

(19) 日本国特許庁(JP)

(12) 特 許 公 報(B2)

(11) 特許番号

特許第3757318号

(P3757318)

(45) 発行日 平成18年3月22日(2006.3.22)

(24) 登録日 平成18年1月13日(2006.1.13)

(51) Int. Cl.	F I	
C 1 2 N 15/09 (2006.01)	C 1 2 N 15/00	Z N A A
C O 7 K 14/11 (2006.01)	C O 7 K 14/11	
C O 7 K 19/00 (2006.01)	C O 7 K 19/00	
C 1 2 P 21/02 (2006.01)	C 1 2 P 21/02	C
C 1 2 N 5/10 (2006.01)	C 1 2 N 5/00	B
請求項の数 15 (全 34 頁)		

(21) 出願番号	特願平8-535617	(73) 特許権者	プロテイン サイエンス
(86) (22) 出願日	平成7年5月26日(1995.5.26)		アメリカ合衆国 コネティカット州 O 6
(65) 公表番号	特表2000-513922 (P2000-513922A)		4 5 0-7 1 5 9 メリディアン リサー
(43) 公表日	平成12年10月24日(2000.10.24)		チ パークウェイ 1 0 0 0
(86) 国際出願番号	PCT/US1995/006750	(74) 代理人	弁理士 柳田 征史
(87) 国際公開番号	W01996/037624	(74) 代理人	弁理士 佐久間 剛
(87) 国際公開日	平成8年11月28日(1996.11.28)	(72) 発明者	スミス, ゲイル ユージーン
審査請求日	平成14年5月27日(2002.5.27)		アメリカ合衆国 コネティカット州 O 6
			4 5 5 ミドルフィールド ハーヴェスト
			ウッド ロード 3 6
			最終頁に続く

(54) 【発明の名称】 インフルエンザ血球凝集素多価ワクチンの製造方法

(57) 【特許請求の範囲】

【請求項 1】

配列番号 7、9、13、15、17、または 21 記載の配列より成る群から選択されるポリペプチド。

【請求項 2】

配列番号 6、8、12、14、16、または 20 記載の配列より成る群から選択される核酸。

【請求項 3】

ポリヘドリンプロモーター、配列番号 6 または 8 のヌクレオチド 19-72 の配列を有するバキュロウイルス 61 K 遺伝子由来のシグナルペプチド配列、および前記シグナル配列に続く成熟血球凝集素タンパク質の完全コード配列を含んでなるバキュロウイルス組換えベクター。

【請求項 4】

配列番号 6、8、12、14、16、または 20 記載の配列より成る群から選択される配列を含んでなる、請求項 3 記載のベクター。

【請求項 5】

組換えインフルエンザ血球凝集素タンパク質を生産する方法であって、請求項 3 記載のベクターを昆虫細胞に感染させる工程を含んでなる方法。

【請求項 6】

異種アミノ酸配列に作動可能に結合した、配列番号 7 または 9 の配列のアミノ酸位置 1 -

18のアミノ酸を有するバキュロウイルスシグナルペプチドを含んでなるポリペプチド。

【請求項7】

請求項6記載のポリペプチドをコードする単離核酸。

【請求項8】

請求項7記載の核酸を含んでなるベクター。

【請求項9】

バキュロウイルス発現系におけるベクターとして請求項8記載のベクターを用いることを含んでなる、外来タンパク質を発現させる方法。

【請求項10】

異種コード配列に作動可能に結合した、バキュロウイルスシグナルペプチドをコードする配列番号6または8の配列のヌクレオチド19-72のヌクレオチド配列を含んでなる単離核酸。

10

【請求項11】

請求項10記載の核酸を含んでなるベクター。

【請求項12】

バキュロウイルス発現系におけるベクターとして請求項11記載のベクターを用いる工程を含む、外来タンパク質を発現させる方法。

【請求項13】

前記異種コード配列が、インフルエンザ赤血球凝集素コード配列であることを特徴とする請求項8または11記載のベクター。

20

【請求項14】

請求項8または11記載のベクターでトランスフェクトまたは感染させた昆虫細胞。

【請求項15】

請求項13記載のベクターでトランスフェクトまたは感染させた昆虫細胞。

【発明の詳細な説明】

発明の背景

本発明は一般に組換えインフルエンザワクチンの領域にある。

卵中での繁殖を要求しないインフルエンザワクチンの製造方法は、好ましくない免疫反応を引き起こす恐れが少ないであろうより純粋な製品という結果となる。さらに、より純粋なワクチン繁殖は、ウイルスの不活性化またはウイルス膜成分の有機的抽出を要求しないであろうから、それにより、抗原性エピトープの変性およびワクチン中の残存化合物による安全性の懸念を回避するものである。

30

付加的には、卵繁殖なしで生産されたインフルエンザワクチンは、卵を通しての適応および継代の間に生じる遺伝的非相同性を回避するであろう。これにより、インフルエンザ感染病株により適合したワクチンという結果となり、改善された効率となるであろう。

従って、卵中での複製を必要としないインフルエンザワクチンの製造方法を提供することが本発明の目的である。

迅速で、経費効率が良く、高度に精製された、インフルエンザの1次給源からのワクチン製造を可能とするインフルエンザワクチンの製造方法を提供することが本発明のさらなる目的である。

40

発明の概要

組換えインフルエンザ血球凝集素タンパク質の、バキュロウイルス発現系を用いた昆虫細胞中での発現による調整方法が提供されている。得られたタンパク質は多価インフルエンザは、伝染病の可能性のあるインフルエンザウイルスからクローン化された組換え血球凝集素抗原の混合物に基づくインフルエンザワクチンである。組換え血球凝集素抗原は、全長で、HA1およびHA2の両方のサブユニット(HA0)を有する、非変性条件下で95%より高い純度、好ましくは99%の純度まで精製された分解されていない(HA0)糖タンパク質である。

【図面の簡単な説明】

図1はインフルエンザA株由来のHA遺伝子のウイルスRNA調製物からのクローニング

50

、発現された r H A の精製、および r H A の生物学的な活性を示す図である。

略語：F D A、食品薬品局；M D C K、マディン ダービー (M a d i n D a r b y) イヌ腎臓；T P C K、トシルフェニルアラニルクロロメチルケトン；R N A、リボ核酸；H A、血球凝集素；F B S、胎児ウシ血清；P C R複製連鎖反応；B V、バキュロウイルス。

図 2 は、インフルエンザ A / テキサス / 3 6 / 9 1 株の H A 遺伝子のクローニングおよび発現に応用された図 1 の方法のより詳細な図である。インフルエンザ H A 遺伝子は、インフルエンザ A / テキサス / 3 6 / 9 1 株に感染した M D C K 細胞から精製された R N A より、逆転写酵素およびユニバーサルプライマー (配列番号 1) を用いて、続いて 2 ラウンドの P C R 増幅およびクローニングにより得られた。示されているように、第 1 のラウンドの P C R 反応においては、5 ' 末端プライマー配列番号 2 および 3 ' 末端プライマー配列番号 3 が用いられた。第 2 ラウンドの P C R 反応においては、5 ' 末端プライマー配列番号 4 および 3 ' 末端プライマー配列番号 5 が用いられた。バキュロウイルス組換えベクターはポリヘドリン (p o l y h e d r i n) プロモーター、および成熟 H A タンパク質の完全コード配列が続いているバキュロウイルス 6 1 K 遺伝子 (約 6 1 0 0 0 の分子量を有するシグナルペプチドをコードしているバキュロウイルス遺伝子) 由来のシグナルペプチド配列を含んで構築された。この組合せのベクターは、続いてこのウイルス株から H A を生産するバキュロウイルス発現ベクターを作成するために用いられた、

図 3 は、4 2 日、n = 5 のマウスにおける抗 H A 免疫反応のグラフであり、r H A 0 - ニート (n e a t) ; F l u z o n e (登録商標) ワクチンおよび r H A - アルム (a l u m) についての抗体価を、投与量 0 . 5 μ g (黒いバー)、0 . 1 μ g (影付きバー)、0 . 0 2 μ g (水玉バー)、0 . 0 0 4 μ g (白いバー) で図示している。

図 4 a、4 b、4 c は、r H A または許可された 3 個ワクチンで免疫化されたネズミにおける抗 H A 免疫反応、1 9 9 4 - 1 9 9 5 規格、ワクチン化以降の週を H I A 力価に対し、H A I A / テキサス / 3 6 / 9 1 (図 4 a)、H A I A / シャンドン (S h a n g d o n g) / 9 / 9 3 (図 4 b)、H A I B / パナマ / 4 5 / 9 0 (図 4 c)、r H A (菱形) および卵中で培養された弱毒化ワクチン F L U V I R O N (登録商標) (正方形) に関して図示している。

発明の詳細な説明

組換えインフルエンザワクチンの調製方法が記載されている。インフルエンザウイルス由来の、全長の、分解されていない (H A 0) 血球凝集素抗原がバキュロウイルス発現系により昆虫細胞中で生産され、非変性条件下で精製された。インフルエンザ A および / またはインフルエンザ B 株由来の 2 またはより多くの精製された血球凝集素と一緒に混合され、多価インフルエンザワクチンを形成した。組換え抗原は、効率を増加させるためにアジュバント担体と組み合わされても良い。

配列番号 6 は、バキュロウイルス 6 1 K シグナルペプチドをコードするポリヌクレオチド配列に結合した A / 北京 / 3 2 / 9 2 の H A をコードするポリヌクレオチド配列を含む核酸配列である。配列番号 7 は対応するアミノ酸配列であり、バキュロウイルス 6 1 K シグナルペプチド (アミノ酸 1 - 1 8) に結合した H A のアミノ酸配列を示す。

配列番号 8 は、バキュロウイルス 6 1 K シグナルペプチドをコードするポリヌクレオチド配列に結合した A / テキサス / 3 6 / 9 1 の H A をコードするポリヌクレオチド配列を含む核酸配列である。配列番号 9 は対応するアミノ酸配列であり、バキュロウイルス 6 1 K シグナルペプチド (アミノ酸 1 - 1 8) に結合した H A のアミノ酸配列を示す。

配列番号 1 0 は、B / パナマ / 4 5 / 9 0 の H A をコードするポリヌクレオチド配列を含む核酸配列である。配列番号 1 1 は対応するアミノ酸配列である。

配列番号 1 2 は、バキュロウイルス 6 1 K シグナルペプチドをコードするポリヌクレオチド配列に結合した B / オランダ / 1 3 / 9 4 の H A をコードするポリヌクレオチド配列を含む核酸配列である。配列番号 1 3 は対応するアミノ酸配列であり、バキュロウイルス 6 1 K シグナルペプチド (アミノ酸 1 - 1 8) に結合した H A のアミノ酸配列を示す。

配列番号 1 4 は、バキュロウイルス 6 1 K シグナルペプチドをコードするポリヌクレオチ

10

20

30

40

50

ド配列に結合したA／山東／9／93のHAをコードするポリヌクレオチド配列を含む核酸配列である。配列番号15は対応するアミノ酸配列であり、バキュロウィルス61Kシグナルペプチド（アミノ酸1－18）に結合したHAのアミノ酸配列を示す。

配列番号16は、バキュロウィルス61Kシグナルペプチドをコードするポリヌクレオチド配列に結合したB／上海／4／94のHAをコードするポリヌクレオチド配列を含む核酸配列である。配列番号17は対応するアミノ酸配列であり、バキュロウィルス61Kシグナルペプチド（アミノ酸1－18）に結合したHAのアミノ酸配列を示す。

配列番号18は、B／ハルビン／7／94のHAをコードするポリヌクレオチド配列を含む核酸配列である。配列番号19は対応するアミノ酸配列である。

配列番号20は、バキュロウィルス61Kシグナルペプチドをコードするポリヌクレオチド配列に結合したA／ヨハネスブルグ／33／94HAをコードするポリヌクレオチド配列を含む核酸配列である。配列番号18は対応するアミノ酸配列であり、バキュロウィルス61Kシグナルペプチド（アミノ酸1－18）に結合したHAのアミノ酸配列を示す。

