DESCRIPTION

Anti-(Influenza A Virus Subtype H5 Hemagglutinin) Monoclonal Antibody

TECHNICAL FIELD

[0001]

The present invention relates to an anti-H5 subtype influenza A virus hemagglutinin monoclonal antibody, and a method of immunoassay of anti-H5 subtype influenza A virus and an immunoassay kit, which method and kit use the monoclonal antibody.

BACKGROUND ART

[0002]

Influenza viruses of H5 and H7 types have caused heavy damage to the poultry industry mainly in Asia, and, in recent years, avian influenza virus was confirmed to be infectious also to human. In particular, in terms of avian influenza viruses belonging to H5 subtype, there are many reports as from 2003 on their infection to human and high lethality mainly in Asia, so that there is a worldwide concern of their pandemic due to absence of immunity against the viruses in human. Therefore, prophylaxis of, and countermeasures against them are being studied.

[0003]

In order to prevent infection of avian influenza virus to human, or in order to prevent at least its outbreak in human, it is important to specifically and rapidly detect avian influenza virus that is infectious also to human. As a method for rapid detection of a virus in a sample, immunoassay has been conventionally widely used, and immunochromatography carried out by a sandwich immunoassay, wherein a solid phase in which an anti-virus antibody is immobilized on a part of a porous substrate through which a liquid is allowed to flow is used, has been especially

widely used at clinical sites such as hospitals since viruses can be very simply detected in a short time thereby. Immunochromatography kits with which human influenza viruses can be detected are also commercially available.

[0004]

In order to detect by immunoassay avian influenza virus that is also infectious to human, an antibody against the avian influenza virus is of course necessary. The surface antigens of influenza viruses are known to contain proteins called hemagglutinin and neuraminidase. As the hemagglutinin (HA), 16 types having different antigenicities, H1 to H16, are known, and, as the neuraminidase, 9 types having different antigenicities, N1 to N9, are known. The subtype of each influenza virus is represented by description of the types of these hemagglutinin and neuraminidase, such as "H5N1". Most of the avian influenza viruses that have been so far confirmed to have been infected from bird to human are those having hemagglutinin of H5 type. Therefore, as an antibody to detect a highly pathogenic influenza virus that is infectious from bird to human, an antibody specific to H5 subtype influenza virus is demanded.

[0005]

Hemagglutinin of H5 subtype influenza A virus has been studied well, and not only the amino acid sequence but also the spatial structure thereof are known (Non-patent Document 1). Further, various monoclonal antibodies against hemagglutinin of H5 subtype influenza A virus have been known (Non-patent Documents 2 to 4). Further, measurement of H5 subtype influenza A virus by a sandwich immunoassay using 2 types of hemagglutinin monoclonal antibodies has been known (Non-patent Documents 5 and 6).

[0006]

[Non-patent Document 1] Ya Ha et al; The EMBO Journal, 21(5), 865-875, 2002

[Non-patent Document 2] Nikolai V.K. et al., J. Gen. Virol. 83, 2497, 2002

[Non-patent Document 3] James Stevens et al., SCIENCE VOL 312, 21 APRIL 2006

[Non-patent Document 4] Zhi-Yong Yang et al., SCIENCE VOL 317, 10 AUGUST 2007

[Non-patent Document 5] Tsuda Y. et al., Microbiol. Immunol. 51(9), 903, 2007

[Non-patent Document 6] Qigai He et al., Clin. Vacc. Immnol. 617, 2007

SUMMARY

[0006a]

In a first aspect, there is provided an anti-H5 subtype influenza A virus hemagglutinin monoclonal antibody or an antigen-binding fragment thereof which undergoes antigen-antibody reaction with hemagglutinin of H5 subtype influenza A virus, whose corresponding epitope does not exist in the receptor subdomain (excluding C-terminal region thereof consisting of 11 amino acids) and which des not have neutralizing activity against said influenza A virus; wherein said monoclonal antibody or an antigen-binding fragment thereof is suibstantially non-cross-reactive with hemagglutinins of H1 to H4 subtypes and H6 to H15 subtypes; and wherein said corresponding epitope exits in: (1) the regions of 41 to 60 aa and 312 to 322 aa; (2) the regions of 61 to 80 aa and 290 to 300 aa; or (3) the regions of 101 to 113 aa and 268 to 278 aa, based on the amino acid sequence shown in SEQ ID NO: 2.

[0006b]

In a second aspect, there is provided a method of immunoassay of H5 subtype influenza A virus, comprising measurement of H5 subtype influenza A virus in a sample by immunoassay using antigen-antibody reaction of the monoclonal antibody or an antigen-binding fragment thereof as defined above with hemagglutinin of the H5 subtype influenza A virus.

[0006c]

In a third aspect, there is provided an immunoassay kit for H5 subtype influenza A virus, comprising 2 types of the monoclonal antibody and/or an antigen-binding fragment thereof as defined above, said 2 types of the antibody and/or the antigen-binding fragment thereof being capable of binding at the same time to hemagglutinin of H5 subtype influenza A virus.

DISCLOSURE OF THE INVENTION

PROBLEMS TO BE SOLVED BY THE INVENTION

[0007]

As monoclonal antibodies against hemagglutinin of H5 subtype influenza A virus, neutralizing antibodies having neutralizing activity as antibodies that suppress and inhibit the infectivity of the virus have been mainly studied so far. In order to develop a vaccine against the virus, a neutraliizing antibody is necessary, and the monoclonal antibodies described in the above Non-Patent Documents 2 to 4 are also neutralizing antibodies. Further, in terms of the monoclonal antibodies used for the immunoassays described in Non-patent Documents 5 and 6, there is no description on the result of analysis of the epitopes and neutralizing activity of the antibodies.

[0008]

Using such a known neutralizing antibody, an immunoassay system for H5 subtype influenza virus can of course be constructed. However, the present inventors noticed that, in cases where an immunoassay system was constructed using a neutralizing antibody, it may be impossible to keep up with mutation of the virus. That is, the present inventors noticed that, since influenza virus is known to cause

mutation in the epitope recognized by a neutralizing antibody to escape from immunological surveillance of the host, construction of an immunoassay system using a known neutralizing antibody may lead to loss of reactivity with the mutant virus or decrease in the binding affinity, resulting in inability to detect the virus or drastic decrease in the measured value relative to the correct value. In view of the fact that viruses frequently mutate, it is preferred to be able to accurately carry out immunoassay of a virus even in cases where a certain level of mutation has occurred.

[0009]

Accordingly, an object of the present invention is to provide a method of immunoassay of H5 subtype influenza A virus by which the virus can be accurately assayed even in cases where a certain level of mutation has occurred in the H5 subtype influenza A virus, and a kit therefor, and a novel anti-H5 subtype influenza A virus monoclonal antibody which can be used for the immunoassay.

MEANS FOR SOLVING THE PROBLEMS

[0010]

Influenza virus is known to be first bound to a receptor on the cell surface and then incorporated into the inside of the cell, upon its infection. Therefore, for growth of influenza virus in a host cell, the virus needs to be bound to the receptor on the cell surface, so that, if this process is inhibited, growth of the virus does not occur. The corresponding epitopes of known neutralizing antibodies are located in the receptor binding region of influenza virus, and the neutralizing antibodies are bound to the virus to prevent the virus from being bound to the receptor. On the other hand, viruses are known to be prone to mutation in circumstances where a neutralizing antibody produced by the natural immunity of the host or by administration of a vaccine exists, in order to escape from growth inhibition by the neutralizing antibody. Although the mutation itself may occur at random, only

viruses mutated such that their growth is not inhibited by the neutralizing antibody can grow well, so that, as a result, viruses having such a mutation(s) increase among the growing viruses. This phenomenon is called escape mutation, and the fact that a neutralization antibody makes such mutation more easily occur is called antibody pressure or immune pressure. The present inventors inferred that a method of immunoassay by which a virus can be assayed even in cases where a certain level of mutation has occurred in the virus can be constructed by using a monoclonal antibody whose corresponding epitope is located in a region other than the region where the corresponding epitopes of neutralizing antibodies exist, and determined the region where the corresponding epitope of such a monoclonal antibody exists, which monoclonal antibody was then actually provided, thereby completing the present invention.

[0011]

That is, the present invention provides an anti-H5 subtype influenza A virus hemagglutinin monoclonal antibody or an antigen-binding fragment thereof which undergoes antigen-antibody reaction with hemagglutinin of H5 subtype influenza A virus, whose corresponding epitope does not exist in the receptor subdomain (excluding C-terminal region thereof consisting of 11 amino acids) and which does not have neutralizing activity against the influenza A virus. Further, the present invention provides a method of immunoassay of H5 subtype influenza A virus, comprising measurement of H5 subtype influenza A virus in a sample by immunoassay using antigen-antibody reaction of the above-described monoclonal antibody or an antigen-binding fragment thereof of the present invention with hemagglutinin of the H5 subtype influenza A virus. Further, the present invention provides an immunoassay kit for H5 subtype influenza A virus, comprising 2 types of the above-described monoclonal antibody and/or an antigen-binding fragment thereof of the present invention, the 2 types of the antibody and/or the antigen-

binding fragment thereof being capable of binding at the same time to hemagglutinin of H5 subtype influenza A virus.

EFFECT OF THE INVENTION

[0012]

By the present invention, anti-H5 subtype influenza A virus hemagglutinin monoclonal antibodies whose binding affinities do not change even in cases where H5 subtype influenza A virus caused escape mutation were first provided. Therefore, by immunoassay using a monoclonal antibody of the present invention, it is possible to assay H5 subtype influenza A virus in which escape mutation occurred, and it is also possible to rapidly assay avian influenza virus which is pathogenic also to human. Thus, the present invention is thought to largely contribute to prevention of prevalence of avian influenza virus which is pathogenic also to human.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013]

Fig. 1 is a diagram showing an alignment of the amino acid sequences of hemagglutinin in 2 types of strains of H5 subtype influenza A virus, wherein the distribution of each subdomain and the corresponding epitopes of the 3 types of monoclonal antibodies prepared in Examples are shown.

Fig. 2 is a diagram showing alignment of the amino acid sequences of hemagglutinin in 2 types of strains of H5 subtype influenza A virus.

Fig. 3 is a diagram showing the spatial structure of hemagglutinin of the H5 subtype influenza A virus strain, wherein the corresponding epitope regions of the 3 types of monoclonal antibodies prepared in Examples are shown.

Fig. 4 is a diagram showing the results obtained during the epitope analysis of the 3 types of monoclonal antibodies, which was carried out in Examples.

Fig. 5 is a diagram showing results obtained during the epitope analysis of the 3 types of monoclonal antibodies, which was carried out in Examples.

Fig. 6 is a schematic cross-sectional view of the main part of the immunoassay device (immunochromatographic device) prepared in Examples.

Fig. 7 is a schematic plan view of the immunoassay device (immunochromatographic device) prepared in Examples.

Fig. 8 is a schematic cross-sectional view of the immunoassay device (immunochromatographic device) prepared in Examples.

Fig. 9 is a schematic cross-sectional view of the main part of another immunoassay device (immunochromatographic device) prepared in Examples.

Fig. 10 is a schematic plan view of another immunoassay device (immunochromatographic device) prepared in Examples.

BEST MODE FOR CARRYING OUT THE INVENTION

[0014]

As described above, the monoclonal antibody of the present invention undergoes antigen-antibody reaction with hemagglutinin of H5 subtype influenza A virus, and the corresponding epitope of the monoclonal antibody is located in a region other than the receptor subdomain (excluding C-terminal region thereof consisting of 11 amino acids).

[0015]

Examples of the base sequence of the gene of hemagglutinin of H5 subtype influenza A virus (this may be hereinafter referred to as "H5 HA" for short) and the amino acid sequence encoded thereby are shown in SEQ ID NOs: 1 and 2. The sequences shown in SEQ ID NOs: 1 and 2 are known and registered in GenBank under the Accession No. AB263192.

[0016]

Several base sequences of genes and amino acid sequences of H5 HA other than those described above are also known, and examples thereof include the base sequence of the gene and the amino acid sequence of HA of H5N3 described in the above-described Non-patent Document 1, registered in GenBank under Accession No. of AF303057 (the amino acid sequence is registered also under Accession No. Q9DLP3) (SEQ ID NOs. 3 and 4). A monoclonal antibody which undergoes antigen-antibody reaction with one of the known H5 subtype HAs is included within the scope of the monoclonal antibody of the present invention, and, since the homologies among the H5 subtype HAs are high, it usually undergoes antigen-antibody reaction with any of the H5 subtype HAs.

[0017]

An alignment of the amino acid sequence shown in SEQ ID NO:2 and the amino acid sequence shown in SEQ ID NO:4 is shown in Fig. 1. In Fig. 1, each domain in the amino acid sequences is also shown (Non-patent Document 1). Fig. 2 shows only the alignment of the amino acid sequences. Since, as shown well in Fig.2, the homology between the both amino acid sequences is very high (about 96.8%) and the numbers of amino acids are the same, the distribution of the various domains in the amino acid sequence shown in SEQ ID NO:2 can be easily seen from the distribution of the various domains (Non-patent Document 1) known for SEQ ID NO:4 (Fig. 1). In the present specification and claims, positions in the amino acid sequence of H5 HA are specified based on the amino acid sequence shown in SEQ ID NO:2. Since, as described above, the homologies among the amino acid sequences of HAs of H5 influenza A are very high, the amino acid sequence of another H5 HA can be easily aligned with the amino acid sequence shown in SEQ ID NO:2, so that the corresponding position in the amino acid sequence of the another H5 HA can be easily specified based on the amino acid sequence shown in SEQ ID NO:2. Further, the term "based on the amino acid sequence shown in SEQ ID

NO:2" means usage of the amino acid sequence shown in SEQ ID NO:2 as the basis for specifying the position, and does not only mean a monoclonal antibody prepared using HA having the amino acid sequence shown in SEQ ID NO:2 as an immunogen.

[0018]

As can be seen from Fig. 1, based on the amino acid sequence shown in SEQ ID NO:2, the receptor subdomain corresponds to 278 aa from the 126th amino acid from the N-terminus (hereinafter referred to as "126 aa"). The corresponding epitope of the monoclonal antibody of the present invention does not exist in the receptor subdomain (excluding C-terminal region thereof consisting of 11 amino acids). When the antibody is bound to the receptor subdomain, influenza virus cannot be bound to the receptor on the cell surface, and hence cannot enter the cell, so that the virus cannot grow in the host. That is, the antibody has neutralizing activity against influenza virus. However, it should be noted that a part of the corresponding epitope of one (IFH5-115) of the monoclonal antibodies actually prepared in the Examples below is located in the region of 11 amino acids (268-278 aa) in the C-terminus of the receptor subdomain, but the antibody does not have neutralizing activity, so that the C-terminus region of the receptor subdomain is not indispensable for binding of the virus to the receptor. Therefore, from the region defined in the present invention where the corresponding epitope does not exist (which is basically the receptor subdomain), the 11 amino acids in the C-terminus of the receptor subdomain are excluded.

[0019]

The corresponding epitope of the monoclonal antibody of the present invention is not restricted as long as it is located in a region other than the above-described receptor subdomain (excluding C-terminal region thereof consisting of 16 amino acids), and the corresponding epitope preferably exists in:

(1) the region of 41 to 60 aa and 312 to 322 aa;

(2) the region of 61 to 80 aa and 290 to 300 aa; or

(3) the region of 101 to 113 aa and 268 to 278 aa.

[0020]

Here, the corresponding epitope "exists in the region" means that the binding activity to a deletion mutant in which the region is deleted is lost or at least significantly decreases, and its meaning includes not only cases where the corresponding epitope exists in the region, but also cases where the corresponding epitope exists in a region overlapping with this region and the binding activity is lost or at least significantly decreases if the region is deleted. The corresponding epitope regions defined in each of the above (1) to (3) consist of two regions which are largely distant from each other in the amino acid sequence, but these two regions are adjacent to each other in the spatial structure of HA (see Fig. 3). Therefore, for example, existence of the corresponding epitope in the region of 41 to 60 aa and 290 to 300 aa described in the above (1) means existence of the corresponding region over the entire portion consisting of these regions adjacent to each other in the spatial structure, and in cases where either 36 to 65 aa or 307 to 327 aa is deleted, the monoclonal antibody cannot be bound to the partially deleted HA.

[0021]

The region in which the corresponding epitope exists can be known by investigation of the binding ability to deletion mutants as concretely described in the Examples below, which investigation is based on a principle used in conventional methods. That is, it can be investigated by preparing various mutants in which various regions are deleted using the genetic engineering technique, followed by assaying whether or not the binding ability to the monoclonal antibody is lost or significantly decreased in each of the deletion mutants due to the deletion.

[0022]

The monoclonal antibody of the present invention does not have neutralizing

activity against the influenza A virus to which it is bound by antigen-antibody reaction. As described above, the corresponding epitope of the monoclonal antibody of the present invention is located in a region other than the receptor subdomain (excluding C-terminus region thereof consisting of 11 amino acids), and by this constitutional requirement, the neutralizing activity is mostly lost, but monoclonal antibodies whose corresponding epitopes are located in regions other than the receptor subdomain (excluding C-terminal region thereof consisting of 11 amino acids) are also included, which monoclonal antibodies exert neutralizing activity by, for example, inhibition of binding of the receptor subdomain to the receptor due to steric hindrance. Whether or not a monoclonal antibody has neutralizing activity can be investigated by allowing a mixture of H5 subtype influenza A virus and the monoclonal antibody to act on cells and culturing the cells, followed by confirming whether or not the cells are injured, as concretely described in the Examples below.

[0023]

Further, the monoclonal antibody of the present invention is preferably substantially non-cross-reactive with the other HA subtypes (i.e., H1 to H4 and H6 to H15) of influenza A virus. Because of the fact that the monoclonal antibody is substantially non-cross-reactive with the other HA subtypes, H5 subtype influenza A virus which has been confirmed to be infectious from bird to human can be distinguished from other influenza viruses and assayed. Here, the term "substantially non-cross-reactive" means that the cross-reaction does not occur at a detectable level or, even though detection of the cross-reaction is possible, the cross-reaction is very weak and therefore can be clearly distinguished from the antigen-antibody reaction with H5 HA. For example, in the Examples below, cross-reaction with various subtypes of HAs was investigated by immunochromatography using 2 types of anti-H5 HA monoclonal antibodies of the present invention as an

immobilized antibody and a labeled antibody. In such a method, if the label is not detected in the detection zone, the antibodies can be judged to be substantially non-cross-reactive. The base sequences of the genes, as well as the amino acid sequences, of H1 to H4 and H6 to H15 used in the Examples below are shown in SEQ ID NOs:5 to 12 and 15 to 34, respectively. Occurrence of cross-reaction with the other HA subtypes can be investigated using these.

[0024]

The present invention also provides an antigen-binding fragment of the monoclonal antibody of the present invention. Here, the term "antigen-binding fragment" means an antibody fragment maintaining binding ability (antigen-antibody reactivity) to the corresponding antigen of the antibody, such as a Fab fragment or a $F(ab')_2$ fragment of immunoglobulin. It is well-known that such an antigen-binding fragment can also be used for immunoassay. As is well-known, such fragments can be obtained by treating a monoclonal antibody with a protease such as papain or pepsin. The antigen-binding fragment is not restricted to a Fab fragment and a $F(ab')_2$ fragment, and may be any fragment which maintains binding ability to the corresponding antigen. It may further be one prepared by the genetic engineering technique. Further, for example, a single chain fragment of the variable region (scFv) of an antibody may be expressed in *E. coli* by the genetic engineering technique and used. The method for preparing scFv is well-known, and scFv can be prepared by a process wherein mRNA of a hybridoma prepared as described above is extracted to prepare single-stranded cDNAs, and PCR is carried out using primers specific to the heavy chain and the light chain of immunoglobulin to amplify the heavy chain gene and the light chain gene, which genes are then linked to each other with a linker and given an appropriate restriction site, followed by introduction of the resultant to a plasmid vector, transformation of *E. coli* with the resulting plasmid vector, and recovery of scFv from the *E. coli*. Such scFv is also included in the

"antigen-binding fragment" defined in the present invention.

[0025]

The monoclonal antibody of the present invention can be obtained by a process wherein anti-H5 subtype influenza A virus monoclonal antibodies are prepared by a conventional method using H5 subtype influenza A virus as an immunogen, and monoclonal antibodies having binding ability to HA are screened, followed by screening of those which do not have neutralizing activity against H5 subtype influenza A virus and analysis of the corresponding epitopes of the screened monoclonal antibodies, to select an antibody that satisfies the above-described requirement for the epitope. The monoclonal antibodies themselves can be prepared by the well-known hybridoma method, and the method is also concretely described in the Examples below. Further, the neutralizing activity against influenza A virus can be investigated by the above method wherein a mixture of the virus and a monoclonal antibody is allowed to act on cells to see if the cells are injured, which method is also concretely described in the Examples below. Further, the analysis of the corresponding epitopes can be carried out by the above method wherein various deletion mutants of H5 HA are prepared and their binding ability to each monoclonal antibody is investigated, which method is also concretely described in the Examples below.

[0026]

The present invention also provides a method of immunoassay of H5 subtype influenza A virus, comprising measurement of H5 subtype influenza A virus in a sample by immunoassay using antigen-antibody reaction of the above-described monoclonal antibody or an antigen-binding fragment thereof of the present invention with hemagglutinin of the H5 subtype influenza A virus. In the present invention, the term "measurement" include detection, quantification and semi-quantification.

[0027]

Methods of immunoassay themselves are well-known in the art and the monoclonal antibody or an antigen-binding fragment thereof of the present invention can be used in any of the well-known methods of immunoassay. That is, based on the reaction type, known immunoassays include sandwich immunoassays, competition immunoassays, agglutination immunoassays and the like. Based on the label employed, known immunoassays include enzyme immunoassays, radio immunoassays, fluorescence immunoassays, chemiluminescence immunoassays and the like. Any of these immunoassays are included in the "immunoassay" defined in the present invention and can be used as the method of immunoassay of the present invention. The reagents necessary for each type of immunoassay are also well-known in the art. Except for the monoclonal antibody or an antigen-binding fragment thereof used which is characteristic, the immunoassay can be carried out using an ordinary immunoassay kit. That is, the present invention also provides an immunoassay kit for carrying out the method of measurement of the present invention, which kit contains the above-described monoclonal antibody or an antigen-binding fragment thereof of the present invention.

[0028]

Among the methods of immunoassay, a sandwich immunoassay is advantageous for highly sensitive and rapid measurement of H5 subtype influenza A virus, which immunoassay uses 2 types of the monoclonal antibody and/or an antigen-binding fragment thereof of the present invention which can be bound to hemagglutinin of the virus at the same time. Usually, in a sandwich immunoassay, one of the 2 types of monoclonal antibodies used is immobilized on beads or wells of a microplate, or a solid phase such as a porous matrix for immunochromatography, and the other is labeled by enzyme labeling, fluorescence labeling, chemiluminescence labeling or the like. The virus antigen to be measured is sandwiched between the immobilized antibody and the labeled antibody, and the

label bound to the solid phase is measured. In cases where H5 subtype influenza A virus is to be detected, detection of the label bound to the solid phase allows detection of the virus. In cases where the virus is to be quantified, the label is measured for standard samples of various different known amounts by the immunoassay system and the correlation between the amount of the label and the amount of the virus is plotted to prepare a calibration curve (standard curve). By the same operation, the amount of the label of an unknown sample is then measured, and the measured value is applied to the calibration curve to measure the virus quantitatively. These sandwich immunoassays themselves are well-known.

[0029]

In the sandwich immunoassay of the present invention, 2 types of anti-H5 HA monoclonal antibodies of the present invention which can be bound to a single H5 HA molecule at the same time are used. In this case, the immunoassay is preferably carried out using 2 types out of the 3 types of monoclonal antibodies whose corresponding epitopes exist in:

(1) the region of 41 to 60 aa and 312 to 322 aa;

(2) the region of 61 to 80 aa and 290 to 300 aa; and

(3) the region of 101 to 113 aa and 268 to 278 aa,

based on the amino acid sequence shown in SEQ ID NO:2, since, by this, immunoassay which is excellent in the sensitivity and the specificity is possible.

[0030]

In cases where H5 subtype influenza A virus in a sample is to be quantified, a sandwich immunoassay using wells of a microplate or beads as a solid phase, such as ELISA, can be preferably used. On the other hand, in cases where H5 subtype influenza A virus is to be detected rapidly and simply at clinical sites, immunochromatography (often referred to as "immunochromato" for short) is preferably used. Immunochromatography itself and devices (this may be

hereinafter referred to as "immunochromatographic device") used therefor are well-known, and also concretely described in the Examples below.

[0031]

Briefly, lateral flow-based immunochromatography is carried out using a device having, usually on a belt-like matrix comprising a porous material such as nitrocellulose membrane, a detection zone on which a first anti-H5 HA monoclonal antibody was immobilized, and a labeled reagent zone on which a labeled second anti-H5 HA monoclonal antibody was spotted positioned in the upstream (upstream with respect to the direction of the flow of the later-mentioned developer) of the detection zone. Since the sample is added to the labeled reagent zone, and since it is necessary for the labeled antibody to be discharged from the labeled reagent zone and flow in the matrix, the labeled reagent zone is usually constituted by a porous pad to which the labeled antibody was spotted. At the upstream end of the matrix, a developer tank storing a developer is provided. The device usually further has: a development confirmation section on which an anti-labeled antibody was immobilized, for confirmation of whether or not development of the labeled antibody occurred, in the downstream of the above detection zone; and a developer absorption zone on which a porous absorption pad to absorb the developer flown to this zone is provided, in the further downstream of the development confirmation section. Further, in cases where the label is an enzyme label, a substrate zone on which the substrate of the label enzyme was spotted is provided in the upstream of the labeled reagent zone.

[0032]

In operation, the sample is added to the labeled reagent zone, and the developer is applied to the upper end of the matrix by breaking the developer tank. The developer flows to the downstream by capillary action of the matrix. When the developer flows through the substrate zone, the substrate is eluted into the developer,

and the resulting developer containing the substrate continues to flow. When the developer passes through the labeled reagent zone, the labeled antibody and the sample are eluted into the developer, and the resulting developer containing the substrate, the labeled antibody and the sample continues to flow. In cases where H5 subtype influenza A virus is contained in the sample, HA of the virus is bound to the labeled antibody by antigen-antibody reaction. When the mixture of these has reached the detection zone, the immobilized antibody is bound to HA of the virus by antigen-antibody reaction. As a result, the labeled antibody is immobilized on the detection zone via HA of the virus. Therefore, by measuring the label immobilized on the detection zone, the virus can be detected. In cases where H5 subtype influenza A virus is not contained in the sample, nothing is bound to the immobilized antibody, so that the labeled antibody is not immobilized to the detection zone, and continues to flow to the downstream. Therefore, the label is not detected on the detection zone. Since the anti-labeled antibody is immobilized on the developer confirmation section in the downstream of the detection zone, the labeled antibody is immobilized on the developer confirmation section. In cases where the label is detected on the developer confirmation section, it can be confirmed that the developer has reached this section properly. The developer is absorbed to the absorption pad in the further downstream of the developer confirmation section.

