gly Pro Leu  Thr Val Gly Gly Ser  Cys Leu Leu
    1070                1075                1080

Ser Gly  His Asn Leu Ala Lys  Lys Cys Leu His Val  Val Gly Pro
    1085                1090                1095

Asn Leu  Asn Ala Gly Glu Asp  Ile Gln Leu Leu Lys  Ala Ala Tyr
    1100                1105                1110

Glu Asn  Phe Asn Ser Gln Asp  Ile Leu Leu Ala Pro  Leu Leu Ser
    1115                1120                1125

Ala Gly  Ile Phe Gly Ala Lys  Pro Leu Gln Ser Leu  Gln Val Cys
    1130                1135                1140

Val Gln  Thr Val Arg Thr Gln  Val Tyr Ile Ala Val  Asn Asp Lys
    1145                1150                1155

Ala Leu  Tyr Glu Gln Val Val  Met Asp Tyr Leu Asp  Asn Leu Lys
    1160                1165                1170

Pro Arg  Val Glu Ala Pro Lys  Gln Glu Glu Pro Pro  Asn Thr Glu
    1175                1180                1185

Asp Ser  Lys Thr Glu Glu Lys  Ser Val Val Gln Lys  Pro Val Asp
    1190                1195                1200

Val Lys  Pro Lys Ile Lys Ala  Cys Ile Asp Glu Val  Thr Thr Thr
    1205                1210                1215

Leu Glu  Glu Thr Lys Phe Leu  Thr Asn Lys Leu Leu  Leu Phe Ala
    1220                1225                1230

Asp Ile  Asn Gly Lys Leu Tyr  His Asp Ser Gln Asn  Met Leu Arg
    1235                1240                1245

Gly Glu  Asp Met Ser Phe Leu  Glu Lys Asp Ala Pro  Tyr Met Val
    1250                1255                1260

Gly Asp  Val Ile Thr Ser Gly  Asp Ile Thr Cys Val  Val Ile Pro
    1265                1270                1275

Ser Lys  Lys Ala Gly Gly Thr  Thr Glu Met Leu Ser  Arg Ala Leu
    1280                1285                1290

Lys Lys  Val Pro Val Asp Glu  Tyr Ile Thr Thr Tyr  Pro Gly Gln
    1295                1300                1305

Gly Cys  Ala Gly Tyr Thr Leu  Glu Glu Ala Lys Thr  Ala Leu Lys
    1310                1315                1320

Lys Cys  Lys Ser Ala Phe Tyr  Val Leu Pro Ser Glu  Ala Pro Asn
    1325                1330                1335

Ala Lys  Glu Glu Ile Leu Gly  Thr Val Ser Trp Asn  Leu Arg Glu
    1340                1345                1350

Met Leu  Ala His Ala Glu Glu  Thr Arg Lys Leu Met  Pro Ile Cys
    1355                1360                1365

Met Asp  Val Arg Ala Ile Met  Ala Thr Ile Gln Arg  Lys Tyr Lys
    1370                1375                1380

Gly Ile  Lys Ile Gln Glu Gly  Ile Val Asp Tyr Gly  Val Arg Phe
    1385                1390                1395

Phe Phe  Tyr Thr Ser Lys Glu  Pro Val Ala Ser Ile  Ile Thr Lys
    1400                1405                1410

Leu Asn  Ser Leu Asn Glu Pro  Leu Val Thr Met Pro  Ile Gly Tyr
    1415                1420                1425

Val Thr  His Gly Phe Asn Leu  Glu Glu Ala Ala Arg  Cys Met Arg
    1430                1435                1440

Ser Leu  Lys Ala Pro Ala Val  Val Ser Val Ser Ser  Pro Asp Ala
    1445                1450                1455
```

```
Val Thr Thr Tyr Asn Gly Tyr Leu Thr Ser Ser Ser Lys Thr Ser
    1460                1465                1470

Glu Glu His Phe Val Glu Thr Val Ser Leu Ala Gly Ser Tyr Arg
    1475                1480                1485

Asp Trp Ser Tyr Ser Gly Gln Arg Thr Glu Leu Gly Val Glu Phe
    1490                1495                1500

Leu Lys Arg Gly Asp Lys Ile Val Tyr His Thr Leu Glu Ser Pro
    1505                1510                1515

Val Glu Phe His Leu Asp Gly Glu Val Leu Ser Leu Asp Lys Leu
    1520                1525                1530

Lys Ser Leu Leu Ser Leu Arg Glu Val Lys Thr Ile Lys Val Phe
    1535                1540                1545

Thr Thr Val Asp Asn Thr Asn Leu His Thr Gln Leu Val Asp Met
    1550                1555                1560

Ser Met Thr Tyr Gly Gln Gln Phe Gly Pro Thr Tyr Leu Asp Gly
    1565                1570                1575

Ala Asp Val Thr Lys Ile Lys Pro His Val Asn His Glu Gly Lys
    1580                1585                1590

Thr Phe Phe Val Leu Pro Ser Asp Asp Thr Leu Arg Ser Glu Ala
    1595                1600                1605

Phe Glu Tyr Tyr His Thr Leu Asp Glu Ser Phe Leu Gly Arg Tyr
    1610                1615                1620

Met Ser Ala Leu Asn His Thr Lys Lys Trp Lys Phe Pro Gln Val
    1625                1630                1635

Gly Gly Leu Thr Ser Ile Lys Trp Ala Asp Asn Asn Cys Tyr Leu
    1640                1645                1650

Ser Ser Val Leu Leu Ala Leu Gln Gln Leu Glu Val Lys Phe Asn
    1655                1660                1665

Ala Pro Ala Leu Gln Glu Ala Tyr Tyr Arg Ala Arg Ala Gly Asp
    1670                1675                1680

Ala Ala Asn Phe Cys Ala Leu Ile Leu Ala Tyr Ser Asn Lys Thr
    1685                1690                1695

Val Gly Glu Leu Gly Asp Val Arg Glu Thr Met Thr His Leu Leu
    1700                1705                1710

Gln His Ala Asn Leu Glu Ser Ala Lys Arg Val Leu Asn Val Val
    1715                1720                1725

Cys Lys His Cys Gly Gln Lys Thr Thr Thr Leu Thr Gly Val Glu
    1730                1735                1740

Ala Val Met Tyr Met Gly Thr Leu Ser Tyr Asp Asn Leu Lys Thr
    1745                1750                1755

Gly Val Ser Ile Pro Cys Val Cys Gly Arg Asp Ala Thr Gln Tyr
    1760                1765                1770

Leu Val Gln Gln Glu Ser Ser Phe Val Met Met Ser Ala Pro Pro
    1775                1780                1785

Ala Glu Tyr Lys Leu Gln Gln Gly Thr Phe Leu Cys Ala Asn Glu
    1790                1795                1800

Tyr Thr Gly Asn Tyr Gln Cys Gly His Tyr Thr His Ile Thr Ala
    1805                1810                1815

Lys Glu Thr Leu Tyr Arg Ile Asp Gly Ala His Leu Thr Lys Met
    1820                1825                1830

Ser Glu Tyr Lys Gly Pro Val Thr Asp Val Phe Tyr Lys Glu Thr
    1835                1840                1845
```

-continued

```
Ser Tyr  Thr Thr Thr Ile Lys  Pro Val Ser Tyr Lys  Leu Asp Gly
    1850                 1855                 1860

Val Thr  Tyr Thr Glu Ile Glu  Pro Lys Leu Asp Gly  Tyr Tyr Lys
    1865                 1870                 1875

Lys Asp  Asn Ala Tyr Tyr Thr  Glu Gln Pro Ile Asp  Leu Val Pro
    1880                 1885                 1890

Thr Gln  Pro Leu Pro Asn Ala  Ser Phe Asp Asn Phe  Lys Leu Thr
    1895                 1900                 1905

Cys Ser  Asn Thr Lys Phe Ala  Asp Asp Leu Asn Gln  Met Thr Gly
    1910                 1915                 1920

Phe Thr  Lys Pro Ala Ser Arg  Glu Leu Ser Val Thr  Phe Phe Pro
    1925                 1930                 1935

Asp Leu  Asn Gly Asp Val Val  Ala Ile Asp Tyr Arg  His Tyr Ser
    1940                 1945                 1950

Ala Ser  Phe Lys Lys Gly Ala  Lys Leu Leu His Lys  Pro Ile Val
    1955                 1960                 1965

Trp His  Ile Asn Gln Ala Thr  Thr Lys Thr Thr Phe  Lys Pro Asn
    1970                 1975                 1980

Thr Trp  Cys Leu Arg Cys Leu  Trp Ser Thr Lys Pro  Val Asp Thr
    1985                 1990                 1995

Ser Asn  Ser Phe Glu Val Leu  Ala Val Glu Asp Thr  Gln Gly Met
    2000                 2005                 2010

Asp Asn  Leu Ala Cys Glu Ser  Gln Gln Pro Thr Ser  Glu Glu Val
    2015                 2020                 2025

Val Glu  Asn Pro Thr Ile Gln  Lys Glu Val Ile Glu  Cys Asp Val
    2030                 2035                 2040

Lys Thr  Thr Glu Val Val Gly  Asn Val Ile Leu Lys  Pro Ser Asp
    2045                 2050                 2055

Glu Gly  Val Lys Val Thr Gln  Glu Leu Gly His Glu  Asp Leu Met
    2060                 2065                 2070

Ala Ala  Tyr Val Glu Asn Thr  Ser Ile Thr Ile Lys  Lys Pro Asn
    2075                 2080                 2085

Glu Leu  Ser Leu Ala Leu Gly  Leu Lys Thr Ile Ala  Thr His Gly
    2090                 2095                 2100

Ile Ala  Ala Ile Asn Ser Val  Pro Trp Ser Lys Ile  Leu Ala Tyr
    2105                 2110                 2115

Val Lys  Pro Phe Leu Gly Gln  Ala Ala Ile Thr Thr  Ser Asn Cys
    2120                 2125                 2130

Ala Lys  Arg Leu Ala Gln Arg  Val Phe Asn Asn Tyr  Met Pro Tyr
    2135                 2140                 2145

Val Phe  Thr Leu Leu Phe Gln  Leu Cys Thr Phe Thr  Lys Ser Thr
    2150                 2155                 2160

Asn Ser  Arg Ile Arg Ala Ser  Leu Pro Thr Thr Ile  Ala Lys Asn
    2165                 2170                 2175

Ser Val  Lys Ser Val Ala Lys  Leu Cys Leu Asp Ala  Gly Ile Asn
    2180                 2185                 2190

Tyr Val  Lys Ser Pro Lys Phe  Ser Lys Leu Phe Thr  Ile Ala Met
    2195                 2200                 2205

Trp Leu  Leu Leu Leu Ser Ile  Cys Leu Gly Ser Leu  Ile Cys Val
    2210                 2215                 2220

Thr Ala  Ala Phe Gly Val Leu  Leu Ser Asn Phe Gly  Ala Pro Ser
    2225                 2230                 2235

Tyr Cys  Asn Gly Val Arg Glu  Leu Tyr Leu Asn Ser  Ser Asn Val
```

-continued

```
    2240                2245                2250

Thr Thr  Met Asp Phe Cys Glu  Gly Ser Phe Pro Cys  Ser Ile Cys
    2255                2260                2265

Leu Ser  Gly Leu Asp Ser Leu  Asp Ser Tyr Pro Ala  Leu Glu Thr
    2270                2275                2280

Ile Gln  Val Thr Ile Ser Ser  Tyr Lys Leu Asp Leu  Thr Ile Leu
    2285                2290                2295

Gly Leu  Ala Ala Glu Trp Val  Leu Ala Tyr Met Leu  Phe Thr Lys
    2300                2305                2310

Phe Phe  Tyr Leu Leu Gly Leu  Ser Ala Ile Met Gln  Val Phe Phe
    2315                2320                2325

Gly Tyr  Phe Ala Ser His Phe  Ile Ser Asn Ser Trp  Leu Met Trp
    2330                2335                2340

Phe Ile  Ile Ser Ile Val Gln  Met Ala Pro Val Ser  Ala Met Val
    2345                2350                2355

Arg Met  Tyr Ile Phe Phe Ala  Ser Phe Tyr Tyr Ile  Trp Lys Ser
    2360                2365                2370

Tyr Val  His Ile Met Asp Gly  Cys Thr Ser Ser Thr  Cys Met Met
    2375                2380                2385

Cys Tyr  Lys Arg Asn Arg Ala  Thr Arg Val Glu Cys  Thr Thr Ile
    2390                2395                2400

Val Asn  Gly Met Lys Arg Ser  Phe Tyr Val Tyr Ala  Asn Gly Gly
    2405                2410                2415

Arg Gly  Phe Cys Lys Thr His  Asn Trp Asn Cys Leu  Asn Cys Asp
    2420                2425                2430

Thr Phe  Cys Thr Gly Ser Thr  Phe Ile Ser Asp Glu  Val Ala Arg
    2435                2440                2445

Asp Leu  Ser Leu Gln Phe Lys  Arg Pro Ile Asn Pro  Thr Asp Gln
    2450                2455                2460

Ser Ser  Tyr Ile Val Asp Ser  Val Ala Val Lys Asn  Gly Ala Leu
    2465                2470                2475

His Leu  Tyr Phe Asp Lys Ala  Gly Gln Lys Thr Tyr  Glu Arg His
    2480                2485                2490

Pro Leu  Ser His Phe Val Asn  Leu Asp Asn Leu Arg  Ala Asn Asn
    2495                2500                2505

Thr Lys  Gly Ser Leu Pro Ile  Asn Val Ile Val Phe  Asp Gly Lys
    2510                2515                2520

Ser Lys  Cys Asp Glu Ser Ala  Ser Lys Ser Ala Ser  Val Tyr Tyr
    2525                2530                2535

Ser Gln  Leu Met Cys Gln Pro  Ile Leu Leu Leu Asp  Gln Ala Leu
    2540                2545                2550

Val Ser  Asp Val Gly Asp Ser  Thr Glu Val Ser Val  Lys Met Phe
    2555                2560                2565

Asp Ala  Tyr Val Asp Thr Phe  Ser Ala Thr Phe Ser  Val Pro Met
    2570                2575                2580

Glu Lys  Leu Lys Ala Leu Val  Ala Thr Ala His Ser  Glu Leu Ala
    2585                2590                2595

Lys Gly  Val Ala Leu Asp Gly  Val Leu Ser Thr Phe  Val Ser Ala
    2600                2605                2610

Ala Arg  Gln Gly Val Val Asp  Thr Asp Val Asp Thr  Lys Asp Val
    2615                2620                2625

Ile Glu  Cys Leu Lys Leu Ser  His His Ser Asp Leu  Glu Val Thr
    2630                2635                2640
```

-continued

```
Gly Asp  Ser Cys Asn Asn Phe  Met Leu Thr Tyr Asn  Lys Val Glu
    2645                 2650                 2655

Asn Met  Thr Pro Arg Asp Leu  Gly Ala Cys Ile Asp  Cys Asn Ala
    2660                 2665                 2670

Arg His  Ile Asn Ala Gln Val  Ala Lys Ser His Asn  Val Ser Leu
    2675                 2680                 2685

Ile Trp  Asn Val Lys Asp Tyr  Met Ser Leu Ser Glu  Gln Leu Arg
    2690                 2695                 2700

Lys Gln  Ile Arg Ser Ala Ala  Lys Lys Asn Asn Ile  Pro Phe Arg
    2705                 2710                 2715

Leu Thr  Cys Ala Thr Thr Arg  Gln Val Val Asn Val  Ile Thr Thr
    2720                 2725                 2730

Lys Ile  Ser Leu Lys Gly Gly  Lys Ile Val Ser Thr  Cys Phe Lys
    2735                 2740                 2745

Leu Met  Leu Lys Ala Thr Leu  Leu Cys Val Leu Ala  Ala Leu Val
    2750                 2755                 2760

Cys Tyr  Ile Val Met Pro Val  His Thr Leu Ser Ile  His Asp Gly
    2765                 2770                 2775

Tyr Thr  Asn Glu Ile Ile Gly  Tyr Lys Ala Ile Gln  Asp Gly Val
    2780                 2785                 2790

Thr Arg  Asp Ile Ile Ser Thr  Asp Asp Cys Phe Ala  Asn Lys His
    2795                 2800                 2805

Ala Gly  Phe Asp Ala Trp Phe  Ser Gln Arg Gly Gly  Ser Tyr Lys
    2810                 2815                 2820

Asn Asp  Lys Ser Cys Pro Val  Val Ala Ala Ile Ile  Thr Arg Glu
    2825                 2830                 2835

Ile Gly  Phe Ile Val Pro Gly  Leu Pro Gly Thr Val  Leu Arg Ala
    2840                 2845                 2850

Ile Asn  Gly Asp Phe Leu His  Phe Leu Pro Arg Val  Phe Ser Ala
    2855                 2860                 2865

Val Gly  Asn Ile Cys Tyr Thr  Pro Ser Lys Leu Ile  Glu Tyr Ser
    2870                 2875                 2880

Asp Phe  Ala Thr Ser Ala Cys  Val Leu Ala Ala Glu  Cys Thr Ile
    2885                 2890                 2895

Phe Lys  Asp Ala Met Gly Lys  Pro Val Pro Tyr Cys  Tyr Asp Thr
    2900                 2905                 2910

Asn Leu  Leu Glu Gly Ser Ile  Ser Tyr Ser Glu Leu  Arg Pro Asp
    2915                 2920                 2925