10

実施例1

インフルエンザウイルスの繁殖と精製

以下のインフルエンザワクチン株が、FDAから鶏卵尿液中に得られた：

A／北京／353／89様（H3N2）

A／北京／32／92様（H3N2）

A／テキサス／36／91様（H1N1）

B／パナマ／45／90

20

実施例2

インフルエンザA／テキサス／36／91 HA遺伝子のクローニング

インフルエンザHA遺伝子の1つのためのクローニングの手順の特別な例が図2に示されている。

実施例3

細菌プラスミドへのHA遺伝子のクローニング

PCR増幅されたrHA遺伝子はpUC様プラスミドベクター中にTAクローニングシステム（Invitrogen、Inc.）を用いてクローン化された。

実施例4

組換えHA遺伝子の昆虫細胞中での発現

クローン化されたHA遺伝子を含むキメラ組換えプラスミドは精製され、2μgを、1μgのAcNPV野生型DNAと混合した。

30

実施例5

組換えHAの生産および精製

インフルエンザA／北京／353／89の遺伝子を含むバキュロウィルス発現ベクター、A8611が、A／北京／32／92血液凝集素をポリヘドリンプロモーターについて上に記載されたものと実質的に同様に作られ、S. frugiperda細胞を感染させるために用いられた。

実施例6

rHAプロテアーゼ抵抗性の分析

成熟HAは、HAモノマーを分解するトリプシンを含む酵素に対して抵抗性である3次構造に集合する（Murphy and Webster、1990）。

40

実施例7

標準化されたマウス効力アッセイを用いたrHAの免疫原性

ある抗原の免疫原性を測定するための方法の1つに、マウス中において検出可能な抗体反応を誘導するために必要な量を決定することがある（マウス効力アッセイ）。

実施例8

アジュバントと組合せたrHAの投与および入手可能なインフルエンザワクチンとの比較
インフルエンザA／北京／353／89由来の精製されたrHAのマウス効力がアルムとともに、またはアルム無し（ニート）で試験され、市販のインフルエンザワクチンで、イ

50

ンフルエンザ A／北京／353／89 を含んでいる Fluzone (登録商標) (Connaught Laboratories, Inc. Swiftwater, PA) と比較した。

実施例 9

血液凝集素阻害の研究

血液凝集素阻害 (HAI) 抗体は、4つの公知の抗体のうちの3つに結合し、インフルエンザの赤血球を凝集する能力を妨害する (Wilson et al., "Structure of the hemagglutinin membrane glycoprotein of influenza virus at 3 Å resolution" Nature, 289:366-378 (1981))。

10

実施例 10

1993／1994 インフルエンザワクチンの系統的記述および診療効率

一連のヒト診療の試みが、組換え HA を含む実験インフルエンザワクチンのヒト中での安全性および免疫原性を特徴づけるために、および、そのようなワクチンの伝染病の季節の間の天然感染に対しての防御効率についての予備的データを得るために行った。

実施例 11

改善された HA0 クローニングベクターを作成するための方法

成熟 HA の発現のための改善されたクローニングベクターであって、HA をコードしている遺伝子はキチナーゼシグナルペプチドの配列をコードしている配列の直後に位置されているものが設計された。

20

実施例 12

1995-1996 インフルエンザウイルスワクチン A および B 3 価型の調製および効率
インフルエンザウイルスワクチン、精製された組換え血球凝集素、3 価、A および B 型 (A／テキサス／36／92／1 (H1N1)、A／ヨハネスブルグ／33／94 (H3N2) および B／ハービン／7／94) は、精製された、組換えインフルエンザ血球凝集素抗原 (HA) から派生された非感染性サブユニットである。

配列表

(1) GENERAL INFORMATION:

- (i) APPLICANT: MicroGeneSys, Inc.
- (ii) TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
HEMAGGLUTININ MULTIVALENT VACCINES
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Patrea L. Pabst
 - (B) STREET: 2800 One Atlantic Center
1201 West Peachtree Street
 - (C) CITY: Atlanta
 - (D) STATE: GA
 - (E) COUNTRY: USA
 - (F) ZIP: 30309-3450
- (v) COMPUTER READABLE FORM: 10
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US95/06750
 - (B) FILING DATE: 26-MAY-1995
 - (C) CLASSIFICATION:
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (404)-873-8794
 - (B) TELEFAX: (404)-873-8795

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS: 20
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Davis, et al.
 - (B) TITLE: Construction and Characterization of a
Bacterial Clone Containing the Hemagglutinin Gene
of the WSN Strain (HON1) of Influenza Virus
 - (C) JOURNAL: Gene
 - (D) VOLUME: 10 30
 - (F) PAGES: 205-218
 - (G) DATE: 1980
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAAAAGCA GG 12

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: 40

GGGGGTACCC CCGGGAGCAA AAGCAGGGGA AAATAAAAA 39

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGGTACCT CAKATKCATA TTCTGCACTG CAAAG

35

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10

GGGGGTACCC CCGGGGACAC AATATGTATA GGCTACCAT

39

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCGGTACCT CAKATKCATA TTCTGCACTG CAAAG

35

20

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1793 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
 - (ix) FEATURE
 - (A) NAME/KEY: polyhedrin mRNA leader (partial)
 - (B) LOCATION: 1 to 18
 - (ix) FEATURE
 - (A) NAME/KEY: coding region for AcNPV 61K protein signal sequence
 - (B) LOCATION: 19 to 72
 - (ix) FEATURE
 - (A) NAME/KEY: SmaI restriction site
 - (B) LOCATION: 76 to 81
 - (ix) FEATURE
 - (A) NAME/KEY: coding region for mature rHA
 - (B) LOCATION: 73 to 1728
 - (ix) FEATURE
 - (A) NAME/KEY: KpnI restriction site
 - (B) LOCATION: 1771 to 1777
 - (ix) FEATURE
 - (A) NAME/KEY: BglIII restriction site
 - (B) LOCATION: 1776 to 1782
 - (ix) FEATURE
 - (A) NAME/KEY: universal translation termination signal
 - (B) LOCATION: 1783 to 1793
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

30

40

TAAAAAACC TATAAATAAT GCCCTTGTAC AAATTGTTAA ACGTTTTGTG GTTGGTCGCC

60

GTTTCTAACG CGATTCCCGG GGACTTTCCA GGAAATGACA ACAGCACAGC AACGCTGTGC

120

CTGGGACATC ATGCAGTGCC AAACGGAACG CTAGTGAAAA CAATCACGAA TGATCAAATT	180
GAAGTGAATA ATGCTACTGA GCTGGTTCAG AGTTCCTCAA CAGGTAGAAT ATGCGACAGT	240
CCTCACCGAA TCCTTGATGG AAAAACTGC AACTTGATAG ATGCTCTATT GGGAGACCCT	300
CATTGTGATG GCTTCCAAAA TAAGGAATGG GACCTTTTTG TTGAACGCAG CAAAGCTTAC	360
AGCAACTGTT ACCCTTATGA TGTACCGGAT TATGCCTCCC TTAGGTCACT AGTTGCCTCA	420
TCAGGCACCC TGGAGTTTAT CAATGAAGAC TTCAATTGGA CTGGAGTCGC TCAGGATGGG	480
GGAAGCTATG CTTGCAAAAAG GGGATCTGTT AACAGTTTCT TTAGTAGATT GAATTGGTTG	540
CACAAATCAG AATACAAATA TCCAGCGCTG AACGTGACTA TGCCAAACAA TGGCAAATTT	600
GACAAATTGT ACATTTGGGG GGTTCACCAC CCGAGCACGG ACAGAGACCA AACCAGCCTA	660
TATGTTTCGAG CATCAGGGAG AGTCACAGTC TCTACCAAAA GAAGCCAACA AACTGTAACC	720
CCGAATATCG GGTCTAGACC CTGGGTAAGG GGTCACTCCA GTAGAATAAG CATCTATTGG	780
ACAATAGTAA AACCGGGAGA CATACTTTTG ATTAATAGCA CAGGGAATCT AATTGCTCCT	840
CGGGGTACT TCAAAATACG AAATGGGAAA AGCTCAATAA TGAGGTCAGA TGCACCCATT	900
GGCACCTGCA GTTCTGAATG CATCACTCCA AATGGAAGCA TTCCCAATGA CAAACCTTTT	960
CAAAATGTAA ACAGGATCAC ATATGGGGCC TGCCCCAGAT ATGTTAAGCA AAACACTCTG	1020
AAATTGGCAA CAGGGATGCG GAATGTACCA GAGAAACAAA CTAGAGGCAT ATTCGGCGCA	1080
ATCGCAGGTT TCATAGAAAA TGGTTGGGAG GGAATGGTAG ACGGTTGGTA CGGTTTCAGG	1140
CATCAAAATT CTGAGGGCAC AGGACAAGCA GCAGATCTTA AAAGCACTCA AGCAGCAATC	1200
GACCAATCA ACGGGAAACT GAATAGGTTA ATCGAGAAAA CGAACGAGAA ATTCCATCAA	1260
ATCGAAAAAG AATTCTCAGA AGTAGAAGGG AGAATTCAGG ACCTCGAGAA ATATGTTGAA	1320
GACACTAAAA TAGATCTCTG GTCTTACAAC GCGGAGCTTC TTGTTGCCCT GGAGAACCAA	1380
CATACAATTG ATCTAACTGA CTCAGAAATG AACAACTGT TTGAAAAAAC AAGGAAGCAA	1440
CTGAGGGAAA ATGCTGAGGA CATGGGCAAT GGTGCTTCA AAATATACCA CAAATGTGAC	1500
AATGCCTGCA TAGGGTCAAT CAGAAATGGA ACTTATGACC ATGATGTATA CAGAGACGAA	1560
GCATTAAACA ACCGGTTCCTA GATCAAAGGT GTTGAGCTGA AGTCAGGATA CAAAGATTGG	1620
ATCCTATGGA TTTCCTTTGC CATATCATGC TTTTGTCTTT GTGTTGTTTT GCTGGGGTTC	1680
ATCATGTGGG CCTGCCAAAA AGGCAACATT AGGTGCAACA TTTGCATTG AGTGTATTAA	1740
TTAAAAACAC CTTGTTTCT AGGATGATTC GGTACCAGAT CTTAATTAAT TAA	1793

10

20

30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: Influenza virus
 (C) INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
 (ix) FEATURE
 (A) NAME/KEY: AcNPV 61K protein signal sequence
 (B) LOCATION: 1 to 18
 (ix) FEATURE
 (A) NAME/KEY: mature rHA
 (B) LOCATION: 19 to 552
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1      5      10      15
Asn Ala Ile Pro Gly Asp Phe Pro Gly Asn Asp Asn Ser Thr Ala Thr
20      25      30
Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys Thr
35      40      45
Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln
50      55      60
Ser Ser Ser Thr Gly Arg Ile Cys Asp Ser Pro His Arg Ile Leu Asp
65      70      75      80
Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His Cys
85      90      95
Asp Gly Phe Gln Asn Lys Glu Trp Asp Leu Phe Val Glu Arg Ser Lys
100     105     110
Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu
115     120     125
Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe Ile Asn Glu Asp
130     135     140
Phe Asn Trp Thr Gly Val Ala Gln Asp Gly Gly Ser Tyr Ala Cys Lys
145     150     155     160
Arg Gly Ser Val Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu His Lys
165     170     175
Ser Glu Tyr Lys Tyr Pro Ala Leu Asn Val Thr Met Pro Asn Asn Gly
180     185     190
Lys Phe Asp Lys Leu Tyr Ile Trp Gly Val His His Pro Ser Thr Asp
195     200     205
Arg Asp Gln Thr Ser Leu Tyr Val Arg Ala Ser Gly Arg Val Thr Val
210     215     220
Ser Thr Lys Arg Ser Gln Gln Thr Val Thr Pro Asn Ile Gly Ser Arg
225     230     235     240
Pro Trp Val Arg Gly Gln Ser Ser Arg Ile Ser Ile Tyr Trp Thr Ile
245     250     255
Val Lys Pro Gly Asp Ile Leu Leu Ile Asn Ser Thr Gly Asn Leu Ile
260     265     270
Ala Pro Arg Gly Tyr Phe Lys Ile Arg Asn Gly Lys Ser Ser Ile Met
275     280     285
Arg Ser Asp Ala Pro Ile Gly Thr Cys Ser Ser Glu Cys Ile Thr Pro
290     295     300
Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Arg Ile
305     310     315     320
Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn Thr Leu Lys Leu
325     330     335
Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Ile Phe
340     345     350
Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Val Asp
355     360     365
Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln Ala
370     375     380

Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys
385     390     395     400
Leu Asn Arg Leu Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile Glu
405     410     415
Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr
420     425     430
Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu
435     440     445

```

10

20

30

40