[0033]

The sample to be applied to the method of immunoassay of the present invention is not restricted as long as whether or not H5 subtype influenza A virus is contained in the sample is to be detected, and examples of the sample include, but are not limited to, body fluids such as blood (including whole blood, plasma and serum), saliva and sputum; mucosal swabs; and swabs of tools and equipments.

[0034]

The present invention will now be described more concretely by way of

Examples. However, the present invention is not restricted to the Examples below.

EXAMPLES

[0035]

Reference Example 1

Preparation of a H5 Subtype Influenza A Virus (H5N1) Antigen for Immunization and ELISA/Western Blotting (WB)

Chorioallantoic fluid derived from an embryonated egg infected with an attenuated influenza virus strain A/duck/Hokkaido/Vac-1/04(H5N1) (GenBank accession No.: AB259712; SEQ ID NOs:49 and 50) was subjected to ultracentrifugation at 27000 rpm at 4°C for 1.5 hours, and the virus was recovered as a pellet. The pellet was dissolved into PBS, followed by recovery of the virus-containing fraction by sucrose gradient centrifugation. Ultracentrifugation was carried out again to remove sucrose, thereby obtaining a purified virus solution. The purified virus was inactivated with formalin or Triton X-100 (trademark) to be used as an antigen for immunization and ELISA/WB. The formalin treatment was carried out by adding formalin to the purified virus solution to a final concentration of 0.2% and leaving the resulting mixture to stand at 4°C for 1 week, and the Triton X-100 (trademark) treatment was carried out by adding 3 volumes of cell extraction buffer (0.05M Tris-HCl (pH8.0), 0.6 M KCl, 0.5% Triton X-100 (trademark)) to the purified virus solution. Inactivation of the virus was confirmed by inoculating the virus subjected to the inactivation treatment to an embryonated egg at 10 days of age and culturing the egg for 2 days, followed by confirming that no HA titer was detected by a hemagglutination (HA) test on chorioallantoic fluid derived from an embryonated egg infected with the virus.

[0036]

Reference Example 2

Preparation of a H5 Subtype Influenza A Virus (H5N1) Antigen for Confirmation of Specificity (IF, WB)

The virus-infected Madin-Darby canine kidney (MDCK) cells (source of supply: Hokkaido University) to be used for confirmation of the specificity of the established antibody, and cell extract thereof were prepared as follows. For preparation of the antibody for immunofluorescence (IF), MDCK cells were cultured on a chamber slide to obtain a full sheet of the cells, and each influenza virus was optimally diluted with MEM supplemented with trypsin (serum-free) and inoculated to the cells. The cells were then cultured in a CO_2 incubator at 35°C for 16 hours, and the cultured cells were fixed with cold acetone to provide a slide for IF for confirmation of the specificity.

[0037]

For preparation of the antigen for WB, MCDK cells were cultured in a petri dish to obtain a full sheet of the cells, and serum-free MEM supplemented with trypsin was added to a virus solution optimized in the same manner as in the preparation of the antibody for IF, followed by culturing the cells at 35°C for 16 hours. Thereafter, cell lysis buffer was added to the petri dish to lyse the cells, and the resulting lysate was centrifuged at 14000 rpm for 5 minutes, to obtain the supernatant as the antigen for WB for confirmation of the specificity.

[0038]

Example 1

Establishment of Monoclonal Antibodies Specific to Influenza A Virus (H5) Hemagglutinin

The monoclonal antibodies were prepared by immunizing mice with the purified inactivated influenza virus A/duck/Hokkaido/Vac-1/04(H5N1) prepared in Reference Example 1, followed by fusing lymphocytes derived from hind limbs of the mice and myeloma cells. That is, BALB/C mice were first immunized in their

footpads with the purified inactivated influenza virus A/duck/Hokkaido/Vac-1/04(H5N1) emulsified with Freund's complete adjuvant in an amount of 50 to 100 μg/mouse, and 2 to 3 weeks later, the mice were subjected to second immunization with the purified inactivated influenza virus A/duck/Hokkaido/Vac-1/04(H5N1) antigen which is adjuvant-free in an amount of 50 to 100 μg/mouse. The antibody titer was confirmed by solid-phase ELISA using a 96-well ELISA plate coated with Triton X100-treated purified influenza virus A/duck/Hokkaido/Vac-1/04(H5N1), and by WB with the same antigen. Mice in which increase in the antibody titer was confirmed were immunized in their footpads with the purified inactivated influenza virus A/duck/Hokkaido/Vac-1/04(H5N1) in an amount of 25 to 50 μg/mouse, and 3 to 4 days later, lymphocytes were prepared from lymph nodes of hinder limbs of the mice. Mouse myeloma cells (P3U1) preliminarily cultured in RPMI-1640 medium were mixed with spleen cells at ratios of 1:2 to 1:5, and cell fusion was carried out using polyethylene glycol (PEG; manufactured by Boehringer). The fused cells were suspended in HAT medium and aliquoted to a 96-well culture plate, followed by culturing the cells in a CO_2 incubator at 37°C.

[0039]

Screening of the produced antibodies was carried out by the above-described solid-phase ELISA. That is, the Triton X-100 (trademark)-treated purified influenza virus A/duck/Hokkaido/Vac-1/04(H5N1) antigen was aliquoted to a 96-well ELISA plate (manufactured by Nunc) at a concentration of 1 μg/ml in a volume of 50 μl/well, and left to stand at 4°C overnight to allow its adsorption. The wells were blocked with 1% skim milk and washed 3 times with washing buffer (PBS supplemented with 0.05% Tween 20), followed by adding 50 μl of the culture supernatant from the plate in which the cell fusion was carried out, and allowing the reaction to proceed at 37°C for 1 hour. After washing the wells 3 times with washing buffer in the same manner, a POD-labeled anti-mouse immunoglobulin

antibody (manufactured by DACO) was added, followed by allowing the reaction to proceed at 37°C for 1 hour. After washing the wells 4 times with washing buffer, the substrate ABTS was added, followed by selecting the wells in which coloring was observed. Subsequently, the cells in the selected wells were transferred to a 48-well or 24-well culture plate and cultured in a CO2 incubator at 37°C, followed by confirming their reactivity with hemagglutinin by WB. The WB was carried out according to a conventional method using a membrane prepared by subjecting the Triton X-100 (trademark)-treated purified influenza virus A/duck/Hokkaido/Vac-1/04(H5N1) antigen to SDS-PAGE, followed by transferring it to a nitrocellulose membrane. The cells in the wells in which reactivity to hemagglutinin was confirmed by WB were made into single clones by the limiting dilution method to establish the various hybridomas described below which produce monoclonal antibodies reactive with influenza (H5N1) hemagglutinin.

[0040]

In order to exclude clones having cross-reactivity with epitopes, competing monoclonal antibodies were first excluded by an inhibition test, and only monoclonal antibodies that are not competitive with one another were selected. More particularly, this inhibition test was carried out as follows. A 96-well ELISA plate to which purified influenza virus was adsorbed was prepared in the same manner as in the screening of the Mabs, and a Mab for inhibition at a several-fold higher concentration and an equal amount of an alkaline phosphatase-labeled Mab were added to each well at the same time, followed by allowing the reaction to proceed at 37°C for 1 hour. After washing, the substrate pNPP was added, and whether the reaction of the labeled Mab with the solid phase was inhibited by each Mab was confirmed. Selected 14 types of monoclonal antibodies were used in various combinations as the solid phase antibody and the labeled antibody for the later-mentioned immunochromatographic device which was actually prepared by the late-

mentioned method. Using the prepared immunochromatographic device, influenza A virus in a sample was actually detected, and 3 types of monoclonal antibodies IFH5-115, IFH5-136 and IFH5-26 showing excellent sensitivities and specificities (absence of cross-reaction with other HA subtypes, as mentioned later), and 3 types of hybridomas IFH5-115, IFH5-136 and IFH5-26 producing them were established (the monoclonal antibodies IFH5-115, IFH5-136 and IFH5-26 may be hereinafter referred to as the monoclonal antibody 115 (or Mab 115), monoclonal antibody 136 (or Mab 136) and monoclonal antibody 26 (or Mab 26), respectively). These monoclonal antibodies did not have neutralizing activity against influenza A virus, as mentioned later.

[0041]

Example 2

Confirmation of the Reaction Specificities of the Monoclonal Antibodies by IF and WB

The IF was carried out as follows. That is, to the slide for IF for confirmation of the specificity which was prepared in Reference Example 2, the culture supernatant for each monoclonal antibody or ascites (diluted with 1% BSA in PBST) was added, and the reaction was allowed to proceed for 1 hour at room temperature. The resultant was washed with PBS and allowed to react with a fluorescent dye-labeled anti-mouse IgG (1000-fold diluted with 1% BSA in PBST) at room temperature for 30 minutes. This was followed by washing with PBS, mounting in glycerol and observation under a fluorescence microscope. WB was carried out using the antigen prepared in Reference Example 2 according to a conventional method.

[0042]

The monoclonal antibodies IFH5-115, IFH5-136 and IFH5-26 were confirmed in either assay to be reactive with attenuated H5N1 influenza HA, but the

results on the reactivities against HAs of other substrains and virulent H5N1 were different between the assays. Therefore, the actual assay system (EL) was used for confirmation of these.

[0043]

Example 3

Analysis of the Corresponding Epitopes of the Anti-influenza H5N1 Virus Monoclonal Antibodies

3-1: Preparation of N-terminus Deletion Plasmids

In order to determine the recognition sites of Mab 26, 115 and 136 in the N-terminus side, HA of the influenza H5N1 strain A/duck/Hokkaido/Vac-1/04(H5N1) (SEQ ID NO:2) consisting of 564 amino acids was subjected to PCR to amplify 6 types of fragments: 1 to 564 aa (A fragment), 1 to 514 aa (B fragment), 21 to 514 aa (C fragment), 101 to 500 aa (D fragment), 151 to 500 aa (E fragment), and 201 to 500 aa (F fragment). A *Bam*HI or *Xba*I site had been preliminarily added to each primer. Each amplified fragment was purified with PCR Purification Kit manufactured by QIAGEN and inserted into the *Bam*HI-*Xba*I site in an expression plasmid pWG6A which was prepared by incorporating GST into the *Nde*I-*Eco*RI site in an expression plasmid pW6A, to prepare the plasmids pWGInf.H5N1-N-A, pWGInf.H5N1-N-B, pWGInf.H5N1-N-C, pWGInf.H5N1-N-D, pWGInf.H5N1-N-E and pWGInf.H5N1-N-F. Using these plasmids, *E. coli* BL21(DE3) (supplied from Brookhaven National Laboratory) was transformed to obtain ampicillin-resistant *E. coli* transformants BL21(DE3)pWGInf.H5N1-N-A, BL21(DE3)pWGInf.H5N1-N-B, BL21(DE3)pWGInf.H5N1-N-C, BL21(DE3)pWGInf.H5N1-N-D, BL21(DE3)pWGInf.H5N1-N-E and BL21(DE3)pWGInf.H5N1-N-F.

[0044]

3-2 Expression and Western Blotting of Recombinant Proteins (GST+Inf.H5N1-N-A, GST+Inf.H5N1-N-B, GST+Inf.H5N1-N-C, GST+Inf.H5N1-N-D, GST+Inf.H5N1-

N-E and GST+Inf.H5N1-N-F)

Each of the transformants prepared in 3-1 was cultured in 2 ml of LB medium supplemented with 50 μg/ml ampicillin at 37°C. Preculture was carried out until an OD of 0.6 to 0.8 at 600 nm was attained, and 1 mM IPTG was then added to the culture to induce expression, followed by culturing for additional 3 hours. The bacterial cells were collected by centrifuging 1.5 ml of the bacterial cell culture at 5,000 rpm for 2 minutes, and the collected bacterial cells were suspended in 100 μl of a buffer (10 mM Tris-HCl (pH 8.0), 0.1 M sodium chloride, 1 mM EDTA), followed by completely disrupting the bacterial cells by sonication for 15 minutes. The resultant was used as a bacterial cell sample.

[0045]

To 8 μl of the bacterial sample, 4 μl of 3× SDS polyacrylamide buffer (0.15 M Tris-HCl (pH 6.8), 6% SDS, 24% glycerol, 6 mM EDTA, 2% 2-mercaptoethanol, 0.03% bromophenol blue) was added, and the resulting mixture was stirred sufficiently, followed by heat treatment at 100°C before being subjected to electrophoresis. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) was carried according to a conventional method using e-PAGEL, 12.5% gel concentration (trademark; manufactured by ATTO). Thereafter, the sample was transferred to a PVDF membrane (manufactured by ATTO) and blocked with 1% BSA at 4°C overnight. The blocking solution was removed, and the membrane was washed with PBS-Tween (trademark), followed by adding the monoclonal antibodies 26, 115 and 136 whose concentrations were adjusted to 2 μg/ml and allowing the reaction to proceed at room temperature for 60 minutes. The membrane was washed sufficiently with PBS-Tween (trademark) and subjected to a reaction with a peroxidase-labeled anti-mouse immunoglobulin rabbit polyclonal antibody (manufactured by DAKO) 5000-fold diluted with a reaction buffer. After washing, the membrane was exposed to instant film (manufactured by FUJIFILM) for 1 to 15

minutes using ECL Western Blotting Detection System (manufactured by GE Healthcare Bio-Sciences KK) to detect signals. The results are shown in Fig. 4. The monoclonal antibodies 26 and 115 reacted with the A, B and C fragments, but not reacted with the D fragment. The monoclonal antibody 136 reacted with the A, B, C and D fragments, but not reacted with the E fragment. Accordingly, the monoclonal antibodies 26 and 115, and the monoclonal antibody 136 were revealed to recognize the region of 21 to 100 aa and the region of 101 to 150 aa, respectively.

[0046]

3-3: Preparation of N-terminus Deletion Plasmids

Subsequently, shorter fragments of the amino acid fragment of 21 to 400 of influenza H5N1: N1 (21 to 400 aa), N2 (41 to 400 aa), N3 (61 to 400 aa), N4 (81 to 400 aa), N5 (101 to 400 aa), N6 (114 to 400 aa), N7 (127 to 400 aa) and N8 (139 to 400 aa) were amplified by PCR. Each amplified fragment was purified with PCR Purification Kit manufactured by QIAGEN and inserted into the *Bam*HI-*Xba*I site in an insect cell expression plasmid pBac-EGTs-6A (manufactured by Invitrogen; modified from pFastBac1 vector), to prepare plasmids pBacInf.H5N1-N1, pBacInf.H5N1-N2, pBacInf.H5N1-N3, pBacInf.H5N1-N4, pBacInf.H5N1-N5, pBacInf.H5N1-N6, pBacInf.H5N1-N7 and pBacInf.H5N1-N8. Using these plasmids, *E. coli* DH10Bac for Bacmid preparation was transformed, to prepare Bacmid-Inf.H5N1-N1, Bacmid-Inf.H5N1-N2, Bacmid-Inf.H5N1-N3, Bacmid-Inf.H5N1-N4, Bacmid-Inf.H5N1-N5, Bacmid-Inf.H5N1-N6, Bacmid-Inf.H5N1-N7 and Bacmid-Inf.H5N1-N8.

[0047]

3-4 Expression of Recombinant Proteins (Inf.H5N1-N1, Inf.H5N1-N2, Inf.H5N1-N3, Inf.H5N1-N4, Inf.H5N1-N5, Inf.H5N1-N6, Inf.H5N1-N7 and Inf.H5N1-N8)

Transfection of insect cells, Sf-21 (manufactured by Invitrogen), with each of the 8 types of Bacmid DNAs prepared in 3-3 was carried out to prepare recombinant

viruses P1-N1, P1-N2, P1-N3, P1-N4, P1-N5, P1-N6, P1-N7 and P1-N8. Sf21 cells were infected with a part of each of these P1s and cultured at 27°C for 4 days, followed by collecting the culture supernatant by centrifugation at 3000 rpm for 20 minutes. This was used as the sample for ELISA.

[0048]

The monoclonal antibody 254 which reacts with the amino acid region of 139 to 400 was immobilized and used for ELISA. That is, the monoclonal antibody 254 was diluted to a concentration of 2 μg/mL, and 50 μl of the diluted monoclonal antibody was placed in each well of a microplate module (manufactured by Nunc), followed by incubation at 4°C overnight to immobilize the monoclonal antibody. Subsequently, each well was washed with PBS supplemented with 0.1% Tween 20 (trademark) (PBS-Tween (trademark)), and 100 μL of 1% bovine serum albumin (BSA) prepared by dilution with PBS was added to the well, followed by blocking at 37°C for 1 hour. After removing the blocking solution, 50 μl of a biotinylated monoclonal antibody 26, 115 or 126 was added, and the reaction was allowed to proceed at 37°C for 1 hour. After washing sufficiently with PBS-Tween (trademark), 50 μL of alkaline phosphatase-labeled streptavidin (manufactured by DAKO) 2,000-fold diluted with a reaction buffer was added to each well, and the reaction was allowed to proceed at 37°C for 1 hour. Thereafter, the wells were washed sufficiently with PBS-Tween (trademark), and 50 μl of p-nitrophenyl phosphate was added to each well. The reaction was allowed to proceed at room temperature for 30 minutes, and 50 μl of a stop solution was added to each well, followed by measuring the coloring level (absorbance) at a wave length of 405 nm. As shown in Table 1, it can be assumed that the monoclonal antibody 26 has its epitope in the region of amino acids 61 to 80; the monoclonal antibody 115 has its epitope in the region of amino acids 41 to 60; and the monoclonal antibody 136 has its epitope in the region of amino acids 101 to 113.

[0049]

[Table 1]

	26		115		136	
21-400	1.98	1.89	0.68	0.67	1.48	1.39
41-100	1.94	1.88	0.84	0.64	1.54	1.50
61-400	1.92	1.93	0.29	0.28	1.21	1.20
81-400	0.15	0.15	0.30	0.27	0.78	0.74
101-400	0.15	0.16	0.28	0.27	0.57	0.50
114-400	0.16	0.16	0.30	0.29	0.16	0.17
127-400	0.16	0.16	0.28	0.29	0.17	0.17
139-400	0.15	0.15	0.28	0.29	0.16	0.16
1-514	1.00	0.70	1.10	0.87	1.38	1.44
HBs wt	0.14	0.13	0.24	0.26	0.14	0.14
control	0.13	0.13	0.26	0.26	0.14	0.15

[0050]

3-5 Preparation of C-terminus Deletion Plasmids

In order to determine the recognition sites of Mab 26, 115 and 136 in the C-terminus side, HA of the influenza H5N1 strain A/duck/Hokkaido/Vac-1/04(H5N1) (SEQ ID NO:2) consisting of 564 amino acids was subjected to PCR to amplify 5 types of fragments: 21 to 400 aa (A fragment), 21 to 333 aa (B fragment), 21 to 266 aa (C fragment), 21 to 200 aa (D fragment), and 21 to 133 aa (E fragment). A *Bam*HI or *Xba*I site had been preliminarily added to each primer. Each amplified fragment was purified with PCR Purification Kit manufactured by QIAGEN and inserted into the *Bam*HI-*Xba*I site in an expression plasmid pWG6A which was prepared by incorporating GST into the *Nde*I-*Eco*RI site in an expression plasmid pW6A, to prepare the plasmids pWGInf.H5N1-C-A, pWGInf.H5N1-C-B, pWGInf.H5N1-C-C, pWGInf.H5N1-C-D and pWGInf.H5N1-C-E. Using these, *E. coli* BL21(DE3) (supplied from Brookhaven National Laboratory) was transformed to obtain ampicillin-resistant *E. coli* transformants BL21(DE3)pWGInf.H5N1-C-A, BL21(DE3)pWGInf.H5N1-C-B, BL21(DE3)pWGInf.H5N1-C-C, BL21(DE3)pWGInf.H5N1-C-D and BL21(DE3)pWGInf.H5N1-C-E.

[0051]

3-6 Expression and Western Blotting of Recombinant Proteins (GST+Inf.H5N1-C-A, GST+Inf.H5N1-C-B, GST+Inf.H5N1-C-C, GST+Inf.H5N1-C-D and GST+Inf.H5N1-C-E)

Each of the transformants prepared in 3-5 was cultured in 2 ml of LB medium supplemented with 50 μg/ml ampicillin at 37°C. Preculture was carried out until an OD of 0.6 to 0.8 at 600 nm was attained, and 1 mM IPTG was then added to the culture to induce expression, followed by culturing for additional 3 hours. The bacterial cells were collected by centrifuging 1.5 ml of the bacterial cell culture at 5,000 rpm for 2 minutes, and the collected bacterial cells were suspended in 100 μl of a buffer (10 mM Tris-HCl (pH 8.0), 0.1 M sodium chloride, 1 mM EDTA), followed by completely disrupting the bacterial cells by sonication for 15 minutes. The resultant was used as a bacterial cell sample.

[0052]

To 8 μl of the bacterial sample, 4 μl of 3× SDS polyacrylamide buffer (0.15 M Tris-HCl (pH 6.8), 6% SDS, 24% glycerol, 6 mM EDTA, 2% 2-mercaptoethanol, 0.03% bromophenol blue) was added, and the resulting mixture was stirred sufficiently, followed by heat treatment at 100°C before being subjected to electrophoresis. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) was carried according to a conventional method using e-PAGEL, 12.5% gel concentration (trademark; manufactured by ATTO). Thereafter, the sample was transferred to a PVDF membrane (manufactured by ATTO) and blocked with 1% BSA at 4°C overnight. The blocking solution was removed, and the membrane was washed with PBS-Tween (trademark), followed by adding the monoclonal antibodies 26, 115 and 136 whose concentrations were adjusted to 2 μg/ml and allowing the reaction to proceed at room temperature for 60 minutes. The membrane was washed sufficiently with PBS-Tween (trademark) and subjected to a reaction with a

peroxidase-labeled anti-mouse immunoglobulin rabbit polyclonal antibody (manufactured by DAKO) 5000-fold diluted with a reaction buffer. After washing, the membrane was exposed to instant film (manufactured by FUJIFILM) for 1 to 15 minutes using ECL Western Blotting Detection System (manufactured by GE Healthcare Bio-Sciences KK) to detect signals. The results are shown in Fig. 5. The monoclonal antibodies 26, 115 and 136 reacted with the A and B fragments, but not reacted with the C fragment. Accordingly, the monoclonal antibodies 26, 115 and 136 were revealed to recognize the region of 267 to 333aa.

[0053]

3-7: Preparation of C-terminus Deletion Plasmids

Subsequently, shorter fragments of the amino acid fragment of 267 to 333 aa of influenza H5N1: C1 (41 to 333 aa), C2 (41 to 322 aa), C3 (41 to 311 aa), C4 (41 to 300 aa), C5 (41 to 289 aa), C6 (41 to 278 aa) and C7 (41 to 267 aa) were amplified by PCR. Each amplified fragment was purified with PCR Purification Kit manufactured by QIAGEN and inserted into the *Bam*HI-*Xba*I site in an insect cell expression plasmid pBac-EGTs-6A (manufactured by Invitrogen; modified from pFastBac1 vector), to prepare plasmids pBacInf.H5N1-C1, pBacInf.H5N1-C2, pBacInf.H5N1-C3, pBacInf.H5N1-C4, pBacInf.H5N1-C5, pBacInf.H5N1-C6 and pBacInf.H5N1-C7. Using these plasmids, *E. coli* DH10Bac for Bacmid preparation was transformed, to prepare Bacmid-Inf.H5N1-C1, Bacmid-Inf.H5N1-C2, Bacmid-Inf.H5N1-C3, Bacmid-Inf.H5N1-C4, Bacmid-Inf.H5N1-C5, Bacmid-Inf.H5N1-C6 and Bacmid-Inf.H5N1-C7

[0054]

3-8 Expression of Recombinant Proteins (Inf.H5N1-C1, Inf.H5N1-C2, Inf.H5N1-C3, Inf.H5N1-C4, Inf.H5N1-C5, Inf.H5N1-C6 and Inf.H5N1-C7)

Transfection of insect cells, Sf-21 (manufactured by Invitrogen) with each of the 7 types of Bacmid DNAs prepared in 3-7 was carried out to prepare recombinant

viruses P1-C1, P1-C2, P1-C3, P1-C4, P1-C5, P1-C6 and P1-C7. Sf21 cells were infected with a part of each of these P1s and cultured at 27°C for 4 days, followed by collecting the culture supernatant by centrifugation at 3000 rpm for 20 minutes. This was used as the sample for Enzyme Linked Immunosorbent Assay (ELISA).

[0055]

The monoclonal antibody 270 which reacts with the amino acid region of 41 to 333 aa was immobilized and used for ELISA. That is, the monoclonal antibody 270 was diluted to a concentration of 2 μg/mL, and 50 μl of the diluted monoclonal antibody was placed in each well of a microplate module (manufactured by Nunc), followed by incubation at 4°C overnight to immobilize the monoclonal antibody. Subsequently, each well was washed with PBS supplemented with 0.1% Tween 20 (trademark) (PBS-Tween (trademark)), and 100 μL of 1% bovine serum albumin (BSA) prepared by dilution with PBS was added to the well, followed by blocking at 37°C for 1 hour. After removing the blocking solution, 50 μl of a biotinylated monoclonal antibody 26, 115 or 126 was added, and the reaction was allowed to proceed at 37°C for 1 hour. After washing sufficiently with PBS-Tween (trademark), 50 μL of alkaline phosphatase-labeled streptavidin (manufactured by DAKO) 2,000-fold diluted with a reaction buffer was added to each well, and the reaction was allowed to proceed at 37°C for 1 hour. Thereafter, the wells were washed sufficiently with PBS-Tween (trademark), and 50 μl of p-nitrophenyl phosphate was added to each well. The reaction was allowed to proceed at room temperature for 30 minutes, and 50 μl of a stop solution was added to each well, followed by measuring the coloring level (absorbance) at a wave length of 405 nm. As shown in Table 2, it can be assumed that the monoclonal antibody 26 has its epitope in the region of amino acids 290 to 300; the monoclonal antibody 115 has its epitope in the region of amino acids 312 to 322; and the monoclonal antibody 136 has its epitope in the region of amino acids 268 to 278.

[0056]

[Table 2]

Mutant	26		115		136	
41-333	0.22	0.23	0.94	0.96	0.95	0.96
41-322	0.55	0.52	0.87	0.78	1.10	1.12
41-311	0.53	0.50	0.15	0.14	1.15	1.18
41-300	0.57	0.61	0.14	0.14	1.13	1.21
41-289	0.17	0.17	0.15	0.14	1.01	1.07
41-278	0.17	0.16	0.13	0.14	0.99	1.01
41-267	0.14	0.13	0.14	0.14	0.19	0.15
1-514	1.60	1.47	1.55	1.34	1.10	1.11
HBs wt	0.13	0.13	0.17	0.13	0.12	0.14
Sf21	0.13	0.13	0.13	0.15	0.09	0.16

[0057]

In summary, from 3-1 to 3-8, it is assumed that the monoclonal antibody 26 recognizes the regions of 61 to 88 aa and 290 to 300 aa; the monoclonal antibody 115 recognizes the regions of 41 to 60 aa and 312 to 322 aa; and the monoclonal antibody 136 recognizes the regions of 101 to 113 aa and 268 to 278 aa. That is, it is assumed that these monoclonal antibodies recognize the spatial structure (see Fig. 3).