Thr Arg  Tyr Val Leu Met Asp  Gly Ser Ile Ile Gln  Phe Pro Asn
    2930                 2935                 2940

Thr Tyr  Leu Glu Gly Ser Val  Arg Val Val Thr Thr  Phe Asp Ala
    2945                 2950                 2955

Glu Tyr  Cys Arg His Gly Thr  Cys Glu Arg Ser Glu  Val Gly Ile
    2960                 2965                 2970

Cys Leu  Ser Thr Ser Gly Arg  Trp Val Leu Asn Asn  Glu His Tyr
    2975                 2980                 2985

Arg Ala  Leu Ser Gly Val Phe  Cys Gly Val Asp Ala  Met Asn Leu
    2990                 2995                 3000

Ile Ala  Asn Ile Phe Thr Pro  Leu Val Gln Pro Val  Gly Ala Leu
    3005                 3010                 3015

Asp Val  Ser Ala Ser Val Val  Ala Gly Gly Ile Ile  Ala Ile Leu
    3020                 3025                 3030
```

-continued

```
Val Thr  Cys Ala Ala Tyr Tyr  Phe Met Lys Phe Arg  Arg Val Phe
    3035                 3040                 3045

Gly Glu  Tyr Asn His Val Val  Ala Ala Asn Ala Leu  Leu Phe Leu
    3050                 3055                 3060

Met Ser  Phe Thr Ile Leu Cys  Leu Val Pro Ala Tyr  Ser Phe Leu
    3065                 3070                 3075

Pro Gly  Val Tyr Ser Val Phe  Tyr Leu Tyr Leu Thr  Phe Tyr Phe
    3080                 3085                 3090

Thr Asn  Asp Val Ser Phe Leu  Ala His Leu Gln Trp  Phe Ala Met
    3095                 3100                 3105

Phe Ser  Pro Ile Val Pro Phe  Trp Ile Thr Ala Ile  Tyr Val Phe
    3110                 3115                 3120

Cys Ile  Ser Leu Lys His Cys  His Trp Phe Phe Asn  Asn Tyr Leu
    3125                 3130                 3135

Arg Lys  Arg Val Met Phe Asn  Gly Val Thr Phe Ser  Thr Phe Glu
    3140                 3145                 3150

Glu Ala  Ala Leu Cys Thr Phe  Leu Leu Asn Lys Glu  Met Tyr Leu
    3155                 3160                 3165

Lys Leu  Arg Ser Glu Thr Leu  Leu Pro Leu Thr Gln  Tyr Asn Arg
    3170                 3175                 3180

Tyr Leu  Ala Leu Tyr Asn Lys  Tyr Lys Tyr Phe Ser  Gly Ala Leu
    3185                 3190                 3195

Asp Thr  Thr Ser Tyr Arg Glu  Ala Ala Cys Cys His  Leu Ala Lys
    3200                 3205                 3210

Ala Leu  Asn Asp Phe Ser Asn  Ser Gly Ala Asp Val  Leu Tyr Gln
    3215                 3220                 3225

Pro Pro  Gln Thr Ser Ile Thr  Ser Ala Val Leu Gln  Ser Gly Phe
    3230                 3235                 3240

Arg Lys  Met Ala Phe Pro Ser  Gly Lys Val Glu Gly  Cys Met Val
    3245                 3250                 3255

Gln Val  Thr Cys Gly Thr Thr  Thr Leu Asn Gly Leu  Trp Leu Asp
    3260                 3265                 3270

Asp Thr  Val Tyr Cys Pro Arg  His Val Ile Cys Thr  Ala Glu Asp
    3275                 3280                 3285

Met Leu  Asn Pro Asn Tyr Glu  Asp Leu Leu Ile Arg  Lys Ser Asn
    3290                 3295                 3300

His Ser  Phe Leu Val Gln Ala  Gly Asn Val Gln Leu  Arg Val Ile
    3305                 3310                 3315

Gly His  Ser Met Gln Asn Cys  Leu Leu Arg Leu Lys  Val Asp Thr
    3320                 3325                 3330

Ser Asn  Pro Lys Thr Pro Lys  Tyr Lys Phe Val Arg  Ile Gln Pro
    3335                 3340                 3345

Gly Gln  Thr Phe Ser Val Leu  Ala Cys Tyr Asn Gly  Ser Pro Ser
    3350                 3355                 3360

Gly Val  Tyr Gln Cys Ala Met  Arg Pro Asn His Thr  Ile Lys Gly
    3365                 3370                 3375

Ser Phe  Leu Asn Gly Ser Cys  Gly Ser Val Gly Phe  Asn Ile Asp
    3380                 3385                 3390

Tyr Asp  Cys Val Ser Phe Cys  Tyr Met His His Met  Glu Leu Pro
    3395                 3400                 3405

Thr Gly  Val His Ala Gly Thr  Asp Leu Glu Gly Lys  Phe Tyr Gly
    3410                 3415                 3420

Pro Phe  Val Asp Arg Gln Thr  Ala Gln Ala Ala Gly  Thr Asp Thr
```

-continued

```
    3425                3430                3435

Thr Ile  Thr Leu Asn Val Leu  Ala Trp Leu Tyr Ala  Ala Val Ile
    3440                3445                3450

Asn Gly  Asp Arg Trp Phe Leu  Asn Arg Phe Thr Thr  Thr Leu Asn
    3455                3460                3465

Asp Phe  Asn Leu Val Ala Met  Lys Tyr Asn Tyr Glu  Pro Leu Thr
    3470                3475                3480

Gln Asp  His Val Asp Ile Leu  Gly Pro Leu Ser Ala  Gln Thr Gly
    3485                3490                3495

Ile Ala  Val Leu Asp Met Cys  Ala Ala Leu Lys Glu  Leu Leu Gln
    3500                3505                3510

Asn Gly  Met Asn Gly Arg Thr  Ile Leu Gly Ser Thr  Ile Leu Glu
    3515                3520                3525

Asp Glu  Phe Thr Pro Phe Asp  Val Val Arg Gln Cys  Ser Gly Val
    3530                3535                3540

Thr Phe  Gln Gly Lys Phe Lys  Lys Ile Val Lys Gly  Thr His His
    3545                3550                3555

Trp Met  Leu Leu Thr Phe Leu  Thr Ser Leu Leu Ile  Leu Val Gln
    3560                3565                3570

Ser Thr  Gln Trp Ser Leu Phe  Phe Phe Val Tyr Glu  Asn Ala Phe
    3575                3580                3585

Leu Pro  Phe Thr Leu Gly Ile  Met Ala Ile Ala Ala  Cys Ala Met
    3590                3595                3600

Leu Leu  Val Lys His Lys His  Ala Phe Leu Cys Leu  Phe Leu Leu
    3605                3610                3615

Pro Ser  Leu Ala Thr Val Ala  Tyr Phe Asn Met Val  Tyr Met Pro
    3620                3625                3630

Ala Ser  Trp Val Met Arg Ile  Met Thr Trp Leu Glu  Leu Ala Asp
    3635                3640                3645

Thr Ser  Leu Ser Gly Tyr Arg  Leu Lys Asp Cys Val  Met Tyr Ala
    3650                3655                3660

Ser Ala  Leu Val Leu Leu Ile  Leu Met Thr Ala Arg  Thr Val Tyr
    3665                3670                3675

Asp Asp  Ala Ala Arg Arg Val  Trp Thr Leu Met Asn  Val Ile Thr
    3680                3685                3690

Leu Val  Tyr Lys Val Tyr Tyr  Gly Asn Ala Leu Asp  Gln Ala Ile
    3695                3700                3705

Ser Met  Trp Ala Leu Val Ile  Ser Val Thr Ser Asn  Tyr Ser Gly
    3710                3715                3720

Val Val  Thr Thr Ile Met Phe  Leu Ala Arg Ala Ile  Val Phe Val
    3725                3730                3735

Cys Val  Glu Tyr Tyr Pro Leu  Leu Phe Ile Thr Gly  Asn Thr Leu
    3740                3745                3750

Gln Cys  Ile Met Leu Val Tyr  Cys Phe Leu Gly Tyr  Cys Cys Cys
    3755                3760                3765

Cys Tyr  Phe Gly Leu Phe Cys  Leu Leu Asn Arg Tyr  Phe Arg Leu
    3770                3775                3780

Thr Leu  Gly Val Tyr Asp Tyr  Leu Val Ser Thr Gln  Glu Phe Arg
    3785                3790                3795

Tyr Met  Asn Ser Gln Gly Leu  Leu Pro Pro Lys Ser  Ser Ile Asp
    3800                3805                3810

Ala Phe  Lys Leu Asn Ile Lys  Leu Leu Gly Ile Gly  Gly Lys Pro
    3815                3820                3825
```

-continued

```
Cys Ile  Lys Val Ala Thr Val  Gln Ser Lys Met Ser  Asp Val Lys
    3830                 3835                 3840

Cys Thr  Ser Val Val Leu Leu  Ser Val Leu Gln Gln  Leu Arg Val
    3845                 3850                 3855

Glu Ser  Ser Ser Lys Leu Trp  Ala Gln Cys Val Gln  Leu His Asn
    3860                 3865                 3870

Asp Ile  Leu Leu Ala Lys Asp  Thr Thr Glu Ala Phe  Glu Lys Met
    3875                 3880                 3885

Val Ser  Leu Leu Ser Val Leu  Leu Ser Met Gln Gly  Ala Val Asp
    3890                 3895                 3900

Ile Asn  Arg Leu Cys Glu Glu  Met Leu Asp Asn Arg  Ala Thr Leu
    3905                 3910                 3915

Gln Ala  Ile Ala Ser Glu Phe  Ser Ser Leu Pro Ser  Tyr Ala Ala
    3920                 3925                 3930

Tyr Ala  Thr Ala Gln Glu Ala  Tyr Glu Gln Ala Val  Ala Asn Gly
    3935                 3940                 3945

Asp Ser  Glu Val Val Leu Lys  Lys Leu Lys Lys Ser  Leu Asn Val
    3950                 3955                 3960

Ala Lys  Ser Glu Phe Asp Arg  Asp Ala Ala Met Gln  Arg Lys Leu
    3965                 3970                 3975

Glu Lys  Met Ala Asp Gln Ala  Met Thr Gln Met Tyr  Lys Gln Ala
    3980                 3985                 3990

Arg Ser  Glu Asp Lys Arg Ala  Lys Val Thr Ser Ala  Met Gln Thr
    3995                 4000                 4005

Met Leu  Phe Thr Met Leu Arg  Lys Leu Asp Asn Asp  Ala Leu Asn
    4010                 4015                 4020

Asn Ile  Ile Asn Asn Ala Arg  Asp Gly Cys Val Pro  Leu Asn Ile
    4025                 4030                 4035

Ile Pro  Leu Thr Thr Ala Ala  Lys Leu Met Val Val  Val Pro Asp
    4040                 4045                 4050

Tyr Gly  Thr Tyr Lys Asn Thr  Cys Asp Gly Asn Thr  Phe Thr Tyr
    4055                 4060                 4065

Ala Ser  Ala Leu Trp Glu Ile  Gln Gln Val Val Asp  Ala Asp Ser
    4070                 4075                 4080

Lys Ile  Val Gln Leu Ser Glu  Ile Asn Met Asp Asn  Ser Pro Asn
    4085                 4090                 4095

Leu Ala  Trp Pro Leu Ile Val  Thr Ala Leu Arg Ala  Asn Ser Ala
    4100                 4105                 4110

Val Lys  Leu Gln Asn Asn Glu  Leu Ser Pro Val Ala  Leu Arg Gln
    4115                 4120                 4125

Met Ser  Cys Ala Ala Gly Thr  Thr Gln Thr Ala Cys  Thr Asp Asp
    4130                 4135                 4140

Asn Ala  Leu Ala Tyr Tyr Asn  Asn Ser Lys Gly Gly  Arg Phe Val
    4145                 4150                 4155

Leu Ala  Leu Leu Ser Asp His  Gln Asp Leu Lys Trp  Ala Arg Phe
    4160                 4165                 4170

Pro Lys  Ser Asp Gly Thr Gly  Thr Ile Tyr Thr Glu  Leu Glu Pro
    4175                 4180                 4185

Pro Cys  Arg Phe Val Thr Asp  Thr Pro Lys Gly Pro  Lys Val Lys
    4190                 4195                 4200

Tyr Leu  Tyr Phe Ile Lys Gly  Leu Asn Asn Leu Asn  Arg Gly Met
    4205                 4210                 4215
```

-continued

```
Val Leu  Gly Ser Leu Ala Ala  Thr Val Arg Leu Gln  Ala Gly Asn
    4220                4225                4230

Ala Thr  Glu Val Pro Ala Asn  Ser Thr Val Leu Ser  Phe Cys Ala
    4235                4240                4245

Phe Ala  Val Asp Pro Ala Lys  Ala Tyr Lys Asp Tyr  Leu Ala Ser
    4250                4255                4260

Gly Gly  Gln Pro Ile Thr Asn  Cys Val Lys Met Leu  Cys Thr His
    4265                4270                4275

Thr Gly  Thr Gly Gln Ala Ile  Thr Val Thr Pro Glu  Ala Asn Met
    4280                4285                4290

Asp Gln  Glu Ser Phe Gly Gly  Ala Ser Cys Cys Leu  Tyr Cys Arg
    4295                4300                4305

Cys His  Ile Asp His Pro Asn  Pro Lys Gly Phe Cys  Asp Leu Lys
    4310                4315                4320

Gly Lys  Tyr Val Gln Ile Pro  Thr Thr Cys Ala Asn  Asp Pro Val
    4325                4330                4335

Gly Phe  Thr Leu Arg Asn Thr  Val Cys Thr Val Cys  Gly Met Trp
    4340                4345                4350

Lys Gly  Tyr Gly Cys Ser Cys  Asp Gln Leu Arg Glu  Pro Leu Met
    4355                4360                4365

Gln Ser  Ala Asp Ala Ser Thr  Phe
    4370                4375


<210> SEQ ID NO 64
<211> LENGTH: 2697
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 64

Phe Lys Arg Val Cys Gly Val Ser Ala Ala Arg Leu Thr Pro Cys Gly
1               5                   10                  15

Thr Gly Thr Ser Thr Asp Val Val Tyr Arg Ala Phe Asp Ile Tyr Asn
            20                  25                  30

Glu Lys Val Ala Gly Phe Ala Lys Phe Leu Lys Thr Asn Cys Cys Arg
        35                  40                  45

Phe Gln Glu Lys Asp Glu Glu Gly Asn Leu Leu Asp Ser Tyr Phe Val
    50                  55                  60

Val Lys Arg His Thr Met Ser Asn Tyr Gln His Glu Glu Thr Ile Tyr
65                  70                  75                  80

Asn Leu Val Lys Asp Cys Pro Ala Val Ala Val His Asp Phe Phe Lys
                85                  90                  95

Phe Arg Val Asp Gly Asp Met Val Pro His Ile Ser Arg Gln Arg Leu
            100                 105                 110

Thr Lys Tyr Thr Met Ala Asp Leu Val Tyr Ala Leu Arg His Phe Asp
        115                 120                 125

Glu Gly Asn Cys Asp Thr Leu Lys Glu Ile Leu Val Thr Tyr Asn Cys
    130                 135                 140

Cys Asp Asp Asp Tyr Phe Asn Lys Lys Asp Trp Tyr Asp Phe Val Glu
145                 150                 155                 160

Asn Pro Asp Ile Leu Arg Val Tyr Ala Asn Leu Gly Glu Arg Val Arg
                165                 170                 175

Gln Ser Leu Leu Lys Thr Val Gln Phe Cys Asp Ala Met Arg Asp Ala
            180                 185                 190

Gly Ile Val Gly Val Leu Thr Leu Asp Asn Gln Asp Leu Asn Gly Asn
        195                 200                 205
```

-continued

```
Trp Tyr Asp Phe Gly Asp Phe Val Gln Val Ala Pro Gly Cys Gly Val
    210                 215                 220

Pro Ile Val Asp Ser Tyr Tyr Ser Leu Leu Met Pro Ile Leu Thr Leu
225                 230                 235                 240

Thr Arg Ala Leu Ala Ala Glu Ser His Met Asp Ala Asp Leu Ala Lys
                245                 250                 255

Pro Leu Ile Lys Trp Asp Leu Leu Lys Tyr Asp Phe Thr Glu Glu Arg
            260                 265                 270

Leu Cys Leu Phe Asp Arg Tyr Phe Lys Tyr Trp Asp Gln Thr Tyr His
        275                 280                 285

Pro Asn Cys Ile Asn Cys Leu Asp Asp Arg Cys Ile Leu His Cys Ala
    290                 295                 300

Asn Phe Asn Val Leu Phe Ser Thr Val Phe Pro Pro Thr Ser Phe Gly
305                 310                 315                 320

Pro Leu Val Arg Lys Ile Phe Val Asp Gly Val Pro Phe Val Val Ser
                325                 330                 335

Thr Gly Tyr His Phe Arg Glu Leu Gly Val Val His Asn Gln Asp Val
            340                 345                 350

Asn Leu His Ser Ser Arg Leu Ser Phe Lys Glu Leu Leu Val Tyr Ala
        355                 360                 365

Ala Asp Pro Ala Met His Ala Ala Ser Gly Asn Leu Leu Leu Asp Lys
    370                 375                 380

Arg Thr Thr Cys Phe Ser Val Ala Ala Leu Thr Asn Asn Val Ala Phe
385                 390                 395                 400

Gln Thr Val Lys Pro Gly Asn Phe Asn Lys Asp Phe Tyr Asp Phe Ala
                405                 410                 415