```

Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu Met
  450                               455                               460
Asn Lys Leu Phe Glu Lys Thr Arg Lys Gln Leu Arg Glu Asn Ala Glu
  465                               470                               475                               480
Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn Ala
                               485                               490                               495
Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr Arg
                               500                               505                               510
Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu Lys
                               515                               520                               525
Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser Cys
                               530                               535                               540
Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys Gln
  545                               550                               555                               560
Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
                               565                               570

```

10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
- (ix) FEATURE
 - (A) NAME/KEY: polyhedrin mRNA leader (partial)
 - (B) LOCATION: 1 to 18
- (ix) FEATURE
 - (A) NAME/KEY: coding region for AcNPV 61K protein signal peptide
 - (B) LOCATION: 19 to 72
- (ix) FEATURE
 - (A) NAME/KEY: SmaI restriction site
 - (B) LOCATION: 76 to 81
- (ix) FEATURE
 - (A) NAME/KEY: KpnI restriction site
 - (B) LOCATION: 82 to 87
- (ix) FEATURE
 - (A) NAME/KEY: SmaI restriction site
 - (B) LOCATION: 88 to 93
- (ix) FEATURE
 - (A) NAME/KEY: coding region for mature rHA
 - (B) LOCATION: 73 to 1734
- (ix) FEATURE
 - (A) NAME/KEY: KpnI restriction site
 - (B) LOCATION: 1744 to 1749
- (ix) FEATURE
 - (A) NAME/KEY: BglII restriction site
 - (B) LOCATION: 1750 to 1755
- (ix) FEATURE
 - (A) NAME/KEY: universal translation termination signal
 - (B) LOCATION: 1756 to 1766
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20

30

40

```

TAAAAAACC TATAATAAT GCCCTTGAC AAATTGTAA ACGTTTGTG GTTGGTCGCC      60
GTTTCTAACG CGATTCCCGG GGGTACCCCC GGGGACACAA TATGTATAGG CTACCATGCG      120
AACAACTCAA CCGACACTGT TGACACAGTA CTTGAGAAGA ACGTGACAGT GACACACTCT      180
GTCAACCTAC TTGAGGACAG TCACAACGGA AAATATGTC GACTAAAGGG AATAGCCCCA      240

```

CTACAATTGG	GTAATTGCAG	CGTTGCCCGGA	TGGATCTTAG	GAAACCCAAA	ATGCGAATCA	300		
CTGTTTTCTA	AGGAATCATG	GTCCTACATT	GCAGAAACAC	CAAACCCTGA	GAATGGAACA	360		
TGTTACCCAG	GGTATTTTCGC	CGACTATGAG	GAACTGAGGG	AGCAATTGAG	TTCAGTATCA	420		
TCATTTCGAGA	GATTTCGAAAT	ATTCCCCAAA	GAAAGCTCAT	GGCCCAACCA	CACCGTAACC	480		
AAAGGAGTAA	CGAGATCATG	CTCCCATAAT	GGGAAAAGCA	GTTTTTACAG	AAATTTGCTA	540		
TGGCTGACGG	AGAAGAATGG	CTTGTACCCA	AATCTGAGCA	AGTCCTATGT	AAACAACAAA	600		
GAGAAAGAAG	TCCTTGTA	ACT	ATGGGGTGT	T	CATCACCCGT	CTAACATAAG	GGACCAAAGG	660
GCCATCTATC	ATACAGAAAA	TGCTTATGTC	TCTGTAGTGT	CTTCACATTA	TAGCAGAAGA	720		
TTCACCCCAG	AAATAGCAAA	AAGACCCAAA	GTAAGAGATC	AAGAAGGAAG	AATTA	ACTAC	780	
TACTGGACTC	TGCTGGAACC	CGGGGACACA	ATAATATTTG	AGGCAAATGG	AAATCTAATA	840		
GCGCCATGGT	ATGCTTTCGC	ACTGAGTAGA	GGCTTTGGGT	CAGGAATCAT	CACCTCAAAC	900		
GCATCAATGG	ATGAATGTGA	CGCGAAGTGT	CAAACACCCC	AGGGAGCTAT	AAACAGTAGT	960		
CTTCCTTTCC	AGAATGTACA	CCCAGTCACA	ATAGGAGAGT	GTCCAAAGTA	TGTCAGGAGT	1020		
ACAAAATTAA	GGATGGTTAC	AGGACTAAGG	AACATCCCAT	CCATTCAATC	CAGAGGTTTG	1080		
TTTGGAGCCA	TTGCCGTTT	CATTGAAGGG	GGGTGGACTG	GAATGATAGA	TGGATGGTAT	1140		
GGTTATCATC	ATCAGAATGA	ACAAGGATCT	GGCTATGCTG	CGGACCAAAA	AAGCACACAA	1200		
AATGCCATTA	ACGGGATTAC	AAACAAGGTG	AATTCTGTAA	TCGAGAAAAT	GAACACTCAA	1260		
TTCACAGCTG	TGGGCAAAGA	ATTCAACAAA	TTAGAAAGAA	GGATGGAAAA	CTTAAATAAA	1320		
AAAGTTGATG	ATGGATTTCT	GGACATTTGG	ACATATAATG	CAGAATTGTT	GGTTCTACTG	1380		
GAAAATGGAA	GGACTTTGGA	TTTTTCATGAC	TCAAATGTGA	AGAATCTGTA	TGAGAAAGTA	1440		
AAAAGCCAAT	TGAAGAATAA	TGCCAAAGAA	ATAGGGAACG	GGTGTTTTGA	ATTCTATCAC	1500		
AAGTGTAACA	ATGAATGCAT	GGAAAGTGTG	AAAAATGGAA	CTTATGACTA	TCCAAAATAT	1560		
TCCGAAGAAT	CAAAGTTAAA	CAGGGGAAAA	ATTGATGGAG	TGAAATTGGA	ATCAATGGGA	1620		
GTCTATCAGA	TTCTGGCGAT	CTACTCAACT	GTCGCCAGTT	CACTGGTGCT	TTTGGTCTCC	1680		
CTGGGGGCAA	TCAGCTTCTG	GATGTGTTCT	AATGGGTCTT	TGCAGTGCAG	AATATGAATC	1740		
TGAGGTACCA	GATCTTAATT	AATTAA				1766		

10

20

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(C) INDIVIDUAL ISOLATE: A/Texas/36/91 rHA

(ix) FEATURE

(A) NAME/KEY: AcNPV 61K protein signal sequence

40

(B) LOCATION: 1 to 18
 (ix) FEATURE
 (A) NAME/KEY: mature rHA
 (B) LOCATION: 19 to 554
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Pro	Leu	Tyr	Lys	Leu	Leu	Asn	Val	Leu	Trp	Leu	Val	Ala	Val	Ser	
1				5					10					15		
Asn	Ala	Ile	Pro	Gly	Gly	Thr	Pro	Gly	Asp	Thr	Ile	Cys	Ile	Gly	Tyr	
			20					25					30			
His	Ala	Asn	Asn	Ser	Thr	Asp	Thr	Val	Asp	Thr	Val	Leu	Glu	Lys	Asn	
			35				40					45				
Val	Thr	Val	Thr	His	Ser	Val	Asn	Leu	Leu	Glu	Asp	Ser	His	Asn	Gly	
	50					55				60						
Lys	Leu	Cys	Arg	Leu	Lys	Gly	Ile	Ala	Pro	Leu	Gln	Leu	Gly	Asn	Cys	
65				70					75					80		
Ser	Val	Ala	Gly	Trp	Ile	Leu	Gly	Asn	Pro	Lys	Cys	Glu	Ser	Leu	Phe	
			85					90						95		
Ser	Lys	Glu	Ser	Trp	Ser	Tyr	Ile	Ala	Glu	Thr	Pro	Asn	Pro	Glu	Asn	
			100					105					110			
Gly	Thr	Cys	Tyr	Pro	Gly	Tyr	Phe	Ala	Asp	Tyr	Glu	Glu	Leu	Arg	Glu	
			115				120					125				
Gln	Leu	Ser	Ser	Val	Ser	Ser	Phe	Glu	Arg	Phe	Glu	Ile	Phe	Pro	Lys	
	130					135					140					
Glu	Ser	Ser	Trp	Pro	Asn	His	Thr	Val	Thr	Lys	Gly	Val	Thr	Arg	Ser	
145				150					155						160	
Cys	Ser	His	Asn	Gly	Lys	Ser	Ser	Phe	Tyr	Arg	Asn	Leu	Leu	Trp	Leu	
			165					170						175		
Thr	Glu	Lys	Asn	Gly	Leu	Tyr	Pro	Asn	Leu	Ser	Lys	Ser	Tyr	Val	Asn	
			180				185						190			
Asn	Lys	Glu	Lys	Glu	Val	Leu	Val	Leu	Trp	Gly	Val	His	His	Pro	Ser	
			195				200					205				
Asn	Ile	Arg	Asp	Gln	Arg	Ala	Ile	Tyr	His	Thr	Glu	Asn	Ala	Tyr	Val	
	210			215							220					
Ser	Val	Val	Ser	Ser	His	Tyr	Ser	Arg	Arg	Phe	Thr	Pro	Glu	Ile	Ala	
225				230						235				240		
Lys	Arg	Pro	Lys	Val	Arg	Asp	Gln	Glu	Gly	Arg	Ile	Asn	Tyr	Tyr	Trp	
			245					250					255			
Thr	Leu	Leu	Glu	Pro	Gly	Asp	Thr	Ile	Ile	Phe	Glu	Ala	Asn	Gly	Asn	
			260				265					270				
Leu	Ile	Ala	Pro	Trp	Tyr	Ala	Phe	Ala	Leu	Ser	Arg	Gly	Phe	Gly	Ser	
	275					280						285				
Gly	Ile	Ile	Thr	Ser	Asn	Ala	Ser	Met	Asp	Glu	Cys	Asp	Ala	Lys	Cys	
	290				295					300						
Gln	Thr	Pro	Gln	Gly	Ala	Ile	Asn	Ser	Ser	Leu	Pro	Phe	Gln	Asn	Val	
305				310						315				320		
His	Pro	Val	Thr	Ile	Gly	Glu	Cys	Pro	Lys	Tyr	Val	Arg	Ser	Thr	Lys	
			325					330					335			
Leu	Arg	Met	Val	Thr	Gly	Leu	Arg	Asn	Ile	Pro	Ser	Ile	Gln	Ser	Arg	
			340				345					350				
Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Thr	Gly	
	355					360					365					
Met	Ile	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Gln	Asn	Glu	Gln	Gly	Ser	
	370					375					380					
Gly	Tyr	Ala	Ala	Asp	Gln	Lys	Ser	Thr	Gln		Ala	Ile	Asn	Gly	Ile	
385				390										400		
Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys		Asn	Thr	Gln	Phe	Thr	
			405					410						415		
Ala	Val	Gly	Lys	Glu	Phe	Asn	Lys	Leu	Glu	Arg	Arg	Met	Glu	Asn	Leu	
			420					425				430				
Asn	Lys	Lys	Val	Asp	Asp	Gly	Phe	Leu	Asp	Ile	Trp	Thr	Tyr	Asn	Ala	
		435				440					445					
Glu	Leu	Leu	Val	Leu	Leu	Glu	Asn	Gly	Arg	Thr	Leu	Asp	Phe	His	Asp	
	450				455					460						
Ser	Asn	Val	Lys	Asn	Leu	Tyr	Glu	Lys	Val	Lys	Ser	Gln	Leu	Lys	Asn	
465				470				475						480		

10

20

30

40