[0058]

Example 4

Assay of Neutralizing Antibody Activity

Whether or not the monoclonal antibodies IFH5-115, IFH5-136 and IFH5-26 have neutralizing activity against H5 subtype influenza A viruses was tested. As the influenza viruses, A/dk/Hokkaido/84/02(H5N3) and A/PR/8/34(H1N1) were used. A 2-fold dilution series of each monoclonal antibody was prepared with Eagle's MEM, and 50 μl of each antibody dilution was placed in a 96-well plate. Each of the A/dk/Hokkaido/84/02(H5N3) and A/PR/8/34(H1N1) was diluted such that 200 $TCID_{50}$/25μL was attained, and 25 μl of the virus dilution was added to each

well containing the antibody dilution (protein concentration: 0 to 160 μg/25 μL). The resulting mixture was incubated at room temperature for 1 hour (virus-antibody mixture). On the other hand, in a 48-well plate, MDCK cells were preliminarily cultured in Eagle's MEM supplemented with 10% fetal calf serum to confluence, and the culture supernatant was removed. The plate was washed once with Eagle's MEM, and 75 μl of the above-described virus-antibody mixture was added thereto, followed by incubation at 35°C for 1 hour. Subsequently, 150 μl of Eagle's MEM supplemented with 0.0005% trypsin was added to each well, and culture was started at 35°C in the presence of 5% carbon dioxide gas. On day 3 of the culture, whether or not cell injury by the virus was inhibited by neutralizing antibody activity was investigated under the microscope to confirm whether or not the neutralizing activity was exerted. In cases where cell injury has occurred, cell rounding due to cell fusion by virus infection is observed. In cases where cell injury has not occurred, it can be judged that the monoclonal antibody has neutralizing activity against the virus.

[0059]

In terms of controls for this measurement system, a well to which no antibody was added was used as the virus activity control, and chicken antiserum of A/duck/Hokkaido/Vac-1/04 (SEQ ID NO:2) having neutralizing activity was used as the neutralizing antibody control. The test results are shown in Table 3 to Table 6.

[0060]

The chicken antiserum (obtained by immunization with A/duck/Hokkaido/Vac-1/04 (SEQ ID NO:2)) used as the neutralizing antibody control showed neutralizing antibody activity against A/dk/Hokkaido/84/02(H5N3) and A/PR/8/34(H1N1) up to 64-fold dilution, but the monoclonal antibodies IFH5-115, IFH5-136 and IFH5-26 showed no neutralizing activity.

[0061]

[Table 3]

Virus: A/dk/Hokkaido/84/02(H5N3) 10^2 TCID50/25μL(well)

CPE

Antibody	Antibody concentration (μg/mL)					
	160	80	40	20	10	0
IFH5-115	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
IFH5-136	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
IFH5-26	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+

[0062]

[Table 4]

Virus: A/PR/8/34(H1N1) 10^2 TCID50/25μL(well)

CPE

Antibody	Antibody concentration (μg/mL)					
	160	80	40	20	10	0
IFH5-115	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
IFH5-136	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
IFH5-26	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+
	+	+	+	+	+	+

[0063]

[Table 5]

CPE

Immune serum	Chicken immune serum dilution rate								
	2	4	6	8	16	32	64	128	256
A/duck/Hokkaido/Vac-1/04 (H5N1) chicken immune serum	-	-	-	-	-	-	-	+	+
	-	-	-	-	-	-	-	+	+
	-	-	-	-	-	-	-	+	+
	-	-	-	-	-	-	-	+	+

[0064]

[Table 6]

CPE

Immune serum	Chicken immune serum dilution rate								
	2	4	6	8	16	32	64	128	256
A/duck/Hokkaido/Vac-1/04 (H5N1) chicken immune serum	-	-	-	-	-	-	-	+	+
	-	-	-	-	-	-	-	+	+
	-	-	-	-	-	-	-	+	+
	-	-	-	-	-	-	-	+	+

[0065]

Example 5 Preparation of the Influenza A H5 Immunoassay (Immunochromatography) Device 1

As shown in Fig. 6, at the position 15 mm distant from the end of the developer-absorption zone 5-side of a matrix 2 which is a nitrocellulose membrane having a width of 5 mm and a length of 50 mm (manufactured by Millipore), 0.7 μl of an aqueous solution containing an anti-influenza A H5-specific antibody (IFH5-26) was spotted, and the spot was dried, thereby preparing a detection zone 6. Further, at the position 12 mm distant from the end of the developer-absorption zone 5-side of the matrix 2, anti-alkaline phosphatase antibody (rabbit) was spotted, and the spot was dried, thereby preparing a development confirmation section 10. Subsequently, 5 μl of an alkaline phosphatase-labeled anti-influenza A H5-specific antibody which was produced by labeling IFH5-115 antibody with alkaline

phosphatase (ALP- IFH5-115, 10 μg/ml) was spotted on the matrix, and the spot was dried, thereby preparing a labeled reagent zone comprising an enzyme labeling reagent pad 4.

[0066]

In a developer pad 3, 100 μg of 5-bromo-4-chloro-3-indolyl phosphate (BCIP) was spotted as a substrate in the form of a line having a width of 6.0 mm on a filter paper having a width of 6 mm and length of 20 mm (manufactured by Millipore), and the spot was dried, to prepare a substrate zone 7. The matrix 2, the developer pad 3, the enzyme labeling reagent pad 4 and an absorption pad 5 (filter paper of 10 mm width, 15 mm length and 1 mm thickness (manufactured by Whatman)) were immobilized in a plastic case having a developer tank 11, to produce the influenza A H5 immunoassay device 1 shown in Figs. 7 and 8.

[0067]

Example 6

Preparation of the Influenza A H5 Immunoassay Device 2

In the same manner as shown in Fig. 6 in Example 5, at the position 15 mm distant from the end of the developer-absorption zone 5-side of a matrix 2 which is a nitrocellulose membrane having a width of 5 mm and a length of 50 mm (manufactured by Millipore), 0.7 μl of an aqueous solution containing an anti-influenza A H5-specific antibody (IFH5-136) was spotted, and the spot was dried, thereby preparing a detection zone 6. Further, at the position 12 mm distant from the end of the developer-absorption zone 5-side of the matrix 2, anti-alkaline phosphatase antibody (rabbit) was spotted, and the spot was dried, thereby preparing a development confirmation section 10. Subsequently, 5 μl of an alkaline phosphatase-labeled anti-influenza A H5-specific antibody which was produced by labeling IFH5-115 antibody with alkaline phosphatase (ALP- IFH5-115, 10 μg/ml) was spotted on the matrix, and the spot was dried, thereby preparing a labeled

reagent zone comprising an enzyme labeling reagent pad 4.

[0068]

Further, in the same manner as in Example 5, the substrate was spotted and dried to prepare a developer pad 3, which was then immobilized, together with the matrix 2, the enzyme labeling reagent pad 4 and the absorption pad 5, in a plastic case having a developer tank 11, to produce the influenza A H5 immunoassay device 2 similar to the device shown in Figs. 6 and 7.

[0069]

Example 7

Preparation of the Influenza A H5 Immunoassay Device 3

In the same manner as shown in Fig. 6 in Example 5, at the position 15 mm distant from the end of the developer-absorption zone 5-side of a matrix 2 which is a nitrocellulose membrane having a width of 5 mm and a length of 50 mm (manufactured by Millipore), 0.7 μl of an aqueous solution containing an anti-influenza A H5-specific antibody (IFH5-136) was spotted, and the spot was dried, thereby preparing a detection zone 6. Further, at the position 12 mm distant from the end of the developer-absorption zone 5-side of the matrix 2, an anti-alkaline phosphatase antibody (rabbit) was spotted, and the spot was dried, thereby preparing a development confirmation section 10. Subsequently, 5 μl of an alkaline phosphatase-labeled anti-influenza A H5-specific antibody which was produced by labeling IFH5-26 antibody with alkaline phosphatase (ALP- IFH5-26, 10 μg/ml) was spotted on the matrix, and the spot was dried, thereby preparing a labeled reagent zone comprising an enzyme labeling reagent pad 4.

[0070]

Further, in the same manner as in Example 5, the substrate was spotted and dried to prepare a developer pad 3, which was then immobilized, together with the matrix 2, the enzyme labeling reagent pad 4 and the absorption pad 5, in a plastic

case having a developer tank 11, to produce the influenza A H5 immunoassay device 3 similar to the device shown in Figs. 6 and 7.

[0071]

Example 8

Assay of Each Subtype of Influenza A with the Immunoassay Devices 1, 2 and 3

Using the influenza A H5 immunoassay (immunochromatography) devices 1, 2 and 3 (measurement devices of the present invention) produced in Examples 5, 6 and 7, and various influenza A virus subtype samples, the reaction specificities of the immunoassay devices against the influenza A virus subtype (H1-15) were tested. As each influenza A virus subtype sample, chorioallantoic fluid whose hemagglutination titer (HA titer) was known was used, which chorioallantoic fluid was obtained by culturing each virus in an embryonated egg and recovering the chorioallantoic fluid (see Table 4). Each chorioallantoic fluid was 10-fold diluted with a sample diluent (Tris buffer (pH 8.0) containing a surfactant), and 30 μL of the dilution was added to a sample spotting zone 8. A pushing area 12 provided in a deformable member was then pushed down to be deformed, thereby inserting, with a projection 13 provided in the deformable member, the developer pad 3 into the developer tank 11 to supply the developer to the developer pad 3 to start the measurement. Fifteen minutes after the start of the measurement, development of the developer was confirmed by coloring of the subject reagent zone 10, and coloring of the detection zone 6 was visually observed. The results are shown in Table 7. It was confirmed that all of the immunoassay devices specifically detect the influenza A virus H5 subtype and are not reactive with the other subtypes (H1 to 4 and H6 to 15) of influenza A virus.

[0072]

[Table 7]

Reactivity of the immunoassay devices against influenza A virus substrains

Influenza A virus substrain (H1-15)	HA titer		Immunoassay device 1	Immunoassay device 2	Immunoassay device 3	GenBank Accession No.	SEQ ID NO: base/amino acid
		Solid phase antibody	IFH5-26	IFH5-136	IFH5-136		
		Labeled antibody	IFH5-115	IFH5-115	IFH5-26		
A/PR/8/34 (H1N1)	512		-	-	-	J02144	5/6
A/Singapore/1/57 (H2N2)	64		-	-	-	L11142	7/8
A/duck/Ukraine/63 (H3N8)	512		-	-	-	V01087, J02109	9/10
A/duck/Czech/56 (H4N6)	256		-	-	-	AB295611	11/12
A/swan/Hokkaido/51/96 (H5N3)	64		+	+	+	AB241617	13/14
A/turkey/Massachusetts/3740/65 (H6N2)	64		-	-	-	AB296072	15/16
A/seal/Massachusetts/1/80 (H7N7)	256		-	-	-	AB269696	17/18
A/turkey/Ontario/6118/68 (H8N4)	128		-	-	-	AB289343	19/20
A/turkey/Wisconsin/66 (H9N2)	128		-	-	-	AB295601	21/22
A/chicken/Germany/N/49 (H10N7)	512		-	-	-	AB292666	23/24
A/duck/England/1/56 (H11N6)	128		-	-	-	J02107	25/26
A/duck/Alberta/60/76 (H12N5)	256		-	-	-	J02104	27/28
A/gull/Maryland/704/77 (H13N6)	128		-	-	-	AB292664	29/30
A/mallard/Astrakhan/263/82 (H14N5)	256		-	-	-	AB289335	31/32
A/duck/Australian/341/83 (H15N8)	128		-	-	-	AB295613	33/34

[0073]

Further, the specificities and the detection sensitivities against influenza A virus H5 substrains were tested. As each influenza A virus H5 substrain, chorioallantoic fluid whose hemagglutination titer (HA titer) was known was used, which chorioallantoic fluid was obtained by culturing each virus in an embryonated egg and recovering the chorioallantoic fluid (see Table 7). Each chorioallantoic fluid was serially diluted with a sample diluent (Tris buffer (pH 8.0) containing a surfactant), and 30 μl of each resulting dilution was added to the sample addition zone 8. The pushing area 12 provided in the deformable member was then pushed down to be deformed, thereby inserting, with a projection 13 provided in the deformable member, the developer pad 3 into the developer tank 11 to supply the developer to the developer pad 3 to start the measurement. Fifteen minutes after the start of the measurement, development of the developer was confirmed by coloring of the development confirmation section 10, and coloring of the detection zone 6 was visually observed. The results are shown in Table 8. Each detection sensitivity was represented as the maximum dilution rate of each chorioallantoic fluid at which the virus was detectable, which chorioallantoic fluid had been serially diluted. All of the immunoassay devices detected the influenza A virus H5 substrains that were tested.

[0074]

[Table 8]

Reactivities and detection sensitivities of the immunoassay devices against the influenza A virus H5 subtype

Influenza A virus substrain (H1-15)	HA titer		Immunoassay device 1	Immunoassay device 2	Immunoassay device 3	GenBank Accession No.	SEQ ID NO: base/amino acid
		Solid phase antibody	IFH5-26	IFH5-136	IFH5-136		
		Labeled antibody	IFH5-115	IFH5-115	IFH5-26		
A/swan/Hokkaido/51/96 (H5N3)	256		10000	10000	1000	AB241617	13/14
A/Tern/South Africa/61 (H5N3)	2048		4000	4000	10	U20460	35/36
A/Hong Kong/483/97 (H5N1)	2048		40000	40000	1000	AF084280	37/38
A/Duck/Yokohama/aq10/03 (H5N1)	128		1000	1000	1000	AB212280	39/40
A/Viet Nam/1184/04 (H5N1)	512		8000	8000	1000	EF541402	41/42
A/Chicken/Yamaguchi/7/04 (H5N1)	1024		2000	2000	1000	AB166862	43/44
A/Whooper Swan/Mongolia/3/05 (H5N1)	16		2000	100	100	AB233320	45/46
A/Whooper Swan/Mongolia/2/06 (H5N1)	256		2000	2000	1000	AB263752	47/48

[0075]

Example 9

Preparation of the Immunoassay Device 4 for Simultaneous Assay of Influenza A and Influenza A H5

As shown in Fig. 9, at the positions 16 mm and 13.5 mm distant from the end of the developer-absorption zone 5-side of a matrix 2 which is a nitrocellulose membrane having a width of 5 mm and a length of 50 mm (manufactured by Millipore), 0.7 μl each of aqueous solutions containing the anti-H5 subtype influenza A virus hemagglutinin H5-specific antibody (IFH5-26) produced in Reference Example 2 and an anti-influenza A virus antibody (FVA2-11) (Literature: Gui-Rong BAI et.al.: Improvement of a Rapid Diagnosis Kit to Detect Either Influenza A or B Virus Infection. J.Vet.Med.Sci.68(1);1-6,2006), respectively, was spotted, and the spots were dried, thereby preparing detection zones 6a and 6b. Further, at the position 11 mm distant from the end of the developer-absorption zone 5-side of the matrix 2, an anti-alkaline phosphatase antibody (rabbit) was spotted, and the spot was dried, thereby preparing a development confirmation section 10. Subsequently, 5 μl of a mixed aqueous solution of the alkaline phosphatase-labeled anti-influenza A virus antibody (5 μg/mL) produced in Reference Example 1 and an alkaline phosphatase-labeled anti-influenza A H5-specific antibody (ALP-IFH-115 (10 μg/mL)) was spotted on the matrix, and the spot was dried, thereby preparing a labeled reagent zone comprising an enzyme labeling reagent pad 4.

[0076]

On a filter paper having a width of 6 mm and length of 20 mm (manufactured by Millipore), 100 μg of 5-bromo-4-chloro-3-indolyl phosphate (BCIP) was spotted as a substrate in the form of a line having a width of 6.0 mm, and the spot was dried, to prepare a developer pad 3. The matrix 2, the developer pad 3, the enzyme labeling reagent pad 4 and an absorption pad 5 (filter paper of 10 mm width, 15 mm

length and 1 mm thickness (manufactured by Whatman)) were immobilized in a plastic case having a developer tank 11, to produce the simultaneous immunoassay device 4 for influenza A virus and influenza A H5 virus shown in Fig. 10 and Fig. 8.

[0077]

Example 10

Assay of Each Subtype of Influenza A with the Simultaneous Immunoassay Device 4

To the sample addition zone 8 of the simultaneous immunoassay device 4 (immunoassay device according to the present invention) for influenza A virus and A H5 virus prepared in Example 9, 30 μL each of the samples of influenza A virus subtypes described in Tables 7 and 8 (Tris buffer (pH 8.0) containing a surfactant was used as the sample diluent) was added, and the pushing area 12 provided in the deformable member was then pushed down to be deformed, thereby inserting, with the projection 13 provided in the deformable member, the developer pad 3 into the developer tank 11 to supply the developer to the developer pad 3 to start the measurement. Fifteen minutes after the start of the measurement, development of the developer was confirmed by coloring of the development confirmation section 10, and coloring of the detection zones 6a and 6b was visually observed.

[0078]

As a result of testing of the influenza A subtypes H1 to H15 using chorioallantoic fluid obtained by culture with embryonated eggs, coloring of the both 6a and 6b lines in the detection zone was observed for the H5 strain, and the strains other than H5, that is, the H1 to H4 and the H6 to H15 strains, showed coloring of only the 6b line (line for detection of the entire A type) in the detection zone. With uninfected chorioallantoic fluid, no coloration was detected in the 6a and 6b lines in the detection zone.

CLAIMS

1. An anti-H5 subtype influenza A virus hemagglutinin monoclonal antibody or an antigen-binding fragment thereof which undergoes antigen-antibody reaction with hemagglutinin of H5 subtype influenza A virus, whose corresponding epitope does not exist in the receptor subdomain (excluding C-terminal region thereof consisting of 11 amino acids) and which does not have neutralizing activity against said influenza A virus;

wherein said monoclonal antibody or an antigen-binding fragment thereof is substantially non-cross-reactive with hemagglutinins of H1 to H4 subtypes and H6 to H15 subtypes; and

wherein said corresponding epitope exists in:

(1) the regions of 41 to 60 aa and 312 to 322 aa;

(2) the regions of 61 to 80 aa and 290 to 300 aa; or

(3) the regions of 101 to 113 aa and 268 to 278 aa,

based on the amino acid sequence shown in SEQ ID NO:2.

2. A method of immunoassay of H5 subtype influenza A virus, comprising measurement of H5 subtype influenza A virus in a sample by immunoassay using antigen-antibody reaction of the monoclonal antibody or an antigen-binding fragment thereof according to claim 1 with hemagglutinin of the H5 subtype influenza A virus.

3. The method according to claim 2, carried out by a sandwich immunoassay using 2 types of the monoclonal antibody and/or an antigen-binding fragment thereof according to any one of claims 1 or 2, said 2 types of the monoclonal antibody and/or the antigen-binding fragment thereof being capable of binding at the same time to a single hemagglutinin molecule of H5 subtype influenza A virus.

4. The method according to claim 3, carried out using 2 types out of the 3 types of monoclonal antibodies whose corresponding epitopes exist in:

(1) the regions of 41 to 60 aa and 312 to 322 aa;

(2) the regions of 61 to 80 aa and 290 to 300 aa; and

(3) the regions of 101 to 113 aa and 268 to 278 aa,

based on the amino acid sequence shown in SEQ ID NO:2.

5. The method according to claim 4, carried out by an immunochromatography.

6. An immunoassay kit for H5 subtype influenza A virus, comprising 2 types of the monoclonal antibody and/or an antigen-binding fragment thereof according to claim 1, said 2 types of the antibody and/or the antigen-binding fragment thereof being capable of binding at the same time to hemagglutinin of H5 subtype influenza A virus.

7. The kit according to claim 6, wherein one of said 2 types of the monoclonal antibody and/or the antigen-binding fragment thereof is immobilized on a solid phase and the other is labeled.

8. The kit according to claim 7, wherein said solid phase is a solid phase for immunochromatography.

SEQUENCE LISTING

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Thr Glu Gln Val Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His
    30                  35                  40

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Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu
45                  50                  55                  60

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Asn Gly Val Lys Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp
                65                  70                  75

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tct tac ata gtg gag aag gac agc cca atc aat ggc ctc tgc tac cca      338
Ser Tyr Ile Val Glu Lys Asp Ser Pro Ile Asn Gly Leu Cys Tyr Pro
        95                  100                 105

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Gly Asp Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Thr
    110                 115                 120

aac cat ttt gag aaa att caa atc atc ccc agg agt tct tgg tcc gat      434
Asn His Phe Glu Lys Ile Gln Ile Ile Pro Arg Ser Ser Trp Ser Asp
125                 130                 135                 140

cat gat gcc tca tca gga gtg agc tcc gca tgt cca tat aat ggg agg      482
His Asp Ala Ser Ser Gly Val Ser Ser Ala Cys Pro Tyr Asn Gly Arg
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tcc tcc ttt ttc aga aat gta gtg tgg ctc atc aaa aag aac aat gca      530
Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Ala
            160                 165                 170

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Leu Val Leu Trp Gly Ile His His Pro Asn Asp Ala Thr Glu Gln Thr
    190                 195                 200

aag ctc tat caa aac cca acc acc tat gtt tct gtt gga aca tca aca      674
Lys Leu Tyr Gln Asn Pro Thr Thr Tyr Val Ser Val Gly Thr Ser Thr
205                 210                 215                 220

ctg aac cag aga tcg gtc cca gaa ata gct acc agg ccc aaa gta aat      722
Leu Asn Gln Arg Ser Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn
                225                 230                 235

ggg caa agt gga aga ata gag ttt ttc tgg aca atc tta aag cca aat      770
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            240                 245                 250

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Asp Ala Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr
        255                 260                 265

gca tac aaa att gcc aag aaa gga gac tca gca atc atg aaa agt gga      866
Ala Tyr Lys Ile Ala Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Gly
    270                 275                 280

ttg gag tat ggt aac tgc aac acc aag tgt caa act cca atg ggt gca      914
Leu Glu Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala
285                 290                 295                 300

ata aac tcc agc atg cca ttt cac aac ata cac cct ctc acc att ggg      962
Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly
                305                 310                 315

gaa tgc ccc aga tac gtg aag tca gat aga tta gtc ctt gca aca ggg     1010
Glu Cys Pro Arg Tyr Val Lys Ser Asp Arg Leu Val Leu Ala Thr Gly
            320                 325                 330

ctc agg aat gtc cct caa aga gaa aca aga gga cta ttt ggg gcc ata     1058
Leu Arg Asn Val Pro Gln Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile
        335                 340                 345

gca ggc ttc ata gaa gga ggg tgg caa gga atg gta gac ggt tgg tat     1106
Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
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Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
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Glu Ser Thr Gln Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser
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Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Lys Glu Phe
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Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
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Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
                465                 470                 475

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Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asp Glu Cys Met Glu
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Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
        495                 500                 505

aga cta aac aga gag gaa ata agt gga gta aaa ttg gaa tca ata gga     1586
Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
    510                 515                 520

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Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
525                 530                 535                 540

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        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asn Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
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Glu Lys Asp Ser Pro Ile Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn
            100                 105                 110

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15 20 25

aac tcg aca gag cag gtt gac aca ata atg gaa aag aat gtt act gtt 149
Asn Ser Thr Glu Gln Val Asp Thr Ile Met Glu Lys Asn Val Thr Val

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                30                  35                  40

aca cat gct caa gac ata ttg gaa aag aca cac aac ggg aag ctc tgc      197
Thr His Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys
        45                  50                  55

agt cta aat gga gtg aaa cct ctc att ttg agg gat tgt agt gta gct      245
Ser Leu Asn Gly Val Lys Pro Leu Ile Leu Arg Asp Cys Ser Val Ala
    60                  65                  70

gga tgg ctc ctc gga aac cct atg tgt gac gaa ttc ctc aat gtg ccg      293
Gly Trp Leu Leu Gly Asn Pro Met Cys Asp Glu Phe Leu Asn Val Pro
75                  80                  85                  90

gaa tgg tct tac ata gtg gag aag gac aat cca gtc aat ggc ctc tgc      341
Glu Trp Ser Tyr Ile Val Glu Lys Asp Asn Pro Val Asn Gly Leu Cys
                95                 100                 105

tac cca gga gat ttc aac gac tat gaa gaa ctg aaa cac cta ttg agc      389
Tyr Pro Gly Asp Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser
            110                 115                 120

agc aca aac cat ttt gag aaa atc cga atc atc ccc aga agc tct tgg      437
Ser Thr Asn His Phe Glu Lys Ile Arg Ile Ile Pro Arg Ser Ser Trp
        125                 130                 135

tcc aat cat gat gcc tca tca gga gtg agc tct gca tgt cca tat aat      485
Ser Asn His Asp Ala Ser Ser Gly Val Ser Ser Ala Cys Pro Tyr Asn
    140                 145                 150

ggg agg tcc tcc ttt ttc aga aat gtg gta tgg ctt atc aaa aag aac      533
Gly Arg Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asn
155                 160                 165                 170

aat gca tac cca aca ata aag agg agt tac aat aac acc aac caa gaa      581
Asn Ala Tyr Pro Thr Ile Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu
                175                 180                 185

gat ctt ttg ata ctg tgg ggg att cac cat cct aat gat gcg gca gag      629
Asp Leu Leu Ile Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu
            190                 195                 200

cag aca aag ctc tat caa aac cca act acc tac gtt tcc gtt gga aca      677
Gln Thr Lys Leu Tyr Gln Asn Pro Thr Thr Tyr Val Ser Val Gly Thr
        205                 210                 215

tca aca ctg aac cag aga tcg gtc cca gaa ata gct acc agg ccc aaa      725
Ser Thr Leu Asn Gln Arg Ser Val Pro Glu Ile Ala Thr Arg Pro Lys
    220                 225                 230

gtg aac ggg caa agt gga aga atg gag ttc ttc tgg aca att tta aag      773
Val Asn Gly Gln Ser Gly Arg Met Glu Phe Phe Trp Thr Ile Leu Lys
235                 240                 245                 250

ccg aat gat gcc atc aat ttt gag agt aat gga aat ttc att gct cca      821
Pro Asn Asp Ala Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro
                255                 260                 265

gaa tat gca tac aaa att gtt aaa aaa gga ggc tca gca atc atg aaa      869
Glu Tyr Ala Tyr Lys Ile Val Lys Lys Gly Gly Ser Ala Ile Met Lys
            270                 275                 280

agt gga ttg gaa tat ggt aac tgc aac acc aag tgt caa act cca atg      917
Ser Gly Leu Glu Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Met
        285                 290                 295

ggt gcg ata aac tct agt atg cca ttc cat aac ata cac cct ctc acc      965
Gly Ala Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr
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    300                 305                 310

att gga gaa tgc ccc aaa tat gtg aaa tca ggt aga tta gtc ctt gca      1013
Ile Gly Glu Cys Pro Lys Tyr Val Lys Ser Gly Arg Leu Val Leu Ala
315                 320                 325                 330

act gga ctc aga aat gtc cct caa aga gaa aca aga gga cta ttt ggg      1061
Thr Gly Leu Arg Asn Val Pro Gln Arg Glu Thr Arg Gly Leu Phe Gly
                335                 340                 345

gct ata gca ggc ttt ata gaa gga gga tgg caa gga atg gta gac ggt      1109
Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly
            350                 355                 360

tgg tat ggg tac cac cat agc aac gag cag ggg agt gga tac gct gca      1157
Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala
        365                 370                 375

gac aaa gaa tcc act caa aag gca ata gat gga atc act aat aag gtc      1205
Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp Gly Ile Thr Asn Lys Val
    380                 385                 390

aac tca atc att gac aaa atg aac act cag ttt gag gcc gtt gga aag      1253
Asn Ser Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Lys
395                 400                 405                 410

gaa ttt aat aac ttg gaa agg agg ata gag aat ttg aat aag aaa atg      1301
Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met
                415                 420                 425

gaa gac gga ttt cta gat gtc tgg act tat aat gct gaa ctt ttg gtt      1349
Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val
            430                 435                 440

cta atg gaa aat gag aga acc cta gac ttt cat gac tca aat gtc aag      1397
Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys
        445                 450                 455

aac ctt tat gac aag gtt cga cta cag ctt agg gat aat gca aag gag      1445
Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu
    460                 465                 470

ctg ggt aat ggt tgt ttc gag ttc tac cat aaa tgt gat aat gaa tgt      1493
Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys
475                 480                 485                 490

atg gaa agt gta aaa aac ggg acg tat gac tac ccg cag tat tca gaa      1541
Met Glu Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu
                495                 500                 505

gag gca aga cta aac aga gag gaa ata agt ggg gtg aaa ttg gaa tca      1589
Glu Ala Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser
            510                 515                 520

atg gga att tac caa ata ctg tca att tat tca aca gtg gcg agt tcc      1637
Met Gly Ile Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser
        525                 530                 535

cta gca ctg gca atc atg ata gct ggt cta tct ttc tgg atg tgc tcc      1685
Leu Ala Leu Ala Ile Met Ile Ala Gly Leu Ser Phe Trp Met Cys Ser
    540                 545                 550

aat gga tca ttg cag tgc aga att tgc att taa atctgtgagt tcagattgta    1738
Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
555                 560

gttaaaaaca cccttgtttc tac                                            1761
```

<210> 4
<211> 564
<212> PRT
<213> Influenza A virus

<400> 4

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Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1               5                  10                  15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asn Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Asp Asn Pro Val Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn
            100                 105                 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Thr Asn His Phe Glu
        115                 120                 125

Lys Ile Arg Ile Ile Pro Arg Ser Ser Trp Ser Asn His Asp Ala Ser
    130                 135                 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Asn Gly Arg Ser Ser Phe Phe
145                 150                 155                 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Ala Tyr Pro Thr Ile
                165                 170                 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
            180                 185                 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

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

Ser Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240
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```
Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Gly Ser Ala Ile Met Lys Ser Gly Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Gly Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Val
                325                 330                 335

Pro Gln Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile
            340                 345                 350

Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His
        355                 360                 365

Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln
    370                 375                 380

Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser Ile Ile Asp Lys
385                 390                 395                 400

Met Asn Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Asn Asn Leu Glu
                405                 410                 415

Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp
            420                 425                 430

Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg
        435                 440                 445

Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val
    450                 455                 460

Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn Gly Cys Phe
465                 470                 475                 480

Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser Val Lys Asn
                485                 490                 495

Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Asn Arg
            500                 505                 510
```

```
Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Met Gly Ile Tyr Gln Ile
        515                 520                 525

Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met
    530                 535                 540

Ile Ala Gly Leu Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys
545                 550                 555                 560

Arg Ile Cys Ile
```