Val Ser Lys Gly Phe Phe Lys Glu Gly Ser Ser Val Glu Leu Lys His
            420                 425                 430

Phe Phe Phe Ala Gln Asp Gly Asn Ala Ala Ile Ser Asp Tyr Asp Tyr
        435                 440                 445

Tyr Arg Tyr Asn Leu Pro Thr Met Cys Asp Ile Arg Gln Leu Leu Phe
    450                 455                 460

Val Val Glu Val Val Asp Lys Tyr Phe Asp Cys Tyr Asp Gly Gly Cys
465                 470                 475                 480

Ile Asn Ala Asn Gln Val Ile Val Asn Asn Leu Asp Lys Ser Ala Gly
                485                 490                 495

Phe Pro Phe Asn Lys Trp Gly Lys Ala Arg Leu Tyr Tyr Asp Ser Met
            500                 505                 510

Ser Tyr Glu Asp Gln Asp Ala Leu Phe Ala Tyr Thr Lys Arg Asn Val
        515                 520                 525

Ile Pro Thr Ile Thr Gln Met Asn Leu Lys Tyr Ala Ile Ser Ala Lys
    530                 535                 540

Asn Arg Ala Arg Thr Val Ala Gly Val Ser Ile Cys Ser Thr Met Thr
545                 550                 555                 560

Asn Arg Gln Phe His Gln Lys Leu Leu Lys Ser Ile Ala Ala Thr Arg
                565                 570                 575

Gly Ala Thr Val Val Ile Gly Thr Ser Lys Phe Tyr Gly Gly Trp His
            580                 585                 590

Asn Met Leu Lys Thr Val Tyr Ser Asp Val Glu Thr Pro His Leu Met
        595                 600                 605

Gly Trp Asp Tyr Pro Lys Cys Asp Arg Ala Met Pro Asn Met Leu Arg
    610                 615                 620
```

-continued

```
Ile Met Ala Ser Leu Val Leu Ala Arg Lys His Asn Thr Cys Cys Asn
625                 630                 635                 640

Leu Ser His Arg Phe Tyr Arg Leu Ala Asn Glu Cys Ala Gln Val Leu
                645                 650                 655

Ser Glu Met Val Met Cys Gly Gly Ser Leu Tyr Val Lys Pro Gly Gly
            660                 665                 670

Thr Ser Ser Gly Asp Ala Thr Thr Ala Tyr Ala Asn Ser Val Phe Asn
        675                 680                 685

Ile Cys Gln Ala Val Thr Ala Asn Val Asn Ala Leu Leu Ser Thr Asp
    690                 695                 700

Gly Asn Lys Ile Ala Asp Lys Tyr Val Arg Asn Leu Gln His Arg Leu
705                 710                 715                 720

Tyr Glu Cys Leu Tyr Arg Asn Arg Asp Val Asp His Glu Phe Val Asp
                725                 730                 735

Glu Phe Tyr Ala Tyr Leu Arg Lys His Phe Ser Met Met Ile Leu Ser
            740                 745                 750

Asp Asp Ala Val Val Cys Tyr Asn Ser Asn Tyr Ala Ala Gln Gly Leu
        755                 760                 765

Val Ala Ser Ile Lys Asn Phe Lys Ala Val Leu Tyr Tyr Gln Asn Asn
    770                 775                 780

Val Phe Met Ser Glu Ala Lys Cys Trp Thr Glu Thr Asp Leu Thr Lys
785                 790                 795                 800

Gly Pro His Glu Phe Cys Ser Gln His Thr Met Leu Val Lys Gln Gly
                805                 810                 815

Asp Asp Tyr Val Tyr Leu Pro Tyr Pro Asp Pro Ser Arg Ile Leu Gly
            820                 825                 830

Ala Gly Cys Phe Val Asp Asp Ile Val Lys Thr Asp Gly Thr Leu Met
        835                 840                 845

Ile Glu Arg Phe Val Ser Leu Ala Ile Asp Ala Tyr Pro Leu Thr Lys
    850                 855                 860

His Pro Asn Gln Glu Tyr Ala Asp Val Phe His Leu Tyr Leu Gln Tyr
865                 870                 875                 880

Ile Arg Lys Leu His Asp Glu Leu Thr Gly His Met Leu Asp Met Tyr
                885                 890                 895

Ser Val Met Leu Thr Asn Asp Asn Thr Ser Arg Tyr Trp Glu Pro Glu
            900                 905                 910

Phe Tyr Glu Ala Met Tyr Thr Pro His Thr Val Leu Gln Ala Val Gly
        915                 920                 925

Ala Cys Val Leu Cys Asn Ser Gln Thr Ser Leu Arg Cys Gly Ala Cys
    930                 935                 940

Ile Arg Arg Pro Phe Leu Cys Cys Lys Cys Cys Tyr Asp His Val Ile
945                 950                 955                 960

Ser Thr Ser His Lys Leu Val Leu Ser Val Asn Pro Tyr Val Cys Asn
                965                 970                 975

Ala Pro Gly Cys Asp Val Thr Asp Val Thr Gln Leu Tyr Leu Gly Gly
            980                 985                 990

Met Ser Tyr Tyr Cys Lys Ser His  Lys Pro Pro Ile Ser  Phe Pro Leu
        995                 1000                 1005

Cys Ala  Asn Gly Gln Val Phe  Gly Leu Tyr Lys Asn  Thr Cys Val
    1010                 1015                 1020

Gly Ser  Asp Asn Val Thr Asp  Phe Asn Ala Ile Ala  Thr Cys Asp
    1025                 1030                 1035

Trp Thr  Asn Ala Gly Asp Tyr  Ile Leu Ala Asn Thr  Cys Thr Glu
```

-continued

1040 1045 1050

Arg Leu Lys Leu Phe Ala Ala Glu Thr Leu Lys Ala Thr Glu Glu
1055 1060 1065

Thr Phe Lys Leu Ser Tyr Gly Ile Ala Thr Val Arg Glu Val Leu
1070 1075 1080

Ser Asp Arg Glu Leu His Leu Ser Trp Glu Val Gly Lys Pro Arg
1085 1090 1095

Pro Pro Leu Asn Arg Asn Tyr Val Phe Thr Gly Tyr Arg Val Thr
1100 1105 1110

Lys Asn Ser Lys Val Gln Ile Gly Glu Tyr Thr Phe Glu Lys Gly
1115 1120 1125

Asp Tyr Gly Asp Ala Val Val Tyr Arg Gly Thr Thr Thr Tyr Lys
1130 1135 1140

Leu Asn Val Gly Asp Tyr Phe Val Leu Thr Ser His Thr Val Met
1145 1150 1155

Pro Leu Ser Ala Pro Thr Leu Val Pro Gln Glu His Tyr Val Arg
1160 1165 1170

Ile Thr Gly Leu Tyr Pro Thr Leu Asn Ile Ser Asp Glu Phe Ser
1175 1180 1185

Ser Asn Val Ala Asn Tyr Gln Lys Val Gly Met Gln Lys Tyr Ser
1190 1195 1200

Thr Leu Gln Gly Pro Pro Gly Thr Gly Lys Ser His Phe Ala Ile
1205 1210 1215

Gly Leu Ala Leu Tyr Tyr Pro Ser Ala Arg Ile Val Tyr Thr Ala
1220 1225 1230

Cys Ser His Ala Ala Val Asp Ala Leu Cys Glu Lys Ala Leu Lys
1235 1240 1245

Tyr Leu Pro Ile Asp Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala
1250 1255 1260

Arg Val Glu Cys Phe Asp Lys Phe Lys Val Asn Ser Thr Leu Glu
1265 1270 1275

Gln Tyr Val Phe Cys Thr Val Asn Ala Leu Pro Glu Thr Thr Ala
1280 1285 1290

Asp Ile Val Val Phe Asp Glu Ile Ser Met Ala Thr Asn Tyr Asp
1295 1300 1305

Leu Ser Val Val Asn Ala Arg Leu Arg Ala Lys His Tyr Val Tyr
1310 1315 1320

Ile Gly Asp Pro Ala Gln Leu Pro Ala Pro Arg Thr Leu Leu Thr
1325 1330 1335

Lys Gly Thr Leu Glu Pro Glu Tyr Phe Asn Ser Val Cys Arg Leu
1340 1345 1350

Met Lys Thr Ile Gly Pro Asp Met Phe Leu Gly Thr Cys Arg Arg
1355 1360 1365

Cys Pro Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val Tyr Asp
1370 1375 1380

Asn Lys Leu Lys Ala His Lys Asp Lys Ser Ala Gln Cys Phe Lys
1385 1390 1395

Met Phe Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile
1400 1405 1410

Asn Arg Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn
1415 1420 1425

Pro Ala Trp Arg Lys Ala Val Phe Ile Ser Pro Tyr Asn Ser Gln
1430 1435 1440

-continued

```
Asn Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
    1445                1450                1455

Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln
    1460                1465                1470

Thr Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val
    1475                1480                1485

Ala Ile Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp
    1490                1495                1500

Arg Asp Leu Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro
    1505                1510                1515

Arg Arg Asn Val Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu
    1520                1525                1530

Phe Lys Asp Cys Ser Lys Ile Ile Thr Gly Leu His Pro Thr Gln
    1535                1540                1545

Ala Pro Thr His Leu Ser Val Asp Ile Lys Phe Lys Thr Glu Gly
    1550                1555                1560

Leu Cys Val Asp Ile Pro Gly Ile Pro Lys Asp Met Thr Tyr Arg
    1565                1570                1575

Arg Leu Ile Ser Met Met Gly Phe Lys Met Asn Tyr Gln Val Asn
    1580                1585                1590

Gly Tyr Pro Asn Met Phe Ile Thr Arg Glu Glu Ala Ile Arg His
    1595                1600                1605

Val Arg Ala Trp Ile Gly Phe Asp Val Glu Gly Cys His Ala Thr
    1610                1615                1620

Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln Leu Gly Phe Ser
    1625                1630                1635

Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr Val Asp Thr
    1640                1645                1650

Glu Asn Asn Thr Glu Phe Thr Arg Val Asn Ala Lys Pro Pro Pro
    1655                1660                1665

Gly Asp Gln Phe Lys His Leu Ile Pro Leu Met Tyr Lys Gly Leu
    1670                1675                1680

Pro Trp Asn Val Val Arg Ile Lys Ile Val Gln Met Leu Ser Asp
    1685                1690                1695

Thr Leu Lys Gly Leu Ser Asp Arg Val Val Phe Val Leu Trp Ala
    1700                1705                1710

His Gly Phe Glu Leu Thr Ser Met Lys Tyr Phe Val Lys Ile Gly
    1715                1720                1725

Pro Glu Arg Thr Cys Cys Leu Cys Asp Lys Arg Ala Thr Cys Phe
    1730                1735                1740

Ser Thr Ser Ser Asp Thr Tyr Ala Cys Trp Asn His Ser Val Gly
    1745                1750                1755

Phe Asp Tyr Val Tyr Asn Pro Phe Met Ile Asp Val Gln Gln Trp
    1760                1765                1770

Gly Phe Thr Gly Asn Leu Gln Ser Asn His Asp Gln His Cys Gln
    1775                1780                1785

Val His Gly Asn Ala His Val Ala Ser Cys Asp Ala Ile Met Thr
    1790                1795                1800

Arg Cys Leu Ala Val His Glu Cys Phe Val Lys Arg Val Asp Trp
    1805                1810                1815

Ser Val Glu Tyr Pro Ile Ile Gly Asp Glu Leu Arg Val Asn Ser
    1820                1825                1830
```

-continued

```
Ala Cys  Arg Lys Val Gln His  Met Val Val Lys Ser  Ala Leu Leu
    1835                 1840                 1845

Ala Asp  Lys Phe Pro Val Leu  His Asp Ile Gly Asn  Pro Lys Ala
    1850                 1855                 1860

Ile Lys  Cys Val Pro Gln Ala  Glu Val Glu Trp Lys  Phe Tyr Asp
    1865                 1870                 1875

Ala Gln  Pro Cys Ser Asp Lys  Ala Tyr Lys Ile Glu  Glu Leu Phe
    1880                 1885                 1890

Tyr Ser  Tyr Ala Thr His His  Asp Lys Phe Thr Asp  Gly Val Cys
    1895                 1900                 1905

Leu Phe  Trp Asn Cys Asn Val  Asp Arg Tyr Pro Ala  Asn Ala Ile
    1910                 1915                 1920

Val Cys  Arg Phe Asp Thr Arg  Val Leu Ser Asn Leu  Asn Leu Pro
    1925                 1930                 1935

Gly Cys  Asp Gly Gly Ser Leu  Tyr Val Asn Lys His  Ala Phe His
    1940                 1945                 1950

Thr Pro  Ala Phe Asp Lys Ser  Ala Phe Thr Asn Leu  Lys Gln Leu
    1955                 1960                 1965

Pro Phe  Phe Tyr Tyr Ser Asp  Ser Pro Cys Glu Ser  His Gly Lys
    1970                 1975                 1980

Gln Val  Val Ser Asp Ile Asp  Tyr Val Pro Leu Lys  Ser Ala Thr
    1985                 1990                 1995

Cys Ile  Thr Arg Cys Asn Leu  Gly Gly Ala Val Cys  Arg His His
    2000                 2005                 2010

Ala Asn  Glu Tyr Arg Gln Tyr  Leu Asp Ala Tyr Asn  Met Met Ile
    2015                 2020                 2025

Ser Ala  Gly Phe Ser Leu Trp  Ile Tyr Lys Gln Phe  Asp Thr Tyr
    2030                 2035                 2040

Asn Leu  Trp Asn Thr Phe Thr  Arg Leu Gln Ser Leu  Glu Asn Val
    2045                 2050                 2055

Ala Tyr  Asn Val Val Asn Lys  Gly His Phe Asp Gly  His Ala Gly
    2060                 2065                 2070

Glu Ala  Pro Val Ser Ile Ile  Asn Asn Ala Val Tyr  Thr Lys Val
    2075                 2080                 2085

Asp Gly  Ile Asp Val Glu Ile  Phe Glu Asn Lys Thr  Thr Leu Pro
    2090                 2095                 2100

Val Asn  Val Ala Phe Glu Leu  Trp Ala Lys Arg Asn  Ile Lys Pro
    2105                 2110                 2115

Val Pro  Glu Ile Lys Ile Leu  Asn Asn Leu Gly Val  Asp Ile Ala
    2120                 2125                 2130

Ala Asn  Thr Val Ile Trp Asp  Tyr Lys Arg Glu Ala  Pro Ala His
    2135                 2140                 2145

Val Ser  Thr Ile Gly Val Cys  Thr Met Thr Asp Ile  Ala Lys Lys
    2150                 2155                 2160

Pro Thr  Glu Ser Ala Cys Ser  Ser Leu Thr Val Leu  Phe Asp Gly
    2165                 2170                 2175

Arg Val  Glu Gly Gln Val Asp  Leu Phe Arg Asn Ala  Arg Asn Gly
    2180                 2185                 2190

Val Leu  Ile Thr Glu Gly Ser  Val Lys Gly Leu Thr  Pro Ser Lys
    2195                 2200                 2205

Gly Pro  Ala Gln Ala Ser Val  Asn Gly Val Thr Leu  Ile Gly Glu
    2210                 2215                 2220

Ser Val  Lys Thr Gln Phe Asn  Tyr Phe Lys Lys Val  Asp Gly Ile
```

-continued

2225 2230 2235

Ile Gln Gln Leu Pro Glu Thr Tyr Phe Thr Gln Ser Arg Asp Leu
2240 2245 2250

Glu Asp Phe Lys Pro Arg Ser Gln Met Glu Thr Asp Phe Leu Glu
2255 2260 2265

Leu Ala Met Asp Glu Phe Ile Gln Arg Tyr Lys Leu Glu Gly Tyr
2270 2275 2280

Ala Phe Glu His Ile Val Tyr Gly Asp Phe Ser His Gly Gln Leu
2285 2290 2295

Gly Gly Leu His Leu Met Ile Gly Leu Ala Lys Arg Ser Gln Asp
2300 2305 2310

Ser Pro Leu Lys Leu Glu Asp Phe Ile Pro Met Asp Ser Thr Val
2315 2320 2325

Lys Asn Tyr Phe Ile Thr Asp Ala Gln Thr Gly Ser Ser Lys Cys
2330 2335 2340

Val Cys Ser Val Ile Asp Leu Leu Leu Asp Asp Phe Val Glu Ile
2345 2350 2355

Ile Lys Ser Gln Asp Leu Ser Val Ile Ser Lys Val Val Lys Val
2360 2365 2370

Thr Ile Asp Tyr Ala Glu Ile Ser Phe Met Leu Trp Cys Lys Asp
2375 2380 2385

Gly His Val Glu Thr Phe Tyr Pro Lys Leu Gln Ala Ser Gln Ala
2390 2395 2400

Trp Gln Pro Gly Val Ala Met Pro Asn Leu Tyr Lys Met Gln Arg
2405 2410 2415

Met Leu Leu Glu Lys Cys Asp Leu Gln Asn Tyr Gly Glu Asn Ala
2420 2425 2430

Val Ile Pro Lys Gly Ile Met Met Asn Val Ala Lys Tyr Thr Gln
2435 2440 2445

Leu Cys Gln Tyr Leu Asn Thr Leu Thr Leu Ala Val Pro Tyr Asn
2450 2455 2460

Met Arg Val Ile His Phe Gly Ala Gly Ser Asp Lys Gly Val Ala
2465 2470 2475

Pro Gly Thr Ala Val Leu Arg Gln Trp Leu Pro Thr Gly Thr Leu
2480 2485 2490

Leu Val Asp Ser Asp Leu Asn Asp Phe Val Ser Asp Ala Asp Ser
2495 2500 2505

Thr Leu Ile Gly Asp Cys Ala Thr Val His Thr Ala Asn Lys Trp
2510 2515 2520

Asp Leu Ile Ile Ser Asp Met Tyr Asp Pro Arg Thr Lys His Val
2525 2530 2535

Thr Lys Glu Asn Asp Ser Lys Glu Gly Phe Phe Thr Tyr Leu Cys
2540 2545 2550

Gly Phe Ile Lys Gln Lys Leu Ala Leu Gly Gly Ser Ile Ala Val
2555 2560 2565

Lys Ile Thr Glu His Ser Trp Asn Ala Asp Leu Tyr Lys Leu Met
2570 2575 2580

Gly His Phe Ser Trp Trp Thr Ala Phe Val Thr Asn Val Asn Ala
2585 2590 2595

Ser Ser Ser Glu Ala Phe Leu Ile Gly Ala Asn Tyr Leu Gly Lys
2600 2605 2610

Pro Lys Glu Gln Ile Asp Gly Tyr Thr Met His Ala Asn Tyr Ile
2615 2620 2625