```

Asn Ala Lys Glu Ile Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys
      485      490      495
Asn Asn Glu Cys Met Glu Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro
      500      505      510
Lys Tyr Ser Glu Glu Ser Lys Leu Asn Arg Gly Lys Ile Asp Gly Val
      515      520      525
Lys Leu Glu Ser Met Gly Val Tyr Gln Ile Leu Ala Ile Tyr Ser Thr
      530      535      540
Val Ala Ser Ser Leu Val Leu Leu Val Ser Leu Gly Ala Ile Ser Phe
      545      550      555      560
Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
      565      570

```

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1799 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: B/Panama/45/90 rHA
- (ix) FEATURE
 - (A) NAME/KEY: polyhedrin mRNA leader (partial)
 - (B) LOCATION: 1 to 18
- (ix) FEATURE
 - (A) NAME/KEY: coding region for HA signal peptide sequence
 - (B) LOCATION: 19 to 69
- (ix) FEATURE
 - (A) NAME/KEY: SmaI restriction site
 - (B) LOCATION: 22 to 27
- (ix) FEATURE
 - (A) NAME/KEY: coding region for mature rHA
 - (B) LOCATION: 70 to 1773
- (ix) FEATURE
 - (A) NAME/KEY: KpnI restriction site
 - (B) LOCATION: 1777 to 1782
- (ix) FEATURE
 - (A) NAME/KEY: BglII restriction site
 - (B) LOCATION: 1783 to 1788
- (ix) FEATURE
 - (A) NAME/KEY: universal translation termination signal
 - (B) LOCATION: 1789 to 1799
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

TAAAAAACC TATAAATAAT GCCCGGAAG GCAATAATTG TACTACTCAT GGTAGTAACA      60
TCCAACGCAG ATCGAATCTG CACTGGGATA ACATCTTCAA ACTCACCTCA TGTGGTCAAA      120
ACAGCTACTC AAGGGGAAGT CAATGTGACT GGTGTGATAC CACTGACAAC AACACCAACA      180
AAATCTCATT TTGCAAACTT AAAAGGAACA AAGACCAGAG GGAAACTATG CCCAAACTGT      240
CTCAACTGCA CAGATCTGGA TGTGGCCTTG GGCAGACCAA TGTGTGTGGG GACCACACCT      300
TCGGCAAAAG CTTCAATACT CCACGAAGTC AGACCTGTTA CATCCGGGTG CTTTCCTATA      360
ATGCACGACA GAACAAAAAT CAGACAGCTA CCCAATCTTC TCAGAGGATA TGAAAATATC      420
AGATTATCAA CCCAAACGT TATCAACGCA GAAAGAGCAC CAGGAGGACC CTACAGACTT      480
GGAACCTCAG GATCTTGCCC TAACGTTACC AGTAGAGACG GATTCTTCGC AACAATGGCT      540

```

TGGGCTGTCC CAAGGGACAA CAAAACAGCA ACGAATCCAC TAACAGTAGA AGTACCATAC 600
 ATTTGTACCA AAGGAGAAGA CCAAATTACT GTTTGGGGGT TCCATTCTGA TAACAAAATC 660
 CAAATGAAAA ACCTCTATGG AGACTCAAAT CCTCAAAAGT TCACCTCATC TGCCAATGGA 720
 GTAACCACAC ATTATGTTTC TCAGATTGGT GGCTTCCCAA ATCAAACAGA AGACGGAGGG 780
 CTACCACAAA GCGGCAGAAT TGTGTGTGAT TACATGGTGC AAAAACCTGG GAAAACAGGA 840
 ACAATTGTCT ATCAAAGAGG TGTTTTGTG CCTCAAAAGG TGTGGTGCGC AAGTGGCAGG 900
 AGCAAGGTAA TAAAAGGGTC CTTGCCTTTA ATTGGTGAAG CAGATTGCCT TCACGAAAAA 960
 TACGGTGGAT TAAACAAAAG CAAGCCTTAC TACACAGGAG AACATGCAAA AGCCATAGGA 1020
 AATTGCCCAA TATGGGTGAA AACACCTTTG AAGCTTGCCA ATGGAACCAA ATATAGACCT 1080
 CCTGCAAAAC TATTAAAGGA AAGGGGTTTC TTCGGAGCTA TTGCTGGTTT CTTAGAAGGA 1140
 GGATGGGAAG GAATGATTGC AGGTTGGCAC GGATACACAT CTCATGGAGC ACATGGAGTG 1200
 GCAGTGGCAG CAGACCTTAA GAGTACGCAA GAAGCCATAA ACAAGATAAC AAAAAATCTC 1260
 AATTCTTTGA GTGAGCTAGA AGTAAAGAAT CTTCAAAGAC TAAGTGGTGC CATGGATGAA 1320
 CTCCACAACG AAATACTCGA GCTGGATGAG AAAGTGGATG ATCTCAGAGC TGACACAATA 1380
 AGCTCGCAAA TAGAGCTTGC AGTCTTGCTT TCCAACGAAG GAATAATAAA CAGTGAAGAT 1440
 GAGCATCTAT TGGCACTTGA GAGAAAATA AAGAAAATGC TGGGTCCCTC TGCTGTAGAC 1500
 ATAGGGAATG GATGCTTCGA AACCAAACAC AAGTGCAACC AGACCTGCTT AGACAGGATA 1560
 GCTGCTGGCA CCTTTAATGC AGGAGAATTT TCTCTTCCCA CTTTGTATTC ACTGAATATT 1620
 ACTGCTGCAT CTTTAAATGA TGATGGATTG GATAATCATA CTATACTGCT CTACTACTCA 1680
 ACTGCTGCTT CTAGTTTGGC TGTAACATTG ATGATAGCTA TTTTATTGT TTATATGGTC 1740
 TCCAGAGACA ATGTTTCTTG TTCCATCTGT CTGTGAGGTA CCAGATCTTA ATTAATTAA 1799

10

20

(2) INFORMATION FOR SEQ ID NO:11:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: B/Panama/45/90 rHA
- (ix) FEATURE
 - (A) NAME/KEY: HA signal peptide
 - (B) LOCATION: 1 to 17
- (ix) FEATURE
 - (A) NAME/KEY: mature rHA
 - (B) LOCATION: 18 to 568
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40

Met Pro Gly Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
 1 5 10 15
 Ala Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val
 20 25 30

Val Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro
 35 40 45
 Leu Thr Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr
 50 55 60
 Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu
 65 70 75 80
 Asp Val Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala
 85 90 95
 Lys Ala Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe
 100 105 110
 Pro Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu
 115 120 125
 Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn Val Ile Asn Ala
 130 135 140
 Glu Arg Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys
 145 150 155 160
 Pro Asn Val Thr Ser Arg Asp Gly Phe Phe Ala Thr Met Ala Trp Ala
 165 170 175
 Val Pro Arg Asp Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu Val
 180 185 190
 Pro Tyr Ile Cys Thr Lys Gly Glu Asp Gln Ile Thr Val Trp Gly Phe
 195 200 205
 His Ser Asp Asn Lys Ile Gln Met Lys Asn Leu Tyr Gly Asp Ser Asn
 210 215 220
 Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val
 225 230 235 240
 Ser Gln Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Gly Gly Leu Pro
 245 250 255
 Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys
 260 265 270
 Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val
 275 280 285
 Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu
 290 295 300
 Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys
 305 310 315 320
 Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys
 325 330 335
 Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr
 340 345 350
 Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile
 355 360 365
 Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His
 370 375 380
 Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu
 385 390 395 400
 Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser
 405 410 415
 Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met
 420 425 430
 Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp
 435 440 445
 Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu
 450 455 460
 Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu
 465 470 475 480
 Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly
 485 490 495

 Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp
 500 505 510
 Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro Thr
 515 520 525
 Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu
 530 535 540
 Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu
 545 550 555 560

10

20

30

40

Ala Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg
565 570 575
Asp Asn Val Ser Cys Ser Ile Cys Leu
580 585