<210> 5
<211> 1015
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (2)..(1015)
<223>

<400> 5

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c cta ctg gtc ctg tta tgt gca ctt gca gct gca gat gca gac aca ata      49
  Leu Leu Val Leu Leu Cys Ala Leu Ala Ala Ala Asp Ala Asp Thr Ile
  1               5                  10                  15

tgt ata ggc tac cat gcg aac aat tca acc gac act gtt gac aca gta      97
Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Asp Thr Val Asp Thr Val
            20                  25                  30

ctc gag aag aat gtg aca gtg aca cac tct gtt aac ctg ctc gaa gac     145
Leu Glu Lys Asn Val Thr Val Thr His Ser Val Asn Leu Leu Glu Asp
        35                  40                  45

agc cac aac gga aaa cta tgt aga tta aaa gga ata gcc cca cta caa     193
Ser His Asn Gly Lys Leu Cys Arg Leu Lys Gly Ile Ala Pro Leu Gln
    50                  55                  60

ttg ggg aaa tgt aac atc gcc gga tgg ctc ttg gga aac cca gaa tgc     241
Leu Gly Lys Cys Asn Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys
65                  70                  75                  80

gac cca ctg ctt cca gtg aga tca tgg tcc tac att gta gaa aca cca     289
Asp Pro Leu Leu Pro Val Arg Ser Trp Ser Tyr Ile Val Glu Thr Pro
                85                  90                  95

aac tct gag aat gga ata tgt tat cca gga gat ttc atc gac tat gag     337
Asn Ser Glu Asn Gly Ile Cys Tyr Pro Gly Asp Phe Ile Asp Tyr Glu
            100                 105                 110

gag ctg agg gag caa ttg agc tca gtg tca tca ttc gaa aga ttc gaa     385
Glu Leu Arg Glu Gln Leu Ser Ser Val Ser Ser Phe Glu Arg Phe Glu
        115                 120                 125

ata ttt ccc aaa gaa agc tca tgg ccc aac cac aac aca aac gga gta     433
Ile Phe Pro Lys Glu Ser Ser Trp Pro Asn His Asn Thr Asn Gly Val
    130                 135                 140

acg gca gca tgc tcc cat gag ggg aaa agc agt ttt tac aga aat ttg     481
Thr Ala Ala Cys Ser His Glu Gly Lys Ser Ser Phe Tyr Arg Asn Leu
145                 150                 155                 160

cta tgg ctg acg gag aag gag ggc tca tac cca aag ctg aaa aat tct     529
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```
Leu Trp Leu Thr Glu Lys Glu Gly Ser Tyr Pro Lys Leu Lys Asn Ser
                165                 170                 175

tat gtg aac aaa aaa ggg aaa gaa gtc ctt gta ctg tgg ggt att cat      577
Tyr Val Asn Lys Lys Gly Lys Glu Val Leu Val Leu Trp Gly Ile His
            180                 185                 190

cac ccg cct aac agt aag gaa caa cag aat ctc tat cag aat gaa aat      625
His Pro Pro Asn Ser Lys Glu Gln Gln Asn Leu Tyr Gln Asn Glu Asn
        195                 200                 205

gct tat gtc tct gta gtg act tca aat tat aac agg aga ttt acc ccg      673
Ala Tyr Val Ser Val Val Thr Ser Asn Tyr Asn Arg Arg Phe Thr Pro
    210                 215                 220

gaa ata gca gaa aga ccc aaa gta aga gat caa gct ggg agg atg aac      721
Glu Ile Ala Glu Arg Pro Lys Val Arg Asp Gln Ala Gly Arg Met Asn
225                 230                 235                 240

tat tac tgg acc ttg cta aaa ccc gga gac aca ata ata ttt gag gca      769
Tyr Tyr Trp Thr Leu Leu Lys Pro Gly Asp Thr Ile Ile Phe Glu Ala
                245                 250                 255

aat gga aat cta ata gca cca atg tat gct ttc gca ctg agt aga ggc      817
Asn Gly Asn Leu Ile Ala Pro Met Tyr Ala Phe Ala Leu Ser Arg Gly
            260                 265                 270

ttt ggg tcc ggc atc atc acc tca aac gca tca atg cat gag tgt aac      865
Phe Gly Ser Gly Ile Ile Thr Ser Asn Ala Ser Met His Glu Cys Asn
        275                 280                 285

acg aag tgt caa aca ccc ctg gga gct ata aac agc agt ctc cct tac      913
Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Ser Ser Leu Pro Tyr
    290                 295                 300

cag aat ata cac cca gtc aca ata gga gag tgc cca aaa tac gtc agg      961
Gln Asn Ile His Pro Val Thr Ile Gly Glu Cys Pro Lys Tyr Val Arg
305                 310                 315                 320

agt gcc aaa ttg agg atg gtt aca gga cta agg aac att ccg tcc att     1009
Ser Ala Lys Leu Arg Met Val Thr Gly Leu Arg Asn Ile Pro Ser Ile
                325                 330                 335

caa tcc                                                            1015
Gln Ser
```

<210> 6
<211> 338
<212> PRT
<213> Influenza A virus

<400> 6

```
Leu Leu Val Leu Leu Cys Ala Leu Ala Ala Ala Asp Ala Asp Thr Ile
1               5                   10                  15

Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Asp Thr Val Asp Thr Val
            20                  25                  30

Leu Glu Lys Asn Val Thr Val Thr His Ser Val Asn Leu Leu Glu Asp
        35                  40                  45

Ser His Asn Gly Lys Leu Cys Arg Leu Lys Gly Ile Ala Pro Leu Gln
```

50 55 60

Leu Gly Lys Cys Asn Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys
65 70 75 80

Asp Pro Leu Leu Pro Val Arg Ser Trp Ser Tyr Ile Val Glu Thr Pro
85 90 95

Asn Ser Glu Asn Gly Ile Cys Tyr Pro Gly Asp Phe Ile Asp Tyr Glu
100 105 110

Glu Leu Arg Glu Gln Leu Ser Ser Val Ser Ser Phe Glu Arg Phe Glu
115 120 125

Ile Phe Pro Lys Glu Ser Ser Trp Pro Asn His Asn Thr Asn Gly Val
130 135 140

Thr Ala Ala Cys Ser His Glu Gly Lys Ser Ser Phe Tyr Arg Asn Leu
145 150 155 160

Leu Trp Leu Thr Glu Lys Glu Gly Ser Tyr Pro Lys Leu Lys Asn Ser
165 170 175

Tyr Val Asn Lys Lys Gly Lys Glu Val Leu Val Leu Trp Gly Ile His
180 185 190

His Pro Pro Asn Ser Lys Glu Gln Gln Asn Leu Tyr Gln Asn Glu Asn
195 200 205

Ala Tyr Val Ser Val Val Thr Ser Asn Tyr Asn Arg Arg Phe Thr Pro
210 215 220

Glu Ile Ala Glu Arg Pro Lys Val Arg Asp Gln Ala Gly Arg Met Asn
225 230 235 240

Tyr Tyr Trp Thr Leu Leu Lys Pro Gly Asp Thr Ile Ile Phe Glu Ala
245 250 255

Asn Gly Asn Leu Ile Ala Pro Met Tyr Ala Phe Ala Leu Ser Arg Gly
260 265 270

Phe Gly Ser Gly Ile Ile Thr Ser Asn Ala Ser Met His Glu Cys Asn
275 280 285

Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Ser Ser Leu Pro Tyr
290 295 300

Gln Asn Ile His Pro Val Thr Ile Gly Glu Cys Pro Lys Tyr Val Arg
305 310 315 320

Ser Ala Lys Leu Arg Met Val Thr Gly Leu Arg Asn Ile Pro Ser Ile

325 330 335

Gln Ser

<210> 7
<211> 1773
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (44)..(1732)
<223>

<400> 7

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agcaaaagca ggggttatac catagacaac caaaagcaaa aca atg gcc atc att       55
                                                Met Ala Ile Ile
                                                1

tat ctc att ctc ctg ttc aca gca gtg aga ggg gac cag ata tgc att      103
Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp Gln Ile Cys Ile
5                   10                  15                  20

gga tac cat gcc aat aat tcc aca gag aag gtc gac aca att cta gag      151
Gly Tyr His Ala Asn Asn Ser Thr Glu Lys Val Asp Thr Ile Leu Glu
                25                  30                  35

cgg aac gtc act gtg act cat gcc aag gac att ctt gag aag acc cat      199
Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu Glu Lys Thr His
            40                  45                  50

aac gga aag tta tgc aaa cta aac gga atc cct cca ctt gaa cta ggg      247
Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro Leu Glu Leu Gly
        55                  60                  65

gac tgt agc att gcc gga tgg ctc ctt gga aat cca gaa tgt gat agg      295
Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys Asp Arg
    70                  75                  80

ctt cta agt gtg cca gaa tgg tcc tat ata atg gag aaa gaa aac ccg      343
Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu Lys Glu Asn Pro
85                  90                  95                  100

aga gac ggt ttg tgt tat cca ggc agc ttc aat gat tat gaa gaa ttg      391
Arg Asp Gly Leu Cys Tyr Pro Gly Ser Phe Asn Asp Tyr Glu Glu Leu
                105                 110                 115

aaa cat ctc ctc agc agc gtg aaa cat ttc gag aaa gta aag att ctg      439
Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu
            120                 125                 130

ccc aaa gat aga tgg aca cag cat aca aca act gga ggt tca cgg gcc      487
Pro Lys Asp Arg Trp Thr Gln His Thr Thr Thr Gly Gly Ser Arg Ala
        135                 140                 145

tgc gcg gtg tct ggt aat cca tca ttc ttc agg aac atg gtc tgg ctg      535
Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn Met Val Trp Leu
    150                 155                 160

aca gag aaa gga tca aat tat ccg gtt gcc aaa gga tcg tac aac aat      583
Thr Glu Lys Gly Ser Asn Tyr Pro Val Ala Lys Gly Ser Tyr Asn Asn
165                 170                 175                 180

aca agc gga gaa caa atg cta ata att tgg ggg gtg cac cat ccc aat      631
Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val His His Pro Asn
```

```
                    185                 190                 195

gat gag aaa gaa caa aga aca ttg tac cag aat gtg gga acc tat gtt      679
Asp Glu Lys Glu Gln Arg Thr Leu Tyr Gln Asn Val Gly Thr Tyr Val
            200                 205                 210

tcc gta ggc aca tca aca ttg aac aaa agg tca acc cca gac ata gca      727
Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr Pro Asp Ile Ala
        215                 220                 225

aca agg cct aaa gtg aat gga cta gga agt aga atg gaa ttc tct tgg      775
Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met Glu Phe Ser Trp
    230                 235                 240

acc cta ttg gat atg tgg gac acc ata aat ttt gag agt act ggt aat      823
Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu Ser Thr Gly Asn
245                 250                 255                 260

cta att gca cca gag tat gga ttc aaa ata tcg aaa aga ggt agt tca      871
Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys Arg Gly Ser Ser
                265                 270                 275

ggg atc atg aaa aca gaa gga aca ctt gag aac tgt gag acc aaa tgc      919
Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys Glu Thr Lys Cys
            280                 285                 290

caa act cct ttg gga gca ata aat aca aca ttg cct ttt cac aat gtc      967
Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro Phe His Asn Val
        295                 300                 305

cac cca ctg aca ata ggt gag tgc ccc aaa tat gta aaa tcg gag aag     1015
His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val Lys Ser Glu Lys
    310                 315                 320

ttg gtc tta gca aca gga cta agg aat gtt ccc cag att gaa tca aga     1063
Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln Ile Glu Ser Arg
325                 330                 335                 340

gga ttg ttt ggg gca ata gct ggt ttt ata gaa gga gga tgg caa gga     1111
Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly
                345                 350                 355

atg att gat ggt tgg tat gga tac cat cac agc aat gac cag gga tca     1159
Met Ile Asp Gly Trp Tyr Gly Tyr His His Ser Asn Asp Gln Gly Ser
            360                 365                 370

ggg tat gca gca gac aaa gaa tcc act caa aag gca ttt gat gga atc     1207
Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Phe Asp Gly Ile
        375                 380                 385

acc aac aag gta aat tct gtg att gaa aag atg aac acc caa ttt gaa     1255
Thr Asn Lys Val Asn Ser Val Ile Glu Lys Met Asn Thr Gln Phe Glu
    390                 395                 400

gct gtt ggg aaa gaa ttc agt aac tta gag aga aga ctg gag aac ttg     1303
Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg Leu Glu Asn Leu
405                 410                 415                 420

aac aaa aag atg gaa gac ggg ttt cta gat gtg tgg aca tac aat gct     1351
Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala
                425                 430                 435

gag ctt cta gtt ctg atg gaa aat gag agg aca ctt gac ttt cat gat     1399
Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp
            440                 445                 450

tct aat gtc aag aat ctg tat gat aaa gtc aga atg cag ctg aga gac     1447
Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met Gln Leu Arg Asp
```

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        455                 460                 465

aac gtc aaa gaa cta gga aat gga tgt ttt gaa ttt tat cac aaa tgt     1495
Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys
    470                 475                 480

gat gat gaa tgc atg aat agt gtg aaa aac ggg acg tat gat tat ccc     1543
Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro
485                 490                 495                 500

aag tat gaa gaa gag tct aaa cta aat aga aat gaa atc aaa ggg gta     1591
Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu Ile Lys Gly Val
                505                 510                 515

aaa ttg agc agc atg ggg gtt tat caa atc ctt gcc att tat gct aca     1639
Lys Leu Ser Ser Met Gly Val Tyr Gln Ile Leu Ala Ile Tyr Ala Thr
            520                 525                 530

gta gca ggt tct ctg tca ctg gca atc atg atg gct ggg atc tct ttc     1687
Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala Gly Ile Ser Phe
        535                 540                 545

tgg atg tgc tcc aac ggg tct ctg cag tgc agg atc tgc ata tga         1732
Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
    550                 555                 560

ttataagtca ttttataatt aaaaacactc ttgtttctac t                       1773
```

<210> 8
<211> 562
<212> PRT
<213> Influenza A virus

<400> 8

```
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp
1               5                   10                  15

Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Lys Val Asp
            20                  25                  30

Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu
        35                  40                  45

Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro
    50                  55                  60

Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro
65                  70                  75                  80

Glu Cys Asp Arg Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu
                85                  90                  95

Lys Glu Asn Pro Arg Asp Gly Leu Cys Tyr Pro Gly Ser Phe Asn Asp
            100                 105                 110

Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys
        115                 120                 125
```

```
Val Lys Ile Leu Pro Lys Asp Arg Trp Thr Gln His Thr Thr Thr Gly
    130                 135                 140

Gly Ser Arg Ala Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn
145                 150                 155                 160

Met Val Trp Leu Thr Glu Lys Gly Ser Asn Tyr Pro Val Ala Lys Gly
                165                 170                 175

Ser Tyr Asn Asn Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val
            180                 185                 190

His His Pro Asn Asp Glu Lys Glu Gln Arg Thr Leu Tyr Gln Asn Val
        195                 200                 205

Gly Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr
    210                 215                 220

Pro Asp Ile Ala Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met
225                 230                 235                 240

Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu
                245                 250                 255

Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys
            260                 265                 270

Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys
        275                 280                 285

Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro
    290                 295                 300

Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val
305                 310                 315                 320

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

Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
            340                 345                 350

Gly Trp Gln Gly Met Ile Asp Gly Trp Tyr Gly Tyr His His Ser Asn
        355                 360                 365

Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala
    370                 375                 380

Phe Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys Met Asn
385                 390                 395                 400
```

```
Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg
                405                 410                 415

Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
            420                 425                 430

Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
        435                 440                 445

Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met
    450                 455                 460

Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
465                 470                 475                 480

Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr
                485                 490                 495

Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu
            500                 505                 510

Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Tyr Gln Ile Leu Ala
        515                 520                 525

Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala
    530                 535                 540

Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
545                 550                 555                 560

Cys Ile
```

<210> 9
<211> 1765
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (30)..(1730)
<223>

<400> 9

```
agcaaaagca ggggatactt tcattaatc atg aag acc gtt att gct tta agc       53
                                Met Lys Thr Val Ile Ala Leu Ser
                                1               5

tac att ctc tgt ctg act ttc gga cag gac ctc cca ggg aat gac aac      101
Tyr Ile Leu Cys Leu Thr Phe Gly Gln Asp Leu Pro Gly Asn Asp Asn
    10                  15                  20

agt aca gca aca ctg tgc ctg ggg cac cat gca gtg ccg aat ggg aca      149
Ser Thr Ala Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr
25                  30                  35                  40

ata gtg aag aca atc aca gat gat cag att gag gtg act aat gct act      197
```

```
Ile Val Lys Thr Ile Thr Asp Asp Gln Ile Glu Val Thr Asn Ala Thr
                45                  50                  55

gag cta gtt caa agc tcc tca aca ggg aaa ata tgc aac aat cct cac      245
Glu Leu Val Gln Ser Ser Ser Thr Gly Lys Ile Cys Asn Asn Pro His
            60                  65                  70

agg atc ctt gat gga agg gcc tgc aca tta ata gat gct cta ctg ggg      293
Arg Ile Leu Asp Gly Arg Ala Cys Thr Leu Ile Asp Ala Leu Leu Gly
        75                  80                  85

gat cct cat tgc gat gtc ttt caa aat gag acg tgg gac ctt ttt gtg      341
Asp Pro His Cys Asp Val Phe Gln Asn Glu Thr Trp Asp Leu Phe Val
    90                  95                  100

gag cga agc aat gct ttc agc aac tgt tac cct tat gat ata cca gat      389
Glu Arg Ser Asn Ala Phe Ser Asn Cys Tyr Pro Tyr Asp Ile Pro Asp
105                 110                 115                 120

tat gca tcc ctt agg tcc cta gtt gcc tca tca ggc aca ttg gag ttc      437
Tyr Ala Ser Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe
                125                 130                 135

atc act gag ggt ttc acc tgg aca gga gta act cag aat gga ggg agc      485
Ile Thr Glu Gly Phe Thr Trp Thr Gly Val Thr Gln Asn Gly Gly Ser
            140                 145                 150

agt gct tgc aaa aga gga cct gct aac ggt ttc ttc agt aga ctg aac      533
Ser Ala Cys Lys Arg Gly Pro Ala Asn Gly Phe Phe Ser Arg Leu Asn
        155                 160                 165

tgg ttg act aaa tca gaa agc gca tac cca gtg ctg aac gtg act atg      581
Trp Leu Thr Lys Ser Glu Ser Ala Tyr Pro Val Leu Asn Val Thr Met
    170                 175                 180

cca aat aat gac aat ttt gac aaa cta tac atc tgg gga gta cac cac      629
Pro Asn Asn Asp Asn Phe Asp Lys Leu Tyr Ile Trp Gly Val His His
185                 190                 195                 200

ccg agc aca aat caa gaa caa acc aac ctg tat gtt caa gca tca ggg      677
Pro Ser Thr Asn Gln Glu Gln Thr Asn Leu Tyr Val Gln Ala Ser Gly
                205                 210                 215

aga gtc aca gtc tct acc agg aga agt cag cag act ata atc ccg aat      725
Arg Val Thr Val Ser Thr Arg Arg Ser Gln Gln Thr Ile Ile Pro Asn
            220                 225                 230

att gga tct aga ccc tgg gta agg ggc cag cct ggc aga ata agc atc      773
Ile Gly Ser Arg Pro Trp Val Arg Gly Gln Pro Gly Arg Ile Ser Ile
        235                 240                 245

tat tgg aca ata gtt aaa cct ggg gac gtg ctg gta atc aac agt aat      821
Tyr Trp Thr Ile Val Lys Pro Gly Asp Val Leu Val Ile Asn Ser Asn
    250                 255                 260

gga aac cta atc gct cct cgg ggt tac ttc aag atg cgc act ggg aaa      869
Gly Asn Leu Ile Ala Pro Arg Gly Tyr Phe Lys Met Arg Thr Gly Lys
265                 270                 275                 280

agc tca ata atg agg tca gat gca cct att gac acc tgt atc tct gag      917
Ser Ser Ile Met Arg Ser Asp Ala Pro Ile Asp Thr Cys Ile Ser Glu
                285                 290                 295

tgc atc act cca aat gga agc att ccc aat gac aag ccc ttc caa aat      965
Cys Ile Thr Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn
            300                 305                 310

gta aac aag atc aca tac gga gca tgt ccc aag tat gtt aag cag aac     1013
```

```
Val Asn Lys Ile Thr Tyr Gly Ala Cys Pro Lys Tyr Val Lys Gln Asn
        315                 320                 325

acc ctg aag ttg gca aca ggg atg cgg aat gta cca gag aaa caa acc     1061
Thr Leu Lys Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr
    330                 335                 340

aga ggc cta ttc ggt gca ata gca ggt ttt ata gaa aat gga tgg gag     1109
Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu
345                 350                 355                 360

gga atg ata gat ggc tgg tat ggc ttc agg cat caa aat tct gag ggt     1157
Gly Met Ile Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly
                365                 370                 375

aca gga caa gca gca gac ctt aaa agc act cag gca gcc att gac caa     1205
Thr Gly Gln Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln
            380                 385                 390

atc aat agg aaa ttg aac aga gtg att gaa aag acg aat gag aag ttc     1253
Ile Asn Arg Lys Leu Asn Arg Val Ile Glu Lys Thr Asn Glu Lys Phe
        395                 400                 405

cat caa atc gaa aag gaa ttc tcc gaa gta gaa ggg agg att cag gac     1301
His Gln Ile Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp
    410                 415                 420

ctt gag aaa tac gtt gaa gac acg aaa ata gat ctc tgg tct tac aat     1349
Leu Glu Lys Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn
425                 430                 435                 440

gcg gaa ctt ctt gtt gcc cta gag aat cag cat aca atc gat ctg gct     1397
Ala Glu Leu Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Ala
                445                 450                 455

gat tca gaa atg aac aaa tta ttt gaa aaa acc agg agg caa ctg agg     1445
Asp Ser Glu Met Asn Lys Leu Phe Glu Lys Thr Arg Arg Gln Leu Arg
            460                 465                 470

gaa aat gct gaa gac atg ggc aat ggt tgt ttc aag ata tac cac aaa     1493
Glu Asn Ala Glu Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys
        475                 480                 485

tgt gac aat gct tgc ata gag tca att aga aac ggg act tat gat cat     1541
Cys Asp Asn Ala Cys Ile Glu Ser Ile Arg Asn Gly Thr Tyr Asp His
    490                 495                 500

gat ata tac aga gac gag gca ttg aac aac cgg ttc cag atc aaa ggt     1589
Asp Ile Tyr Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly
505                 510                 515                 520

gtc gaa cta aaa tct gga tac aaa gac tgg atc ctg tgg att tcc ttt     1637
Val Glu Leu Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe
                525                 530                 535

gcc ata tca tgc ctt ttg ctt tgt gtt gtt ttg ctg ggt ttc att atg     1685
Ala Ile Ser Cys Leu Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met
            540                 545                 550

tgg gcc tgc cag aga ggc aac att agg tgc aac att tgc att tga         1730
Trp Ala Cys Gln Arg Gly Asn Ile Arg Cys Asn Ile Cys Ile
        555                 560                 565

gtatactaat gattaaaaac acccttgttt ctact                             1765
```

<210> 10
<211> 566

<212> PRT
<213> Influenza A virus

<400> 10

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

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

His His Ala Val Pro Asn Gly Thr Ile Val Lys Thr Ile Thr Asp Asp
        35                  40                  45

Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser Thr
    50                  55                  60

Gly Lys Ile Cys Asn Asn Pro His Arg Ile Leu Asp Gly Arg Ala Cys
65                  70                  75                  80

Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His Cys Asp Val Phe Gln
                85                  90                  95

Asn Glu Thr Trp Asp Leu Phe Val Glu Arg Ser Asn Ala Phe Ser Asn
            100                 105                 110

Cys Tyr Pro Tyr Asp Ile Pro Asp Tyr Ala Ser Leu Arg Ser Leu Val
        115                 120                 125

Ala Ser Ser Gly Thr Leu Glu Phe Ile Thr Glu Gly Phe Thr Trp Thr
    130                 135                 140

Gly Val Thr Gln Asn Gly Gly Ser Ser Ala Cys Lys Arg Gly Pro Ala
145                 150                 155                 160

Asn Gly Phe Phe Ser Arg Leu Asn Trp Leu Thr Lys Ser Glu Ser Ala
                165                 170                 175

Tyr Pro Val Leu Asn Val Thr Met Pro Asn Asn Asp Asn Phe Asp Lys
            180                 185                 190

Leu Tyr Ile Trp Gly Val His His Pro Ser Thr Asn Gln Glu Gln Thr
        195                 200                 205

Asn Leu Tyr Val Gln Ala Ser Gly Arg Val Thr Val Ser Thr Arg Arg
    210                 215                 220

Ser Gln Gln Thr Ile Ile Pro Asn Ile Gly Ser Arg Pro Trp Val Arg
225                 230                 235                 240

Gly Gln Pro Gly Arg Ile Ser Ile Tyr Trp Thr Ile Val Lys Pro Gly
                245                 250                 255
```

```
Asp Val Leu Val Ile Asn Ser Asn Gly Asn Leu Ile Ala Pro Arg Gly
            260                 265                 270

Tyr Phe Lys Met Arg Thr Gly Lys Ser Ser Ile Met Arg Ser Asp Ala
        275                 280                 285

Pro Ile Asp Thr Cys Ile Ser Glu Cys Ile Thr Pro Asn Gly Ser Ile
    290                 295                 300

Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Lys Ile Thr Tyr Gly Ala
305                 310                 315                 320

Cys Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Gly Met
                325                 330                 335

Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Leu Phe Gly Ala Ile Ala
            340                 345                 350

Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Ile Asp Gly Trp Tyr Gly
        355                 360                 365

Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln Ala Ala Asp Leu Lys
    370                 375                 380

Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Arg Lys Leu Asn Arg Val
385                 390                 395                 400

Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile Glu Lys Glu Phe Ser
                405                 410                 415

Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val Glu Asp Thr
            420                 425                 430

Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Leu Glu
        435                 440                 445

Asn Gln His Thr Ile Asp Leu Ala Asp Ser Glu Met Asn Lys Leu Phe
    450                 455                 460

Glu Lys Thr Arg Arg Gln Leu Arg Glu Asn Ala Glu Asp Met Gly Asn
465                 470                 475                 480

Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn Ala Cys Ile Glu Ser
                485                 490                 495

Ile Arg Asn Gly Thr Tyr Asp His Asp Ile Tyr Arg Asp Glu Ala Leu
            500                 505                 510

Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu Lys Ser Gly Tyr Lys
        515                 520                 525
```

```
Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser Cys Leu Leu Leu Cys
    530                 535                 540

Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys Gln Arg Gly Asn Ile
545                 550                 555                 560

Arg Cys Asn Ile Cys Ile
                565
```