```
Phe Trp  Arg Asn Thr Asn Pro  Ile Gln Leu Ser Ser  Tyr Ser Leu
    2630                 2635                 2640

Phe Asp  Met Ser Lys Phe Pro  Leu Lys Leu Arg Gly  Thr Ala Val
    2645                 2650                 2655

Met Ser  Leu Lys Glu Asn Gln  Ile Asn Asp Met Ile  Tyr Ser Leu
    2660                 2665                 2670

Leu Glu  Lys Gly Arg Leu Ile  Ile Arg Glu Asn Asn  Arg Val Val
    2675                 2680                 2685

Val Ser  Ser Asp Ile Leu Val  Asn Asn
    2690                 2695


<210> SEQ ID NO 65
<211> LENGTH: 274
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 65

Met Asp Leu Phe Met Arg Phe Phe Thr Leu Arg Ser Ile Thr Ala Gln
1               5                   10                  15

Pro Val Lys Ile Asp Asn Ala Ser Pro Ala Ser Thr Val His Ala Thr
            20                  25                  30

Ala Thr Ile Pro Leu Gln Ala Ser Leu Pro Phe Gly Trp Leu Val Ile
        35                  40                  45

Gly Val Ala Phe Leu Ala Val Phe Gln Ser Ala Thr Lys Ile Ile Ala
    50                  55                  60

Leu Asn Lys Arg Trp Gln Leu Ala Leu Tyr Lys Gly Phe Gln Phe Ile
65                  70                  75                  80

Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser His Leu Leu Leu
                85                  90                  95

Val Ala Ala Gly Met Glu Ala Gln Phe Leu Tyr Leu Tyr Ala Leu Ile
            100                 105                 110

Tyr Phe Leu Gln Cys Ile Asn Ala Cys Arg Ile Ile Met Arg Cys Trp
        115                 120                 125

Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu Tyr Asp Ala Asn
    130                 135                 140

Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr Cys Ile Pro Tyr
145                 150                 155                 160

Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly Asp Gly Ile Ser
                165                 170                 175

Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly Tyr Ser Glu Asp
            180                 185                 190

Arg His Ser Gly Val Lys Asp Tyr Val Val Val His Gly Tyr Phe Thr
        195                 200                 205

Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr Thr Asp Thr Gly
    210                 215                 220

Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu Val Lys Asp Pro
225                 230                 235                 240

Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser Gly Val Ala Asn
                245                 250                 255

Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr Thr Thr Ser Val
            260                 265                 270

Pro Leu


<210> SEQ ID NO 66
```

<211> LENGTH: 154
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 66

```
Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
1               5                   10                  15

Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu Ser Leu Leu Lys Val
            20                  25                  30

Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr Thr Lys Leu Val Val
        35                  40                  45

Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr Met Ser Leu Tyr Met
    50                  55                  60

Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser Leu His Lys Leu Leu
65                  70                  75                  80

Gln Thr Leu Val Leu Lys Met Leu His Ser Ser Ser Leu Thr Ser Leu
                85                  90                  95

Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln Ser Thr Ala Leu Gln
            100                 105                 110

Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met Met Ser Arg Arg Arg
        115                 120                 125

Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val Ser Thr Asn Leu Cys
    130                 135                 140

Thr His Ser Phe Arg Lys Lys Gln Val Arg
145                 150
```

<210> SEQ ID NO 67
<211> LENGTH: 63
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 67

```
Met Phe His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile
1               5                   10                  15

Ile Ile Met Arg Thr Phe Arg Ile Ala Ile Trp Asn Leu Asp Val Ile
            20                  25                  30

Ile Ser Ser Ile Val Arg Gln Leu Phe Lys Pro Leu Thr Lys Lys Asn
        35                  40                  45

Tyr Ser Glu Leu Asp Asp Glu Glu Pro Met Glu Leu Asp Tyr Pro
    50                  55                  60
```

<210> SEQ ID NO 68
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 68

```
Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu
1               5                   10                  15

Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys
            20                  25                  30

Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro
        35                  40                  45

Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala
    50                  55                  60

Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg
65                  70                  75                  80
```

-continued

Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu
85 90 95

Leu Tyr Ser Pro Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile
100 105 110

Leu Cys Phe Thr Ile Lys Arg Lys Thr Glu
115 120

<210> SEQ ID NO 69
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 69

Met Asn Glu Leu Thr Leu Ile Asp Phe Tyr Leu Cys Phe Leu Ala Phe
1 5 10 15

Leu Leu Phe Leu Val Leu Ile Met Leu Ile Ile Phe Trp Phe Ser Leu
20 25 30

Glu Ile Gln Asp Leu Glu Glu Pro Cys Thr Lys Val
35 40

<210> SEQ ID NO 70
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 70

Met Lys Leu Leu Ile Val Leu Thr Cys Ile Ser Leu Cys Ser Cys Ile
1 5 10 15

Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val Leu Glu
20 25 30

Asp Pro Cys Lys Val Gln His
35

<210> SEQ ID NO 71
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 71

Met Cys Leu Lys Ile Leu Val Arg Tyr Asn Thr Arg Gly Asn Thr Tyr
1 5 10 15

Ser Thr Ala Trp Leu Cys Ala Leu Gly Lys Val Leu Pro Phe His Arg
20 25 30

Trp His Thr Met Val Gln Thr Cys Thr Pro Asn Val Thr Ile Asn Cys
35 40 45

Gln Asp Pro Ala Gly Gly Ala Leu Ile Ala Arg Cys Trp Tyr Leu His
50 55 60

Glu Gly His Gln Thr Ala Ala Phe Arg Asp Val Leu Val Val Leu Asn
65 70 75 80

Lys Arg Thr Asn

<210> SEQ ID NO 72
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 72

Met Asp Pro Asn Gln Thr Asn Val Val Pro Pro Ala Leu His Leu Val
1 5 10 15

-continued

```
Asp Pro Gln Ile Gln Leu Thr Ile Thr Arg Met Glu Asp Ala Met Gly
            20                  25                  30

Gln Gly Gln Asn Ser Ala Asp Pro Lys Val Tyr Pro Ile Ile Leu Arg
        35                  40                  45

Leu Gly Ser Gln Leu Ser Leu Ser Met Ala Arg Arg Asn Leu Asp Ser
    50                  55                  60

Leu Glu Ala Arg Ala Phe Gln Ser Thr Pro Ile Val Val Gln Met Thr
65                  70                  75                  80

Lys Leu Ala Thr Thr Glu Glu Leu Pro Asp Glu Phe Val Val Val Thr
                85                  90                  95

Ala Lys


<210> SEQ ID NO 73
<211> LENGTH: 70
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 73

Met Leu Pro Pro Cys Tyr Asn Phe Leu Lys Glu Gln His Cys Gln Lys
1               5                   10                  15

Ala Ser Thr Gln Arg Glu Ala Glu Ala Ala Val Lys Pro Leu Leu Ala
            20                  25                  30

Pro His His Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala
        35                  40                  45

Val Gly Glu Ile Leu Leu Leu Glu Trp Leu Ala Glu Val Val Lys Leu
    50                  55                  60

Pro Ser Arg Tyr Cys Cys
65                  70


<210> SEQ ID NO 74
<211> LENGTH: 6
<212> TYPE: RNA
<213> ORGANISM: Coronavirus

<400> SEQUENCE: 74

cuaaac                                                                  6


<210> SEQ ID NO 75
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 75

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly
1               5                   10


<210> SEQ ID NO 76
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 76

Thr Ile Pro Leu Gln Ala Ser Leu Pro Phe Gly Trp Leu Val Ile Gly
1               5                   10                  15

Val Ala Phe Leu Ala Val Phe
            20


<210> SEQ ID NO 77
<211> LENGTH: 23
<212> TYPE: PRT
```

-continued

<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 77

```
Phe Gln Phe Ile Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser
1               5                   10                  15

His Leu Leu Leu Val Ala Ala
            20
```

<210> SEQ ID NO 78
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 78

```
Ala Gln Phe Leu Tyr Leu Tyr Ala Leu Ile Tyr Phe Leu Gln Cys Ile
1               5                   10                  15

Asn Ala Cys Arg Ile Ile Met
            20
```

<210> SEQ ID NO 79
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 79

```
Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
1               5                   10                  15

Ile Leu
```

<210> SEQ ID NO 80
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 80

```
Leu Leu Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp
1               5                   10                  15

Ile Met Leu Leu Gln Phe Ala
            20
```

<210> SEQ ID NO 81
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 81

```
Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe Val
1               5                   10                  15

Leu Ala Ala Val Tyr Arg Ile
            20
```

<210> SEQ ID NO 82
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 82

```
Gly Gly Ile Ala Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu
1               5                   10                  15

Ser Tyr Phe Val Ala Ser Phe
            20
```

```
<210> SEQ ID NO 83
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 83

His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile Ile Ile
1               5                   10                  15

Met Arg Thr Phe
            20


<210> SEQ ID NO 84
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 84

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


<210> SEQ ID NO 85
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 85

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

Phe Thr Ile


<210> SEQ ID NO 86
<211> LENGTH: 83
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 86

Glu Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu
1               5                   10                  15

Lys Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His
            20                  25                  30

Pro Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe
        35                  40                  45

Ala Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala
    50                  55                  60

Arg Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln
65                  70                  75                  80

Glu Leu Tyr


<210> SEQ ID NO 87
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 87

caggaaacag ctatgacacc aagaacaagg ctctcca                              37


<210> SEQ ID NO 88
<211> LENGTH: 37
<212> TYPE: DNA
```

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 88

caggaaacag ctatgacgat agggcctctt ccacaga 37

<210> SEQ ID NO 89
<211> LENGTH: 496
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 89

acctacccag ngaaaagcca accaacctcg atctcttgta gatctgttct ctaaacgaac 60

tttaaaatct gtgtagctgt cgctcggctg catgcctagt gcacctacgc agtataaaca 120

ataataaatt ttactgtcgt tgacaagaaa cgagtaactc gtccctcttc tgcagactgc 180

ttacggtttc gtccgtgttg cagtcgatca tcagcatacc taggtttcgt ccgggtgtga 240

ccgaaaggta agatggagag ccttgttctt ggtgtcaacg agaaaacaca cgtccaactc 300

agtttgcctg tccttcaggt tagagacgtg ctagtgcgtg gcttcgggga ctctgtggaa 360

gaggccctat cggaggcacg tgaacacctc aaaaatggca cttgtggtct agtagagctg 420

gaaaaaggcg tactgcccca gcttgaacag ccctatgtgt tcattaaacg ttctgatgcc 480

ttaagcacca atcacg 496

<210> SEQ ID NO 90
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 90

gtcgacaaca atttctgtgg cccagatggg taccctcttg attgcatcaa agattttctc 60

gcacgcgcgg gcaagtcaat gtgcactctt tccgaacaac ttgattacat cgagtcgaag 120

agaggtgtct actgctgccg tgaccatgag catgaaattg cctggttcac tgagcgctct 180

gataagagct acgagcacca gacacccttc gaaattaaga gtgccaagaa atttgacact 240

ttcaaagggg aatgcccaaa gtttgtgttt cctcttaact caaaagtcaa agtcattcaa 300

ccacgtgttg aaaagaaaaa gactgagggt ttcatggggc gtatacgctc tgtgtaccct 360

gttgcatctc cacaggagtg taacaatatg cacttgtcta ccttgatgaa atgtaatcat 420

tgcgatgaag tttcatggca gacgtgcgac tttctgaaag ccacttgtga acattgtggc 480

actgaaaatt tagttattga aggacctact acatgtgggt acc 523

<210> SEQ ID NO 91
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 91

cttaggtgac gagcttggca ctgatcccat tgaagattat gaacaaaact ggaacactaa 60

gcatggcagt ggtgcactcc gtgaactcac tcgtgagctc aatggaggtg cagtcactcg 120

ctatgtcgac aacaatttct gtggcccaga tgggtaccct cttgattgca tcaaagattt 180

tctcgcacgc gcgggcaagt caatgtgcac tctttccgaa caacttgatt acatcgagtc 240

-continued

```
gaagagaggt gtctactgct gccgtgacca tgagcatgaa attgcctggt tcactgagcg    300

ctcctgataa gagctacgag cacc                                            324
```

<210> SEQ ID NO 92
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 92

```
tgctataata agcgtgccta ctgggttcct cgtgctagtg ctgatattgg gctcaggcca     60

tactggcatt actggtgaca atgtggagac cttgaatgag gatctccttg agatactgag    120

tcgtgaacgt gttaacatta acattgttgg cgattttcat ttgaatgaag aggttgccat    180

cattttggca tctttctctg cttctacaag tgcctttatt gacactataa agagtcttga    240

ttacaagtct ttcaaaacca ttgttgagtc ctgcggtaac tataaagtta ccaagggaaa    300

gcccgtaaaa ggtgcttgga acattggaca acagagatca gttttaacac cactgtgtgg    360

ttttccctca caggctgctg gtgttatcag atcaattttt gcgcgcacac ttgatgcagc    420

aaaccactca attcctgatt tgcaaagagc agctgtcacc atacttgatg gtatttctga    480

acagtcatta cgtct                                                      495
```

<210> SEQ ID NO 93
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 93

```
gccactcaaa cattgaaact cgactccgca agggaggtag gactagatgt tttggaggct     60

gtgtgtttgc ctatgttggc tgctataata agcgtgccta ctgggttcct cgtgctagtg    120

ctgatattgg ctcaggccat actggcatta ctggtgacaa tgtggagacc ttgaatgagg    180

atctccttga gatactgagt cgtgaacgtg ttaacattaa cattgttggc gattttcatt    240

tgaatgaaga ggttgccatc attttggcat ctttctctgc ttctacaagt gcctttattg    300

acactataaa gagtcttgat tacaagtctt tcaaaaccat tgttgagtcc tgcggtaact    360

ataaagttac caagggaaag cccgtaaaag gtgcttggaa cattggacaa cagagatcag    420

ttttaacacc actgtgtggt tttccctcac aggctgctgg tgttatcaga tcaatttttg    480

cgcgca                                                                486
```

<210> SEQ ID NO 94
<211> LENGTH: 567
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 94

```
cactactgtg gaaaaactca ggcctatctt tgaatggatt gaggcgaaac ttagtgcagg     60

agttgaattt ctcaaggatg cttgggagat tctcaaattt ctcattacag gtgtttttga    120

catcgtcaag ggtcaaatac aggttgcttc agataacatc aaggattgtg taaaatgctt    180

cattgatgtt gttaacaagg cactcgaaat gtgcattgat caagtcacta tcgctggcgc    240

aaagttgcga tcactcaact taggtgaagt cttcatcgct caaagcaagg gactttaccg    300

tcagtgtata cgtggcaagg agcagctgca actactcatg cctcttaagg caccaaaaga    360

agtaaccttt cttgaaggtg attcacatga cacagtactt acctctgagg aggttgttct    420
```

-continued

```
caagaacggt gaactcgaag cactcgagac gcccgttgat agcttcacaa atggagctat    480

cgttggcaca ccagtctgtg taaatggcct catgctctta gagattaagg acaaagaaca    540

atactgcgca ttgtctcctg gtttact                                        567
```

<210> SEQ ID NO 95
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 95

```
gggagattct caaatttctc attacaggtg tttttgacat cgtcaagggt caaatacagg     60

ttgcttcaga taacatcaag gattgtgtaa aatgcttcat tgatgttgtt aacaaggcac    120

tcgaaatgtg cattgatcaa gtcactatcg ctggcgcaaa gttgcgatca ctcaacttag    180

gtgaagtctt catcgctcaa agcaagggac tttaccgtca gtgtatacgt ggcaaggagc    240

agctgcaact actcatgcct cttaaggcac caaaagaagt aacctttctt gaaggtgatt    300

cacatgacac agtacttacc tctgaggagg ttgttctcaa gaacggtgaa ctcgaagcac    360

tcgagacgcc cgttgatagc ttcacaaatg gagctatcgt tggcacacca gtctgtgtaa    420

atggcctcat gctcttagag attaaggaca aagaacaata ctgcgcattg tctcctggtt    480

tactggctac aaacaatgtc tttcgcttaa aagggg                              516
```

<210> SEQ ID NO 96
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 96