(2) INFORMATION FOR SEQ ID NO:12:

- ```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1811 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Influenza virus
 (C) INDIVIDUAL ISOLATE: B/Netherlands/13/94 rHA
(ix) FEATURE
 (A) NAME/KEY: polyhedrin mRNA leader (partial)
 (B) LOCATION: 1 to 18
(ix) FEATURE
 (A) NAME/KEY: coding region for AcNPV 61K protein signal
 sequence
 (B) LOCATION: 19 to 72
(ix) FEATURE
 (A) NAME/KEY: SmaI restriction site
 (B) LOCATION: 76 to 81
(ix) FEATURE
 (A) NAME/KEY: coding region for mature rHA
 (B) LOCATION: 73 to 1785
(ix) FEATURE
 (A) NAME/KEY: KpnI restriction site
 (B) LOCATION: 1789 to 1794
(ix) FEATURE
 (A) NAME/KEY: BglII restriction site
 (B) LOCATION: 1795 to 1800
(ix) FEATURE
 (A) NAME/KEY: universal translation termination signal
 (B) LOCATION: 1801 to 1811
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| TAAAAAAACC | TATAAATAAT | GCCCTTGTAC | AAATTGTTAA | ACGTTTTTGTG | GTTGGTCGCC | 60  |
| GTTTCTAACG | CGATTCCCCG | GGATCGAATC | TGCACTGGGA | TAACATCTTC  | AAAATCACCT | 120 |
| CATGTAGTCA | AAACAGCTAC | TCAAGGGGAG | GTCAATGTGA | CTGGTGTGAT  | ACCACTGACG | 180 |
| ACAACACCAA | CAAAATCTCA | TTTTGCAAAT | CTCAAAGGAA | CAAAGACCAG  | AGGGAAACTA | 240 |
| TGCCCCAACT | GTCTCAACTG | CACAGATCTG | GATGTGGCCT | TGGGCAGACC  | AATGTGTGTG | 300 |
| GGGATCACAC | CTTCGGCAAA | AGCTTCAATA | CTCCACGAAG | TCAGACCTGT  | TACATCCGGG | 360 |
| TGCTTTCCTA | TAATGCATGA | CAGAACAAA  | ATCAGACAGC | TACCCAATCT  | TCTCAGAGGA | 420 |
| TATGAAAACA | TCAGACTATC | AACCCAAAAC | GTTATCAACG | CAGAAAAGGC  | ACCAGGAGGA | 480 |
| CCCTACAGAC | TTGGAACCTC | AGGATCTTGC | CCTAACGTTA | CCAGTAGAAC  | CGGATTCTTC | 540 |
| GCAACAATGG | CTTGGGCTGT | CCCAAGGGAC | AACAAAACAG | CAACGAATCC  | ACTAACAGTA | 600 |
| GAAGTACCAT | ACATTGTGAC | GAAAGGAGAA | GACCAAATTA | CTGTTTGGGG  | GTTCCATTCT | 660 |
| GATAACAAAA | CCCAAATGAA | AAACCTCTAT | GGAGACTCAA | ATCCTCAAAA  | GTTACCTCA  | 720 |
| TCTGCCAATG | GAGTAACCAC | ACATTATGTT | TCTCAGATTG | GTGGCTTCCC  | AGATCAAACA | 780 |

GAAGACGGAG GACTACCACA AAGCGGCAGA ATTGTTGTTG ATTACATGGT GCAAAAACCT 840  
 GGGAAAACAG GAACAATTGT CTATCAAAGA GGTATTTTGT TGCCTCAAAA GGTGTGGTGC 900  
 GCAAGTGGCA GGAGCAAGGT AATAAAGGG TCCTTGCCCTT TAATTGGTGA AGCAGATTGC 960  
 CTTACAGAAA AATACGGTGG ATTAACAAA AGCAAGCCTT ACTACACAGG AGAACATGCA 1020  
 AAAGCCATAG GAAATTGCCC AATATGGGTG AAAACACCTT TGAAGCTTGC CAATGGAACC 1080  
 AGATATAGAC CTCCTGCAAA ACTATTAAAG GAAAGGGGTT TCTTCGGAGC TATTGCTGGT 1140  
 TTCTTAGAAG GAGGATGGGA AGGAATGATT GCAGGTTGGC ACGGATACAC ATCTCACGGG 1200  
 GCACATGGAG TGGCAGTGGC AGCAGACCTT AAGAGTACGC AAGAAGCCAT AAACAAGATA 1260  
 ACAAAAAATC TCAATTCTTT GAGTGAGCTA GAAGTAAAGA ACCTTCAAAG ACTAAGTGGT 1320  
 GCCATGGATG AACTCCACAA CGAAATACTC GAGCTGGATG AGAAAGTGGG TGATCTCAGA 1380  
 GCTGACACAA TAAGCTCGCA AATAGAGCTT GCAGTCTTAC TTTCCAACGA AGGAATAATA 1440  
 AACAGTGAAG ATGAGCATCT ATTGGCACTT GAGAGAAAAC TAAAGAAAAT GCTGGGTCCC 1500  
 TCTGCTGTAG ACATAGGGAA TGGATGCTTC GAAACAAAAC ACAAGTGCAA CCAGACCTGC 1560  
 TTAGACAGGA TAGCTGCTGG CACCTTTAAT GCAGGAGAAT TTTCTCTTCC CACTTTTGTAT 1620  
 TCACTGAATA TTAGCTGCTG ATCTTTAAAT GATGATGGAT TGGATAATCA TACTATACTG 1680  
 CTCTACTACT CAACTGCTGC TTCTAGTTTG GCTGTAACAT TGATGATAGC TATTTTTATT 1740  
 GTTTATATGG TCTCCAGAGA CAATGTTTCT TGTTCATCT GTCTGTGAGG TACCAGATCT 1800  
 TAATTAATTA A 1811

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 589 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: B/Netherlands/13/94 rHA
- (ix) FEATURE
  - (A) NAME/KEY: AcNPV 61K protein signal sequence
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: mature rHA
  - (B) LOCATION: 19 to 571
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser  
 1 5 10 15  
 Asn Ala Ile Pro Gly Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Lys  
 20 25 30  
 Ser Pro His Val Val Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr  
 35 40 45  
 Gly Val Ile Pro Leu Thr Thr Thr Pro Thr Lys Ser His Phe Ala Asn  
 50 55 60  
 Leu Lys Gly Thr Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn  
 65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Cys | Thr | Asp | Leu | Asp | Val | Ala | Leu | Gly | Arg | Pro | Met | Cys | Val | Gly | Ile |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Thr | Pro | Ser | Ala | Lys | Ala | Ser | Ile | Leu | His | Glu | Val | Arg | Pro | Val | Thr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |
| Ser | Gly | Cys | Phe | Pro | Ile | Met | His | Asp | Arg | Thr | Lys | Ile | Arg | Gln | Leu |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Pro | Asn | Leu | Leu | Arg | Gly | Tyr | Glu | Asn | Ile | Arg | Leu | Ser | Thr | Gln | Asn |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Ile | Asn | Ala | Glu | Lys | Ala | Pro | Gly | Gly | Pro | Tyr | Arg | Leu | Gly | Thr |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Ser | Gly | Ser | Cys | Pro | Asn | Val | Thr | Ser | Arg | Thr | Gly | Phe | Phe | Ala | Thr |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Met | Ala | Trp | Ala | Val | Pro | Arg | Asp | Asn | Lys | Thr | Ala | Thr | Asn | Pro | Leu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Thr | Val | Glu | Val | Pro | Tyr | Ile | Cys | Thr | Lys | Gly | Glu | Asp | Gln | Ile | Thr |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Val | Trp | Gly | Phe | His | Ser | Asp | Asn | Lys | Thr | Gln | Met | Lys | Asn | Leu | Tyr |  |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Gly | Asp | Ser | Asn | Pro | Gln | Lys | Phe | Thr | Ser | Ser | Ala | Asn | Gly | Val | Thr |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Thr | His | Tyr | Val | Ser | Gln | Ile | Gly | Gly | Phe | Pro | Asp | Gln | Thr | Glu | Asp |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Gly | Gly | Leu | Pro | Gln | Ser | Gly | Arg | Ile | Val | Val | Asp | Tyr | Met | Val | Gln |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Lys | Pro | Gly | Lys | Thr | Gly | Thr | Ile | Val | Tyr | Gln | Arg | Gly | Ile | Leu | Leu |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Pro | Gln | Lys | Val | Trp | Cys | Ala | Ser | Gly | Arg | Ser | Lys | Val | Ile | Lys | Gly |  |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Ser | Leu | Pro | Leu | Ile | Gly | Glu | Ala | Asp | Cys | Leu | His | Glu | Lys | Tyr | Gly |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Gly | Leu | Asn | Lys | Ser | Lys | Pro | Tyr | Tyr | Thr | Gly | Glu | His | Ala | Lys | Ala |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Ile | Gly | Asn | Cys | Pro | Ile | Trp | Val | Lys | Thr | Pro | Leu | Lys | Leu | Ala | Asn |  |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Gly | Thr | Arg | Tyr | Arg | Pro | Pro | Ala | Lys | Leu | Leu | Lys | Glu | Arg | Gly | Phe |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Phe | Gly | Ala | Ile | Ala | Gly | Phe | Leu | Glu | Gly | Gly | Trp | Glu | Gly | Met | Ile |  |  |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |
| Ala | Gly | Trp | His | Gly | Tyr | Thr | Ser | His | Gly | Ala | His | Gly | Val | Ala | Val |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Ala | Ala | Asp | Leu | Lys | Ser | Thr | Gln | Glu | Ala | Ile | Asn | Lys | Ile | Thr | Lys |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |
| Asn | Leu | Asn | Ser | Leu | Ser | Glu | Leu | Glu | Val | Lys | Asn | Leu | Gln | Arg | Leu |  |  |
|     |     |     |     | 420 |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Ser | Gly | Ala | Met | Asp | Glu | Leu | His | Asn | Glu | Ile | Leu | Glu | Leu | Asp | Glu |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |
| Lys | Val | Asp | Asp | Leu | Arg | Ala | Asp | Thr | Ile | Ser | Ser | Gln | Ile | Glu | Leu |  |  |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |
| Ala | Val | Leu | Leu | Ser | Asn | Glu | Gly | Ile | Ile | Asn | Ser | Glu | Asp | Glu | His |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |
| Leu | Leu | Ala | Leu | Glu | Arg | Lys | Leu | Lys | Lys | Met | Leu | Gly | Pro | Ser | Ala |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |
| Val | Asp | Ile | Gly | Asn | Gly | Cys | Phe | Glu | Thr | Lys | His | Lys | Cys | Asn | Gln |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |
| Thr | Cys | Leu | Asp | Arg | Ile | Ala | Ala | Gly | Thr | Phe | Asn | Ala | Gly | Glu | Phe |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |
| Ser | Leu | Pro | Thr | Phe | Asp | Ser | Leu | Asn | Ile | Thr | Ala | Ala | Ser | Leu | Asn |  |  |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |
| Asp | Asp | Gly | Leu | Asp | Asn | His | Thr | Ile | Leu | Leu | Tyr | Tyr | Ser | Thr | Ala |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |
| Ala | Ser | Ser | Leu | Ala | Val | Thr | Leu | Met | Ile | Ala | Ile | Phe | Ile | Val | Tyr |  |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |
| Met | Val | Ser | Arg | Asp | Asn | Val | Ser | Cys | Ser | Ile | Cys | Leu |     |     |     |  |  |
|     |     |     |     | 580 |     |     |     | 585 |     |     |     |     |     |     |     |  |  |

10

20

30

40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1757 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
- (ix) FEATURE
  - (A) NAME/KEY: polyhedrin mRNA leader (partial)
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: coding region for AcNPV 61K protein signal sequence
  - (B) LOCATION: 19 to 72
- (ix) FEATURE
  - (A) NAME/KEY: SmaI restriction site
  - (B) LOCATION: 76 to 81
- (ix) FEATURE
  - (A) NAME/KEY: coding region for mature rHA
  - (B) LOCATION: 73 to 1728
- (ix) FEATURE
  - (A) NAME/KEY: KpnI restriction site
  - (B) LOCATION: 1735 to 1740
- (ix) FEATURE
  - (A) NAME/KEY: BglII restriction site
  - (B) LOCATION: 1741 to 1746
- (ix) FEATURE
  - (A) NAME/KEY: universal translation termination signal
  - (B) LOCATION: 1747 to 1757
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAAAAAACC TATAAATAAT GCCCTTGTAC AAATTGTTAA ACGTTTTGTG GTTGGTCGCC  | 60  |
| GTTTCTAACG CGATTCCCGG GCAAGACCTT CCAGGAAATG ACAACAGCAC AGCAACGCTG | 120 |
| TGCCTGGGAC ATCATGCAGT GCCAAACGGA ACGCTAGTGA AAACAATCAC GAATGATCAA | 180 |
| ATTGAAGTGA CTAATGCTAC TGAGTTGGTT CAGAGTTCCT CAACAGGTAG AATATGCGGC | 240 |
| AGTCCTCACC GAATCCTTGA TGGAAAAAC TGCACACTGA TAGATGCTCT ATTGGGAGAC  | 300 |
| CCTCATTGTG ATGGCTTCCA AAATAAGGAA TGGGACCTTT TTGTTGAACG CAGCAAAGCT | 360 |
| TACAGCAACT GTTACCCTTA TGATGTGCCG GATTATGCCT CCCTTAGGTC ACTAGTTGCC | 420 |
| TCATCAGGCA CCCTGGAGTT TATCAATGAA GACTTCAATT GGACTGGAGT CGCTCAGGAT | 480 |
| GGGGGAAGCT ATGCTTGCAA AAGAGGATCT GTTAACAGTT TCTTTAGTAG ATTGAATTGG | 540 |
| TTGCACAAAT TAGAATACAA ATATCCAGCG CTGAACGTGA CTATGCCAAA CAATGGCAAA | 600 |
| TTTGACAAAT TGTACATTG GGGGGTTCAC CACCCGAGCA CGGACAGTGA CCAAACCAGC  | 660 |
| CTATATGTTC GAGCATCAGG GAGAGTCACA GTCTCTACCA AAAGAAGCCA ACAAACTGTA | 720 |
| ACCCCGAATA TCGGGTCTAG ACCCTGGGTA AGGGGTCAGT CCAGTAGAAT AAGCATCTAT | 780 |
| TGGACAATAG TAAAACCGGG AGACATACTT TTGATTGATA GCACAGGGAA TCTAATTGCT | 840 |
| CCTCGGGGTT ACTTCAAAAT ACGAAATGGG AAAAGCTCAA TAATGAGGTC AGATGCACCC | 900 |
| ATTGGCAACT GCAGTTCTGA ATGCATCACT CCAAATGGAA GCATTCCCAA TGACAAACCT | 960 |

10

20

30

40

```

TTTCAAAATG TAAACAGAAT CACATATGGG GCCTGCCCCA GATATGTTAA GCAAAACACT 1020
CTGAAATTGG CAACAGGGAT GCGGAATGTA CCAGAGAAAC AAAC TAGAGG CATATTCGGC 1080
GCAATCGCAG GTTTCATAGA AAATGGTTGG GAGGGAATGG TAGACGGTTG GTACGGTTTC 1140
AGGCATCAAA ATTCTGAGGG CACAGGACAA GCAGCAGATC TAAAAGCAC TCAAGCAGCA 1200
ATCGACCAAA TCAACGGGAA ACTGAATAGG TTAATCGAGA AAACGAACGA GAAATTCCAT 1260
CAAATCGAAA AAGAATTCTC AGAAGTAGAA GGGAGAATTC AGGACCTCGA GAAATATGTT 1320
GAAGACACTA AAATAGATCT CTGGTCTTAC AACGCGGAGC TTCTTGTTGC CCTGGAGAAC 1380
CAACATACAA TTGATCTAAC TGAATCAGAA ATGAACAAAC TGTTTGAAAA AACAAGGAAG 1440
CAACTGAGGG AAAATGCTGA GGACATGGGC AATGGTTGCT TCAAAATATA CCACAAATGT 1500
GACAATGCCT GCATAGGGTC AATCAGAAAT GGAACCTTATG ACCATGATGT ATACAGAGAC 1560
GAAGCATTAA ACAACCGGTT CCAGATCAAA GGTGTTGAGC TGAAGTCAGG ATACAAAGAT 1620
TGGATCCTAT GGATTCCTT TGCCATATCA TGCTTTTTC TTTGTGTTGT TTTGCTGGGG 1680
TTCATCATGT GGCCTGCCA AAAAGGCAAC ATTAGGTGCA ACATTTCAT TTGAGGTACC 1740
AGATCTTAAT TAATTAA 1757

```

10

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 571 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
- (ix) FEATURE
  - (A) NAME/KEY: AcNPV 61K protein signal sequence
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: mature rHA
  - (B) LOCATION: 19 to 553
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20

30

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1 5 10 15
Asn Ala Ile Pro Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala
20 25 30
Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys
35 40 45
Thr Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val
50 55 60
Gln Ser Ser Ser Thr Gly Arg Ile Cys Gly Ser Pro His Arg Ile Leu
65 70 75 80
Asp Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His
85 90 95
Cys Asp Gly Phe Gln Asn Lys Glu Trp Asp Leu Phe Val Glu Arg Ser
100 105 110
Lys Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
115 120 125
Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe Ile Asn Glu
130 135 140

```

40

```

Asp Phe Asn Trp Thr Gly Val Ala Gln Asp Gly Gly Ser Tyr Ala Cys
145 150 155
Lys Arg Gly Ser Val Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu His
 165 170
Lys Leu Glu Tyr Lys Tyr Pro Ala Leu Asn Val Thr Met Pro Asn Asn
 180 185 190
Gly Lys Phe Asp Lys Leu Tyr Ile Trp Gly Val His His Pro Ser Thr
 195 200 205
Asp Ser Asp Gln Thr Ser Leu Tyr Val Arg Ala Ser Gly Arg Val Thr
 210 215 220
Val Ser Thr Lys Arg Ser Gln Gln Thr Val Thr Pro Asn Ile Gly Ser
 225 230 235
Arg Pro Trp Val Arg Gly Gln Ser Ser Arg Ile Ser Ile Tyr Trp Thr
 245 250 255
Ile Val Lys Pro Gly Asp Ile Leu Leu Ile Asp Ser Thr Gly Asn Leu
 260 265 270
Ile Ala Pro Arg Gly Tyr Phe Lys Ile Arg Asn Gly Lys Ser Ser Ile
 275 280 285
Met Arg Ser Asp Ala Pro Ile Gly Asn Cys Ser Ser Glu Cys Ile Thr
 290 295 300
Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Arg
 305 310 315
Ile Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn Thr Leu Lys
 325 330 335
Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Ile
 340 345 350
Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Val
 355 360 365
Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln
 370 375 380
Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly
 385 390 395
Lys Leu Asn Arg Leu Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile
 405 410 415
Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys
 420 425 430
Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu
 435 440 445
Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu
 450 455 460
Met Asn Lys Leu Phe Glu Lys Thr Arg Lys Gln Leu Arg Glu Asn Ala
 465 470 475
Glu Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn
 485 490 495
Ala Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr
 500 505 510
Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu
 515 520 525
Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser
 530 535 540
Cys Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys
 545 550 555
Gln Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
 565 570