<210> 11
<211> 1704
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (6)..(1700)
<223>

<400> 11

```
aaaca atg cta tca att gtg att ttg ttt ctg ctc ata gca gag aac tct     50
      Met Leu Ser Ile Val Ile Leu Phe Leu Leu Ile Ala Glu Asn Ser
      1               5                   10                  15

tcc caa aac tac aca gga aac cct gtg ata tgc atg gga cat cat gct      98
Ser Gln Asn Tyr Thr Gly Asn Pro Val Ile Cys Met Gly His His Ala
                20                  25                  30

gtg gcc aat ggg acc atg gta aag acc cta gcc gat gat caa gtg gaa     146
Val Ala Asn Gly Thr Met Val Lys Thr Leu Ala Asp Asp Gln Val Glu
            35                  40                  45

gtg gtc acc gca cag gaa ctg gta gaa tca caa aat ctc ccg gaa cta     194
Val Val Thr Ala Gln Glu Leu Val Glu Ser Gln Asn Leu Pro Glu Leu
        50                  55                  60

tgt ccg agc cct ctg aga cta gtt gac ggc cag acc tgt gat atc atc     242
Cys Pro Ser Pro Leu Arg Leu Val Asp Gly Gln Thr Cys Asp Ile Ile
    65                  70                  75

aat gga gca ttg ggg agc cca ggg tgt gac cat ttg aat ggt gca gaa     290
Asn Gly Ala Leu Gly Ser Pro Gly Cys Asp His Leu Asn Gly Ala Glu
80                  85                  90                  95

tgg gac gtt ttc ata gag agg ccc aat gca gta gac act tgc tat cca     338
Trp Asp Val Phe Ile Glu Arg Pro Asn Ala Val Asp Thr Cys Tyr Pro
                100                 105                 110

ttt gat gtg cca gag tac cag agt ctg aga agc ata ctc gcc aac aat     386
Phe Asp Val Pro Glu Tyr Gln Ser Leu Arg Ser Ile Leu Ala Asn Asn
            115                 120                 125

ggg aaa ttc gaa ttc att gcc gaa gaa ttc caa tgg aac acg gtg aag     434
Gly Lys Phe Glu Phe Ile Ala Glu Glu Phe Gln Trp Asn Thr Val Lys
        130                 135                 140

caa aat gga aaa tcc gga gcc tgc aag agg gca aat gtg aat gat ttc     482
Gln Asn Gly Lys Ser Gly Ala Cys Lys Arg Ala Asn Val Asn Asp Phe
    145                 150                 155

ttt aac agg cta aac tgg ctg gtg aag tca gat ggg aat gcg tac ccc     530
Phe Asn Arg Leu Asn Trp Leu Val Lys Ser Asp Gly Asn Ala Tyr Pro
160                 165                 170                 175
```

```
ctt cag aat ttg aca aag ata aac aat ggg gat tat gca agg ctt tac      578
Leu Gln Asn Leu Thr Lys Ile Asn Asn Gly Asp Tyr Ala Arg Leu Tyr
                180                 185                 190

atc tgg gga gtt cat cac cct tcg aca gac aca gag caa acc aac ctg      626
Ile Trp Gly Val His His Pro Ser Thr Asp Thr Glu Gln Thr Asn Leu
            195                 200                 205

tac aag aat aac cct gga gga gtc act gtg tct acc aaa act agt caa      674
Tyr Lys Asn Asn Pro Gly Gly Val Thr Val Ser Thr Lys Thr Ser Gln
        210                 215                 220

aca agt gta gtg cct aac att ggc agc aga ccc ttg gtg aga gga caa      722
Thr Ser Val Val Pro Asn Ile Gly Ser Arg Pro Leu Val Arg Gly Gln
    225                 230                 235

agt ggc aga gta agt ttc tac tgg act att gta gag cct gga gac ttg      770
Ser Gly Arg Val Ser Phe Tyr Trp Thr Ile Val Glu Pro Gly Asp Leu
240                 245                 250                 255

ata gtc ttc aac aca ata ggg aat cta att gcc ccg aga ggg cat tac      818
Ile Val Phe Asn Thr Ile Gly Asn Leu Ile Ala Pro Arg Gly His Tyr
                260                 265                 270

aag tta aac aat cag aag aag agc aca att cta aat act gca att ccc      866
Lys Leu Asn Asn Gln Lys Lys Ser Thr Ile Leu Asn Thr Ala Ile Pro
            275                 280                 285

ata ggc tca tgt gtc agc aaa tgt cac aca gac aaa ggt tct ctc tct      914
Ile Gly Ser Cys Val Ser Lys Cys His Thr Asp Lys Gly Ser Leu Ser
        290                 295                 300

aca act aag ccc ttc caa aat atc tcg agg ata gca gtt gga gac tgc      962
Thr Thr Lys Pro Phe Gln Asn Ile Ser Arg Ile Ala Val Gly Asp Cys
    305                 310                 315

ccc aga tat gtc aaa cag ggc tct cta aaa ctt gca aca ggg atg agg     1010
Pro Arg Tyr Val Lys Gln Gly Ser Leu Lys Leu Ala Thr Gly Met Arg
320                 325                 330                 335

aac att cct gaa aag gca tca aga ggg ctt ttt gga gca ata gct ggg     1058
Asn Ile Pro Glu Lys Ala Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly
                340                 345                 350

ttc ata gag aat ggc tgg caa ggt cta atc gat ggt tgg tat gga ttc     1106
Phe Ile Glu Asn Gly Trp Gln Gly Leu Ile Asp Gly Trp Tyr Gly Phe
            355                 360                 365

aga cac cag aat gca gaa gga aca gga aca gcg gca gat ctc aaa tcc     1154
Arg His Gln Asn Ala Glu Gly Thr Gly Thr Ala Ala Asp Leu Lys Ser
        370                 375                 380

act cag gca gcc att gat caa atc aat ggg aaa ctt aac cgt ctt att     1202
Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys Leu Asn Arg Leu Ile
    385                 390                 395

gag aag aca aac gat aaa tac cat caa atc gaa aaa gag ttc gag caa     1250
Glu Lys Thr Asn Asp Lys Tyr His Gln Ile Glu Lys Glu Phe Glu Gln
400                 405                 410                 415

gtt gaa gga aga att caa gat ctg gaa aag tat gtt gag gac aca aag     1298
Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val Glu Asp Thr Lys
                420                 425                 430

att gat tta tgg tca tat aat gca gag cta tta gtc gct cta gaa aac     1346
Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Leu Glu Asn
            435                 440                 445
```

```
caa cac act ata gac gtg act gat tca gaa atg aac aaa ctc ttt gaa     1394
Gln His Thr Ile Asp Val Thr Asp Ser Glu Met Asn Lys Leu Phe Glu
        450                 455                 460

aga gta agg cgt caa ctc aga gag aat gct gaa gac aaa gga aat ggg     1442
Arg Val Arg Arg Gln Leu Arg Glu Asn Ala Glu Asp Lys Gly Asn Gly
    465                 470                 475

tgt ttc gaa ata ttc cac aag tgt gat aac aac tgc att gaa agt att     1490
Cys Phe Glu Ile Phe His Lys Cys Asp Asn Asn Cys Ile Glu Ser Ile
480                 485                 490                 495

cgg aat ggg act tat gat cat gat att tat aga gat gaa gca atc aac     1538
Arg Asn Gly Thr Tyr Asp His Asp Ile Tyr Arg Asp Glu Ala Ile Asn
                500                 505                 510

aat cga ttc caa atc cag gga gtc aaa ttg acc cag gga tat atg gac     1586
Asn Arg Phe Gln Ile Gln Gly Val Lys Leu Thr Gln Gly Tyr Met Asp
            515                 520                 525

atc att ctt tgg att tca ttc tcc ata tca tgc ttt ttg ctc gta gca     1634
Ile Ile Leu Trp Ile Ser Phe Ser Ile Ser Cys Phe Leu Leu Val Ala
        530                 535                 540

cta ctt tta gcc ttc att ttg tgg gct tgt cag aac gga aac atc cgg     1682
Leu Leu Leu Ala Phe Ile Leu Trp Ala Cys Gln Asn Gly Asn Ile Arg
    545                 550                 555

tgc cag att tgt att tag agaa                                       1704
Cys Gln Ile Cys Ile
560
```

<210> 12
<211> 564
<212> PRT
<213> Influenza A virus

<400> 12

```
Met Leu Ser Ile Val Ile Leu Phe Leu Leu Ile Ala Glu Asn Ser Ser
1               5                   10                  15

Gln Asn Tyr Thr Gly Asn Pro Val Ile Cys Met Gly His His Ala Val
            20                  25                  30

Ala Asn Gly Thr Met Val Lys Thr Leu Ala Asp Asp Gln Val Glu Val
        35                  40                  45

Val Thr Ala Gln Glu Leu Val Glu Ser Gln Asn Leu Pro Glu Leu Cys
    50                  55                  60

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

Gly Ala Leu Gly Ser Pro Gly Cys Asp His Leu Asn Gly Ala Glu Trp
                85                  90                  95

Asp Val Phe Ile Glu Arg Pro Asn Ala Val Asp Thr Cys Tyr Pro Phe
            100                 105                 110
```

```
Asp Val Pro Glu Tyr Gln Ser Leu Arg Ser Ile Leu Ala Asn Asn Gly
        115                 120                 125

Lys Phe Glu Phe Ile Ala Glu Glu Phe Gln Trp Asn Thr Val Lys Gln
    130                 135                 140

Asn Gly Lys Ser Gly Ala Cys Lys Arg Ala Asn Val Asn Asp Phe Phe
145                 150                 155                 160

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

Gln Asn Leu Thr Lys Ile Asn Asn Gly Asp Tyr Ala Arg Leu Tyr Ile
            180                 185                 190

Trp Gly Val His His Pro Ser Thr Asp Thr Glu Gln Thr Asn Leu Tyr
        195                 200                 205

Lys Asn Asn Pro Gly Gly Val Thr Val Ser Thr Lys Thr Ser Gln Thr
    210                 215                 220

Ser Val Val Pro Asn Ile Gly Ser Arg Pro Leu Val Arg Gly Gln Ser
225                 230                 235                 240

Gly Arg Val Ser Phe Tyr Trp Thr Ile Val Glu Pro Gly Asp Leu Ile
                245                 250                 255

Val Phe Asn Thr Ile Gly Asn Leu Ile Ala Pro Arg Gly His Tyr Lys
            260                 265                 270

Leu Asn Asn Gln Lys Lys Ser Thr Ile Leu Asn Thr Ala Ile Pro Ile
        275                 280                 285

Gly Ser Cys Val Ser Lys Cys His Thr Asp Lys Gly Ser Leu Ser Thr
    290                 295                 300

Thr Lys Pro Phe Gln Asn Ile Ser Arg Ile Ala Val Gly Asp Cys Pro
305                 310                 315                 320

Arg Tyr Val Lys Gln Gly Ser Leu Lys Leu Ala Thr Gly Met Arg Asn
                325                 330                 335

Ile Pro Glu Lys Ala Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe
            340                 345                 350

Ile Glu Asn Gly Trp Gln Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg
        355                 360                 365

His Gln Asn Ala Glu Gly Thr Gly Thr Ala Ala Asp Leu Lys Ser Thr
    370                 375                 380
```

```
Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys Leu Asn Arg Leu Ile Glu
385                 390                 395                 400

Lys Thr Asn Asp Lys Tyr His Gln Ile Glu Lys Glu Phe Glu Gln Val
                405                 410                 415

Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val Glu Asp Thr Lys Ile
            420                 425                 430

Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Leu Glu Asn Gln
        435                 440                 445

His Thr Ile Asp Val Thr Asp Ser Glu Met Asn Lys Leu Phe Glu Arg
    450                 455                 460

Val Arg Arg Gln Leu Arg Glu Asn Ala Glu Asp Lys Gly Asn Gly Cys
465                 470                 475                 480

Phe Glu Ile Phe His Lys Cys Asp Asn Asn Cys Ile Glu Ser Ile Arg
                485                 490                 495

Asn Gly Thr Tyr Asp His Asp Ile Tyr Arg Asp Glu Ala Ile Asn Asn
            500                 505                 510

Arg Phe Gln Ile Gln Gly Val Lys Leu Thr Gln Gly Tyr Met Asp Ile
        515                 520                 525

Ile Leu Trp Ile Ser Phe Ser Ile Ser Cys Phe Leu Leu Val Ala Leu
    530                 535                 540

Leu Leu Ala Phe Ile Leu Trp Ala Cys Gln Asn Gly Asn Ile Arg Cys
545                 550                 555                 560

Gln Ile Cys Ile
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<210> 13
<211> 1634
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (3)..(1634)
<223>

<220>
<221> misc_feature
<222> (1634)..(1634)
<223> n is unknown base

<400> 13

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ag aaa ata gtg ctt ctt ctt gca aca gtc agt ctt gtt aaa agt gac        47
   Lys Ile Val Leu Leu Leu Ala Thr Val Ser Leu Val Lys Ser Asp
   1               5                  10                  15
```

```
cag att tgc att ggt tac cat gca aac aac tcg aca gaa cag gtt gac        95
Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val Asp
                20                  25                  30

aca ata atg gaa aag aat gtc act gtt aca cat gcc caa gac ata ttg       143
Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile Leu
            35                  40                  45

gaa aag aca cac aac ggg aag ctc tgc agt cta aat gga gtg aag cct       191
Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asn Gly Val Lys Pro
        50                  55                  60

ctc att ttg agg gat tgt agt gta gct gga tgg ctc ctc gga aac cct       239
Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn Pro
    65                  70                  75

atg tgt gac gaa ttc ctc aat gtg ccg gaa tgg tct tac ata gtg gag       287
Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val Glu
80                  85                  90                  95

aag gac agt cca gtc aat ggc ctc tgc tac cca gga gat ttc aac gac       335
Lys Asp Ser Pro Val Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn Asp
                100                 105                 110

tat gaa gaa ctg aaa cac cta ttg agc agc aca aac cat ttt gag aaa       383
Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Thr Asn His Phe Glu Lys
            115                 120                 125

atc caa atc atc ccc aga agc tct tgg tcc aat cat gat gcc tca tca       431
Ile Gln Ile Ile Pro Arg Ser Ser Trp Ser Asn His Asp Ala Ser Ser
        130                 135                 140

gga gtg agc tct gca tgt cca tat ggt ggg agg tcc tcc ttt ttc aga       479
Gly Val Ser Ser Ala Cys Pro Tyr Gly Gly Arg Ser Ser Phe Phe Arg
    145                 150                 155

aat gtg gta tgg ctt atc aaa aag aac aat gca tac cca aca ata aag       527
Asn Val Val Trp Leu Ile Lys Lys Asn Asn Ala Tyr Pro Thr Ile Lys
160                 165                 170                 175

agg agt tac aat aat acc aac caa gaa gat ctt ttg ata ctg tgg ggg       575
Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp Gly
                180                 185                 190

att cac cat cct aat gat gcg gca gag cag aca aaa ctc tat caa aac       623
Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln Asn
            195                 200                 205

cca act acc tat gtt tcc gtt gga aca tca aca ctg aac cag aga tcg       671
Pro Thr Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Gln Arg Ser
        210                 215                 220

gtt cca gaa ata gct act agg ccc aaa gtg aac ggg caa agt gga aga       719
Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly Arg
    225                 230                 235

atg gag ttc ttc tgg aca att tta aag ccg aat gat gcc atc aat ttc       767
Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn Phe
240                 245                 250                 255

gag agt aat gga aat ttc att gct cca gaa tat gca tac aaa att gtc       815
Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile Val
                260                 265                 270

aaa aaa gga gac tca gca atc atg aaa agt gga ttg gaa tat ggt aac       863
Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Gly Leu Glu Tyr Gly Asn
            275                 280                 285
```

```
tgc aac acc aag tgt caa act cca atg ggt gcg ata aac tct agt atg      911
Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser Met
        290                 295                 300

cca ttc cat aac ata cac cct ctc acc att gga gaa tgc ccc aaa tac      959
Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr
    305                 310                 315

gtg aaa tca gat aga tta gtc ctt gcg act gga ctc aga aat gtc cct     1007
Val Lys Ser Asp Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro
320                 325                 330                 335

caa aga gaa aca aga gga cta ttt ggg gct ata gct ggc ttt ata gag     1055
Gln Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu
                340                 345                 350

gga gga tgg caa gga atg gta gac ggt tgg tat ggg tac cac cat agc     1103
Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser
            355                 360                 365

aac gag cag ggg agt gga tac gct gca gac aaa gaa tcc act caa aag     1151
Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys
        370                 375                 380

gca ata gat gga atc act aat aag gtc aac tca atc att gac aaa atg     1199
Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser Ile Ile Asp Lys Met
    385                 390                 395

aac act cag ttt gag gct gtt gga aag gaa ttt aat aac ttg gaa agg     1247
Asn Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Asn Asn Leu Glu Arg
400                 405                 410                 415

agg ata gag aat ttg aac aag aaa atg gaa gac ggg ttt cta gat gtc     1295
Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val
                420                 425                 430

tgg act tat aat gct gaa ctt ctg gtt ctc atg gaa aat gag aga acc     1343
Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr
            435                 440                 445

cta gac ttt cat gac tca aat gtc aag aac ctt tat gac aag gtt cga     1391
Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg
        450                 455                 460

cta cag ctt agg gat aat gca aag gag ctg ggt aat ggt tgt ttc gag     1439
Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn Gly Cys Phe Glu
    465                 470                 475

ttc tac cac aaa tgt gat aat gaa tgt atg gaa agt gta aaa aac ggg     1487
Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser Val Lys Asn Gly
480                 485                 490                 495

acg tat gac tac ccg cag tat tca gaa gag gca aga cta aac aga gag     1535
Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Asn Arg Glu
                500                 505                 510

gaa ata agt gga gtg aaa ttg gaa tca atg gga act tac caa ata ctg     1583
Glu Ile Ser Gly Val Lys Leu Glu Ser Met Gly Thr Tyr Gln Ile Leu
            515                 520                 525

tca att tat tca aca gtg gcg agt tcc cta gca ctg gca atc atg gta     1631
Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met Val
        530                 535                 540

gcn                                                                1634
Ala
```

<210> 14
<211> 544
<212> PRT
<213> Influenza A virus

<400> 14

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Lys Ile Val Leu Leu Leu Ala Thr Val Ser Leu Val Lys Ser Asp Gln
1               5                   10                  15

Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val Asp Thr
            20                  25                  30

Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile Leu Glu
        35                  40                  45

Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asn Gly Val Lys Pro Leu
    50                  55                  60

Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn Pro Met
65                  70                  75                  80

Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val Glu Lys
                85                  90                  95

Asp Ser Pro Val Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn Asp Tyr
            100                 105                 110

Glu Glu Leu Lys His Leu Leu Ser Ser Thr Asn His Phe Glu Lys Ile
        115                 120                 125

Gln Ile Ile Pro Arg Ser Ser Trp Ser Asn His Asp Ala Ser Ser Gly
    130                 135                 140

Val Ser Ser Ala Cys Pro Tyr Gly Gly Arg Ser Ser Phe Phe Arg Asn
145                 150                 155                 160

Val Val Trp Leu Ile Lys Lys Asn Asn Ala Tyr Pro Thr Ile Lys Arg
                165                 170                 175

Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp Gly Ile
            180                 185                 190

His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln Asn Pro
        195                 200                 205

Thr Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Gln Arg Ser Val
    210                 215                 220

Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly Arg Met
225                 230                 235                 240
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Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn Phe Glu
                245                 250                 255

Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile Val Lys
            260                 265                 270

Lys Gly Asp Ser Ala Ile Met Lys Ser Gly Leu Glu Tyr Gly Asn Cys
        275                 280                 285

Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser Met Pro
    290                 295                 300

Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val
305                 310                 315                 320

Lys Ser Asp Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln
                325                 330                 335

Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
            340                 345                 350

Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn
        355                 360                 365

Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala
    370                 375                 380

Ile Asp Gly Ile Thr Asn Lys Val Asn Ser Ile Ile Asp Lys Met Asn
385                 390                 395                 400

Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Asn Asn Leu Glu Arg Arg
                405                 410                 415

Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
            420                 425                 430

Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
        435                 440                 445

Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Leu
    450                 455                 460

Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
465                 470                 475                 480

Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser Val Lys Asn Gly Thr
                485                 490                 495

Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Asn Arg Glu Glu
            500                 505                 510
```

```
Ile Ser Gly Val Lys Leu Glu Ser Met Gly Thr Tyr Gln Ile Leu Ser
        515                 520                 525

Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met Val Ala
    530                 535                 540