```
agttcgagtt gaggaagaag aagaggaaga ctggctggat gatactactg agcaatcaga     60

gattgagcca gaaccagaac ctacacctga agaaccagtt aatcagttta ctggttattt    120

aaaacttact gacaatgttg ccattaaatg tgttgacatc gttaaggagg cacaaagtgc    180

taatcctatg gtgattgtaa atgctgctaa catacacctg aaacatggtg gtggtgtagc    240

aggtgcactc aacaaggcaa ccaatggtgc catgcaaaag gagagtgatg attacattaa    300

gctaaatggc cctcttacag taggagggtc ttgtttgctt tctggacata atcttgctaa    360

gaagtgtctg catgttgttg gacctaacct aaatgcaggt gaggacatcc agcttcttaa    420

ggcagcatat gaaaatttca attcacag                                       448
```

<210> SEQ ID NO 97
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 97

```
agaggatgat tatcaaggtc tccctctgga atttggtgcc tcagctgaaa cagttcgagt     60

tgaggaagaa gaagaggaag actggctgga tgatactact gagcaatcag agattgagcc    120

agaaccagaa cctacacctg aagaaccagt taatcagttt actggttatt taaaacttac    180

tgacaatgtt gccattaaat gtgttgacat cgttaaggag gcacaaagtg ctaatcctat    240

ggtgattgta aatgctgcta acatacacct gaaacatggt ggtggtgtag caggtgcact    300

caacaaggca accaatggtg ccatgcaaaa gga                                 333
```

<210> SEQ ID NO 98
<211> LENGTH: 399

<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 98

gagatgctct caagagcttt gaagaaagtg ccagttgatg agtatataac cacgtaccct 60

ggacaaggat gtgctggtta tacacttgag gaagctaaga ctgctcttaa gaaatgcaaa 120

tctgcatttt atgtactacc ttcagaagca cctaatgcta aggaagagat tctaggaact 180

gtatcctgga atttgagaga aatgcttgct catgctgaag agacaagaaa attaatgcct 240

atatgcatgg atgttagagc cataatggca accatccaac gtaagtataa aggaattaaa 300

attcaagagg gcatcgttga ctatggtgtc cgattcttct tttatactag taaagagcct 360

gtagcttcta ttattacgaa gctgaactct ctaaatgag 399

<210> SEQ ID NO 99
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 99

agaaatctgt cgtacagaag cctgtcgatg tgaagccaaa aattaaggcc tgcattgatg 60

aggttaccac aacactggaa gaaactaagt ttcttaccaa taagttactc ttgtttgctg 120

atatcaatgg taagctttac catgattctc agaacatgct tagaggtgaa gatatgtctt 180

tccttgagaa ggatgcacct tacatggtag gtgatgttat cactagtggt gatatcactt 240

gtgttgtaat accctccaaa aaggctggtg gcactactga gatgctctca agagctttga 300

agaaagtgcc agttgatgag tatataacca cgtaccctgg acaaggatgt gctggttata 360

cacttgagga agctaagact gctcttaaga aatgcaaatc tgcattttat gtactacctt 420

cagaagcacc taatgct 437

<210> SEQ ID NO 100
<211> LENGTH: 569
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 100

cctctatcgt attgacggag ctcaccttac aaagatgtca gagtacaaag gaccagtgac 60

tgatgttttc tacaaggaaa catcttacac tacaaccatc aagcctgtgt cgtataaact 120

cgatggagtt acttacacag agattgaacc aaaattggat gggtattata aaaaggataa 180

tgcttactat acagagcagc ctatagacct tgtaccaact caaccattac caaatgcgag 240

ttttgataat ttcaaactca catgttctaa cacaaaattt gctgatgatt taaatcaaat 300

gacaggcttc acaaagccag cttcacgaga gctatctgtc acattcttcc cagacttgaa 360

tggcgatgta gtggctattg actatagaca ctattcagcg agtttcaaga aaggtgctaa 420

attactgcat aagccaattg tttggcacat taaccaggct acaaccaaga caacgttcaa 480

accaaacact tggtgtttac gttgtctttg gagtacaaag ccagtagata cttcaaattc 540

atttgaagtt ctggcagtag aagacacat 569

<210> SEQ ID NO 101
<211> LENGTH: 187
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 101

-continued

```
tcagcagata cttcaaattc atttgaagtt ctggcagtag aagacacaca aggaatggac     60

aatcttgctt gtgaaagtca acaacccacc tctgaagaag tagtggaaaa tcctaccata    120

cagaaggaag tcatagagcg tgacgtgaaa actaccgaag ttgtaggcaa tgtcatactt    180

aaaccat                                                              187
```

<210> SEQ ID NO 102
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 102

```
aaatgcgacg agtctgcttc taagtctgct tctgtgtact acagtcagct gatgtgccaa     60

cctattctgt tgcttgacca agctcttgta tcagacgttg gagatagtac tgaagtttcc    120

gttaagatgt ttgatgctta tgtcgacacc ttttcagcaa cttttagtgt tcctatggaa    180

aaacttaagg cacttgttgc tacagctcac agcgagttag caaagggtgt agctttagat    240

ggtgtccttt ctacattcgt gtcagctgcc c                                   271
```

<210> SEQ ID NO 103
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 103

```
catttcatca gcaattcttg gctcatgtgg tttatcatta gtattgtaca aatggcaccc     60

gtttctgcaa tggttaggat gtacatcttc tttgcttctt tctactacat atggaagagc    120

tatgttcata tcatggatgg ttgcacctct tcgacttgca tgatgtgcta taagcgcaat    180

cgtgccacac gcgttgagtg tacaactatt gttaatggca tgaagagatc tttctatgtc    240

tatgcaaatg gaggccgtgg cttctgcaag actcacaatt ggaattgtct caattgtgac    300

acattttgca ctggtagtac attcattagt gatgaagttg ctcgagattt gtcactccag    360

ttt                                                                  363
```

<210> SEQ ID NO 104
<211> LENGTH: 500
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 104

```
agagatcttg gcgcatgtat tgactgtaat gcaaggcata tcaatgccca aggtagcaaa     60

aagtcacaat gtttcactca tctggaatgt aaaagactac atgtctttat ctgaacagct    120

gcgtaaacaa attcgtagtg ctgccaagaa gaacaacata ccttttagac taacttgtgc    180

tacaactaga caggttgtca atgtcataac tactaaaatc tcactcaagg gtggtaagat    240

tgttagtact tgttttaaac ttatgcttaa ggccacatta ttgtgcgttc ttgctgcatt    300

ggtttgttat atcgttatgc cagtacatac attgtcaatc catgatggtt acacaaatga    360

aatcattggt tacaaagcca ttcaggatgg tgtcactcgt gacatcattt ctactgatga    420

ttgttttgca aataaacatg ctggttttga cgcatggttt agccagcgtg gtggttcata    480

caaaaatgac aaaagctgcc                                                500
```

<210> SEQ ID NO 105
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

-continued

<400> SEQUENCE: 105

cattgtcaat ccatgatggt tacacaaatg aaatcattgg ttacaaagcc attcaggatg 60
gtgtcactcg tgacatcatt tctactgatg attgttttgc aaataaacat gctggttttg 120
acgcatggtt tagccagcgt ggtggttcat acaaaaatga caaaagctgc cctgtagtag 180
ctgctatcat tacaagagag attggtttca tagtgcctgg cttaccgggt actgtgctga 240
gagcaatcaa tggtgacttc ttgcattttc tacctcgtgt ttttagtgct gttggcaaca 300
tttgctacac accttccaaa ctcattgagt atagtgattt tgctacctct gcttgcgttc 360
ttgctgctga gtgtacaatt tttaaggatg ctatgggcaa acctgtgcca tattgttatg 420
acactaattt gctagagggt tctatttctt atagtgagct tcgtccagac actcgttatg 480
tgcttatgga tggttccatc atacagtttc ctaacactta cctggagggg tctgtta 537

<210> SEQ ID NO 106
<211> LENGTH: 427
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 106

cacttttgtt tttgatgtct ttcactatac tctgtctggt accagcttac agctttctgc 60
cgggagtcta ctcagtcttt tacttgtact tgacattcta tttcaccaat gatgtttcat 120
tcttggctca ccttcaatgg tttgccatgt tttctcctat tgtgcctttt tggataacag 180
caatctatgt attctgtatt tctctgaagc actgccattg gttctttaac aactatctta 240
ggaaaagagt catgtttaat ggagttacat ttagtacctt cgaggaggct gctttgtgta 300
cctttttgct caacaaggaa atgtacctaa aattgcgtag cgagacactg ttgccactta 360
cacagtataa caggtatctt gctctatata acaagtacaa gtatttcagt ggagccttag 420
atactac 427

<210> SEQ ID NO 107
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 107

agtaacaact tttgatgctg agtactgtag acatggtaca tgcgaaaggt cagaagtagg 60
tatttgccta tctaccagtg gtagatgggt tcttaataat gagcattaca gagctctatc 120
aggagttttc tgtggtgttg atgcgatgaa tctcatagct aacatcttta ctcctcttgt 180
gcaacctgtg ggtgctttag atgtgtctgc ttcagtagtg gctggtggta ttattgccat 240
attggtgact tgtgctgcct actactttat gaaattcaga cgtgtttttg gtgagtacaa 300
ccatgttgtt gctgctaatg cacttttgtt tttgatgtct ttcactatac tctgtctggt 360
accagcttac agctttctgc cgggagtcta ctcagtcttt tacttgtact tgacattcta 420
tttcaccaat gatgtttcat tcttggctca ccttcaatgg tttgccatgt tttctcctat 480
tgtgcctttt tggataacag caatctatgt attctgtatt tctctgaagc actgcca 537

<210> SEQ ID NO 108
<211> LENGTH: 551
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 108

-continued

```
agtatactgt ccaagacatg tcatttgcac agcagaagac atgcttaatc ctaactatga     60

agatctgctc attcgcaaat ccaaccatag ctttcttgtt caggctggca atgttcaact    120

tcgtgttatt ggccattcta tgcaaaattg tctgcttagg cttaaagttg atacttctaa    180

ccctaagaca cccaagtata aatttgtccg tatccaacct ggtcaaacat tttcagttct    240

agcatgctac aatggttcac catctggtgt ttatcagtgt gccatgagac ctaatcatac    300

cattaaaggt tctttcctta atggatcatg tggtagtgtt ggttttaaca ttgattatga    360

ttgcgtgtct ttctgctata tgcatcatat ggagcttcca acaggagtac acgctggtac    420

tgacttagaa ggtaaattct atggtccatt tgttgacaga caaactgcac aggctgcagg    480

tacagacaca accataacat taaatgtttt ggcatggctg tatgctgctg ttatcaatgg    540

tgataggtgg t                                                         551
```

```
<210> SEQ ID NO 109
<211> LENGTH: 593
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 109

acttagcaaa ggctctaaat gactttagca actcaggtgc tgatgttctc taccaaccac     60

cacagacatc aatcacttct gctgttctgc agagtggttt taggaaaatg gcattcccgt    120

caggcaaagt tgaagggtgc atggtacaag taacctgtgg aactacaact cttaatggat    180

tgtggttgga tgacacagta tactgtccaa gacatgtcat ttgcacagca gaagacatgc    240

ttaatcctaa ctatgaagat ctgctcattc gcaaatccaa ccatagcttt cttgttcagg    300

ctggcaatgt tcaacttcgt gttattggcc attctatgca aaattgtctg cttaggctta    360

aagttgatac ttctaaccct aagacaccca agtataaatt tgtccgtatc caacctggtc    420

aaacattttc agttctagca tgctacaatg gttcaccatc tggtgtttat cagtgtgcca    480

tgagacctaa tcataccatt aaaggttctt tccttaatgg atcatgtggt agtgttggtt    540

ttaacattga ttatgattgc gtgtctttct gctatatgca tcatatggag ctt           593
```

```
<210> SEQ ID NO 110
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 110

tgtgctgctt tgaaagagct gctgcagaat gggtatgaat ggtcgtacta tccttggtag     60

cactatttta gaagatgagt ttacaccatt tgatgttgtt agacaatgct ctggtgttac    120

cttccaaggg taagttcaag aaaattgtta agggcactca tcattggatg cttttaactt    180

tcttgacatc actattgatt cttgttcaaa gtacacagtg gtcactgttt ttctttgttt    240

acgagaatgc tttcttgcca tttactcttg gtattatggc aattgctgca tgtgctatgc    300

tgcttgttaa gcataagcac gcattcttgt gcttgtttct gttaccttct cttgcaacag    360

ttgcttactt taatatggtc tacatgcctg ctagctgggt gatgcgtatc atgacatggc    420

ttgaattggc tgacactagc ttgtctggtt ataggcttaa ggattgtgtt atgtatgctt    480

cagctttagt tttgcttatt ctca                                           504
```

```
<210> SEQ ID NO 111
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus
```

<400> SEQUENCE: 111

taggcttaag gattgtgtta tgtatgcttc agctttagtt ttgcttattc tcatgacagc 60

tcgcactgtt tatgatgatg ctgctagacg tgtttggaca ctgatgaatg tcattacact 120

tgtttacaaa gtctactatg gtaatgcttt agatcaagct atttccatgt gggccttagt 180

tatttctgta acctctaact attctggtgt cgttacgact atcatgtttt tagctagagc 240

tatagtgttt gtgtgtgttg agtattaccc attgttattt attacctggc aacacctt 298

<210> SEQ ID NO 112
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 112

aaacaggcaa gatctgagga caagagggca aaagtaacta gtgctatgca aacaatgctc 60

ttcactatgc ttaggaagct tgataatgat gcacttaaca acattatcaa caatgcgcgt 120

gatggttgtg ttccactcaa catcatacca ttgactacag cagccaaact catggttgtt 180

gtccctgatt atggtaccta caagaacact tgtgatggta acacctttac atatgcatct 240

gcactctggg aaatccagca agttgttgat gcggatagca agattgttca acttagtgaa 300

attaacatgg acaattcacc aaatttggct tggcctctta ttgttacagc tctaagagcc 360

aactcagctg ttaaactaca gaataatgaa ctgagtccag tagcactacg acagatgtcc 420

tgtgcggctg gtaccacaca aacagcttgt actgatgaca atgcacttgc ctactataac 480

aattcgaagg gaggtaggtt tgtgctggca ttactatcag accaccaagc 530

<210> SEQ ID NO 113
<211> LENGTH: 605
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 113

gaagtcgttc tcaaaaagtt aaagaaatct ttgaatgtgg ctaaatctga gtttgaccgt 60

gatgctgcca tgcaacgcaa gttggaaaag atggcagatc aggctatgac ccaaatgtac 120

aaacaggcaa gatctgagga caagagggca aaagtaacta gtgctatgca aacaatgctc 180

ttcactatgc ttaggaagct tgataatgat gcacttaaca acattatcaa caatgcgcgt 240

gatggttgtg ttccactcaa catcatacca ttgactacag cagccaaact catggttgtt 300

gtccctgatt atggtaccta caagaacact tgtgatggta acacctttac atatgcatct 360

gcactctggg aaatccagca agttgttgat gcggatagca agattgttca acttagtgaa 420

attaacatgg acaattcacc aaatttggct tggcctctta ttgttacagc tctaagagcc 480

aactcagctg ttaaactaca gaataatgaa ctgagtccag tagcactacg acagatgtcc 540

tgtgcggctg gtaccacaca aacagcttgt actgatgaca atgcacttgc ctactataac 600

aattc 605

<210> SEQ ID NO 114
<211> LENGTH: 176
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 114

acactggtac aggacaggca attactgtaa caccagaagc taacatggac caagagtcct 60

-continued

ttggtggtgc ttcatgttgt ctgtattgta gatgccacat tgaccatcca aatcctaaag 120

gattctgtga cttgaaaggt aagtacgtcc aaatacctac cacttgtgct aatgat 176

<210> SEQ ID NO 115
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 115

actgtaacac cagaagctaa catggaccaa gagtcctttg gtggtgcttc atgttgtctg 60

tattgtagat gccacattga ccatccaaat cctaaaggat tctgtgactt gaaaggtaag 120

tacgtccaaa tacctaccac ttgtgctaat gacccagtgg gttttacact tagaaacaca 180

gtctgtaccg tctgcggaat gtggaaaggt tatggctgta gttgtgacca actccgcgaa 240

cccttgatgc agtctgcgga tgcatcaacg tttttaaacg ggtttgcggt gtaagtgcag 300

cccgtcttac accgtgcggc acaggcacta gtactgatgt cgtctacagg gcttttgata 360

tttacaacga aaaagttgct ggttttgcaa agttcctaaa aactaattgc tgtcgcttcc 420

aggagaagga tgaggaaggc aatttattag actcttactt tgtagttaag aggcatacta 480

tgtctaccta ccaacatgaa gagactattt ataact 516

<210> SEQ ID NO 116
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 116

accacttatt aagtgggatt tgctgaaata tgattttacg gaagagagac tttgtctctt 60

cgaccgttat tttaaatatt gggaccagac ataccatccc aattgtatta actgtttgga 120

tgataggtgt atccttcatt gtgcaaactg taatgtgtta ttttctgctg tgtttccacg 180

tacaagtttt ggaccactag taagaaaaat atttgtagat ggtgttcctt ttgttgtttc 240

aactggatac cattttcgtg agttaggagt cgtacataat caggatgtaa acttacatag 300

ctcgcgtctc agtttcaagg aacttttagt gtatgctgct gatccagcta tgcatgcagc 360

ttctgg 366

<210> SEQ ID NO 117
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 117

tgaaaaagtt gctggttttg caaagttcct aaaaactaat tgctgtcgct tccaggagaa 60

ggatgaggaa ggcaatttat tagactctta ctttgtagtt aagaggcata ctatgtctaa 120

ctaccaacat gaagagacta tttataactt ggttaaagat tgtccagcgg ttgctgtcca 180

tgactttttc aagtttagag tagatggtga catggtacca catatatcac gtcagcgtct 240

aactaaatac acaatggctg atttagtcta tgctctacgt cattttgatg a 291

<210> SEQ ID NO 118
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 118

gagtcccata tggatgctga tctcgcaaaa ccacttatta agtgggattt gctgaaatat 60

-continued

gattttacgg aagagagact ttgtctcttc gaccgttatt ttaaatattg ggaccagaca 120

taccatccca attgtattaa ctgtttggat gataggtgta tccttcattg tgcaaacttt 180

aatgtgttat tttctactgt gtttccacct acaagttttg gaccactagt aagaaaaata 240

tttgtagatg gtgttccttt tgttgtttca actggatacc attttcgtga gttaggagtc 300

gtacataatc aggatgtaaa cttacatagc tcgcgtctca gtttcaagga acttttagtg 360

tatgctgctg atccagctat gcatgcagct tctggcaatt tattgctaga taaacgcact 420

acatgctttt cagtagctgc actaacaaac aatgttgctt ttcaaactgt caaacccggt 480

<210> SEQ ID NO 119
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 119

aatgggaact ggtacgattt cggtgatttc gtacaagtag caccaggctg cggagttcct 60

attgtggatt catattactc attgctgatg cccatcctca ctttgactag ggcattggct 120

gctgagtccc atatggatgc tgatctcgca aaaccactta ttaagtgaga tttgctgaaa 180

tatgatttta cggaagagag actttgtctc ttcgaccgtt attttaaata ttgggaccag 240

acataccatc ccaattgtat taactgtttg gatgataggt gtatccttca ttgtgcaaac 300

tttaatgtgt tattttctac tgtgtttcca cctacaagct ttggaccact agtaagaaaa 360

atatttgtag atggtgttcc ttttgttgtt tcaactggat accat 405

<210> SEQ ID NO 120
<211> LENGTH: 562
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(67)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 120

ctattgatgc ttacccactt acaaaacatc ctaatcagga gtatgctgat gtctttcact 60

tgtattnaca atacattaga aagttacatg atgagcttac tggccacatg ttggacatgt 120

attccgtaat gctaactaat gataacacct cacggtactg ggaacctgag ttttatgagg 180

ctatgtacac accacataca gtcttgcagg ctgtaggtgc ttgtgtattg tgcaattcac 240

agacttcact tcgttgcggt gcctgtatta ggagaccatt cctatgttgc aagtgctgct 300

atgaccatgt catttcaaca tcacacaaat tagtgttgtc tgttaatccc tatgtttgca 360

atgccccagg ttgtgatgtc actgatgtga cacaactgta tctaggaggt atgagctatt 420

attgcaagtc acataagcct cccattagtt ttccattatg tgctaatggt caggtttttg 480

gtttatacaa aaacacatgt gtaggcagtg acaatgtcac tgacttcaat gcgatagcaa 540

catgtgattg gactaatgct gg 562

<210> SEQ ID NO 121
<211> LENGTH: 580
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 121

gctatgtaca caccacatac agtcttgcag gctgtaggtg cttgtgtatt gtgcaattca 60

-continued