```

10

20

30

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1814 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(C) INDIVIDUAL ISOLATE: B/Shanghai/4/94 rHA

40

- (ix) FEATURE
  - (A) NAME/KEY: polyhedrin mRNA leader (partial)
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: coding region for AcNPV 61K protein signal sequence
  - (B) LOCATION: 19 to 72
- (ix) FEATURE
  - (A) NAME/KEY: SmaI restriction site
  - (B) LOCATION: 76 to 81
- (ix) FEATURE
  - (A) NAME/KEY: KpnI restriction site
  - (B) LOCATION: 82 to 87
- (ix) FEATURE
  - (A) NAME/KEY: coding region for mature rHA
  - (B) LOCATION: 73 to 1794
- (ix) FEATURE
  - (A) NAME/KEY: universal translation termination signal
  - (B) LOCATION: 1804 to 1814
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TAAAAAACC TATAATAAT GCCCTGTAC AAATTGTTAA ACGTTTTGTG GTTGGTCGCC    | 60   |
| GTTTCTAACG CGATTCCCGG GGGTACCGAT CGAATCTGCA CTGGGATAAC ATCTTCAAAC | 120  |
| TCACCTCATG TGGTCAAAAC AGCTACTCAA GGGGAGGTCA ATGTGACTGG TGTGATACCA | 180  |
| CTGACAACAA CACCAACAAA ATCTCATTTT GCAAATCTCA AAGGAACAAA GACCAGAGGG | 240  |
| AAACTATGCC CAAACTGTCT CAACTGCACA GATCTGGATG TGGCCTTGGG CAGACCAATG | 300  |
| TGTGTGGGGA CCACACCTTC GGCAAAAGCT TCAATACTCC ACGAAGTCAG ACCTGTTACA | 360  |
| TCCGGGTGCT TTCCTATAAT GCACGACAGA ACAAAAATCA GACAGCTACC CAATCTTCTC | 420  |
| AGAGGATATG AAAATATCAG ATTATCAACC CAAAACGTTA TCAACGCAGA AAAGGCACCA | 480  |
| GGAGGACCCT ACAGACTTGG AACCTCAGGA TCTTGCCCTA ACGCTACCAG TAGAAGCGGA | 540  |
| TTTTTCGCAA CAATGGCTTG GGCTGTCCCA AGGGACAACA ACAAACAGC AACGAATCCA  | 600  |
| CTAACAGTAG AAGTACCATA CATTTCACAA AAAGGAGAAG ACCAAATTAC TGTTTGGGGG | 660  |
| TTCCATTCTG ATAACAAACC CCAAATGAAA AACCTCTATG GAGACTCAA TCCTCAAAAG  | 720  |
| TTCACCTCAT CTGCTAATGG AGTAACCACA CATTATGTTT CTCAGATTGG CGGCTTCCCA | 780  |
| GATCAAACAG AAGACGGAGG GCTACCACAA AGCGGCAGAA TTGTTGTTGA TTACATGGTG | 840  |
| CAAAAACCTG GGAAGACAGG AACAATTGTC TATCAGAGAG GTGTTTTGTT GCCTCAAAAG | 900  |
| GTGTGGTGCG CTAGTGGCAG GAGCAAAGTA ATAAAGGGT CCTTGCCTTT AATTGGTGAA  | 960  |
| GCAGATTGCC TTCACGAAAA ATACGGTGGA TTAAACAAAA GCAAGCCTTA CTACACAGGA | 1020 |
| GAACATGCAA AAGCCATAGG AAATTGCCCA ATATGGGTGA AAACACCTTT GAAGCTTGCC | 1080 |
| AATGGAACCA AATATAGACC TCCTGCAAAA CTATTAAAGG AAAGGGGTTT CTTCGGAGCT | 1140 |
| ATTGCTGGTT TCTTAGAAGG AGGATGGGAA GGAATGATTG CAGGTTGGCA CGGATACACA | 1200 |
| TCTCACGGAG CACATGGAGT GGCAGTGGCA GCAGACCTTA AGAGTACGCA AGAAGCCATA | 1260 |
| AACAAGATAA CAAAAAATCT CAATTCTTTG AGTGAGCTAG AAGTAAAGAA TCTTCAAAGG | 1320 |
| CTAAGTGGTG CCATGGATGA ACTCCACAAC GAAATACTCG AGCTGGATGA GAAAGTGGAT | 1380 |

10

20

30

40

GATCTCAGAG CTGACACAAT AAGCTCGCAA ATAGAACTTG CAGTCTTGCT TTCCAACGAA 1440  
 GGAATAATAA ACAGTGAAGA TGAGCATCTA TTGGCACTTG AGAGAAAACCT AAAGAAAATG 1500  
 CTGGGTCCCT CTGCTGTAGA CATAGGAAAT GGATGCTTCG AAACCAAACA CAAGTGCAAC 1560  
 CAGACCTGCT TAGACAGGAT AGCTGCTGGC ACCTTTAATG CGGGAGAATT TTCTCTTCCC 1620  
 ACTTTTGATT CACTGAATAT TACTGCTGCA TCTTTAAATG ATGATGGATT GGATAACCAT 1680  
 ACTATACTGC TCTACTACTC AACTGCTGCT TCTAGTTTGG CGGTAACATT GATGATAGCT 1740  
 ATTTTTATTG TTTATATGGT CTCCAGAGAC AATGTTTCTT GCTCCATCTG TCTGTGAGGA 1800  
 TCTTAATTAA TTAA 1814

10

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 592 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: B/Shanghai/4/94 rHA
- (ix) FEATURE
  - (A) NAME/KEY: AcNPV 61K protein signal peptide
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: mature rHA
  - (B) LOCATION: 19 to 574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

20

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser  
 1 5 10 15  
 Asn Ala Ile Pro Gly Gly Thr Asp Arg Ile Cys Thr Gly Ile Thr Ser  
 20 25 30  
 Ser Asn Ser Pro His Val Val Lys Thr Ala Thr Gln Gly Glu Val Asn  
 35 40 45  
 Val Thr Gly Val Ile Pro Leu Thr Thr Thr Pro Thr Lys Ser His Phe  
 50 55 60  
 Ala Asn Leu Lys Gly Thr Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys  
 65 70 75 80  
 Leu Asn Cys Thr Asp Leu Asp Val Ala Leu Gly Arg Pro Met Cys Val  
 85 90 95  
 Gly Thr Thr Pro Ser Ala Lys Ala Ser Ile Leu His Glu Val Arg Pro  
 100 105 110  
 Val Thr Ser Gly Cys Phe Pro Ile Met His Asp Arg Thr Lys Ile Arg  
 115 120 125  
 Gln Leu Pro Asn Leu Leu Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr  
 130 135 140  
 Gln Asn Val Ile Asn Ala Glu Lys Ala Pro Gly Gly Pro Tyr Arg Leu  
 145 150 155 160  
 Gly Thr Ser Gly Ser Cys Pro Asn Ala Thr Ser Arg Ser Gly Phe Phe  
 165 170 175  
 Ala Thr Met Ala Trp Ala Val Pro Arg Asp Asn Asn Lys Thr Ala Thr  
 180 185 190  
 Asn Pro Leu Thr Val Glu Val Pro Tyr Ile Cys Thr Lys Gly Glu Asp  
 195 200 205  
 Gln Ile Thr Val Trp Gly Phe His Ser Asp Asn Lys Pro Gln Met Lys  
 210 215 220  
 Asn Leu Tyr Gly Asp Ser Asn Pro Gln Lys Phe Thr Ser Ser Ala Asn  
 225 230 235 240

30

40

Gly Val Thr Thr His Tyr Val Ser Gln Ile Gly Gly Phe Pro Asp Gln  
 245 250 255  
 Thr Glu Asp Gly Leu Pro Gln Ser Gly Arg Ile Val Val Asp Tyr  
 260 265 270  
 Met Val Gln Lys Pro Gly Lys Thr Gly Thr Ile Val Tyr Gln Arg Gly  
 275 280 285  
 Val Leu Leu Pro Gln Lys Val Trp Cys Ala Ser Gly Arg Ser Lys Val  
 290 295 300  
 Ile Lys Gly Ser Leu Pro Leu Ile Gly Glu Ala Asp Cys Leu His Glu  
 305 310 315 320  
 Lys Tyr Gly Gly Leu Asn Lys Ser Lys Pro Tyr Tyr Thr Gly Glu His  
 325 330 335  
 Ala Lys Ala Ile Gly Asn Cys Pro Ile Trp Val Lys Thr Pro Leu Lys  
 340 345 350  
 Leu Ala Asn Gly Thr Lys Tyr Arg Pro Pro Ala Lys Leu Leu Lys Glu  
 355 360 365  
 Arg Gly Phe Phe Gly Ala Ile Ala Gly Phe Leu Glu Gly Gly Trp Glu  
 370 375 380  
 Gly Met Ile Ala Gly Trp His Gly Tyr Thr Ser His Gly Ala His Gly  
 385 390 395 400  
 Val Ala Val Ala Ala Asp Leu Lys Ser Thr Gln Glu Ala Ile Asn Lys  
 405 410 415  
 Ile Thr Lys Asn Leu Asn Ser Leu Ser Glu Leu Glu Val Lys Asn Leu  
 420 425 430  
 Gln Arg Leu Ser Gly Ala Met Asp Glu Leu His Asn Glu Ile Leu Glu  
 435 440 445  
 Leu Asp Glu Lys Val Asp Asp Leu Arg Ala Asp Thr Ile Ser Ser Gln  
 450 455 460  
 Ile Glu Leu Ala Val Leu Leu Ser Asn Glu Gly Ile Ile Asn Ser Glu  
 465 470 475 480  
 Asp Glu His Leu Leu Ala Leu Glu Arg Lys Leu Lys Lys Met Leu Gly  
 485 490 495  
 Pro Ser Ala Val Asp Ile Gly Asn Gly Cys Phe Glu Thr Lys His Lys  
 500 505 510  
 Cys Asn Gln Thr Cys Leu Asp Arg Ile Ala Ala Gly Thr Phe Asn Ala  
 515 520 525  
 Gly Glu Phe Ser Leu Pro Thr Phe Asp Ser Leu Asn Ile Thr Ala Ala  
 530 535 540  
 Ser Leu Asn Asp Asp Gly Leu Asp Asn His Thr Ile Leu Leu Tyr Tyr  
 545 550 555 560  
 Ser Thr Ala Ala Ser Ser Leu Ala Val Thr Leu Met Ile Ala Ile Phe  
 565 570 575  
 Ile Val Tyr Met Val Ser Arg Asp Asn Val Ser Cys Ser Ile Cys Leu  
 580 585 590

10

20

30

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: B/Harbin/7/94 rHA

## (ix) FEATURE

- (A) NAME/KEY: polyhedrin mRNA leader (partial)
- (B) LOCATION: 1 to 18

## (ix) FEATURE

- (A) NAME/KEY: coding region for HA signal peptide sequence
- (B) LOCATION: 19 to 69