<210>  15
<211>  1714
<212>  DNA
<213>  Influenza A virus

<220>
<221>  CDS
<222>  (4)..(1707)
<223>

<400>  15
aaa atg att gca atc ata ata atc gcg gta gtg gcc tct acc agc aaa      48
    Met Ile Ala Ile Ile Ile Ile Ala Val Val Ala Ser Thr Ser Lys
    1               5                  10                  15

tca gac aag atc tgc att ggg tat cat gcc aac aac tcg aca aca caa      96
Ser Asp Lys Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Thr Gln
                20                  25                  30

gtg gac aca ata tta gag aag aat gtg aca gtg acg cac tct gta gag     144
Val Asp Thr Ile Leu Glu Lys Asn Val Thr Val Thr His Ser Val Glu
            35                  40                  45

ctc cta gaa agt cag aag gag gag aga ttc tgc aga gtg ttg aat aaa     192
Leu Leu Glu Ser Gln Lys Glu Glu Arg Phe Cys Arg Val Leu Asn Lys
        50                  55                  60

aca cct ctg gat cta aag ggt tgc acc att gaa gga tgg att ctt gga     240
Thr Pro Leu Asp Leu Lys Gly Cys Thr Ile Glu Gly Trp Ile Leu Gly
    65                  70                  75

aac ccc caa tgt gac atc tta ctt ggt gac caa agt tgg tca tac ata     288
Asn Pro Gln Cys Asp Ile Leu Leu Gly Asp Gln Ser Trp Ser Tyr Ile
80                  85                  90                  95

gta gag agg cct gga gcc caa aat ggg ata tgt tac cca ggg gtg ctg     336
Val Glu Arg Pro Gly Ala Gln Asn Gly Ile Cys Tyr Pro Gly Val Leu
                100                 105                 110

aac gaa gtg gaa gaa ctg aaa gca ttc att ggg tcc gga gag aaa gta     384
Asn Glu Val Glu Glu Leu Lys Ala Phe Ile Gly Ser Gly Glu Lys Val
            115                 120                 125

cag aga ttt gaa atg ttt ccc aag agc acg tgg acc gga gtg gac act     432
Gln Arg Phe Glu Met Phe Pro Lys Ser Thr Trp Thr Gly Val Asp Thr
        130                 135                 140

aac agt gga gtt acg aga gct tgc ccc tat act acc agt gga tca tcc     480
Asn Ser Gly Val Thr Arg Ala Cys Pro Tyr Thr Thr Ser Gly Ser Ser
    145                 150                 155

ttt tac agg aat ctt ttg tgg ata ata aaa aca agg tct gct gca tac     528
Phe Tyr Arg Asn Leu Leu Trp Ile Ile Lys Thr Arg Ser Ala Ala Tyr
160                 165                 170                 175

cca gta att aag gga aca tac aat aat act ggc tcc cag cca atc cta     576
Pro Val Ile Lys Gly Thr Tyr Asn Asn Thr Gly Ser Gln Pro Ile Leu
                180                 185                 190

tat ttc tgg ggt gtg cat cat cct cca aat acc gat gag caa aat acc     624
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```
Tyr Phe Trp Gly Val His His Pro Pro Asn Thr Asp Glu Gln Asn Thr
            195                 200                 205

tta tat ggc tct ggt gac agg tat gtt aga atg gga act gaa agc atg      672
Leu Tyr Gly Ser Gly Asp Arg Tyr Val Arg Met Gly Thr Glu Ser Met
        210                 215                 220

aat ttt gcc aag agt cct gaa ata gca gcc agg cca gct gtg aat ggg      720
Asn Phe Ala Lys Ser Pro Glu Ile Ala Ala Arg Pro Ala Val Asn Gly
    225                 230                 235

caa aga gga aga att gat tat tat tgg tct gta ctg aaa cca gga gaa      768
Gln Arg Gly Arg Ile Asp Tyr Tyr Trp Ser Val Leu Lys Pro Gly Glu
240                 245                 250                 255

acc tta aat gta gaa tcc aat gga aat tta ata gct cct tgg tat gct      816
Thr Leu Asn Val Glu Ser Asn Gly Asn Leu Ile Ala Pro Trp Tyr Ala
                260                 265                 270

tac aag ttc aca agt tcc aac aac aaa gga gct atc ttc aaa tca aac      864
Tyr Lys Phe Thr Ser Ser Asn Asn Lys Gly Ala Ile Phe Lys Ser Asn
            275                 280                 285

ctc cca att gag aat tgt gat gct gta tgt caa act gtt gct gga gca      912
Leu Pro Ile Glu Asn Cys Asp Ala Val Cys Gln Thr Val Ala Gly Ala
        290                 295                 300

cta aag aca aac aaa act ttc caa aat gtt agt cca ctc tgg att gga      960
Leu Lys Thr Asn Lys Thr Phe Gln Asn Val Ser Pro Leu Trp Ile Gly
    305                 310                 315

gaa tgt ccc aaa tat gtt aag agt gag agc cta aga ctg gca act ggt     1008
Glu Cys Pro Lys Tyr Val Lys Ser Glu Ser Leu Arg Leu Ala Thr Gly
320                 325                 330                 335

ctg agg aat gtc cca cag gca gaa aca aga gga ttg ttt gga gcc ata     1056
Leu Arg Asn Val Pro Gln Ala Glu Thr Arg Gly Leu Phe Gly Ala Ile
                340                 345                 350

gct ggg ttt ata gaa gga ggg tgg aca ggt atg ata gac gga tgg tac     1104
Ala Gly Phe Ile Glu Gly Gly Trp Thr Gly Met Ile Asp Gly Trp Tyr
            355                 360                 365

ggg tac cat cat gag aac tca cag ggg tcg ggt tat gca gca gat aaa     1152
Gly Tyr His His Glu Asn Ser Gln Gly Ser Gly Tyr Ala Ala Asp Lys
        370                 375                 380

gaa agt acc cag aaa gca att gac ggg atc acc aat aaa gta aat tcc     1200
Glu Ser Thr Gln Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser
    385                 390                 395

atc att gac aag atg aac aca cag ttt gaa gca gta gag cat gag ttc     1248
Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Glu His Glu Phe
400                 405                 410                 415

tca aat ctc gaa agg aga ata gac aat tta aac aaa aga atg gaa gat     1296
Ser Asn Leu Glu Arg Arg Ile Asp Asn Leu Asn Lys Arg Met Glu Asp
                420                 425                 430

gga ttt ttg gat gtg tgg acg tac aat gct gaa ctt tta gtt cta ctg     1344
Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Leu
            435                 440                 445

gaa aat gaa agg acc ctg gat ctg cac gat gcc aat gtg aag aac cta     1392
Glu Asn Glu Arg Thr Leu Asp Leu His Asp Ala Asn Val Lys Asn Leu
        450                 455                 460

tac gag aag gtg aaa tca caa ttg aga gat aat gca aag gat ttg ggt     1440
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Tyr Glu Lys Val Lys Ser Gln Leu Arg Asp Asn Ala Lys Asp Leu Gly
    465                 470                 475

aat ggg tgt ttt gaa ttt tgg cac aaa tgc gac gat gaa tgc atc aac     1488
Asn Gly Cys Phe Glu Phe Trp His Lys Cys Asp Asp Glu Cys Ile Asn
480                 485                 490                 495

tca gtt aag aat ggc aca tac gat tac cca aag tac caa gac gag agc     1536
Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro Lys Tyr Gln Asp Glu Ser
                500                 505                 510

aaa ctt aac aga cag gag ata gac tca gtg aag ctg gaa aat ctg ggc     1584
Lys Leu Asn Arg Gln Glu Ile Asp Ser Val Lys Leu Glu Asn Leu Gly
            515                 520                 525

gta tat caa att ctt gct att tat agt acg gta tcg agc agt cta gtt     1632
Val Tyr Gln Ile Leu Ala Ile Tyr Ser Thr Val Ser Ser Ser Leu Val
        530                 535                 540

ttg gtg ggg ctg atc att gcc atg ggt ctt tgg atg tgc tca aat ggc     1680
Leu Val Gly Leu Ile Ile Ala Met Gly Leu Trp Met Cys Ser Asn Gly
    545                 550                 555

tca atg caa tgc agg ata tgt ata taa ttaggaa                         1714
Ser Met Gln Cys Arg Ile Cys Ile
560                 565
```

<210> 16
<211> 567
<212> PRT
<213> Influenza A virus

<400> 16

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Met Ile Ala Ile Ile Ile Ile Ala Val Val Ala Ser Thr Ser Lys Ser
1               5                   10                  15

Asp Lys Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Thr Gln Val
            20                  25                  30

Asp Thr Ile Leu Glu Lys Asn Val Thr Val Thr His Ser Val Glu Leu
        35                  40                  45

Leu Glu Ser Gln Lys Glu Glu Arg Phe Cys Arg Val Leu Asn Lys Thr
    50                  55                  60

Pro Leu Asp Leu Lys Gly Cys Thr Ile Glu Gly Trp Ile Leu Gly Asn
65                  70                  75                  80

Pro Gln Cys Asp Ile Leu Leu Gly Asp Gln Ser Trp Ser Tyr Ile Val
                85                  90                  95

Glu Arg Pro Gly Ala Gln Asn Gly Ile Cys Tyr Pro Gly Val Leu Asn
            100                 105                 110

Glu Val Glu Glu Leu Lys Ala Phe Ile Gly Ser Gly Glu Lys Val Gln
        115                 120                 125

Arg Phe Glu Met Phe Pro Lys Ser Thr Trp Thr Gly Val Asp Thr Asn
```

130 135 140

Ser Gly Val Thr Arg Ala Cys Pro Tyr Thr Thr Ser Gly Ser Ser Phe
145 150 155 160

Tyr Arg Asn Leu Leu Trp Ile Ile Lys Thr Arg Ser Ala Ala Tyr Pro
165 170 175

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

Phe Trp Gly Val His His Pro Pro Asn Thr Asp Glu Gln Asn Thr Leu
195 200 205

Tyr Gly Ser Gly Asp Arg Tyr Val Arg Met Gly Thr Glu Ser Met Asn
210 215 220

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

Arg Gly Arg Ile Asp Tyr Tyr Trp Ser Val Leu Lys Pro Gly Glu Thr
245 250 255

Leu Asn Val Glu Ser Asn Gly Asn Leu Ile Ala Pro Trp Tyr Ala Tyr
260 265 270

Lys Phe Thr Ser Ser Asn Asn Lys Gly Ala Ile Phe Lys Ser Asn Leu
275 280 285

Pro Ile Glu Asn Cys Asp Ala Val Cys Gln Thr Val Ala Gly Ala Leu
290 295 300

Lys Thr Asn Lys Thr Phe Gln Asn Val Ser Pro Leu Trp Ile Gly Glu
305 310 315 320

Cys Pro Lys Tyr Val Lys Ser Glu Ser Leu Arg Leu Ala Thr Gly Leu
325 330 335

Arg Asn Val Pro Gln Ala Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala
340 345 350

Gly Phe Ile Glu Gly Gly Trp Thr Gly Met Ile Asp Gly Trp Tyr Gly
355 360 365

Tyr His His Glu Asn Ser Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
370 375 380

Ser Thr Gln Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser Ile
385 390 395 400

Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Glu His Glu Phe Ser

405 410 415

Asn Leu Glu Arg Arg Ile Asp Asn Leu Asn Lys Arg Met Glu Asp Gly
420 425 430

Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu
435 440 445

Asn Glu Arg Thr Leu Asp Leu His Asp Ala Asn Val Lys Asn Leu Tyr
450 455 460

Glu Lys Val Lys Ser Gln Leu Arg Asp Asn Ala Lys Asp Leu Gly Asn
465 470 475 480

Gly Cys Phe Glu Phe Trp His Lys Cys Asp Asp Glu Cys Ile Asn Ser
485 490 495

Val Lys Asn Gly Thr Tyr Asp Tyr Pro Lys Tyr Gln Asp Glu Ser Lys
500 505 510

Leu Asn Arg Gln Glu Ile Asp Ser Val Lys Leu Glu Asn Leu Gly Val
515 520 525

Tyr Gln Ile Leu Ala Ile Tyr Ser Thr Val Ser Ser Ser Leu Val Leu
530 535 540

Val Gly Leu Ile Ile Ala Met Gly Leu Trp Met Cys Ser Asn Gly Ser
545 550 555 560

Met Gln Cys Arg Ile Cys Ile
565

<210> 17
<211> 1697
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (8)..(1690)
<223>

<400> 17
atacaaa atg aac act caa att ctg gta ttc att gcc tgt gtg ctg att 49
Met Asn Thr Gln Ile Leu Val Phe Ile Ala Cys Val Leu Ile
1 5 10

gaa gct aaa gga gac aaa ata tgt ctt gga cac cat gct gtg gca aat 97
Glu Ala Lys Gly Asp Lys Ile Cys Leu Gly His His Ala Val Ala Asn
15 20 25 30

gga aca aag gtg aac acg cta aca gag agg ggg att gaa gta gtg aat 145
Gly Thr Lys Val Asn Thr Leu Thr Glu Arg Gly Ile Glu Val Val Asn
35 40 45

gcc acg gaa aca gtg gaa acc gcg aat atc ggg aaa atc tgc acc caa 193
Ala Thr Glu Thr Val Glu Thr Ala Asn Ile Gly Lys Ile Cys Thr Gln

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                50                  55                  60

ggg aaa agg cca aca gac ctg gga caa tgt ggg ctc cta gga acc cta      241
Gly Lys Arg Pro Thr Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr Leu
        65                  70                  75

ata gga cct ccc caa tgt gat caa ttc ctg gag ttt gaa tca aat ttg      289
Ile Gly Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Glu Ser Asn Leu
    80                  85                  90

ata atc gaa cga agg gaa ggg aac gat gtg tgc tat cct ggg aag ttc      337
Ile Ile Glu Arg Arg Glu Gly Asn Asp Val Cys Tyr Pro Gly Lys Phe
95                  100                 105                 110

aca aat gaa gaa tca ctg agg cag atc ctt cgg ggg tca gga gga gtc      385
Thr Asn Glu Glu Ser Leu Arg Gln Ile Leu Arg Gly Ser Gly Gly Val
                115                 120                 125

gat aaa gag tca atg ggt ttc acc tat agt gga ata aga acc aat gga      433
Asp Lys Glu Ser Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn Gly
            130                 135                 140

gca aca agt gcc tgc aga aga tca ggt tct tcc ttc tat gcg gaa atg      481
Ala Thr Ser Ala Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu Met
        145                 150                 155

aag tgg ttg ctg tcg aat tca gac aat gcg gca ttc cct caa atg acc      529
Lys Trp Leu Leu Ser Asn Ser Asp Asn Ala Ala Phe Pro Gln Met Thr
    160                 165                 170

aaa tca tat aga aat ccc aga aac aaa cca gct ctg ata gtt tgg gga      577
Lys Ser Tyr Arg Asn Pro Arg Asn Lys Pro Ala Leu Ile Val Trp Gly
175                 180                 185                 190

att cac cat tct gga tcg act acc gaa cag acc aga ctc tat gga agt      625
Ile His His Ser Gly Ser Thr Thr Glu Gln Thr Arg Leu Tyr Gly Ser
                195                 200                 205

gga aac aag ttg ata aca gta gga agc tcg aaa tat caa caa tcg ttc      673
Gly Asn Lys Leu Ile Thr Val Gly Ser Ser Lys Tyr Gln Gln Ser Phe
            210                 215                 220

acc cca agt ccg gaa gca cgg cca caa gtg aat gga caa tca ggg aga      721
Thr Pro Ser Pro Glu Ala Arg Pro Gln Val Asn Gly Gln Ser Gly Arg
        225                 230                 235

atc gat ttc cat tgg cta ctc ctt gat ccc aat gac aca gtg act ttc      769
Ile Asp Phe His Trp Leu Leu Leu Asp Pro Asn Asp Thr Val Thr Phe
    240                 245                 250

acc ttc aat gga gca ttc ata gcc cct aat agg gca agt ttc ttt aga      817
Thr Phe Asn Gly Ala Phe Ile Ala Pro Asn Arg Ala Ser Phe Phe Arg
255                 260                 265                 270

gga gaa tca cta gga gtc cag agt gat gtg cct tta gac tct aat tgt      865
Gly Glu Ser Leu Gly Val Gln Ser Asp Val Pro Leu Asp Ser Asn Cys
                275                 280                 285

gga ggg gat tgc ttt cat agt ggg ggc acg ata gtc agt tct ctg cca      913
Gly Gly Asp Cys Phe His Ser Gly Gly Thr Ile Val Ser Ser Leu Pro
            290                 295                 300

ttc caa aac atc aat tct aga acg gtg ggg aaa tgc ccc cga tat gtc      961
Phe Gln Asn Ile Asn Ser Arg Thr Val Gly Lys Cys Pro Arg Tyr Val
        305                 310                 315

aaa cag cca agc ctc ctt tcg gct aca gga atg aga aat gtc cca gag     1009
Lys Gln Pro Ser Leu Leu Ser Ala Thr Gly Met Arg Asn Val Pro Glu
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    320                 325                 330

aat cca aag acc aga gga ctt ttt gga gca att gct gga ttc ata gag     1057
Asn Pro Lys Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu
335                 340                 345                 350

aat gga tgg gag ggt ctc atc gat ggg tgg tat ggt ttc agg cat caa     1105
Asn Gly Trp Glu Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg His Gln
                355                 360                 365

aat gca caa gga gaa gga act gca gct gac tac aaa agc acc caa tct     1153
Asn Ala Gln Gly Glu Gly Thr Ala Ala Asp Tyr Lys Ser Thr Gln Ser
            370                 375                 380

gca ata gat cag atc act ggc aca ttg aat cgt ctg att gac aaa aca     1201
Ala Ile Asp Gln Ile Thr Gly Thr Leu Asn Arg Leu Ile Asp Lys Thr
        385                 390                 395

aat cag cag ttt gag ctg ata gac aat gaa ttc aat gag ata gaa caa     1249
Asn Gln Gln Phe Glu Leu Ile Asp Asn Glu Phe Asn Glu Ile Glu Gln
    400                 405                 410

cag att gga aat gtc att aat tgg aca cga gac tca atg act gaa gta     1297
Gln Ile Gly Asn Val Ile Asn Trp Thr Arg Asp Ser Met Thr Glu Val
415                 420                 425                 430

tgg tcg tat aat gct gag ctg ttg gtg gcc atg gaa aat cag cac aca     1345
Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr
                435                 440                 445

ata gat ctt gcg gat tca gaa atg aac aaa ctt tat gag cgt gtc aga     1393
Ile Asp Leu Ala Asp Ser Glu Met Asn Lys Leu Tyr Glu Arg Val Arg
            450                 455                 460

aaa caa cta agg gag aat gct gaa gaa gat ggg act gga tgt ttt gaa     1441
Lys Gln Leu Arg Glu Asn Ala Glu Glu Asp Gly Thr Gly Cys Phe Glu
        465                 470                 475

ata ttc cat aag tgt gac gac caa tgt atg gag agc ata agg aac aac     1489
Ile Phe His Lys Cys Asp Asp Gln Cys Met Glu Ser Ile Arg Asn Asn
    480                 485                 490

act tat gac cat acc caa tac aga gca gag tca tta cag aat aga ata     1537
Thr Tyr Asp His Thr Gln Tyr Arg Ala Glu Ser Leu Gln Asn Arg Ile
495                 500                 505                 510

cag ata gac cca gtg aaa ttg agt agt gga tac aaa gac ata atc tta     1585
Gln Ile Asp Pro Val Lys Leu Ser Ser Gly Tyr Lys Asp Ile Ile Leu
                515                 520                 525

tgg ttt agc ttc ggg gca tca tgt ttc ctc ctt cta gcc att gca atg     1633
Trp Phe Ser Phe Gly Ala Ser Cys Phe Leu Leu Leu Ala Ile Ala Met
            530                 535                 540

gga ttg gtc ttc att tgc ata aag aat gga aac atg cgg tgc act att     1681
Gly Leu Val Phe Ile Cys Ile Lys Asn Gly Asn Met Arg Cys Thr Ile
        545                 550                 555

tgt ata tag tttgaga                                                 1697
Cys Ile
    560
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<210> 18
<211> 560
<212> PRT
<213> Influenza A virus

<400> 18

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

Lys Gly Asp Lys Ile Cys Leu Gly His His Ala Val Ala Asn Gly Thr
20 25 30

Lys Val Asn Thr Leu Thr Glu Arg Gly Ile Glu Val Val Asn Ala Thr
35 40 45

Glu Thr Val Glu Thr Ala Asn Ile Gly Lys Ile Cys Thr Gln Gly Lys
50 55 60

Arg Pro Thr Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr Leu Ile Gly
65 70 75 80

Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Glu Ser Asn Leu Ile Ile
85 90 95

Glu Arg Arg Glu Gly Asn Asp Val Cys Tyr Pro Gly Lys Phe Thr Asn
100 105 110

Glu Glu Ser Leu Arg Gln Ile Leu Arg Gly Ser Gly Gly Val Asp Lys
115 120 125

Glu Ser Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn Gly Ala Thr
130 135 140

Ser Ala Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu Met Lys Trp
145 150 155 160

Leu Leu Ser Asn Ser Asp Asn Ala Ala Phe Pro Gln Met Thr Lys Ser
165 170 175

Tyr Arg Asn Pro Arg Asn Lys Pro Ala Leu Ile Val Trp Gly Ile His
180 185 190

His Ser Gly Ser Thr Thr Glu Gln Thr Arg Leu Tyr Gly Ser Gly Asn
195 200 205

Lys Leu Ile Thr Val Gly Ser Ser Lys Tyr Gln Gln Ser Phe Thr Pro
210 215 220

Ser Pro Glu Ala Arg Pro Gln Val Asn Gly Gln Ser Gly Arg Ile Asp
225 230 235 240

Phe His Trp Leu Leu Leu Asp Pro Asn Asp Thr Val Thr Phe Thr Phe
245 250 255

Asn Gly Ala Phe Ile Ala Pro Asn Arg Ala Ser Phe Phe Arg Gly Glu
260 265 270

Ser Leu Gly Val Gln Ser Asp Val Pro Leu Asp Ser Asn Cys Gly Gly
275 280 285

Asp Cys Phe His Ser Gly Gly Thr Ile Val Ser Ser Leu Pro Phe Gln
290 295 300

Asn Ile Asn Ser Arg Thr Val Gly Lys Cys Pro Arg Tyr Val Lys Gln
305 310 315 320

Pro Ser Leu Leu Ser Ala Thr Gly Met Arg Asn Val Pro Glu Asn Pro
325 330 335

Lys Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly
340 345 350

Trp Glu Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ala
355 360 365

Gln Gly Glu Gly Thr Ala Ala Asp Tyr Lys Ser Thr Gln Ser Ala Ile
370 375 380

Asp Gln Ile Thr Gly Thr Leu Asn Arg Leu Ile Asp Lys Thr Asn Gln
385 390 395 400

Gln Phe Glu Leu Ile Asp Asn Glu Phe Asn Glu Ile Glu Gln Gln Ile
405 410 415

Gly Asn Val Ile Asn Trp Thr Arg Asp Ser Met Thr Glu Val Trp Ser
420 425 430

Tyr Asn Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr Ile Asp
435 440 445

Leu Ala Asp Ser Glu Met Asn Lys Leu Tyr Glu Arg Val Arg Lys Gln
450 455 460

Leu Arg Glu Asn Ala Glu Glu Asp Gly Thr Gly Cys Phe Glu Ile Phe
465 470 475 480

His Lys Cys Asp Asp Gln Cys Met Glu Ser Ile Arg Asn Asn Thr Tyr
485 490 495

Asp His Thr Gln Tyr Arg Ala Glu Ser Leu Gln Asn Arg Ile Gln Ile
500 505 510

Asp Pro Val Lys Leu Ser Ser Gly Tyr Lys Asp Ile Ile Leu Trp Phe
515 520 525

Ser Phe Gly Ala Ser Cys Phe Leu Leu Leu Ala Ile Ala Met Gly Leu
530 535 540

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Val Phe Ile Cys Ile Lys Asn Gly Asn Met Arg Cys Thr Ile Cys Ile
545                 550                 555                 560


<210>  19
<211>  1710
<212>  DNA
<213>  Influenza A virus

<220>
<221>  CDS
<222>  (6)..(1706)
<223>

<400>  19
tcaca atg gag aaa ttc atc gcc ata gca atg ctc ttg gcg agc aca aat     50
      Met Glu Lys Phe Ile Ala Ile Ala Met Leu Leu Ala Ser Thr Asn
      1               5                  10                  15

gca tac gat agg ata tgc att ggg tac caa tca aac aac tcc aca gac       98
Ala Tyr Asp Arg Ile Cys Ile Gly Tyr Gln Ser Asn Asn Ser Thr Asp
                  20                  25                  30

aca gtg aac act ctc ata gaa cag aat gtg cca gtc acc caa aca atg      146
Thr Val Asn Thr Leu Ile Glu Gln Asn Val Pro Val Thr Gln Thr Met
            35                  40                  45

gag ctc gtg gaa aca gag aaa cat ccc gct tat tgt aac act gat tta      194
Glu Leu Val Glu Thr Glu Lys His Pro Ala Tyr Cys Asn Thr Asp Leu
        50                  55                  60

ggt gcc cca ttg gaa ctg cga gac tgc aag gtt gag gca gta atc tat      242
Gly Ala Pro Leu Glu Leu Arg Asp Cys Lys Val Glu Ala Val Ile Tyr
    65                  70                  75

ggg aac ccc aag tgt gac atc cat ctg aag gat caa ggt tgg tca tac      290
Gly Asn Pro Lys Cys Asp Ile His Leu Lys Asp Gln Gly Trp Ser Tyr
80                  85                  90                  95

ata gtg gag agg ccc agc gca cca gaa ggg atg tgt tac cct gga tct      338
Ile Val Glu Arg Pro Ser Ala Pro Glu Gly Met Cys Tyr Pro Gly Ser
                100                 105                 110

gtg gaa aat cta gaa gaa ctg agg ttt gtc ttc tcc agt gct gca tct      386
Val Glu Asn Leu Glu Glu Leu Arg Phe Val Phe Ser Ser Ala Ala Ser
            115                 120                 125

tac aag aga ata aga cta ttt gac tat tcc agg tgg aat gtg act aga      434
Tyr Lys Arg Ile Arg Leu Phe Asp Tyr Ser Arg Trp Asn Val Thr Arg
        130                 135                 140

tct gga acg agt aaa gca tgc aat gca tca aca ggt ggc caa tcc ttc      482
Ser Gly Thr Ser Lys Ala Cys Asn Ala Ser Thr Gly Gly Gln Ser Phe
    145                 150                 155

tat agg agc atc aat tgg ttg acc aaa aag aaa cca gac act tat gac      530
Tyr Arg Ser Ile Asn Trp Leu Thr Lys Lys Lys Pro Asp Thr Tyr Asp
160                 165                 170                 175

ttc aat gaa gga gct tat gtt aat aat gaa gat gga gac atc att ttc      578
Phe Asn Glu Gly Ala Tyr Val Asn Asn Glu Asp Gly Asp Ile Ile Phe
                180                 185                 190

tta tgg ggg atc cat cat ccg ccg gac aca aaa gag cag aca aca cta      626
Leu Trp Gly Ile His His Pro Pro Asp Thr Lys Glu Gln Thr Thr Leu
            195                 200                 205
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tat aaa aat gca aac act ttg agt agt gtt act act aac act ata aac      674
Tyr Lys Asn Ala Asn Thr Leu Ser Ser Val Thr Thr Asn Thr Ile Asn
        210                 215                 220

aga agc ttt caa cca aat att ggt ccc aga cca tta gta aga gga cag      722
Arg Ser Phe Gln Pro Asn Ile Gly Pro Arg Pro Leu Val Arg Gly Gln
    225                 230                 235

caa ggg agg atg gat tac tat tgg ggc att ctg aaa aga ggg gag act      770
Gln Gly Arg Met Asp Tyr Tyr Trp Gly Ile Leu Lys Arg Gly Glu Thr
240                 245                 250                 255

ctg aag atc agg acc aac gga aat tta atc gca cct gaa ttt ggc tat      818
Leu Lys Ile Arg Thr Asn Gly Asn Leu Ile Ala Pro Glu Phe Gly Tyr
                260                 265                 270

ctg ctc aaa ggt gaa agc tac ggc aga ata att caa aat gag gat ata      866
Leu Leu Lys Gly Glu Ser Tyr Gly Arg Ile Ile Gln Asn Glu Asp Ile
            275                 280                 285

ccc atc ggg aac tgt aac aca aaa tgt caa aca tat gcg gga gca atc      914
Pro Ile Gly Asn Cys Asn Thr Lys Cys Gln Thr Tyr Ala Gly Ala Ile
        290                 295                 300

aat agc agc aaa ccc ttt cag aat gca agt agg cat tac atg gga gaa      962
Asn Ser Ser Lys Pro Phe Gln Asn Ala Ser Arg His Tyr Met Gly Glu
    305                 310                 315

tgt ccc aaa tat gtg aag aag gca agc ttg cga ctt gca gtt ggg ctt     1010
Cys Pro Lys Tyr Val Lys Lys Ala Ser Leu Arg Leu Ala Val Gly Leu
320                 325                 330                 335

agg aat acg cct tct gtt gaa ccc aga gga ctg ttt gga gcc att gct     1058
Arg Asn Thr Pro Ser Val Glu Pro Arg Gly Leu Phe Gly Ala Ile Ala
                340                 345                 350

ggt ttc att gaa gga gga tgg tct gga atg att gat ggg tgg tat gga     1106
Gly Phe Ile Glu Gly Gly Trp Ser Gly Met Ile Asp Gly Trp Tyr Gly
            355                 360                 365

ttt cat cac agc aat tca gag gga aca gga atg gca gct gac cag aaa     1154
Phe His His Ser Asn Ser Glu Gly Thr Gly Met Ala Ala Asp Gln Lys
        370                 375                 380

tca aca caa gaa gcc atc gat aag atc acc aat aaa gtc aac aat ata     1202
Ser Thr Gln Glu Ala Ile Asp Lys Ile Thr Asn Lys Val Asn Asn Ile
    385                 390                 395

gtt gac aag atg aac agg gag ttt gaa gtt gtg aat cat gag ttc tct     1250
Val Asp Lys Met Asn Arg Glu Phe Glu Val Val Asn His Glu Phe Ser
400                 405                 410                 415

gaa gtt gaa aaa aga ata aac atg ata aac gat aaa ata gat gac caa     1298
Glu Val Glu Lys Arg Ile Asn Met Ile Asn Asp Lys Ile Asp Asp Gln
                420                 425                 430

att gaa gat ctt tgg gct tac aat gca gag ctc ctt gtg ctc tta gag     1346
Ile Glu Asp Leu Trp Ala Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu
            435                 440                 445

aac cag aaa acg cta gac gaa cat gat tcc aat gtc aaa aac ctt ttt     1394
Asn Gln Lys Thr Leu Asp Glu His Asp Ser Asn Val Lys Asn Leu Phe
        450                 455                 460

gat gaa gtg aaa agg aga ctg tca gcc aat gca ata gat gct ggg aac     1442
Asp Glu Val Lys Arg Arg Leu Ser Ala Asn Ala Ile Asp Ala Gly Asn
    465                 470                 475
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ggt tgc ttt gac ata ctt cac aaa tgc gac aat gag tgt atg gaa act     1490
Gly Cys Phe Asp Ile Leu His Lys Cys Asp Asn Glu Cys Met Glu Thr
480                 485                 490                 495

ata aag aac gga act tac gat cat aag gaa tat gaa gag gag gct aaa     1538
Ile Lys Asn Gly Thr Tyr Asp His Lys Glu Tyr Glu Glu Glu Ala Lys
                500                 505                 510

cta gaa agg agc aag ata aat gga gta aaa cta gaa gag aac acc act     1586
Leu Glu Arg Ser Lys Ile Asn Gly Val Lys Leu Glu Glu Asn Thr Thr
            515                 520                 525

tac aaa att ctt agc att tac agt aca gtg gcg gcc agt ctt tgc ttg     1634
Tyr Lys Ile Leu Ser Ile Tyr Ser Thr Val Ala Ala Ser Leu Cys Leu
        530                 535                 540

gca atc ctg att gct gga ggt tta atc ctg ggc atg caa aat gga tct     1682
Ala Ile Leu Ile Ala Gly Gly Leu Ile Leu Gly Met Gln Asn Gly Ser
    545                 550                 555

tgt aga tgc atg ttc tgt att tga agaa                               1710
Cys Arg Cys Met Phe Cys Ile
560                 565
```

<210> 20
<211> 566
<212> PRT
<213> Influenza A virus

<400> 20