```
cagacttcac ttcgttgcgg tgcctgtatt aggagaccat tcctatgttg caagtgctgc    120

tatgaccatg tcatttcaac atcacacaaa ttagtgttgt ctgttaatcc ctatgtttgc    180

aatgccccag gttgtgatgt cactgatgtg acacaactgt atctaggagg tatgagctat    240

tattgcaagt cacataagcc tcccattagt tttccattat gtgctaatgg tcaggttttt    300

ggtttataca aaaacacatg tgtaggcagt gacaatgtca ctgacttcaa tgcgatagca    360

acatgtgatt ggactaatgc tggcgattac atacttgcca acacttgtac tgagagactc    420

aagcttttcg cagcagaaac gctcaaagcc actgaggaaa catttaagct gtcatatggt    480

attgccactg tacgcgaagt actctctgac agagaattgc atctttcatg ggaggttgga    540

aaacctagac caccattgaa cagaaactat gtctttactg                          580
```

<210> SEQ ID NO 122
<211> LENGTH: 610
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 122

```
tggtgatgct gttgtgtaca gaggtactac gacatacaag ttgaatgttg gtgattactt     60

tgtgttgaca tctcacactg taatgccact tagtgcacct actctagtgc cacaagagca    120

ctatgtgaga attactggct tgtacccaac actcaacatc tcagatgagt tttctagcaa    180

tgttgcaaat tatcaaaagg tcggcatgca aaagtactct acactccaag gaccacctgg    240

tactggtaag agtcattttg ccatcggact tgctctctat tacccatctg ctcgcatagt    300

gtatacggca tgctctcatg cagctgttga tgccctatgt gaaaaggcat taaaatattt    360

gcccatagat aaatgtagta gaatcatacc tgcgcgtgcg cgcgtagagt gttttgataa    420

attcaaagtg aattcaacac tagaacagta tgttttctgc actgtaaatg cattgccaga    480

aacaactgct gacattgtag tctttgatga aatctctatg gctactaatt atgacttgag    540

tgttgtcaat gctagacttc gtgcaaaaca ctacgtctat attggcgatc ctgctcaatt    600

accagcccct                                                           610
```

<210> SEQ ID NO 123
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 123

```
ccaacactca acatctcaga tgagttttct agcaatgttg caaattatca aaaggtcggc     60

atgcaaaagt actctacact ccaaggacca cctggtactg gtaagagtca ttttgccatc    120

ggacttgctc tctattaccc atctgctcgc atagtgtata cggcatgctc tcatgcagct    180

gttgatgccc tatgtgaaaa ggcattaaaa tatttgccca tagataaatg tagtagaatc    240

atacctgcgc gtgcgcgcgt agagtgtttt gataaattca aagtgaattc aacactagaa    300

cagtatgttt tctgcactgt aaatgcattg ccagaaacaa ctgctgacat tgtagtcttt    360

gatgaaatct ctatggctac taattatgac ttgagtgttg tcaatgctag acttcgtgca    420

aaacactac                                                            429
```

<210> SEQ ID NO 124
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 124

-continued

caatgtggct atcacaaggg caaaaattgg cattttgtgc ataatgtctg atagagatct 60

ttatgacaaa ctgcaattta caagtctaga aataccacgt cgcaatgtgg ctacattaca 120

agcagaaaat gtaactggac tttttaagga ctgtagtaag atcattactg gtcttcatcc 180

tacacaggca cctacacacc tcagcgttga tataaagttc aagactgaag gattatgtgt 240

tgacatacca ggcataccaa aggacatgac ctaccgtaga ctcatctcta tgatgggttt 300

caaaatgaat taccaagtca atggttaccc taatatgttt atcacccgcg aagaagctat 360

tcgtcacgtt cgtgcgtgga ttggctttga tgtagagggc tgtcatgcaa ctagagatgc 420

tgtgggtact aacctacctc tccagctagg attttctaca ggtgttaact tagtagctgt 480

accgac 486

<210> SEQ ID NO 125
<211> LENGTH: 427
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 125

aaaggacatg acctaccgta gactcatctc tatgatgggt ttcaaaatga attaccaagt 60

caatggttac cctaatatgt ttatcacccg cgaagaagct attcgtcacg ttcgtgcgtg 120

gattggcttt gatgtagagg gctgtcatgc aactagagat gctgtgggta ctaacctacc 180

tctccagcta ggattttcta caggtgttaa cttagtagct gtaccgactg gttatgttga 240

cactgaaaat aacacagaat tcaccagagt taatgcaaaa cctccaccag gtgaccagtt 300

taaacatctt ataccactca tgtataaagg cttgccctgg aatgtagtgc gtattaagat 360

agtacaaatg ctcagtgata cactgaaagg attgtcagac agagtcgtgt tcgtcctttg 420

ggcgcat 427

<210> SEQ ID NO 126
<211> LENGTH: 392
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 126

atggaaatgc acatgtggct agttgtgatg ctatcatgac tagatgttta gcagtccatg 60

agtgctttgt taagcgcgtt gattggtctg ttgaataccc tattatagga gatgaactga 120

gggttaattc tgcttgcaga aaagtacaac acatggttgt gaagtctgca ttgcttgctg 180

ataagtttcc agttcttcat gacattggaa atccaaaggc tatcaagtgt gtgcctcagg 240

ctgaagtaga atggaagttc tacgatgctc agccatgtag tgacaaagct tacaaaatag 300

aggaactctt ctattcttat gctacacatc acgataaatt cactgatggt gtttgtttgt 360

tttggaattg taacgttgat cgttacccag cc 392

<210> SEQ ID NO 127
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 127

gcttcatcag atacttatgc ctgctggaat cattctgtgg gttttgacta tgtctataac 60

ccatttatga ttgatgttca gcagtggggc tttacgggta accttcagag taaccatgac 120

caacattgcc aggtacatgg aaatgcacat gtggctagtt gtgatgctat catgactaga 180

-continued

```
tgtttagcag tccatgagtg ctttgttaag cgcgttgatt ggtctgttga ataccctatt    240

ataggagatg aactgagggt taattctgct tgcagaaaag tacaacacat ggttgtgaag    300

tctgcattgc ttgctgataa gtttccagtt cttcatgaca ttggaaatcc aaaggctatc    360

aagtgtgtgc ctcaggctga agtagaatgg aagttctacg atgctcagcc atgtagtgac    420

aaagcttaca aaatagagga actcttctat tcttatgcta cacatcacga taaattcact    480

gat                                                                  483


<210> SEQ ID NO 128
<211> LENGTH: 326
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 128

tcaaagggac cagcacaagc tagcgtcaat ggagtcacat taattggaga atcagtaaaa     60

acacagttta actactttaa gaaagtagac ggcattattc aacagttgcc tgaaacctac    120

tttactcaga gcagagactt agaggatttt aagcccagat cacaaatgga aactgacttt    180

ctcgagctcg ctatggatga attcatacag cgatataagc tcgagggcta tgccttcgaa    240

cacatcgttt atggagattt cagtcatgga caacttggcg gtcttcattt aatgataggc    300

ttagccaagc gctcacaaga ttcact                                         326


<210> SEQ ID NO 129
<211> LENGTH: 457
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 129

acaccttcaa agggaccagc acaagctagc gtcaatggag tcacattaat tggagaatca     60

gtaaaaacac agtttaacta ctttaagaaa gtagacggca ttattcaaca gttgcctgaa    120

acctacttta ctcagagcag agacttagag gattttaagc ccagatcaca aatggaaact    180

gactttctcg agctcgctat ggatgaattc atacagcgat ataagctcga gggctatgcc    240

ttcgaacaca tcgtttatgg agatttcagt catggacaac ttggcggtct tcatttaatg    300

ataggcttag ccaagcgctc acaagattca ccacttaaat tagaggattt tatccctatg    360

gacagcacag tgaaaaatta cttcataaca gatgcgcaaa caggttcatc aaaatgtgtg    420

tgttctgtga ttgatctttt acttgatgac tttgtcg                              457


<210> SEQ ID NO 130
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 130

cgcaaagtat actcaactgt gtcaatactt aaatacactt actttagctg taccctacaa     60

catgagagtt attcactttg gtgctggctc tgataaagga gttgcaccag gtacagctgt    120

gctcagacaa tggttgccaa ctggcacact acttgtcgat tcagatctta atgacttcgt    180

ctccgacgca gattctactt taattggaga ctgtgcaaca gtacatacgg ctaataaatg    240

ggaccttatt attagcgata tgtatgaccc taggaccaaa catgtgacaa aagagaatga    300

ctctaaagaa gggtttttca cttatctgtg tggatttata aagcaaaaac tagccctggg    360

tggttctata gctgtaaaga taacagagca ttcttggaat gctgaccttt acaagcttat    420

gggccatttc tcatggtgga cagcttttgt tacaaatgta aatgcatcat catcggaagc    480
```

-continued

attttaatt ggg 493

<210> SEQ ID NO 131
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 131

acttaaatac acttacttta gctgtaccct acaacatgag agttattcac tttggtgctg 60

gctctgataa aggagttgca ccaggtacag ctgtgctcag acaatggttg ccaactggca 120

cactacttgt cgattcagat cttaatgact tcgtctccga cgcagattct actttaattg 180

gagactgtgc aacagtacat acggctaata aatgggacct tattattagc gatatgtatg 240

accctaggac caaacatgtg acaaaagaga atgactctaa agaagggttt ttcacttatc 300

tgtgtggatt tataaagcaa aaactagccc tgggtggttc tatagctgta aagataacag 360

agcattcttg gaatgctgac ctttacaagc ttatgggcca tttctcatgg tggacagctt 420

ttgttacaaa tgtaaatgca tcatcatcgg aagcattttt aattggggct aactatcttg 480

gcaagccgaa 490

<210> SEQ ID NO 132
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 132

taaggagaat caaatcaatg atatgattta ttctcttctg gaaaaaggta ggcttatcat 60

tagagaaaac aacagagttg tggtttcaag tgatattctt gttaacaact aaacgaacat 120

gtttattttc ttattatttc ttactctcac tagtggtagt gaccttgacc ggtgcaccac 180

ttttgatgat gttcaagctc ctaattacac tcaacatact tcatctatga ggggggttta 240

ctatcctgat gaaattttta gatcagacac tctttattta actcaggatt tatttcttcc 300

attttattct aatgttacag ggtttcatac tattaatcat acgtttggca accctgtcat 360

accttttaag gatggtattt attttgctgc cacagagaaa tcaaatgttg tccgtggttg 420

ggtttttggt tctaccatga acaacaagtc acagtcggtg attattatta acaattctac 480

taatgttgtt atacgagcat gtaactttga attgtgtgac aaccctttct ttgctgtttc 540

taaacccata 550

<210> SEQ ID NO 133
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 133

acttaaatac acttacttta gctgtaccct acaacatgag agttattcac tttggtgctg 60

gctctgataa aggagttgca ccaggtacag ctgtgctcag acaatggttg ccaactggca 120

cactacttgt cgattcagat cttaatgact tcgtctccga cgcagattct actttaattg 180

gagactgtgc aacagtacat acggctaata aatgggacct tattattagc gatatgtatg 240

accctaggac caaacatgtg acaaaagaga atgactctaa agaagggttt ttcacttatc 300

tgtgtggatt tataaagcaa aaactagccc tgggtggttc tatagctgta aagataacag 360

agcattcttg gaatgctgac ctttacaagc ttatgggcca tttctcatgg tggacagctt 420

-continued

```
ttgttacaaa tgtaaatgca tcatcatcgg aagcattttt aattggggct aactatcttg     480

gcaagccgaa                                                            490


<210> SEQ ID NO 134
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 134

taaggagaat caaatcaatg atatgattta ttctcttctg gaaaaaggta ggcttatcat      60

tagagaaaac aacagagttg tggtttcaag tgatattctt gttaacaact aaacgaacat     120

gtttattttc ttattatttc ttactctcac tagtggtagt gaccttgacc ggtgcaccac     180

ttttgatgat gttcaagctc ctaattacac tcaacatact tcatctatga ggggggttta     240

ctatcctgat gaaattttta gatcagacac tctttattta actcaggatt tatttcttcc     300

attttattct aatgttacag ggtttcatac tattaatcat acgtttggca accctgtcat     360

accttttaag gatggtattt attttgctgc cacagagaaa tcaaatgttg tccgtggttg     420

ggtttttggt tctaccatga acaacaagtc acagtcggtg attattatta acaattctac     480

taatgttgtt atacgagcat gtaactttga attgtgtgac aaccctttct ttgctgtttc     540

taaacccata                                                            550


<210> SEQ ID NO 135
<211> LENGTH: 400
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 135

atcaatgata tgatttattc tcttctggaa aaaggtaggc ttatcattag agaaaacaac      60

agagttgtgg tttcaagtga tattcttgtt aacaactaaa cgaacatgtt tattttctta     120

ttatttctta ctctcactag tggtagtgac cttgaccggt gcaccacttt tgatgatgtt     180

caagctccta attacactca acatacttca tctatgaggg gggtttacta tcctgatgaa     240

atttttagat cagacactct ttatttaact caggatttat ttcttccatt ttattctaat     300

gttacagggt ttcatactat taatcatacg tttggcaacc ctgtcatacc ttttaaggat     360

ggtatttatt ttgctgccac agagaaatca aatgttgtcc                           400


<210> SEQ ID NO 136
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 136

tgatctttgc ttctccaatg tctatgcaga ttctttggta gtcaagggag atgatgtaag      60

acaaatagcg ccaggacaaa ctggtgttat tgctgattat aattataaat tgccagatga     120

tttcatgggt tgtgtccttg cttggaatac taggaacatt gatgctactt caactggtaa     180

ttataattat aaatataggt atcttagaca tggcaagctt aggccctttg agagagacat     240

atctaatgtg cctttctcca cctgatggca aaccttgcac cccacctg                  288


<210> SEQ ID NO 137
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 137
```

```
ctttgagaga gacatatcta atgtgccttt ctcccctgat ggcaaacctt gcaccccacc      60
tgctcttaat tgttattggc cattaaatga ttatggtttt tacaccacta ctggcattgg     120
ctaccaacct tacagagttg tagtactttc ttttgaactt ttaaatgcac cggccacggt     180
ttgtggacca aaattatcca ctgaccttat taagaaccag tgtgtcaatt ttaattttaa     240
tggactcact ggtactggtg tgttaactcc ttcttcaaag agatttcaac catttcaaca     300
aattttgccg tgatgtttct gatttcactg attccgttcg agatcctaaa acatctgaaa     360
tattagacat ttcaccctgc gcttttgggg gtgtaagtgt aattacacct g             411
```

<210> SEQ ID NO 138
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 138