## (ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
- (B) LOCATION: 22 to 27

40

- (ix) FEATURE  
 (A) NAME/KEY: coding region for mature rHA  
 (B) LOCATION: 70 to 1776
- (ix) FEATURE  
 (A) NAME/KEY: KpnI restriction site  
 (B) LOCATION: 1780 to 1785
- (ix) FEATURE  
 (A) NAME/KEY: BglII restriction site  
 (B) LOCATION: 1786 to 1791
- (ix) FEATURE  
 (A) NAME/KEY: unversal translation termination signal  
 (B) LOCATION: 1792 to 1802
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|                                                                    |      |  |
|--------------------------------------------------------------------|------|--|
| TAAAAAAACC TATAAATAAT GCCCGGGAAG GCAATAATTG TACTACTCAT GGTAGTAACA  | 60   |  |
| TCCAACGCAG ATCGAATCTG CACTGGGATA ACATCTTCAA ACTCACCTCA TGTGGTCAAA  | 120  |  |
| ACAGCTACTC AAGGGGAAGT CAATGTGACT GGTGTGATAC CACTGACAAC AACACCAACA  | 180  |  |
| AAATCTCATT TTGCAATCT AAAAGGAACA AAGACCAGAG GGAAACTATG CCCAAACTGT   | 240  |  |
| CTCAACTGCA CAGATCTGGA TGTGGCCTTG GGCAGACCAA TGTGTGTGGG GACCACACCT  | 300  |  |
| TCGGCAAAAG CTTCAATACT CCACGAAGTC AGACCTGTTA CATCCGGGTG CTTTCCTATA  | 360  |  |
| ATGCACGACA GAACAAAAAT CAGACAGCTA CCCAATCTTC TCAGAGGATA TGAAAAATATC | 420  |  |
| AGATTATCAA CCCAAACGT TATCAATGCA GAAAAAGCAC CAGGAGGACC CTACAGACTT   | 480  |  |
| GGAACCTCAG GATCTTGCCC TAACGCTACC AGTAGAAGCG GATTTTTTGC AACAATGGCT  | 540  |  |
| TGGGCTGTCC CAAGGGACGA CAACAAAACA GCAACGAATC CACTAACAGT AGAAGTACCA  | 600  |  |
| TACGTTTGTA CAGAAGGAGA AGACCAAATT ACTGTTTGGG GGTTCATTTC TGATAACAAA  | 660  |  |
| GCCCAAATGA AAAACCTCTA TGGAGACTCA AATCCTCAA AGTTCACCTC ATCTGCTAAT   | 720  |  |
| GGAGTAACCA CACATTATGT TTCTCAGATT GCGGCTTCC CAGATCAAAC AGAAGACGGA   | 780  |  |
| GGGCTACCAC AAAGCGGCAG AATTGTTGTT GATTACATGG TGCAAAAACC TGGGAAAACA  | 840  |  |
| GGAACAATTG TCTATCAAAG AGGTGTTTTG TTGCCTCAA AGGTGTGGTG CGCGAGTGGC   | 900  |  |
| AGGAGCAAAG TAATAAAAGG GTCCTTGCC TTAATTGGTG AAGCAGATTG CCTTCACGAA   | 960  |  |
| AAATACGGTG GATTAAACAA AAGCAAGCCT TACTACACAG GAGAACATGC AAAAGCCATA  | 1020 |  |
| GGAAATTGCC CAATATGGGT GAAAACACCT TTGAAGCTTG CCAATGGAAC CAAATATAGA  | 1080 |  |
| CCTCCTGCAA AACTATTAAA GGAAAGGGGT TTCTTCGGAG CTATTGCTGG TTTCTTAGAA  | 1140 |  |
| GGAGGATGGG AAGGAATGAT TGCAGGTTGG CACGGATACA CATCTCACGG AGCACATGGA  | 1200 |  |
| GTGGCAGTGG CAGCAGACCT TAAGAGTACG CAAGAAGCCA TAAACAAGAT AACAAAAAAT  | 1260 |  |
| CTCAATTCTT TGAGTGAGCT AGAAGTAAAG AATCTTCAA GACTAAGTGG TGCCATGGAT   | 1320 |  |
| GAACTCCATA ACGAAATACT CGAGCTGGAT GAGAAAGTGG ATGATCTCAG AGCTGACACT  | 1380 |  |
| ATAAGCTCGC AAATAGAACT TGCAGTCTTG CTTTCCAACG AAGGAATAAT AAACAGTGAA  | 1440 |  |
| GATGAGCATC TATTGGCACT TGAGAGAAAA CTAAAGAAAA TGCTGGGTCC CTCTGCTGTA  | 1500 |  |
| GACATAGGGA ATGGATGCTT CGAAACCAAA CACAAGTGCA ACCAGACCTG CTTAGACAGG  | 1560 |  |
| ATAGCTGCTG GCACCTTTAA TGCAGGAGAA TTTTCTCTCC CCACTTTTGA TTCACTGAAT  | 1620 |  |

10

20

30

40

ATTACTGCTG CATCTTTAAA TGATGATGGA TTGGATAATC ATACTATACT GCTCTACTAC 1680  
TCAACTGCTG CTTCTAGTTT GGCTGTAACA TTGATGATAG CTATTTTAT TGTTTATATG 1740  
GTCTCCAGAG ACAATGTTTC ATGCTCCATC TGTCTGTGAG GTACCAGATC TTAATTAATT 1800  
AA 1802

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 586 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: B/Harbin/7/94 rHA
- (ix) FEATURE
  - (A) NAME/KEY: HA signal peptide
  - (B) LOCATION: 1 to 17
- (ix) FEATURE
  - (A) NAME/KEY: mature rHA
  - (B) LOCATION: 18 to 569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Gly Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn  
1 5 10 15  
Ala Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val  
20 25 30  
Val Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro  
35 40 45  
Leu Thr Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr  
50 55 60  
Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu  
65 70 75 80  
Asp Val Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala  
85 90 95  
Lys Ala Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe  
100 105 110  
Pro Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu  
115 120 125  
Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn Val Ile Asn Ala  
130 135 140  
Glu Lys Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys  
145 150 155 160  
Pro Asn Ala Thr Ser Arg Ser Gly Phe Phe Ala Thr Met Ala Trp Ala  
165 170 175  
Val Pro Arg Asp Asp Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu  
180 185 190  
Val Pro Tyr Val Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly  
195 200 205  
Phe His Ser Asp Asn Lys Ala Gln Met Lys Asn Leu Tyr Gly Asp Ser  
210 215 220  
Asn Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr  
225 230 235 240  
Val Ser Gln Ile Gly Gly Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu  
245 250 255  
Pro Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly  
260 265 270  
Lys Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys  
275 280 285  
Val Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro  
290 295 300

```

Leu Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn
305 310 315 320
Lys Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn
 325 330 335
Cys Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys
 340 345 350
Tyr Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala
 355 360 365
Ile Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp
 370 375 380
His Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp
385 390 395 400
Leu Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn
 405 410 415
Ser Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala
 420 425 430
Met Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp
 435 440 445
Asp Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu
 450 455 460
Leu Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala
465 470 475 480
Leu Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile
 485 490 495
Gly Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu
 500 505 510
Asp Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro
 515 520 525
Thr Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly
 530 535 540
Leu Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser
545 550 555 560
Leu Ala Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser
 565 570 575
Arg Asp Asn Val Ser Cys Ser Ile Cys Leu
 580 585

```

10

20

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1757 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA
- (ix) FEATURE
  - (A) NAME/KEY: polyhedrin mRNA leader (partial)
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: coding region for AcNPV 61K protein signal peptide
  - (B) LOCATION: 19 to 72
- (ix) FEATURE
  - (A) NAME/KEY: SmaI restriction site
  - (B) LOCATION: 76 to 81
- (ix) FEATURE
  - (A) NAME/KEY: coding region for mature rHA
  - (B) LOCATION: 73 to 1731
- (ix) FEATURE
  - (A) NAME/KEY: KpnI restriction site
  - (B) LOCATION: 1735 to 1740
- (ix) FEATURE
  - (A) NAME/KEY: BglIII restriction site

30

40

(B) LOCATION: 1741 to 1747

(ix) FEATURE

(A) NAME/KEY: universal translation termination signal

(B) LOCATION: 1747 to 1757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|                                                                     |      |    |
|---------------------------------------------------------------------|------|----|
| TAAAAAAACC TATAAATAAT GCCCTTGTAC AAATTGTTAA ACGTTTTGTG GTTGGTCGCC   | 60   |    |
| GTTTCTAACG CGATTCCCGG GCAGGACCTT CCAGGAAATG ACAACAGCAC AGCAACGCTG   | 120  |    |
| TGCCTGGGAC ACCATGCAGT GCCAAACGGA ACGCTAGTGA AAACAATCAC GAATGATCAA   | 180  |    |
| ATTGAAGTGA CTAATGCTAC TGAGCTGGTT CAGAGTTCCC CAACAGGTAG AATATGCGAC   | 240  | 10 |
| AGTCCTCACC GAATCCTTGA TGGAAAGAAC TGCACACTGA TAGATGCTCT ATTGGGAGAC   | 300  |    |
| CCTCATTGTG ATGGCTTCCA AAATAAGGAA TGGGACCTTT TTGTTGAACG CAGCAAAGCT   | 360  |    |
| TACAGCAACT GTTACCCTTA TGATGTGCCG GATTATGCCT CCCTTAGGTC ACTAGTTGCC   | 420  |    |
| TCATCAGGCA CCCTGGAGTT TATCAACGAA AACTTCAATT GGACTGGAGT CGCTCAGGAT   | 480  |    |
| GGGAAAAGCT ATGCTTGCAA AAGGGGATCT GTTAACAGTT TCTTTAGTAG ATTGAATTGG   | 540  |    |
| TTGCACAAAT TAGAATACAA ATATCCAGCG CTGAACGTGA CTATGCCAAA CAATGGCAAA   | 600  |    |
| TTTGACAAAT TGTACATTTG GGGGGTTCAC CACCCGAGCA CGGACAGTGA CCAAACCAGC   | 660  |    |
| CTATATGTCC GAGCATCAGG GAGAGTCACA GTCTCTACCA AAAGAAGCCA ACAAACGTGA   | 720  | 20 |
| ATCCCGGATA TCGGGTATAG ACCATGGGTA AGGGGTCAGT CCAGTAGAAT AGGCATCTAT   | 780  |    |
| TGGACAATAG TAAAACCGGG AGACATACTT TTGATTAATA GCACAGGGAA TCTAATTGCT   | 840  |    |
| CCTCGGGGTT ACTTCAAAAT ACGAAATGGG AAAAGCTCAA TAATGAGGTC AGATGCACCC   | 900  |    |
| ATTGGCAACT GCAGTTCTGA ATGCATCACT CCAAATGGAA GCATTCCCAA TGACAAACCT   | 960  |    |
| TTTCAAAATG TAAACAGGAT CACATATGGG GCCTGCCCCA GATATGTTAA GCAAAACACT   | 1020 |    |
| CTGAAATTGG CAACAGGGAT GCGGAATGTA CCAGAGAAAC AAAC TAGAGG CATATTCGGC  | 1080 |    |
| GCAATCGCAG GTTTCATAGA AAATGGTTGG GAGGGAATGG TAGACGGTTG GTACGGTTTC   | 1140 | 30 |
| AGGCATCAAA ATTCTGAGGG CACAGGACAA GCTGCAGATC TTAAAAGCAC TCAAGCAGCA   | 1200 |    |
| ATCGACCAAA TCAACGGGAA ACTGAATAGG TTAGTCGAGA AAACGAACGA GAAATTCCAT   | 1260 |    |
| CAAATCGAAA AAGAATTCTC AGAAGTAGAA GGGAGAATTC AGGACCTCGA GAAATATGTT   | 1320 |    |
| GAAGACACTA AAATAGATCT CTGGTCTTAC AATGCGGAGC TTCTTGTTGC TCTGGAGAAC   | 1380 |    |
| CAACATACAA TTGATCTAAC TGA CTGAGAA ATGAACAAAC TGTGTTGAAAG AACAAGGAAG | 1440 |    |
| CAACTGAGGG AAAATGCTGA GGACATGGGC AATGGTTGTT TCAAAATATA CCACAAATGT   | 1500 |    |
| GACAATGCCT GCATAGGGTC AATCAGAAAT GGAAC TTATG ACCATGATGT ATACAGAGAC  | 1560 | 40 |
| GAAGCATTAA ACAACCGGTT CCAGATCAAA GGTGTTGAGC TGAAGTCAGG ATACAAAGAT   | 1620 |    |
| TGGATTCTAT GGATTTCCTT TGCCATATCA TGCTTTTTGC TTTGTGTTGT TTTGCTTGGG   | 1680 |    |
| TTCATCATGT GGGCCTGCCA AAAAGGCAAC ATTAGGTGCA ACATTTGCAT TTGAGGTACC   | 1740 |    |
| AGATCTTAAT TAATTAA                                                  | 1757 |    |