```
Met Glu Lys Phe Ile Ala Ile Ala Met Leu Leu Ala Ser Thr Asn Ala
1               5                   10                  15

Tyr Asp Arg Ile Cys Ile Gly Tyr Gln Ser Asn Asn Ser Thr Asp Thr
            20                  25                  30

Val Asn Thr Leu Ile Glu Gln Asn Val Pro Val Thr Gln Thr Met Glu
        35                  40                  45

Leu Val Glu Thr Glu Lys His Pro Ala Tyr Cys Asn Thr Asp Leu Gly
    50                  55                  60

Ala Pro Leu Glu Leu Arg Asp Cys Lys Val Glu Ala Val Ile Tyr Gly
65                  70                  75                  80

Asn Pro Lys Cys Asp Ile His Leu Lys Asp Gln Gly Trp Ser Tyr Ile
                85                  90                  95

Val Glu Arg Pro Ser Ala Pro Glu Gly Met Cys Tyr Pro Gly Ser Val
            100                 105                 110

Glu Asn Leu Glu Glu Leu Arg Phe Val Phe Ser Ser Ala Ala Ser Tyr
        115                 120                 125

Lys Arg Ile Arg Leu Phe Asp Tyr Ser Arg Trp Asn Val Thr Arg Ser
    130                 135                 140
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Gly Thr Ser Lys Ala Cys Asn Ala Ser Thr Gly Gly Gln Ser Phe Tyr
145                 150                 155                 160

Arg Ser Ile Asn Trp Leu Thr Lys Lys Lys Pro Asp Thr Tyr Asp Phe
                165                 170                 175

Asn Glu Gly Ala Tyr Val Asn Asn Glu Asp Gly Asp Ile Ile Phe Leu
            180                 185                 190

Trp Gly Ile His His Pro Pro Asp Thr Lys Glu Gln Thr Thr Leu Tyr
        195                 200                 205

Lys Asn Ala Asn Thr Leu Ser Ser Val Thr Thr Asn Thr Ile Asn Arg
    210                 215                 220

Ser Phe Gln Pro Asn Ile Gly Pro Arg Pro Leu Val Arg Gly Gln Gln
225                 230                 235                 240

Gly Arg Met Asp Tyr Tyr Trp Gly Ile Leu Lys Arg Gly Glu Thr Leu
                245                 250                 255

Lys Ile Arg Thr Asn Gly Asn Leu Ile Ala Pro Glu Phe Gly Tyr Leu
            260                 265                 270

Leu Lys Gly Glu Ser Tyr Gly Arg Ile Ile Gln Asn Glu Asp Ile Pro
        275                 280                 285

Ile Gly Asn Cys Asn Thr Lys Cys Gln Thr Tyr Ala Gly Ala Ile Asn
    290                 295                 300

Ser Ser Lys Pro Phe Gln Asn Ala Ser Arg His Tyr Met Gly Glu Cys
305                 310                 315                 320

Pro Lys Tyr Val Lys Lys Ala Ser Leu Arg Leu Ala Val Gly Leu Arg
                325                 330                 335

Asn Thr Pro Ser Val Glu Pro Arg Gly Leu Phe Gly Ala Ile Ala Gly
            340                 345                 350

Phe Ile Glu Gly Gly Trp Ser Gly Met Ile Asp Gly Trp Tyr Gly Phe
        355                 360                 365

His His Ser Asn Ser Glu Gly Thr Gly Met Ala Ala Asp Gln Lys Ser
    370                 375                 380

Thr Gln Glu Ala Ile Asp Lys Ile Thr Asn Lys Val Asn Asn Ile Val
385                 390                 395                 400

Asp Lys Met Asn Arg Glu Phe Glu Val Val Asn His Glu Phe Ser Glu
                405                 410                 415
```

```
Val Glu Lys Arg Ile Asn Met Ile Asn Asp Lys Ile Asp Asp Gln Ile
            420                 425                 430

Glu Asp Leu Trp Ala Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu Asn
        435                 440                 445

Gln Lys Thr Leu Asp Glu His Asp Ser Asn Val Lys Asn Leu Phe Asp
    450                 455                 460

Glu Val Lys Arg Arg Leu Ser Ala Asn Ala Ile Asp Ala Gly Asn Gly
465                 470                 475                 480

Cys Phe Asp Ile Leu His Lys Cys Asp Asn Glu Cys Met Glu Thr Ile
                485                 490                 495

Lys Asn Gly Thr Tyr Asp His Lys Glu Tyr Glu Glu Glu Ala Lys Leu
            500                 505                 510

Glu Arg Ser Lys Ile Asn Gly Val Lys Leu Glu Glu Asn Thr Thr Tyr
        515                 520                 525

Lys Ile Leu Ser Ile Tyr Ser Thr Val Ala Ala Ser Leu Cys Leu Ala
    530                 535                 540

Ile Leu Ile Ala Gly Gly Leu Ile Leu Gly Met Gln Asn Gly Ser Cys
545                 550                 555                 560

Arg Cys Met Phe Cys Ile
                565
```

<210> 21
<211> 1708
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (20)..(1702)
<223>

<400> 21

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aacaacatag ccaatcaag atg gaa aca aaa gca ata att gct gca ctg cta      52
                       Met Glu Thr Lys Ala Ile Ile Ala Ala Leu Leu
                       1               5                   10

atg gta aca gca gcc aat gct gat aaa atc tgc att ggc tat caa tca      100
Met Val Thr Ala Ala Asn Ala Asp Lys Ile Cys Ile Gly Tyr Gln Ser
            15                  20                  25

aca aac tcc acc gaa act gtc gac aca cta aca gag agc aat gtt cct      148
Thr Asn Ser Thr Glu Thr Val Asp Thr Leu Thr Glu Ser Asn Val Pro
        30                  35                  40

gta aca cac act aaa gaa ttg ctc cac aca gaa cac aat ggg atg ttg      196
Val Thr His Thr Lys Glu Leu Leu His Thr Glu His Asn Gly Met Leu
    45                  50                  55
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tgt gca act gat cta gga cat ccc ctc att cta gac acc tgc act att      244
Cys Ala Thr Asp Leu Gly His Pro Leu Ile Leu Asp Thr Cys Thr Ile
60                  65                  70                  75

gaa gga cta atc tat gga aat cct tcc tgt gac ata cta cta gga gga      292
Glu Gly Leu Ile Tyr Gly Asn Pro Ser Cys Asp Ile Leu Leu Gly Gly
                80                  85                  90

aaa gaa tgg tcc tac atc gtt gaa agg tcg tca gcc gtc aat gga atg      340
Lys Glu Trp Ser Tyr Ile Val Glu Arg Ser Ser Ala Val Asn Gly Met
            95                  100                 105

tgt tac cca ggg aat gta gag aac cta gaa gag ctt agg tca ctt ttc      388
Cys Tyr Pro Gly Asn Val Glu Asn Leu Glu Glu Leu Arg Ser Leu Phe
        110                 115                 120

agt tct gca aaa tct tac aaa aga atc caa atc ttt cca gat aaa act      436
Ser Ser Ala Lys Ser Tyr Lys Arg Ile Gln Ile Phe Pro Asp Lys Thr
    125                 130                 135

tgg aat gta aca tac agc gga aca agc aga gca tgc tca aat tca ttc      484
Trp Asn Val Thr Tyr Ser Gly Thr Ser Arg Ala Cys Ser Asn Ser Phe
140                 145                 150                 155

tat agg agc atg aga tgg ctg acc cac aag agt aat tcc tac cct ttt      532
Tyr Arg Ser Met Arg Trp Leu Thr His Lys Ser Asn Ser Tyr Pro Phe
                160                 165                 170

cag aac gct cat tac acc aac aat gag agg gag aac att ctt ttc atg      580
Gln Asn Ala His Tyr Thr Asn Asn Glu Arg Glu Asn Ile Leu Phe Met
            175                 180                 185

tgg ggc ata cac cat cca cct acc gac aca gaa cag aca gac tta tac      628
Trp Gly Ile His His Pro Pro Thr Asp Thr Glu Gln Thr Asp Leu Tyr
        190                 195                 200

aag aat gcc gat aca aca aca agt gtg aca aca gaa gat ata aat cgc      676
Lys Asn Ala Asp Thr Thr Thr Ser Val Thr Thr Glu Asp Ile Asn Arg
    205                 210                 215

act ttc aaa cca gta ata ggg cca agg ccc ctt gtc aac ggc cag cag      724
Thr Phe Lys Pro Val Ile Gly Pro Arg Pro Leu Val Asn Gly Gln Gln
220                 225                 230                 235

gga aga atc gat tac tat tgg tct gta cta aaa cct ggg cag act ttg      772
Gly Arg Ile Asp Tyr Tyr Trp Ser Val Leu Lys Pro Gly Gln Thr Leu
                240                 245                 250

aga ata agg tcc aat gga aat cta att gcc cct tgg tat gga cat gtt      820
Arg Ile Arg Ser Asn Gly Asn Leu Ile Ala Pro Trp Tyr Gly His Val
            255                 260                 265

ctt acg gga gag agc cat gga aga atc cta aag act gat ttg aac aat      868
Leu Thr Gly Glu Ser His Gly Arg Ile Leu Lys Thr Asp Leu Asn Asn
        270                 275                 280

ggt aat tgt gtg gta caa tgt cag act gaa aaa gga gga ctc aat aca      916
Gly Asn Cys Val Val Gln Cys Gln Thr Glu Lys Gly Gly Leu Asn Thr
    285                 290                 295

acc ttg cca ttt cac aat att agc aaa tat gca ttt ggg aat tgt cct      964
Thr Leu Pro Phe His Asn Ile Ser Lys Tyr Ala Phe Gly Asn Cys Pro
300                 305                 310                 315

aag tat gtt gga gtg aaa agt ctc aaa ttg gca gtt ggt tta agg aat     1012
Lys Tyr Val Gly Val Lys Ser Leu Lys Leu Ala Val Gly Leu Arg Asn
                320                 325                 330
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gtg cct gct gta tct agt aga gga ctg ttc gga gca ata gct ggg ttc     1060
Val Pro Ala Val Ser Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe
            335                 340                 345

ata gag gga ggt tgg cca ggg cta gtg gcc gga tgg tat ggt ttt caa     1108
Ile Glu Gly Gly Trp Pro Gly Leu Val Ala Gly Trp Tyr Gly Phe Gln
        350                 355                 360

cat tca aac gat cag gga gtt ggg atg gcc gca gac aag gga tct acc     1156
His Ser Asn Asp Gln Gly Val Gly Met Ala Ala Asp Lys Gly Ser Thr
    365                 370                 375

caa aaa gca atc gat aaa ata aca tca aaa gtg aac aac ata atc gat     1204
Gln Lys Ala Ile Asp Lys Ile Thr Ser Lys Val Asn Asn Ile Ile Asp
380                 385                 390                 395

aaa atg aac aag caa tat gag gtc att gat cat gaa ttc aat gag ctt     1252
Lys Met Asn Lys Gln Tyr Glu Val Ile Asp His Glu Phe Asn Glu Leu
                400                 405                 410

gag gcc agg ctg aac atg atc aac aac aaa att gat gat cag att caa     1300
Glu Ala Arg Leu Asn Met Ile Asn Asn Lys Ile Asp Asp Gln Ile Gln
            415                 420                 425

gac att tgg gct tat aat gca gag ttg ctg gtc ttg ctt gaa aac cag     1348
Asp Ile Trp Ala Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu Asn Gln
        430                 435                 440

aaa act cta gat gag cat gat gca aat gtg aac aac cta tac aac aaa     1396
Lys Thr Leu Asp Glu His Asp Ala Asn Val Asn Asn Leu Tyr Asn Lys
    445                 450                 455

gtg aaa aga gcc ttg ggt tcc aat gct gta gag gat gga aac gga tgc     1444
Val Lys Arg Ala Leu Gly Ser Asn Ala Val Glu Asp Gly Asn Gly Cys
460                 465                 470                 475

ttt gaa ctg tac cac aaa tgt gat gat caa tgc atg gaa aca atc aga     1492
Phe Glu Leu Tyr His Lys Cys Asp Asp Gln Cys Met Glu Thr Ile Arg
                480                 485                 490

aat gga acc tac gac agg cag aaa tac caa gaa gaa tca aga tta gaa     1540
Asn Gly Thr Tyr Asp Arg Gln Lys Tyr Gln Glu Glu Ser Arg Leu Glu
            495                 500                 505

agg cag aaa ata gaa ggg gta aag ctg gaa tct gag ggc act tac aag     1588
Arg Gln Lys Ile Glu Gly Val Lys Leu Glu Ser Glu Gly Thr Tyr Lys
        510                 515                 520

atc ctc acc att tat tcg act gtc gcc tca tct ctt gtg ctt gca atg     1636
Ile Leu Thr Ile Tyr Ser Thr Val Ala Ser Ser Leu Val Leu Ala Met
    525                 530                 535

ggg ttt gct gcc ttc cta ttc tgg gcc atg tcc aat ggc tct tgc aga     1684
Gly Phe Ala Ala Phe Leu Phe Trp Ala Met Ser Asn Gly Ser Cys Arg
540                 545                 550                 555

tgc aac att tgt ata taa ttagca                                     1708
Cys Asn Ile Cys Ile
                560
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<210> 22
<211> 560
<212> PRT
<213> Influenza A virus

<400> 22

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Met Glu Thr Lys Ala Ile Ile Ala Ala Leu Leu Met Val Thr Ala Ala
1               5                  10                  15

Asn Ala Asp Lys Ile Cys Ile Gly Tyr Gln Ser Thr Asn Ser Thr Glu
            20                  25                  30

Thr Val Asp Thr Leu Thr Glu Ser Asn Val Pro Val Thr His Thr Lys
        35                  40                  45

Glu Leu Leu His Thr Glu His Asn Gly Met Leu Cys Ala Thr Asp Leu
    50                  55                  60

Gly His Pro Leu Ile Leu Asp Thr Cys Thr Ile Glu Gly Leu Ile Tyr
65                  70                  75                  80

Gly Asn Pro Ser Cys Asp Ile Leu Leu Gly Gly Lys Glu Trp Ser Tyr
                85                  90                  95

Ile Val Glu Arg Ser Ser Ala Val Asn Gly Met Cys Tyr Pro Gly Asn
            100                 105                 110

Val Glu Asn Leu Glu Glu Leu Arg Ser Leu Phe Ser Ser Ala Lys Ser
        115                 120                 125

Tyr Lys Arg Ile Gln Ile Phe Pro Asp Lys Thr Trp Asn Val Thr Tyr
    130                 135                 140

Ser Gly Thr Ser Arg Ala Cys Ser Asn Ser Phe Tyr Arg Ser Met Arg
145                 150                 155                 160

Trp Leu Thr His Lys Ser Asn Ser Tyr Pro Phe Gln Asn Ala His Tyr
                165                 170                 175

Thr Asn Asn Glu Arg Glu Asn Ile Leu Phe Met Trp Gly Ile His His
            180                 185                 190

Pro Pro Thr Asp Thr Glu Gln Thr Asp Leu Tyr Lys Asn Ala Asp Thr
        195                 200                 205

Thr Thr Ser Val Thr Thr Glu Asp Ile Asn Arg Thr Phe Lys Pro Val
    210                 215                 220

Ile Gly Pro Arg Pro Leu Val Asn Gly Gln Gln Gly Arg Ile Asp Tyr
225                 230                 235                 240

Tyr Trp Ser Val Leu Lys Pro Gly Gln Thr Leu Arg Ile Arg Ser Asn
                245                 250                 255

Gly Asn Leu Ile Ala Pro Trp Tyr Gly His Val Leu Thr Gly Glu Ser
            260                 265                 270
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His Gly Arg Ile Leu Lys Thr Asp Leu Asn Asn Gly Asn Cys Val Val
        275                 280                 285

Gln Cys Gln Thr Glu Lys Gly Gly Leu Asn Thr Thr Leu Pro Phe His
    290                 295                 300

Asn Ile Ser Lys Tyr Ala Phe Gly Asn Cys Pro Lys Tyr Val Gly Val
305                 310                 315                 320

Lys Ser Leu Lys Leu Ala Val Gly Leu Arg Asn Val Pro Ala Val Ser
                325                 330                 335

Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp
            340                 345                 350

Pro Gly Leu Val Ala Gly Trp Tyr Gly Phe Gln His Ser Asn Asp Gln
        355                 360                 365

Gly Val Gly Met Ala Ala Asp Lys Gly Ser Thr Gln Lys Ala Ile Asp
    370                 375                 380

Lys Ile Thr Ser Lys Val Asn Asn Ile Ile Asp Lys Met Asn Lys Gln
385                 390                 395                 400

Tyr Glu Val Ile Asp His Glu Phe Asn Glu Leu Glu Ala Arg Leu Asn
                405                 410                 415

Met Ile Asn Asn Lys Ile Asp Asp Gln Ile Gln Asp Ile Trp Ala Tyr
            420                 425                 430

Asn Ala Glu Leu Leu Val Leu Leu Glu Asn Gln Lys Thr Leu Asp Glu
        435                 440                 445

His Asp Ala Asn Val Asn Asn Leu Tyr Asn Lys Val Lys Arg Ala Leu
    450                 455                 460

Gly Ser Asn Ala Val Glu Asp Gly Asn Gly Cys Phe Glu Leu Tyr His
465                 470                 475                 480

Lys Cys Asp Asp Gln Cys Met Glu Thr Ile Arg Asn Gly Thr Tyr Asp
                485                 490                 495

Arg Gln Lys Tyr Gln Glu Glu Ser Arg Leu Glu Arg Gln Lys Ile Glu
            500                 505                 510

Gly Val Lys Leu Glu Ser Glu Gly Thr Tyr Lys Ile Leu Thr Ile Tyr
        515                 520                 525

Ser Thr Val Ala Ser Ser Leu Val Leu Ala Met Gly Phe Ala Ala Phe
    530                 535                 540
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Leu Phe Trp Ala Met Ser Asn Gly Ser Cys Arg Cys Asn Ile Cys Ile
545                 550                 555                 560


<210>  23
<211>  1694
<212>  DNA
<213>  Influenza A virus

<220>
<221>  CDS
<222>  (6)..(1691)
<223>

<400>  23
tcaca atg tac aaa gta gta gta ata att gcg ctc ctt gga gca gtg aaa     50
      Met Tyr Lys Val Val Val Ile Ile Ala Leu Leu Gly Ala Val Lys
      1               5                  10                  15

ggt ctt gac aga atc tgc cta gga cac cat gcg gtt gcc aat gga acc      98
Gly Leu Asp Arg Ile Cys Leu Gly His His Ala Val Ala Asn Gly Thr
                  20                  25                  30

att gtg aag acc ctt aca aat gaa caa gag gaa gtg acc aat gct act     146
Ile Val Lys Thr Leu Thr Asn Glu Gln Glu Glu Val Thr Asn Ala Thr
              35                  40                  45

gag acg gta gag agc aca aat ttg aat aaa ttg tgt atg aaa gga aga     194
Glu Thr Val Glu Ser Thr Asn Leu Asn Lys Leu Cys Met Lys Gly Arg
          50                  55                  60

agc tac aag gac ttg ggc aat tgt cac ccg gta gga atg ttg ata gga     242
Ser Tyr Lys Asp Leu Gly Asn Cys His Pro Val Gly Met Leu Ile Gly
      65                  70                  75

aca cct gtt tgt gat ccg cac ttg acc ggg acc tgg gac act ctc att     290
Thr Pro Val Cys Asp Pro His Leu Thr Gly Thr Trp Asp Thr Leu Ile
80                  85                  90                  95

gag cga gag aat gcc att gcc cac tgt tat cca ggg gca acc ata aat     338
Glu Arg Glu Asn Ala Ile Ala His Cys Tyr Pro Gly Ala Thr Ile Asn
                 100                 105                 110

gaa gaa gca ttg agg cag aaa ata atg gaa agt gga gga atc agc aag     386
Glu Glu Ala Leu Arg Gln Lys Ile Met Glu Ser Gly Gly Ile Ser Lys
             115                 120                 125

atg agc act ggc ttc act tat ggg tct tcc atc aac tca gct ggg acc     434
Met Ser Thr Gly Phe Thr Tyr Gly Ser Ser Ile Asn Ser Ala Gly Thr
         130                 135                 140

act aag gca tgc atg aga aat gga gga gat agt ttc tat gca gag ctc     482
Thr Lys Ala Cys Met Arg Asn Gly Gly Asp Ser Phe Tyr Ala Glu Leu
     145                 150                 155

aaa tgg cta gtg tca aag aca aag gga caa aat ttc cct cag aca aca     530
Lys Trp Leu Val Ser Lys Thr Lys Gly Gln Asn Phe Pro Gln Thr Thr
160                 165                 170                 175

aac acc tat cgg aat acg gac aca gca gaa cat ctc ata ata tgg gga     578
Asn Thr Tyr Arg Asn Thr Asp Thr Ala Glu His Leu Ile Ile Trp Gly
                 180                 185                 190

att cat cac cct tcc agc aca cag gaa aag aat gac tta tac gga act     626
Ile His His Pro Ser Ser Thr Gln Glu Lys Asn Asp Leu Tyr Gly Thr
             195                 200                 205

cag tca cta tct ata tca gtt gag agt tct aca tat cag aac aac ttt     674
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Gln Ser Leu Ser Ile Ser Val Glu Ser Ser Thr Tyr Gln Asn Asn Phe
        210                 215                 220

gtt cca gtt gtt ggg gca aga cct cag gtc aat gga caa agt ggg cga      722
Val Pro Val Val Gly Ala Arg Pro Gln Val Asn Gly Gln Ser Gly Arg
    225                 230                 235

att gac ttt cac tgg aca cta gta cag ccg ggt gac aac ata acc ttc      770
Ile Asp Phe His Trp Thr Leu Val Gln Pro Gly Asp Asn Ile Thr Phe
240                 245                 250                 255

tca cac aat gga ggt cta ata gca cca agt cga gtt agc aaa tta act      818
Ser His Asn Gly Gly Leu Ile Ala Pro Ser Arg Val Ser Lys Leu Thr
                260                 265                 270

gga agg gga ttg gga atc caa tca gaa gcg ttg ata gac aac agt tgt      866
Gly Arg Gly Leu Gly Ile Gln Ser Glu Ala Leu Ile Asp Asn Ser Cys
            275                 280                 285

gaa tcc aaa tgc ttt tgg aga ggg ggt tct ata aat aca aag ctc cct      914
Glu Ser Lys Cys Phe Trp Arg Gly Gly Ser Ile Asn Thr Lys Leu Pro
        290                 295                 300

ttt caa aat ctg tca ccc aga aca gta ggt caa tgc ccc aaa tac gta      962
Phe Gln Asn Leu Ser Pro Arg Thr Val Gly Gln Cys Pro Lys Tyr Val
    305                 310                 315

aat cag agg agt tta ctg ctt gca aca ggg atg agg aat gtg cca gaa     1010
Asn Gln Arg Ser Leu Leu Leu Ala Thr Gly Met Arg Asn Val Pro Glu
320                 325                 330                 335

gtg gtg cag gga agg ggt ctg ttt ggt gca ata gca ggg ttc ata gaa     1058
Val Val Gln Gly Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu
                340                 345                 350

aac gga tgg gaa gga atg gta gac ggc tgg tat ggt ttc aga cac caa     1106
Asn Gly Trp Glu Gly Met Val Asp Gly Trp Tyr Gly Phe Arg His Gln
            355                 360                 365

aat gcc cag ggc aca ggc caa gct gct gat tac aag agt act caa gca     1154
Asn Ala Gln Gly Thr Gly Gln Ala Ala Asp Tyr Lys Ser Thr Gln Ala
        370                 375                 380

gct att gac caa atc aca ggg aaa ctg aac agg ttg att gag aag acc     1202
Ala Ile Asp Gln Ile Thr Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr
    385                 390                 395

aac act gag ttt gag tca ata gaa tct gaa ttc agt gag act gag cat     1250
Asn Thr Glu Phe Glu Ser Ile Glu Ser Glu Phe Ser Glu Thr Glu His
400                 405                 410                 415

caa att ggt aac gtc att aat tgg acc aaa gat tca ata acc gac att     1298
Gln Ile Gly Asn Val Ile Asn Trp Thr Lys Asp Ser Ile Thr Asp Ile
                420                 425                 430

tgg act tat caa gca gag cta tta gtg gca atg gag aat cag cac aca     1346
Trp Thr Tyr Gln Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr
            435                 440                 445

att gac atg gct gat tca gag atg cta aat ctg tat gaa agg gta aga     1394
Ile Asp Met Ala Asp Ser Glu Met Leu Asn Leu Tyr Glu Arg Val Arg
        450                 455                 460

aag caa ctc aga cag aat gca gaa gaa gac gga aag gga tgt ttt gag     1442
Lys Gln Leu Arg Gln Asn Ala Glu Glu Asp Gly Lys Gly Cys Phe Glu
    465                 470                 475

ata tat cat act tgt gat gat tcg tgc atg gag agt ata agg aac aat     1490
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Ile Tyr His Thr Cys Asp Asp Ser Cys Met Glu Ser Ile Arg Asn Asn
480                 485                 490                 495

act tat gac cat tca caa tac aga gag gag gct ctt ctg aat aga ctg     1538
Thr Tyr Asp His Ser Gln Tyr Arg Glu Glu Ala Leu Leu Asn Arg Leu
                500                 505                 510

aac atc aac tca gtg aaa ctt tct tcg ggg tac aaa gac atc ata ctt     1586
Asn Ile Asn Ser Val Lys Leu Ser Ser Gly Tyr Lys Asp Ile Ile Leu
            515                 520                 525

tgg ttt agc ttc ggg gca tca tgc ttt gtt ctt cta gcc gtt gtt atg     1634
Trp Phe Ser Phe Gly Ala Ser Cys Phe Val Leu Leu Ala Val Val Met
        530                 535                 540

ggt ctt gtt ttc ttc tgc ctg aaa aat gga aac atg cga tgc aca atc     1682
Gly Leu Val Phe Phe Cys Leu Lys Asn Gly Asn Met Arg Cys Thr Ile
    545                 550                 555

tgt att tag tta                                                    1694
Cys Ile
560
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<210> 24
<211> 561
<212> PRT
<213> Influenza A virus

<400> 24

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

Leu Asp Arg Ile Cys Leu Gly His His Ala Val Ala Asn Gly Thr Ile
            20                  25                  30

Val Lys Thr Leu Thr Asn Glu Gln Glu Glu Val Thr Asn Ala Thr Glu
        35                  40                  45

Thr Val Glu Ser Thr Asn Leu Asn Lys Leu Cys Met Lys Gly Arg Ser
    50                  55                  60

Tyr Lys Asp Leu Gly Asn Cys His Pro Val Gly Met Leu Ile Gly Thr
65                  70                  75                  80

Pro Val Cys Asp Pro His Leu Thr Gly Thr Trp Asp Thr Leu Ile Glu
                85                  90                  95

Arg Glu Asn Ala Ile Ala His Cys Tyr Pro Gly Ala Thr Ile Asn Glu
            100                 105                 110

Glu Ala Leu Arg Gln Lys Ile Met Glu Ser Gly Gly Ile Ser Lys Met
        115                 120                 125

Ser Thr Gly Phe Thr Tyr Gly Ser Ser Ile Asn Ser Ala Gly Thr Thr
    130                 135                 140

Lys Ala Cys Met Arg Asn Gly Gly Asp Ser Phe Tyr Ala Glu Leu Lys
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145 150 155 160

Trp Leu Val Ser Lys Thr Lys Gly Gln Asn Phe Pro Gln Thr Thr Asn
165 170 175

Thr Tyr Arg Asn Thr Asp Thr Ala Glu His Leu Ile Ile Trp Gly Ile
180 185 190

His His Pro Ser Ser Thr Gln Glu Lys Asn Asp Leu Tyr Gly Thr Gln
195 200 205

Ser Leu Ser Ile Ser Val Glu Ser Ser Thr Tyr Gln Asn Asn Phe Val
210 215 220

Pro Val Val Gly Ala Arg Pro Gln Val Asn Gly Gln Ser Gly Arg Ile
225 230 235 240

Asp Phe His Trp Thr Leu Val Gln Pro Gly Asp Asn Ile Thr Phe Ser
245 250 255

His Asn Gly Gly Leu Ile Ala Pro Ser Arg Val Ser Lys Leu Thr Gly
260 265 270

Arg Gly Leu Gly Ile Gln Ser Glu Ala Leu Ile Asp Asn Ser Cys Glu
275 280 285

Ser Lys Cys Phe Trp Arg Gly Gly Ser Ile Asn Thr Lys Leu Pro Phe
290 295 300

Gln Asn Leu Ser Pro Arg Thr Val Gly Gln Cys Pro Lys Tyr Val Asn
305 310 315 320

Gln Arg Ser Leu Leu Leu Ala Thr Gly Met Arg Asn Val Pro Glu Val
325 330 335

Val Gln Gly Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn
340 345 350

Gly Trp Glu Gly Met Val Asp Gly Trp Tyr Gly Phe Arg His Gln Asn
355 360 365

Ala Gln Gly Thr Gly Gln Ala Ala Asp Tyr Lys Ser Thr Gln Ala Ala
370 375 380

Ile Asp Gln Ile Thr Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr Asn
385 390 395 400

Thr Glu Phe Glu Ser Ile Glu Ser Glu Phe Ser Glu Thr Glu His Gln
405 410 415

Ile Gly Asn Val Ile Asn Trp Thr Lys Asp Ser Ile Thr Asp Ile Trp

420 425 430

Thr Tyr Gln Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr Ile
435 440 445

Asp Met Ala Asp Ser Glu Met Leu Asn Leu Tyr Glu Arg Val Arg Lys
450 455 460

Gln Leu Arg Gln Asn Ala Glu Glu Asp Gly Lys Gly Cys Phe Glu Ile
465 470 475 480

Tyr His Thr Cys Asp Asp Ser Cys Met Glu Ser Ile Arg Asn Asn Thr
485 490 495

Tyr Asp His Ser Gln Tyr Arg Glu Glu Ala Leu Leu Asn Arg Leu Asn
500 505 510

Ile Asn Ser Val Lys Leu Ser Ser Gly Tyr Lys Asp Ile Ile Leu Trp
515 520 525

Phe Ser Phe Gly Ala Ser Cys Phe Val Leu Leu Ala Val Val Met Gly
530 535 540

Leu Val Phe Phe Cys Leu Lys Asn Gly Asn Met Arg Cys Thr Ile Cys
545 550 555 560

Ile

<210> 25
<211> 281
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (33)..(281)
<223>

<400> 25
agcaaaagca ggggatctat caagaagtcg aa atg gag aaa atc ctg cta ttt 53
Met Glu Lys Ile Leu Leu Phe
1 5

gca gct att ttc ctt tgt gtg aaa gca gat gag atc tgt atc ggg tat 101
Ala Ala Ile Phe Leu Cys Val Lys Ala Asp Glu Ile Cys Ile Gly Tyr
10 15 20

tta agc aac aac tcg aca gac aaa gtt gac aca ata att gag aac aat 149
Leu Ser Asn Asn Ser Thr Asp Lys Val Asp Thr Ile Ile Glu Asn Asn
25 30 35

gtc acg gtc act agc tca gtg gaa ctg gtt gag aca gaa cac act gga 197
Val Thr Val Thr Ser Ser Val Glu Leu Val Glu Thr Glu His Thr Gly
40 45 50 55

tca ttc tgt tca atc aat gga aaa caa cca atc agc ctt gga gat tgt 245
Ser Phe Cys Ser Ile Asn Gly Lys Gln Pro Ile Ser Leu Gly Asp Cys

60 65 70

tca ttt gct gga tgg ata tta ggc aac cct atg tgt 281
Ser Phe Ala Gly Trp Ile Leu Gly Asn Pro Met Cys
75 80

<210> 26
<211> 83
<212> PRT
<213> Influenza A virus

<400> 26

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

Asp Glu Ile Cys Ile Gly Tyr Leu Ser Asn Asn Ser Thr Asp Lys Val
20 25 30

Asp Thr Ile Ile Glu Asn Asn Val Thr Val Thr Ser Ser Val Glu Leu
35 40 45

Val Glu Thr Glu His Thr Gly Ser Phe Cys Ser Ile Asn Gly Lys Gln
50 55 60

Pro Ile Ser Leu Gly Asp Cys Ser Phe Ala Gly Trp Ile Leu Gly Asn
65 70 75 80

Pro Met Cys

<210> 27
<211> 322
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (20)..(322)
<223>

<400> 27
agcaaaagca ggggtcaca atg gaa aaa ttc atc att ttg agt act gtc ttg 52
Met Glu Lys Phe Ile Ile Leu Ser Thr Val Leu
1 5 10

gca gca agc ttt gca tat gac aaa att tgc att gga tac cag aca aac 100
Ala Ala Ser Phe Ala Tyr Asp Lys Ile Cys Ile Gly Tyr Gln Thr Asn
15 20 25

aac tcg act gaa acg gta aac aca cta agt gaa tta aac gtt ccg gtg 148
Asn Ser Thr Glu Thr Val Asn Thr Leu Ser Glu Leu Asn Val Pro Val
30 35 40

acg cag gtg gaa gaa ctt gta cat ggt ggg att gat ccg atc ctg tgt 196
Thr Gln Val Glu Glu Leu Val His Gly Gly Ile Asp Pro Ile Leu Cys
45 50 55

gga acg gaa cta gga tca cca cta gtg ctt gat gac tgt tca tta gag 244
Gly Thr Glu Leu Gly Ser Pro Leu Val Leu Asp Asp Cys Ser Leu Glu
60 65 70 75

ggc cta atc cta ggc aat ccc aaa tgt gat ctt tat ttg aat ggc agg 292
Gly Leu Ile Leu Gly Asn Pro Lys Cys Asp Leu Tyr Leu Asn Gly Arg
80 85 90

gaa tgg tca tac ata gta gag agg ccc aaa 322
Glu Trp Ser Tyr Ile Val Glu Arg Pro Lys
95 100

<210> 28
<211> 101
<212> PRT
<213> Influenza A virus

<400> 28

Met Glu Lys Phe Ile Ile Leu Ser Thr Val Leu Ala Ala Ser Phe Ala
1 5 10 15

Tyr Asp Lys Ile Cys Ile Gly Tyr Gln Thr Asn Asn Ser Thr Glu Thr
20 25 30

Val Asn Thr Leu Ser Glu Leu Asn Val Pro Val Thr Gln Val Glu Glu
35 40 45

Leu Val His Gly Gly Ile Asp Pro Ile Leu Cys Gly Thr Glu Leu Gly
50 55 60

Ser Pro Leu Val Leu Asp Asp Cys Ser Leu Glu Gly Leu Ile Leu Gly
65 70 75 80

Asn Pro Lys Cys Asp Leu Tyr Leu Asn Gly Arg Glu Trp Ser Tyr Ile
85 90 95

Val Glu Arg Pro Lys
100

<210> 29
<211> 1734
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (28)..(1728)
<223>

<400> 29
aaatcttaac aatcagaaac aaacaag atg gct cta aat gtc att gca act ttg 54
Met Ala Leu Asn Val Ile Ala Thr Leu
1 5

aca ctt ata agt gta tgt gta cat gca gac aga ata tgc gtg ggg tat 102
Thr Leu Ile Ser Val Cys Val His Ala Asp Arg Ile Cys Val Gly Tyr
10 15 20 25

ctg agc acc aat tca tca gaa agg gtc gac acg ctc ctt gaa aat ggg 150
Leu Ser Thr Asn Ser Ser Glu Arg Val Asp Thr Leu Leu Glu Asn Gly
30 35 40

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gtc cca gtc acc agc tcc att gat ctg att gag aca aac cac aca gga      198
Val Pro Val Thr Ser Ser Ile Asp Leu Ile Glu Thr Asn His Thr Gly
            45                  50                  55

aca tac tgt tct cta aat gga gtc agt cca gtg cat ttg gga gat tgc      246
Thr Tyr Cys Ser Leu Asn Gly Val Ser Pro Val His Leu Gly Asp Cys
        60                  65                  70

agc ttt gaa gga tgg att gta gga aac cca gcc tgc acc agc aac ttt      294
Ser Phe Glu Gly Trp Ile Val Gly Asn Pro Ala Cys Thr Ser Asn Phe
    75                  80                  85

ggg acc aga gag tgg tca tac ctg att gag gac ccc gcg gcc cct cat      342
Gly Thr Arg Glu Trp Ser Tyr Leu Ile Glu Asp Pro Ala Ala Pro His
90                  95                  100                 105

ggg ctt tgc tac cct gga gaa tta aac aac aat ggt gaa ctc aga cac      390
Gly Leu Cys Tyr Pro Gly Glu Leu Asn Asn Asn Gly Glu Leu Arg His
                110                 115                 120

ttg ttc agt gga atc agg tca ttc agt aga acg gaa ttg atc cca cct      438
Leu Phe Ser Gly Ile Arg Ser Phe Ser Arg Thr Glu Leu Ile Pro Pro
            125                 130                 135

acc tcc tgg ggg gaa gta ctt gac ggt aca aca tct gct tgc aga gat      486
Thr Ser Trp Gly Glu Val Leu Asp Gly Thr Thr Ser Ala Cys Arg Asp
        140                 145                 150

aac acg gga acc aac agc ttc tat cga aat tta gtt tgg ttt ata aag      534
Asn Thr Gly Thr Asn Ser Phe Tyr Arg Asn Leu Val Trp Phe Ile Lys
    155                 160                 165

aag aat aat aga tat cca gtt atc agt aag acc tac aac aat aca acg      582
Lys Asn Asn Arg Tyr Pro Val Ile Ser Lys Thr Tyr Asn Asn Thr Thr
170                 175                 180                 185

gga agg gat gtt tta gtt tta tgg gga ata cat cac cca gtg tct gtg      630
Gly Arg Asp Val Leu Val Leu Trp Gly Ile His His Pro Val Ser Val
                190                 195                 200

gat gag aca aag act ctg tat gtc aat agt gat cca tac aca ctg gtt      678
Asp Glu Thr Lys Thr Leu Tyr Val Asn Ser Asp Pro Tyr Thr Leu Val
            205                 210                 215

tcc acc aag tct tgg agc gag aaa tat aaa cta gaa acg gga gtc cga      726
Ser Thr Lys Ser Trp Ser Glu Lys Tyr Lys Leu Glu Thr Gly Val Arg
        220                 225                 230

cct ggc tat aat gga cag agg agc tgg atg aaa att tat tgg tct ttg      774
Pro Gly Tyr Asn Gly Gln Arg Ser Trp Met Lys Ile Tyr Trp Ser Leu
    235                 240                 245

ata cat cca ggg gag atg att act ttc gag agt aat ggt gga ttt tta      822
Ile His Pro Gly Glu Met Ile Thr Phe Glu Ser Asn Gly Gly Phe Leu
250                 255                 260                 265

gcc cca aga tat ggg tac ata att gaa gaa tat gga aaa gga agg att      870
Ala Pro Arg Tyr Gly Tyr Ile Ile Glu Glu Tyr Gly Lys Gly Arg Ile
                270                 275                 280

ttc cag agt cgc atc aga atg tct agg tgc aac acc aag tgc cag act      918
Phe Gln Ser Arg Ile Arg Met Ser Arg Cys Asn Thr Lys Cys Gln Thr
            285                 290                 295

tcg gtt gga ggg ata aac aca aac aga acg ttc caa aac atc gat aag      966
Ser Val Gly Gly Ile Asn Thr Asn Arg Thr Phe Gln Asn Ile Asp Lys
        300                 305                 310
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aat gct ctt ggt gac tgt ccc aaa tac ata aag tct ggc caa ctc aag      1014
Asn Ala Leu Gly Asp Cys Pro Lys Tyr Ile Lys Ser Gly Gln Leu Lys
    315                 320                 325

cta gcc act gga ctc aga aat gtg cca gct ata tcg aat aga gga ttg      1062
Leu Ala Thr Gly Leu Arg Asn Val Pro Ala Ile Ser Asn Arg Gly Leu
330                 335                 340                 345

ttc gga gca att gca ggg ttc ata gaa gga ggc tgg cca ggt tta atc      1110
Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Pro Gly Leu Ile
                350                 355                 360

aat ggt tgg tac ggt ttt cag cat caa aat gaa cag gga aca gga ata      1158
Asn Gly Trp Tyr Gly Phe Gln His Gln Asn Glu Gln Gly Thr Gly Ile
            365                 370                 375

gct gca gac aaa gaa tca aca cag aaa gct ata gac cag ata aca acc      1206
Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp Gln Ile Thr Thr
        380                 385                 390

aaa ata aat aac att att gat aaa atg aat ggg aac tat gat tca att      1254
Lys Ile Asn Asn Ile Ile Asp Lys Met Asn Gly Asn Tyr Asp Ser Ile
    395                 400                 405

agg ggt gaa ttc aat caa gtt gag aag cgt ata aac atg ctt gca gac      1302
Arg Gly Glu Phe Asn Gln Val Glu Lys Arg Ile Asn Met Leu Ala Asp
410                 415                 420                 425

aga ata gat gat gcc gtg acg gac att tgg tca tac aat gcc aaa ctt      1350
Arg Ile Asp Asp Ala Val Thr Asp Ile Trp Ser Tyr Asn Ala Lys Leu
                430                 435                 440

ctt gta ttg ctg gaa aat gat aaa act tta gat atg cat gat gct aat      1398
Leu Val Leu Leu Glu Asn Asp Lys Thr Leu Asp Met His Asp Ala Asn
            445                 450                 455

gta aag aat tta cat gag caa gta cga aga gaa ttg aag gac aat gca      1446
Val Lys Asn Leu His Glu Gln Val Arg Arg Glu Leu Lys Asp Asn Ala
        460                 465                 470

att gac gaa gga aat ggc tgt ttt gaa ctc ctt cat aaa tgc aat gac      1494
Ile Asp Glu Gly Asn Gly Cys Phe Glu Leu Leu His Lys Cys Asn Asp
    475                 480                 485

tcc tgc atg gaa act ata aga aat gga acg tat gac cac act gag tat      1542
Ser Cys Met Glu Thr Ile Arg Asn Gly Thr Tyr Asp His Thr Glu Tyr
490                 495                 500                 505

gca gag gag tca aag tta aag agg caa gaa atc gat ggg atc aaa ctc      1590
Ala Glu Glu Ser Lys Leu Lys Arg Gln Glu Ile Asp Gly Ile Lys Leu
                510                 515                 520

aaa tca gaa gac aac gtt tac aaa gca tta tca ata tac agt tgc att      1638
Lys Ser Glu Asp Asn Val Tyr Lys Ala Leu Ser Ile Tyr Ser Cys Ile
            525                 530                 535

gca agt agt gtt gta cta gta gga ctc ata ctc tct ttc atc atg tgg      1686
Ala Ser Ser Val Val Leu Val Gly Leu Ile Leu Ser Phe Ile Met Trp
        540                 545                 550

gcc tgt agt agt ggg aat tgc cga ttc aat gtt tgt ata taa gtagaa      1734
Ala Cys Ser Ser Gly Asn Cys Arg Phe Asn Val Cys Ile
    555                 560                 565
```