```
tggaaatatt ttggtggttt taatttttca caaatattac ctgaccctct aaagccaact      60
aagaggtctt ttattgagga cttgctcttt aataaggtga cactcgctga tgctggcttc     120
atgaagcaat atggcgaatg cctaggtgat attaatgcta gagatctcat ttgtgcgcag     180
aagttcaatg gacttacagt gttgccacct ctgctcactg atgatatgat tgctgcctac     240
actgctgctc tagttagtgg tactgccact gctggatgga catttggtgc tggcgctgct     300
cttcaaatac cttttgctat gcaaatggca tataggttca atggcattgg agttact        357
```

<210> SEQ ID NO 139
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 139

```
caatatggcg aatgcctagg tgatattaat gctagagatc tcatttgtgc gcagaagttc      60
aatggactta cagtgttgcc acctctgctc actgatgata tgattgctgc ctacactgct     120
gctctagtta gtggtactgc cactgctgga tggacatttg gtgctggcgc tgctcttcaa     180
ataccttttg ctatgcaaat ggcatatagg ttcaatggca ttggagttac ccaaaatgtt     240
ctctatgaga accaaaaaca aatcgccaac caatttaaca aggcgattag tcaaattcaa     300
gaatcactta caacaacatc aactgcattg ggcaagctgc aagacgttgt taaccagaat     360
gctcaagcat taaacacact tgttaaacaa cttagctcta attttggtgc aatttcaagt     420
gtgctaaatg atat                                                       434
```

<210> SEQ ID NO 140
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 140

```
acagacaata catttgtctc aggaaattgt gatgtcgtta ttggcatcat taacaacaca      60
gtttatgatc ctctgcaacc tgagcttgac tcattcaaag aagagctgga caagtacttc     120
aaaaatcata catcaccaga tgttgatctt ggcgacattt caggcattaa cgcttctgtc     180
gtcaacattc aaaaagaaat tgaccgcctc aatgaggtcg ctaaaaattt aaatgaatca     240
ctcattgacc ttcaagaatt gggaaaatat gagcaatata ttaaatggcc ttggtatgtt     300
tggctcggct tcattgctgg actaattgcc atcgtcatgg ttacaatctt gctttgttgc     360
```

-continued

```
atgactagtt gttgcagttg cctcaagggt gcatgctctt gtggttcttg ctgcaagttt    420

gatgaggatg actctgagcc agttctcaag ggtgtcaaat tacattacac ataaacgaac    480

ttatggattt gtttatgaga ttttttactc ttagatcaat tactgcacag ccagtaaaaa    540

ttgacaatgc ttctcct                                                   557
```

<210> SEQ ID NO 141
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 141

```
atgtttggct cggcttcatt gctggactaa ttgccatcgt catggttaca atcttgcttt     60

gttgcatgac tagttgttgc agttgcctca agggtgcatg ctcttgtggt tcttgctgca    120

agtttgatga ggatgactct gagccagttc tcaagggtgt caaattacat tacacataaa    180

cgaacttatg gatttgttta tgagattttt tactcttaga tcaattactg cacagccagt    240

aaaaattgac aatgcttctc ctgcaagtac tgttcatgct acagcaacga taccgctaca    300

agcctcactc cctttcggat ggcttgttat tggcgttgca tttcttgctg tttttcagag    360

cgctaccaaa ataattgcgc tcaataaaag atggcagcta gccctttata agggcttcca    420

gttcatttgc aatttactgc tgctatttgt taccatctat tcacatcttt tgcttgtcgc    480

tgcaggtatg gaggcgcaat tttgtacct ctatgccttg atatattttc               530
```

<210> SEQ ID NO 142
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 142

```
ttgctcgtac ccgctcaatg tggtcattca acccagaaac aaacattctt ctcaatgtgc     60

ctctccgggg gacaattgtg accagaccgc tcatggaaag tgaacttgtc attggtgctg    120

tgatcattcg tggtcacttg cgaatggccg gacactccct agggcgctgt gacattaagg    180

acctgccaaa agagatcact gtggctacat cacgaacgct ttcttattac aaattaggag    240

cgtcgcagcg tgtaggcact gattcaggtt ttgctgcata caaccgctac cgtattggaa    300

actataaatt aaatacagac                                                320
```

<210> SEQ ID NO 143
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 143

```
cgaacttatg tactcattcg tttcggaaga aacaggtacg ttaatagtta atagcgtact     60

tctttttctt gctttcgtgg tattcttgct agtcacacta gccatcctta ctgcgcttcg    120

attgtgtgcg tactgctgca atattgttaa cgtgagttta gtaaaaccaa cggtttacgt    180

ctactcgcgt gttaaaaatc tgaactcttc tgaaggagtt cctgatcttc tggtctaaac    240

gaactaacta ttattattat tctgtttgga actttaacat tgcttatcat ggcagacaac    300

ggtactatta ccgttgagga gcttaaacaa ctcctggaac aatggaacct agtaataggt    360

ttcctattcc tagcctggat tatgttacta caatttgcct attctaatcg gaacagg       417
```

<210> SEQ ID NO 144
<211> LENGTH: 516

-continued

<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 144

cttgtcattg gtgctgtgat cattcgtggt cacttgcgaa tggccggaca ctccctaggg 60

cgctgtgaca ttaaggacct gccaaaagag atcactgtgg ctacatcacg aacgctttct 120

tattacaaat taggagcgtc gcagcgtgta ggcactgatt caggttttgc tgcatacaac 180

cgctaccgta ttggaaacta taaattaaat acagaccacg ccggtagcaa cgacaatatt 240

gctttgctag tacagtaagt gacaacagat gtttcatctt gttgacttcc aggttacaat 300

agcagagata ttgattatca ttatgaggac tttcaggatt gctatttgga atcttgacgt 360

tataataagt tcaatagtga gacaattatt taagcctcta actaagaaga attattcgga 420

gttagatgat gaagaaccta tggagttaga ttatccataa aacgaacatg aaaattattc 480

tcttcctgac attgatttta tttacatctt gcgagc 516

<210> SEQ ID NO 145
<211> LENGTH: 310
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 145

cgatgtttca tcttgttgac ttccaggtta caatagcaga gatattgatt atcattatga 60

ggactttcag gattgctatt tggaatcttg acgttataat aagttcaata gtgagacaat 120

tatttaagcc tctaactaag aagaattatt cggagttaga tgatgaagaa cctatggagt 180

tagattatcc ataaaacgaa catgaaaatt attctcttcc tgacattgat tgtatttaca 240

tcttgcgagc tatatcacta tcaggagtgt gttagaggta cgactgtact actaaaagaa 300

ccttgcccat 310

<210> SEQ ID NO 146
<211> LENGTH: 556
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 146

agaaagacag aatgaatgag ctcactttaa ttgacttcta tttgtgcttt ttagcctttc 60

tgctattcct tgttttaata atgcttatta tattttggtt ttcactcgaa atccaggatc 120

tagaagaacc ttgtaccaaa gtctaaacga acatgaaact tctcattgtt ttgacttgta 180

tttctctatg cagttgcata tgcactgtag tacagcgctg tgcatctaat aaacctcatg 240

tgcttgaaga tccttgtaag gtacaacact aggggtaata cttatagcac tgcttggctt 300

tgtgctctag gaaaggtttt accttttcat agatggcaca ctatggttca aacatgcaca 360

cctaatgtta ctatcaactg tcaagatcca gctggtggtg cgcttatagc taggtgttgg 420

taccttcatg aaggtcacca aactgctgca tttagagacg tacttgttgt tttaaataaa 480

cgaacaaatt aaaatgtctg ataatggacc ccaatcaaac caacgtagtg ccccccgcat 540

tacatttggt ggaccc 556

<210> SEQ ID NO 147
<211> LENGTH: 110
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 147

-continued

```
acgaacatga aaattattct cttcctgaca ttgattgtat ttacatcttg cgagctatat     60

cactatcagg agtgtgttag aggtacgact gtactactaa aagaaccttg               110


<210> SEQ ID NO 148
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 148

gcatttagag acgtacttgt tgttttaaat aaacgaacaa attaaaatgt ctgataatgg     60

acctcaatca agccaacgta gtgccccccg cattacattt ggtggaccca cagattcaac    120

tgacaataac cagaatggag gacgcaatgg ggcaaggcca aaacagcgcc gaccccaagg    180

tttacccaat aatactgcgt cttggttcac agctctcact cagcatggca aggaggaact    240

tagattccct cgaggccagg gcgttccaat caacaccaat agtggtccag atgaccaaat    300

tggctactac cgaagagcta cccgacgagt tcgtggtggt gacggcaaaa tgaaagagct    360

cag                                                                  363


<210> SEQ ID NO 149
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 149

ctatcagctg cgtgcaagat cagtttcacc aaaacttttc atcagacaag aggaggttca     60

acaagagctc tactcgccac tttttctcat tgttgctgct ctagtatttt taatactttg    120

cttcaccatt aagagaaaga cagaatgaat gagctcactt taattgactt ctatttgtgc    180

tttttagcct ttctgctatt ccttgtttta ataatgctta ttatattttg gttttcactc    240

gaaatccagg atctagaaaa accttgtacc aaaggctaaa cgaacatgaa actt          294


<210> SEQ ID NO 150
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 150

caaactgctg catttagaga cgtacttgtt gtttaaataa acgaacaaat taaaatgtct     60

gataatggac cccaatcaaa ccaacgtagt gccccccgca ttacatttgg tggacccaca    120

gattcaactg acaataacca gaatggagga cgcaatgggg caaggccaaa acagcgccga    180

ccccaaggtt tacccaataa tactgcgtct tggttcacag ctctcactca gcatggcaag    240

gaggaactta gattccctcg aggccagggc gttccaatca acaccaatag tggtccagat    300

gaccaaattg gctactaccg aagagctacc cgacgagttc gtggtggtga cggcaaaatg    360

aaagagctca gccccagatg gtacttctat tacctaggaa ctggcccaga agcttcactt    420

ccctacggcg ctaacaaaga aggcatcgta tgggttgcaa ctgagggagc cttgaataca    480

cccaaagacc acattggcac ccgt                                           504


<210> SEQ ID NO 151
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 151

ctcgccactt tttctcattg ttgctgctct agtattttta atactttgct tcaccattaa     60
```

-continued

```
gagaaagaca gaatgaatga gctcacttta attgacttct atttgtgctt tttagccttt    120
ctgctattcc ttgttttaat aatgcttatt atattttggt tttcactcga aatccaggat    180
ctagaagaac cttgtaccaa agtctaaacg aacatgaaac ttctcattgt tttgacttgt    240
atttctctat gcagttgcat atgcactgta gtacagcgct gtgcatctaa taaacctcat    300
gtgcttgaag atccttgtaa ggtacaacac taggggtaat acttatagca ctgcttggct    360
ttgtgctcta ggaaaggttt taccttttca tagatggcac actatggttc aaacatgcac    420
acctaatgtt actatcaact gtcaagatcc agctggtggt gcgcttatag ctag          474
```

<210> SEQ ID NO 152
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 152

```
cattaagaga aagacagaat gaatgagctc actttaattg acttctattt gtgcttttta     60
gcctttctgc tattccttgt tttaataatg cttattatat tttggttttc actcgaaatc    120
caggatctag aagaaccttg taccaaagtc taaacgaaca tgaaacttct cattgttttg    180
acttgtattt ctctatgcag ttgcatatgc actgtagtac agcgctgtgc atctaataaa    240
cctcatgtgc ttgaagatcc ttgtaaggta caacactagg ggtaatactt atagcactgc    300
ttggctttgt gctctaggaa aggttttacc ttttcataga tggcacacta tggttcaaac    360
atgcacacct aatgttacta tcaactgtca agatccagct ggtggtgcgc ttatagctag    420
gtgttggtac cttcatgaag gtcaccaaac tgctgcattt agagacgtac ttgttgtttt    480
aaataaacga acaaattaaa atgtctgata atggac                              516
```

<210> SEQ ID NO 153
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 153

```
ccaaggttta cccaataata ctgcgtcttg gttcacagct ctcactcagc atggcaagga     60
ggaacttaga ttccctcgag gccagggcgt tccaatcaac accaatagtg gtccagatga    120
ccaaattggc tactaccgaa gagctacccg acgagttcgt ggtggtgacg gcaaaatgaa    180
agagctcagc cccagatggt acttctatta cctaggaact ggcccagaag cttcacttcc    240
ctacggcgct aacaaagaag gcatcgtatg ggttgcaact gagggagcct tgaatacacc    300
caaagaccac attggcaccc gcaatcctaa taacaatgct gccaccgtgc tacaacttcc    360
tcaaggaaca acattgccaa aaggcttcta cgcagaggga agcagaggcg gcagtcaagc    420
ctcttctcgc tcctcatcac gtagtcgcgg t                                   451
```

<210> SEQ ID NO 154
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 154

```
gatgaagctc agcctttgcc gcagagacaa aagaagcagc ccactgtgac tcttcttcct     60
gcggctgaca tggatgattt ctccagacaa cttcaaaatt ccatgagtgg agcttctgct    120
gattcaactc aggcataaac actcatgatg accacacaag gcagatgggc tatgtaaacg    180
```

-continued

```
ttttcgcaat tccgtttacg atacatagtc tactcttgtg cagaatgaat tctcgtaact    240

aaacagcaca agtaggttta gttaacttta atctcacata gcaatcttta atcaatgtgt    300

aacattaggg aggacttgaa agagccacca cattttcatc gaggccacgc ggagtacgat    360

cgagggtaca gtgaataatg ctagggagag ctgcctatat ggaagagccc taatgtgtaa    420

aattaatttt agtagtgcta tccccatgtg attttaatag cttcttagga gaatgacaaa    480

aaaaaaaaaa aaaaa                                                     495


<210> SEQ ID NO 155
<211> LENGTH: 512
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 155

acaaggccaa actgtcacta agaaatctgc tgctgaggca tctaaaaagc ctcgccaaaa     60

acgtactgcc acaaaacagt acaacgtcac tcaagcattt gggagacgtg gtccagaaca    120

aacccaagga aatttcgggg accaagacct aatcagacaa ggaactgatt acaaacattg    180

gccgcaaatt gcacaatttg ctccaagtgc ctctgcattc tttggaatgt cacgcattgg    240

catggaagtc acaccttcgg gaacatggct gacttatcat ggagccatta aattggatga    300

caaagatcca caattcaaag acaacgtcat actgctgaac aagcacattg acgcatacaa    360

aacattccca ccaacagagc ctaaaaagga caaaaagaaa aagactgatg aagctcagcc    420

tttgccgcag agacaaaaga agcagcccac tgtgactctt cttcctgcgg ctgatatgga    480

tgatttctcc agacaacttc aaaattccat ga                                 512


<210> SEQ ID NO 156
<211> LENGTH: 442
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 156

tgtgactctt cttcctgcgg ctgatatgga tgtttctcca gacaacttca aaattccatg     60

agtggagctt ctgctgattc aactcaggca taaacactca tgatgaccac acaaggcaga    120

tgggctatgt aaacgttttc gcaattccgt ttacgataca tagtctactc ttgtgcagaa    180

tgaattctcg taactaaaca gcacaagtag gtttagttaa ctttaatctc acatagcaat    240

ctttaatcaa tgtgtaacat tagggaggac ttgaaagagc caccacattt tcatcgaggc    300

cacgcggagt acgatcgagg gtacagtgaa taatgctagg gagagctgcc tatatggaag    360

agccctaatg tgtaaaatta attttagtag tgctatcccc atgtgatttt aatagcttct    420

taggagaatg acaaaaaaaa aa                                             442


<210> SEQ ID NO 157
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 157

atgaattacc aagtcaatgg ttac                                            24


<210> SEQ ID NO 158
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
```

<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 158

gaagctattc gtcacgttcg 20

<210> SEQ ID NO 159
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 159

ctgtagaaaa tcctagctgg ag 22

<210> SEQ ID NO 160
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 160

cataaccagt cggtacagct a 21

<210> SEQ ID NO 161
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 161

ttatcacccg cgaagaagct 20

<210> SEQ ID NO 162
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 162

ctctagttgc atgacagccc tc 22

<210> SEQ ID NO 163
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 163

tcgtgcgtgg attggctttg atgt 24

<210> SEQ ID NO 164
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 164

gggttgggac tatcctaagt gtga 24

-continued

<210> SEQ ID NO 165
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 165

taacacacaa acaccatcat ca 22

<210> SEQ ID NO 166
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 166

ggttgggact atcctaagtg tga 23

<210> SEQ ID NO 167
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 167

ccatcatcag atagaatcat cata 24

<210> SEQ ID NO 168
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 168

cctctcttgt tcttgctcgc a 21

<210> SEQ ID NO 169
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 169

tatagtgagc cgccacacat g 21

<210> SEQ ID NO 170
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 170

taacacacaa cnccatcatc a 21

<210> SEQ ID NO 171
<211> LENGTH: 21

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 171

ctaacatgct taggataatg g 21

<210> SEQ ID NO 172
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 172

gcctctcttg ttcttgctcg c 21

<210> SEQ ID NO 173
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 173

caggtaagcg taaaactcat c 21

<210> SEQ ID NO 174
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 174

tacacacctc agcgttg 17

<210> SEQ ID NO 175
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 175

cacgaacgtg acgaat 16

<210> SEQ ID NO 176
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 176

gccggagctc tgcagaattc 20

<210> SEQ ID NO 177
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 177

caggaaacag ctatgacttg catcaccact agttgtgcca ccaggtt 47

<210> SEQ ID NO 178
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 178

tgtaaaacga cggccagttg atgggatggg actatcctaa gtgtga 46

<210> SEQ ID NO 179
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 179

gcataggcag tagttgcatc 20

<210> SEQ ID NO 180
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: ATP Binding Domain
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa = A or G
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(5)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa = S or T

<400> SEQUENCE: 180

Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa
1 5

<210> SEQ ID NO 181
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 181

Trp Tyr Val Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met
1 5 10 15

Val Thr Ile Leu Leu Cys Cys
20

<210> SEQ ID NO 182
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 182

Met Asp Leu Phe Met Arg Phe Phe Thr Leu Arg Ser Ile Thr Ala Gln
1 5 10 15

<210> SEQ ID NO 183
<211> LENGTH: 150