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 571 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Influenza virus
  - (C) INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA
- (ix) FEATURE
  - (A) NAME/KEY: AcNPV 61K protein signal sequence
  - (B) LOCATION: 1 to 18
- (ix) FEATURE
  - (A) NAME/KEY: mature rHA
  - (B) LOCATION: 19 to 569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1 5 10 15
Asn Ala Ile Pro Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala
20 25 30
Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys
35 40 45
Thr Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val
50 55 60
Gln Ser Ser Pro Thr Gly Arg Ile Cys Asp Ser Pro His Arg Ile Leu
65 70 75 80
Asp Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His
85 90 95
Cys Asp Gly Phe Gln Asn Lys Glu Trp Asp Leu Phe Val Glu Arg Ser
100 105 110
Lys Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
115 120 125
Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe Ile Asn Glu
130 135 140
Asn Phe Asn Trp Thr Gly Val Ala Gln Asp Gly Lys Ser Tyr Ala Cys
145 150 155 160
Lys Arg Gly Ser Val Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu His
165 170 175
Lys Leu Glu Tyr Lys Tyr Pro Ala Leu Asn Val Thr Met Pro Asn Asn
180 185 190
Gly Lys Phe Asp Lys Leu Tyr Ile Trp Gly Val His His Pro Ser Thr
195 200 205
Asp Ser Asp Gln Thr Ser Leu Tyr Val Arg Ala Ser Gly Arg Val Thr
210 215 220
Val Ser Thr Lys Arg Ser Gln Gln Thr Val Ile Pro Asp Ile Gly Tyr
225 230 235 240
Arg Pro Trp Val Arg Gly Gln Ser Ser Arg Ile Gly Ile Tyr Trp Thr
245 250 255
Ile Val Lys Pro Gly Asp Ile Leu Leu Ile Asn Ser Thr Gly Asn Leu
260 265 270
Ile Ala Pro Arg Gly Tyr Phe Lys Ile Arg Asn Gly Lys Ser Ser Ile
275 280 285
Met Arg Ser Asp Ala Pro Ile Gly Asn Cys Ser Ser Glu Cys Ile Thr
290 295 300
Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Arg
305 310 315 320
Ile Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn Thr Leu Lys
325 330 335
Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Ile
340 345 350
Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Val
355 360 365

```

10

20

30

40

Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln  
 370 375 380  
 Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly  
 385 390 395 400  
 Lys Leu Asn Arg Leu Val Glu Lys Thr Asn Glu Lys Phe His Gln Ile  
 405 410 415  
 Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys  
 420 425 430  
 Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu  
 435 440 445  
 Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu  
 450 455 460  
 Met Asn Lys Leu Phe Glu Arg Thr Arg Lys Gln Leu Arg Glu Asn Ala  
 465 470 475 480  
 Glu Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn  
 485 490 495  
 Ala Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr  
 500 505 510  
 Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu  
 515 520 525  
 Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser  
 530 535 540  
 Cys Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys  
 545 550 555 560  
 Gln Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile  
 565 570

10

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 39 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20

TGGTTGGTCG CCGTTTCTAA CGCGATTCCC GGGGGTACC

39

- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 13 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30

Trp Leu Val Ala Val Ser Asn Ala Ile Pro Gly Gly Thr  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 43 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

40

TGGTTAGTCG CCGTGTCTTG CAGGCCAGAG AGGCCTTGGT ACC

43

- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTCGCCGTGT CCAACGCG

18

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TAATTGGCCA GAGAGGCC

18

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGGGATCCG GTACCAGCAA AAGCAGGGGA TAATTCTAT

39

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGGTACCC CCGGGGACTT TCCAGGAAAT GACAACAG

38

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCGGTACCG AATCATCCTA GAAACAAGGG TGTTTTAAAT TAAT

44

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGAATTCG GTACCCCCCG GAAGGCAATA ATTGTACTAC TCATGGT

47

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTACCCCCG GGGATCGAAT CTGCACTGGG ATAACA

36

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGAATTCG GATCCGGTAC CTCACAGACA GATGGARCAA GAAACATTGT

50

10

20

30

40

50

【図 1】

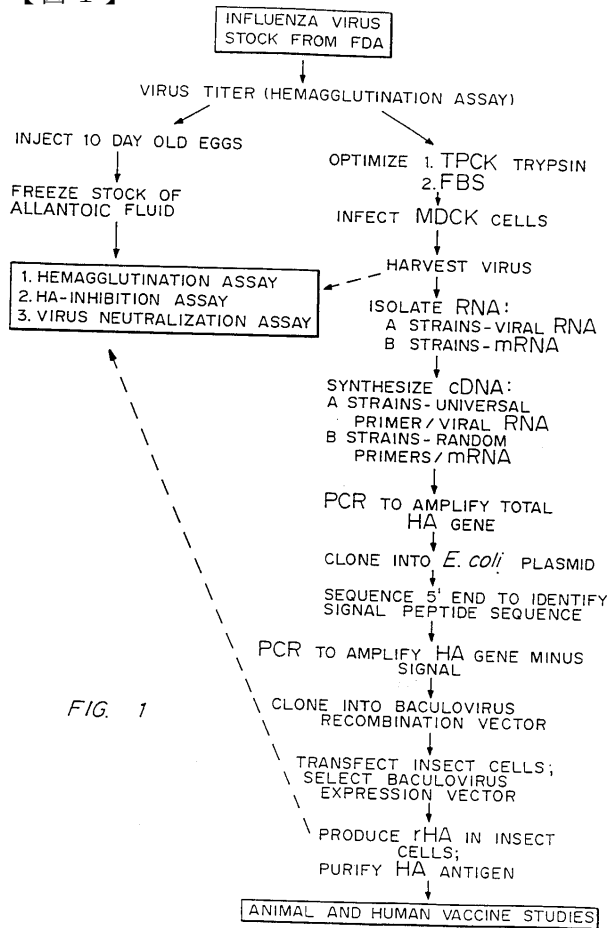


FIG. 1

【図 2】

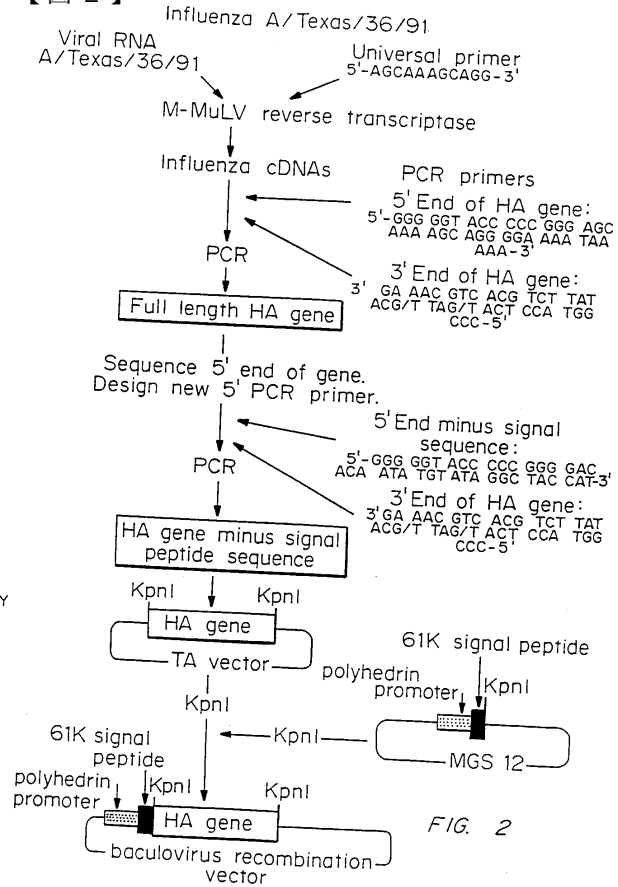


FIG. 2

【図 3】

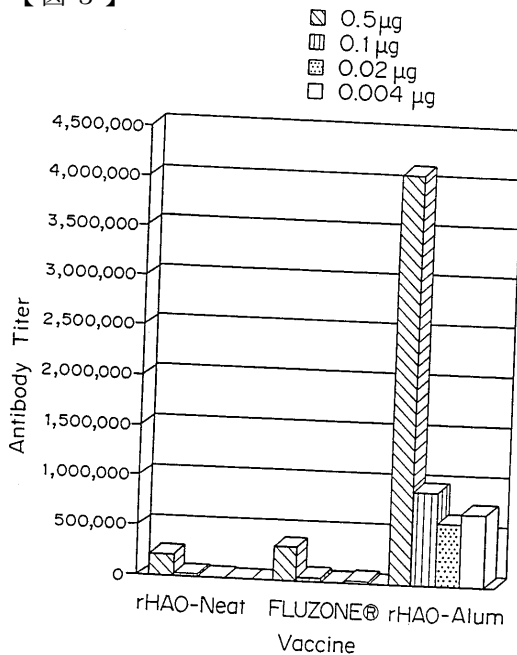
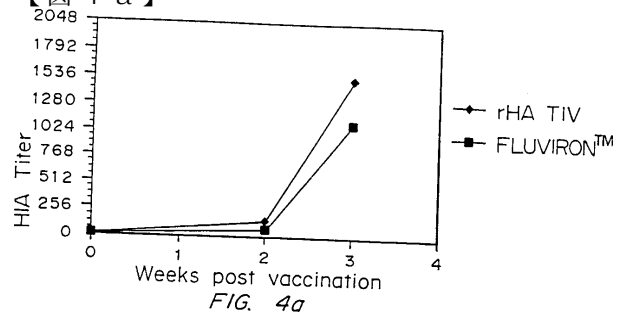
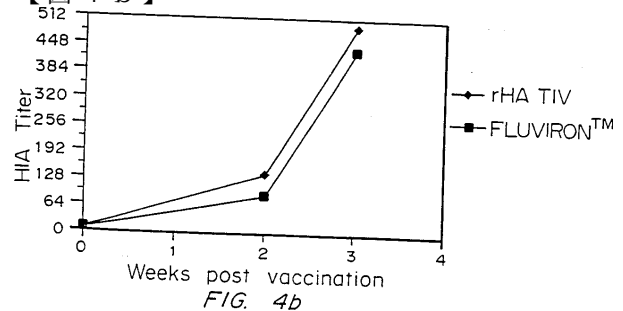


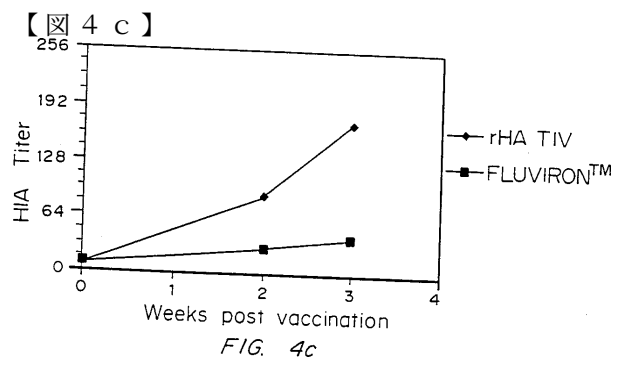
FIG. 3

【図 4 a】



【図 4 b】





フロントページの続き

- (72)発明者 ヴォルヴォヴィッツ, フランクリン  
アメリカ合衆国 コネティカット州 06457 ニュー ヘイヴン ヨーク ストリート 12  
3 アpartment 18イー
- (72)発明者 ウィルキンソン, ベサニー イー  
アメリカ合衆国 コネティカット州 06457 ミドルタウン オレンジ ロード 11
- (72)発明者 ヴォズネゼンスキー, アンドレイ アイ  
アメリカ合衆国 コネティカット州 06107 ウェスト ハートフォード スプリース レー  
ン 15
- (72)発明者 ハケット, クレイグ スタンウェイ  
アメリカ合衆国 コネティカット州 06492 ウォーリングフォード コンドラッキ レーン  
94

審査官 高堀 栄二

- (56)参考文献 米国特許第04752473 (US, A)  
The Journal of Infectious Diseases, 1995, Vol.171, p.1595-1599  
EMBO Journal, 1986, Vol.5, p.1359-1365  
Virus Research, 1986, Vol.5, p.43-59  
Protein Expression Purification, 1993, Vol.4, p.349-357  
Virology, 1994, Vol.202, p.586-605  
Journal of Clinical Microbiology, 1994, Vol.32, p.2468-2473  
Proc. Natl. Acad. Sci. USA, 1983, Vol.80, p.7155-7159  
Vaccine, 1993, Vol.11, p.1185-1187  
Journal of Virology, 1978, Vol.26, p.457-467  
Proc. Natl. Acad. Sci. USA, 1981, Vol.78, p.5488-5492  
Virology, 1990, Vol.174, p.418-429

- (58)調査した分野(Int.Cl., DB名)  
C12N 15/00 - 15/90  
SwissProt/PIR/GeneSeq  
GenBank/EMBL/DDBJ/GeneSeq  
BIOSIS/WPI(DIALOG)  
PubMed