```
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 183

Met Arg Cys Trp Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu
1               5                   10                  15

Tyr Asp Ala Asn Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr
            20                  25                  30

Cys Ile Pro Tyr Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly
        35                  40                  45

Asp Gly Ile Ser Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly
    50                  55                  60

Tyr Ser Glu Asp Arg His Ser Gly Val Lys Asp Tyr Val Val Val His
65                  70                  75                  80

Gly Tyr Phe Thr Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr
                85                  90                  95

Thr Asp Thr Gly Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu
            100                 105                 110

Val Lys Asp Pro Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser
        115                 120                 125

Gly Val Ala Asn Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr
    130                 135                 140

Thr Thr Ser Val Pro Leu
145                 150


<210> SEQ ID NO 184
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 184

Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
1               5                   10                  15

Val Tyr His Ile
            20


<210> SEQ ID NO 185
<211> LENGTH: 42
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 185

Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn Val Ser
1               5                   10                  15

Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn Leu Asn
            20                  25                  30

Ser Ser Glu Gly Val Pro Asp Leu Leu Val
        35                  40


<210> SEQ ID NO 186
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 186

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

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
            20                  25                  30
```

-continued

Leu Leu Gln Phe Ala Tyr Ser
        35

<210> SEQ ID NO 187
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 187

Pro Leu Arg Gly Thr Ile Val Thr Arg Pro Leu Met Glu Ser Glu Leu
1   5   10   15

Val Ile Gly Ala Val Ile Ile Arg Gly His Leu Arg Met Ala Gly His
            20   25   30

Ser Leu Gly Arg Cys Asp Ile Lys Asp Leu Pro Lys Glu Ile Thr Val
        35   40   45

Ala Thr Ser Arg Thr Leu Ser Tyr Tyr Lys Leu Gly Ala Ser Gln Arg
    50   55   60

Val Gly Thr Asp Ser Gly Phe Ala Ala Tyr Asn Arg Tyr Arg Ile Gly
65   70   75   80

Asn Tyr Lys Leu Asn Thr Asp His Ala Gly Ser Asn Asp Asn Ile Ala
                85   90   95

Leu Leu Val Gln
            100

<210> SEQ ID NO 188
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 188

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

Leu Ile Ile Phe Trp Phe Ser
            20

<210> SEQ ID NO 189
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 189

Leu Leu Ile Val Leu Thr Cys Ile Ser Leu Cys Ser Cys Ile Cys Thr
1   5   10   15

Val Val Gln

<210> SEQ ID NO 190
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 190

Ile Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val Leu
1   5   10   15

Glu Asp Pro Cys Lys Val Gln His
            20

<210> SEQ ID NO 191
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 191

Cys Ile Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val
1 5 10 15

Leu Glu Asp Pro Cys Lys
20

<210> SEQ ID NO 192
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 192

Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala Val Gly Glu
1 5 10 15

Ile Leu Leu Leu Glu Trp
20

<210> SEQ ID NO 193
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker

<400> SEQUENCE: 193

aattcgcggc cgcgtcgac 19

<210> SEQ ID NO 194
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker

<400> SEQUENCE: 194

gtcgacgcgg ccgcg 15

<210> SEQ ID NO 195
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 195

aattcgcggc cgcgtcgac 19

<210> SEQ ID NO 196
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 196

ggcctcttcg ctattacgc 19

<210> SEQ ID NO 197
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

-continued

<400> SEQUENCE: 197

```
tgcaggtcga ctctagagga t                                               21
```

<210> SEQ ID NO 198
<211> LENGTH: 410
<212> TYPE: PRT
<213> ORGANISM: Avian infectious bronchitis virus

<400> SEQUENCE: 198

```
Met Ala Ser Gly Lys Ala Ala Gly Lys Thr Asp Ala Pro Ala Pro Val
1               5                   10                  15

Ile Lys Leu Gly Gly Pro Lys Pro Pro Lys Val Gly Ser Ser Gly Asn
            20                  25                  30

Ala Ser Trp Phe Gln Ala Ile Lys Ala Lys Lys Leu Asn Thr Pro Pro
        35                  40                  45

Pro Lys Phe Glu Gly Ser Gly Val Pro Asp Asn Glu Asn Ile Lys Pro
    50                  55                  60

Ser Gln Gln His Gly Tyr Trp Arg Arg Gln Ala Arg Phe Lys Pro Gly
65                  70                  75                  80

Lys Gly Gly Arg Lys Pro Val Pro Asp Ala Trp Tyr Phe Tyr Tyr Thr
                85                  90                  95

Gly Thr Gly Pro Ala Ala Asp Leu Asn Trp Gly Asp Thr Gln Asp Gly
            100                 105                 110

Ile Val Trp Val Ala Ala Lys Gly Ala Asp Thr Lys Ser Arg Ser Asn
        115                 120                 125

Gln Gly Thr Arg Asp Pro Asp Lys Phe Asp Gln Tyr Pro Leu Arg Phe
    130                 135                 140

Ser Asp Gly Gly Pro Asp Gly Asn Phe Arg Trp Asp Phe Ile Pro Leu
145                 150                 155                 160

Lys Asn Arg Gly Arg Ser Gly Arg Ser Thr Ala Ala Ser Ser Ala Ala
                165                 170                 175

Ala Ser Arg Ala Pro Ser Arg Glu Gly Ser Arg Gly Arg Arg Ser Asp
            180                 185                 190

Ser Gly Asp Asp Leu Ile Ala Arg Ala Ala Lys Ile Ile Gln Asp Gln
        195                 200                 205

Gln Lys Lys Gly Ser Arg Ile Thr Lys Ala Lys Ala Asp Glu Met Ala
    210                 215                 220

His Arg Arg Tyr Cys Lys Arg Thr Ile Pro Pro Asn Tyr Arg Val Asp
225                 230                 235                 240

Gln Val Phe Gly Pro Arg Thr Lys Gly Lys Glu Gly Asn Phe Gly Asp
                245                 250                 255

Asp Lys Met Asn Glu Glu Gly Ile Lys Asp Gly Arg Val Thr Ala Met
            260                 265                 270

Leu Asn Leu Val Pro Ser Ser His Ala Cys Leu Phe Gly Ser Arg Val
        275                 280                 285

Thr Pro Lys Leu Gln Leu Asp Gly Leu His Leu Arg Phe Glu Phe Thr
    290                 295                 300

Thr Val Val Pro Cys Asp Asp Pro Gln Phe Asp Asn Tyr Val Lys Ile
305                 310                 315                 320

Cys Asp Gln Cys Val Asp Gly Val Gly Thr Arg Pro Lys Asp Asp Glu
                325                 330                 335

Pro Lys Pro Lys Ser Arg Ser Ser Ser Arg Pro Ala Thr Arg Gly Asn
            340                 345                 350

Ser Pro Ala Pro Arg Gln Gln Arg Pro Lys Lys Glu Lys Lys Leu Lys
```

-continued

355 360 365

Lys Gln Asp Asp Glu Ala Asp Lys Ala Leu Thr Ser Asp Glu Glu Arg
370 375 380

Asn Asn Ala Gln Leu Glu Phe Tyr Asp Glu Pro Lys Val Ile Asn Trp
385 390 395 400

Gly Asp Ala Ala Leu Gly Glu Asn Glu Leu
405 410

<210> SEQ ID NO 199
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: conotoxin

<400> SEQUENCE: 199

Cys Ile Ala Val Gly Gln Leu Cys Val Phe Trp Asn Ile Gly Arg Pro
1 5 10 15

Cys Cys Ser Gly Leu Cys Val Phe Ala Cys Thr Val Lys Leu
20 25 30

<210> SEQ ID NO 200
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 200

Cys Ile Ser Leu Cys Ser Cys Ile Cys Thr Val Val Gln Arg Cys Ala
1 5 10 15

Ser Asn Lys Pro His Val Leu Glu Asp Pro Cys Lys Val Gln His
20 25 30

<210> SEQ ID NO 201
<211> LENGTH: 310
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 201

cgatgtttca tcttgttgac ttccaggtta caatagcaga gatattgatt atcattatga 60

ggactttcag gattgctatt tggaatcttg acgttataat aagttcaata gtgagacaat 120

tatttaagcc tctaactaag aagaattatt cggagttaga tgatgaagaa cctatggagt 180

tagattatcc ataaaacgaa catgaaaatt attctcttcc tgacattgat tgtatttaca 240

tcttgcgagc tatatcacta tcaggagtgt gttagaggta cgactgtact actaaaagaa 300

ccttgcccat 310

<210> SEQ ID NO 202
<211> LENGTH: 556
<212> TYPE: DNA
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 202

agaaagacag aatgaatgag ctcactttaa ttgacttcta tttgtgcttt ttagcctttc 60

tgctattcct tgttttaata atgcttatta tattttggtt ttcactcgaa atccaggatc 120

tagaagaacc ttgtaccaaa gtctaaacga acatgaaact tctcattgtt ttgacttgta 180

tttctctatg cagttgcata tgcactgtag tacagcgctg tgcatctaat aaacctcatg 240

tgcttgaaga tccttgtaag gtacaacact aggggtaata cttatagcac tgcttggctt 300

tgtgctctag gaaaggtttt accttttcat agatggcaca ctatggttca aacatgcaca 360

-continued

```
cctaatgtta ctatcaactg tcaagatcca gctggtggtg cgcttatagc taggtgttgg    420

taccttcatg aaggtcacca aactgctgca tttagagacg tacttgttgt tttaaataaa    480

cgaacaaatt aaaatgtctg ataatggacc ccaatcaaac caacgtagtg ccccccgcat    540

tacatttggt ggaccc                                                    556


<210> SEQ ID NO 203
<211> LENGTH: 1255
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 203

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1               5                   10                  15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
            20                  25                  30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
        35                  40                  45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
    50                  55                  60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65                  70                  75                  80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
                85                  90                  95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
            100                 105                 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
        115                 120                 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
    130                 135                 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145                 150                 155                 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
                165                 170                 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
            180                 185                 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
        195                 200                 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
    210                 215                 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225                 230                 235                 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
                245                 250                 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
            260                 265                 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
        275                 280                 285

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

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305                 310                 315                 320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
                325                 330                 335
```

-continued

```
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
            340                 345                 350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
        355                 360                 365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
    370                 375                 380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385                 390                 395                 400

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
                405                 410                 415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
            420                 425                 430

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
        435                 440                 445

Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
    450                 455                 460

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465                 470                 475                 480

Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
                485                 490                 495

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
            500                 505                 510

Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
        515                 520                 525

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
    530                 535                 540

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545                 550                 555                 560

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
                565                 570                 575

Ala Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
            580                 585                 590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
        595                 600                 605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
    610                 615                 620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625                 630                 635                 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
                645                 650                 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
            660                 665                 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
        675                 680                 685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
    690                 695                 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705                 710                 715                 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
                725                 730                 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740                 745                 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
```

-continued

```
        755                 760                 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
    770                 775                 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785                 790                 795                 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
                805                 810                 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
            820                 825                 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
        835                 840                 845

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
    850                 855                 860

Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865                 870                 875                 880

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
                885                 890                 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
            900                 905                 910

Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
        915                 920                 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
    930                 935                 940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945                 950                 955                 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
                965                 970                 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
            980                 985                 990

Gln Leu Ile Arg Ala Ala Glu Ile  Arg Ala Ser Ala Asn  Leu Ala Ala
        995                 1000                1005

Thr Lys  Met Ser Glu Cys Val  Leu Gly Gln Ser Lys  Arg Val Asp
    1010                1015                1020

Phe Cys  Gly Lys Gly Tyr His  Leu Met Ser Phe Pro  Gln Ala Ala
    1025                1030                1035

Pro His  Gly Val Val Phe Leu  His Val Thr Tyr Val  Pro Ser Gln
    1040                1045                1050

Glu Arg  Asn Phe Thr Thr Ala  Pro Ala Ile Cys His  Glu Gly Lys
    1055                1060                1065

Ala Tyr  Phe Pro Arg Glu Gly  Val Phe Val Phe Asn  Gly Thr Ser
    1070                1075                1080

Trp Phe  Ile Thr Gln Arg Asn  Phe Phe Ser Pro Gln  Ile Ile Thr
    1085                1090                1095

Thr Asp  Asn Thr Phe Val Ser  Gly Asn Cys Asp Val  Val Ile Gly
    1100                1105                1110

Ile Ile  Asn Asn Thr Val Tyr  Asp Pro Leu Gln Pro  Glu Leu Asp
    1115                1120                1125

Ser Phe  Lys Glu Glu Leu Asp  Lys Tyr Phe Lys Asn  His Thr Ser
    1130                1135                1140

Pro Asp  Val Asp Leu Gly Asp  Ile Ser Gly Ile Asn  Ala Ser Val
    1145                1150                1155

Val Asn  Ile Gln Lys Glu Ile  Asp Arg Leu Asn Glu  Val Ala Lys
    1160                1165                1170
```

```
Asn Leu  Asn Glu Ser Leu Ile  Asp Leu Gln Glu Leu  Gly Lys Tyr
    1175                1180                1185

Glu Gln  Tyr Ile Lys Trp Pro  Trp Tyr Val Trp Leu  Gly Phe Ile
    1190                1195                1200

Ala Gly  Leu Ile Ala Ile Val  Met Val Thr Ile Leu  Leu Cys Cys
    1205                1210                1215

Met Thr  Ser Cys Cys Ser Cys  Leu Lys Gly Ala Cys  Ser Cys Gly
    1220                1225                1230

Ser Cys  Cys Lys Phe Asp Glu  Asp Asp Ser Glu Pro  Val Leu Lys
    1235                1240                1245

Gly Val  Lys Leu His Tyr Thr
    1250                1255


<210> SEQ ID NO 204
<211> LENGTH: 422
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 204

Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
1               5                   10                  15

Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
            20                  25                  30

Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
        35                  40                  45

Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
    50                  55                  60

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65                  70                  75                  80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
                85                  90                  95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
            100                 105                 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
        115                 120                 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
    130                 135                 140

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

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
                165                 170                 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
            180                 185                 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
        195                 200                 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
    210                 215                 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
225                 230                 235                 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
                245                 250                 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
            260                 265                 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
```

-continued

```
        275                 280                 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
    290                 295                 300

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

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
                325                 330                 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
            340                 345                 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
        355                 360                 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
    370                 375                 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
385                 390                 395                 400

Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
                405                 410                 415

Ala Asp Ser Thr Gln Ala
            420


<210> SEQ ID NO 205
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: Sars associated coronavirus

<400> SEQUENCE: 205

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

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
            20                  25                  30

Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
        35                  40                  45

Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
    50                  55                  60

Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
65                  70                  75                  80

Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
                85                  90                  95

Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
            100                 105                 110

Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
        115                 120                 125

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

Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
145                 150                 155                 160

Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
                165                 170                 175

Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
            180                 185                 190

Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
        195                 200                 205

His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val Gln
    210                 215                 220
```

-continued

```
<210> SEQ ID NO 206
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Severe acute respiratory syndrome virus

<400> SEQUENCE: 206

Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
1               5                   10                  15

Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
            20                  25                  30

Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
        35                  40                  45

Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
    50                  55                  60

Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
65                  70                  75
```

What is claimed is:

1. An isolated SARS virus nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 2 and 15.

2. The molecule of claim **1**, wherein said molecule is selected from the group consisting of genomic RNA, DNA, cDNA, synthetic DNA and mRNA.

3. The molecule of claim **1**, wherein said molecule comprises a s2m motif.

4. The molecule of claim **1**, wherein said molecule comprises a leader sequence.

5. The molecule of claim **1**, wherein said molecule comprises a transcriptional regulatory sequence.

6. The molecule of claim **1**, wherein said molecule encodes a polyprotein.

7. The molecule of claim **1**, wherein said molecule encodes a polypeptide.

8. A vector comprising the nucleic acid molecule of claim **1**.

9. An isolated host cell comprising the vector of claim **8**.

10. The host cell of claim **9**, wherein said cell is selected from the group consisting of a mammalian cell, a yeast, a bacterium, and a nematode cell.

11. An isolated nucleic acid molecule comprising a sequence complementary to the entire sequence of SEQ ID NOs: 1, 2 or 15.

12. A kit for detecting the presence of a SARS virus in a sample, wherein said kit comprises the isolated SARS virus nucleic acid molecule of claim **1** or **11**.

13. A microarray comprising a plurality of elements, wherein the microarray comprises the nucleic acid of claim **1** or **11**.

14. A composition comprising the nucleic acid of claim **1** or **11**.

* * * * *