<210> 30
<211> 566
<212> PRT

<213> Influenza A virus

<400> 30

```
Met Ala Leu Asn Val Ile Ala Thr Leu Thr Leu Ile Ser Val Cys Val
1               5                  10                  15

His Ala Asp Arg Ile Cys Val Gly Tyr Leu Ser Thr Asn Ser Ser Glu
            20                  25                  30

Arg Val Asp Thr Leu Leu Glu Asn Gly Val Pro Val Thr Ser Ser Ile
        35                  40                  45

Asp Leu Ile Glu Thr Asn His Thr Gly Thr Tyr Cys Ser Leu Asn Gly
    50                  55                  60

Val Ser Pro Val His Leu Gly Asp Cys Ser Phe Glu Gly Trp Ile Val
65                  70                  75                  80

Gly Asn Pro Ala Cys Thr Ser Asn Phe Gly Thr Arg Glu Trp Ser Tyr
                85                  90                  95

Leu Ile Glu Asp Pro Ala Ala Pro His Gly Leu Cys Tyr Pro Gly Glu
            100                 105                 110

Leu Asn Asn Asn Gly Glu Leu Arg His Leu Phe Ser Gly Ile Arg Ser
        115                 120                 125

Phe Ser Arg Thr Glu Leu Ile Pro Pro Thr Ser Trp Gly Glu Val Leu
    130                 135                 140

Asp Gly Thr Thr Ser Ala Cys Arg Asp Asn Thr Gly Thr Asn Ser Phe
145                 150                 155                 160

Tyr Arg Asn Leu Val Trp Phe Ile Lys Lys Asn Asn Arg Tyr Pro Val
                165                 170                 175

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

Trp Gly Ile His His Pro Val Ser Val Asp Glu Thr Lys Thr Leu Tyr
        195                 200                 205

Val Asn Ser Asp Pro Tyr Thr Leu Val Ser Thr Lys Ser Trp Ser Glu
    210                 215                 220

Lys Tyr Lys Leu Glu Thr Gly Val Arg Pro Gly Tyr Asn Gly Gln Arg
225                 230                 235                 240

Ser Trp Met Lys Ile Tyr Trp Ser Leu Ile His Pro Gly Glu Met Ile
                245                 250                 255
```

```
Thr Phe Glu Ser Asn Gly Gly Phe Leu Ala Pro Arg Tyr Gly Tyr Ile
            260                 265                 270

Ile Glu Glu Tyr Gly Lys Gly Arg Ile Phe Gln Ser Arg Ile Arg Met
        275                 280                 285

Ser Arg Cys Asn Thr Lys Cys Gln Thr Ser Val Gly Gly Ile Asn Thr
    290                 295                 300

Asn Arg Thr Phe Gln Asn Ile Asp Lys Asn Ala Leu Gly Asp Cys Pro
305                 310                 315                 320

Lys Tyr Ile Lys Ser Gly Gln Leu Lys Leu Ala Thr Gly Leu Arg Asn
                325                 330                 335

Val Pro Ala Ile Ser Asn Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe
            340                 345                 350

Ile Glu Gly Gly Trp Pro Gly Leu Ile Asn Gly Trp Tyr Gly Phe Gln
        355                 360                 365

His Gln Asn Glu Gln Gly Thr Gly Ile Ala Ala Asp Lys Glu Ser Thr
    370                 375                 380

Gln Lys Ala Ile Asp Gln Ile Thr Thr Lys Ile Asn Asn Ile Ile Asp
385                 390                 395                 400

Lys Met Asn Gly Asn Tyr Asp Ser Ile Arg Gly Glu Phe Asn Gln Val
                405                 410                 415

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

Asp Ile Trp Ser Tyr Asn Ala Lys Leu Leu Val Leu Leu Glu Asn Asp
        435                 440                 445

Lys Thr Leu Asp Met His Asp Ala Asn Val Lys Asn Leu His Glu Gln
    450                 455                 460

Val Arg Arg Glu Leu Lys Asp Asn Ala Ile Asp Glu Gly Asn Gly Cys
465                 470                 475                 480

Phe Glu Leu Leu His Lys Cys Asn Asp Ser Cys Met Glu Thr Ile Arg
                485                 490                 495

Asn Gly Thr Tyr Asp His Thr Glu Tyr Ala Glu Glu Ser Lys Leu Lys
            500                 505                 510

Arg Gln Glu Ile Asp Gly Ile Lys Leu Lys Ser Glu Asp Asn Val Tyr
        515                 520                 525
```

```
Lys Ala Leu Ser Ile Tyr Ser Cys Ile Ala Ser Ser Val Val Leu Val
    530                 535                 540

Gly Leu Ile Leu Ser Phe Ile Met Trp Ala Cys Ser Ser Gly Asn Cys
545                 550                 555                 560

Arg Phe Asn Val Cys Ile
                565
```

<210> 31
<211> 1714
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (4)..(1710)
<223>

<400> 31

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aaa atg att gca ctc ata ttg gtt gca ctg gct ctg agc cac act gct       48
    Met Ile Ala Leu Ile Leu Val Ala Leu Ala Leu Ser His Thr Ala
    1               5                   10                  15

tat tct cag atc aca aat ggg aca aca gga aac ccc att ata tgc ttg       96
Tyr Ser Gln Ile Thr Asn Gly Thr Thr Gly Asn Pro Ile Ile Cys Leu
                20                  25                  30

ggg cat cat gca gtg gaa aac ggc aca tct gtt aaa aca cta aca gac      144
Gly His His Ala Val Glu Asn Gly Thr Ser Val Lys Thr Leu Thr Asp
            35                  40                  45

aat cac gta gaa gtt gtg tca gct aaa gaa tta gtt gag acg aac cac      192
Asn His Val Glu Val Val Ser Ala Lys Glu Leu Val Glu Thr Asn His
        50                  55                  60

act gat gaa ctg tgc cca agc ccc ttg aag ctt gtc gac ggg caa gac      240
Thr Asp Glu Leu Cys Pro Ser Pro Leu Lys Leu Val Asp Gly Gln Asp
    65                  70                  75

tgc gac ctc atc aat ggt gca ttg ggg agt cca ggc tgt gac cgt ttg      288
Cys Asp Leu Ile Asn Gly Ala Leu Gly Ser Pro Gly Cys Asp Arg Leu
80                  85                  90                  95

cag gac acc act tgg gat gtc ttc att gaa agg ccc act gca gta gac      336
Gln Asp Thr Thr Trp Asp Val Phe Ile Glu Arg Pro Thr Ala Val Asp
                100                 105                 110

aca tgt tat cca ttc gac gtc cca gat tac cag agt ctc aga agc atc      384
Thr Cys Tyr Pro Phe Asp Val Pro Asp Tyr Gln Ser Leu Arg Ser Ile
            115                 120                 125

cta gca agc agt ggg agt ttg gag ttc atc gcc gaa caa ttc acc tgg      432
Leu Ala Ser Ser Gly Ser Leu Glu Phe Ile Ala Glu Gln Phe Thr Trp
        130                 135                 140

aat ggt gtc aaa gtt gac gga tca agc agt gct tgt ttg agg ggc ggt      480
Asn Gly Val Lys Val Asp Gly Ser Ser Ser Ala Cys Leu Arg Gly Gly
    145                 150                 155

cgc aac agc ttc ttc tcc cga cta aac tgg cta acc aaa gaa aca aat      528
Arg Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu Thr Lys Glu Thr Asn
160                 165                 170                 175

gga aac tat gga cct att aac gtc act aaa gaa aat acg ggc tct tat      576
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Gly Asn Tyr Gly Pro Ile Asn Val Thr Lys Glu Asn Thr Gly Ser Tyr
                180                 185                 190

gtc agg ctc tat ctc tgg gga gtg cat cac cca tca agc gat aat gag      624
Val Arg Leu Tyr Leu Trp Gly Val His His Pro Ser Ser Asp Asn Glu
            195                 200                 205

caa acg gat ctc tac aag gtg gca aca ggg aga gta aca gta tct acc      672
Gln Thr Asp Leu Tyr Lys Val Ala Thr Gly Arg Val Thr Val Ser Thr
        210                 215                 220

cgc tcg gac caa atc agt att gtt ccc aat ata gga agt aga ccg agg      720
Arg Ser Asp Gln Ile Ser Ile Val Pro Asn Ile Gly Ser Arg Pro Arg
    225                 230                 235

gta agg aat cag agc ggc agg ata agc atc tac tgg acc cta gta aac      768
Val Arg Asn Gln Ser Gly Arg Ile Ser Ile Tyr Trp Thr Leu Val Asn
240                 245                 250                 255

cca ggg gac tcc atc att ttc aac agt att ggg aat ttg att gca cca      816
Pro Gly Asp Ser Ile Ile Phe Asn Ser Ile Gly Asn Leu Ile Ala Pro
                260                 265                 270

aga ggc cac tac aaa ata agc aaa tct act aag agc aca gtg ctt aaa      864
Arg Gly His Tyr Lys Ile Ser Lys Ser Thr Lys Ser Thr Val Leu Lys
            275                 280                 285

agt gac aaa agg att ggg tca tgc aca agc cct tgc tta act gat aaa      912
Ser Asp Lys Arg Ile Gly Ser Cys Thr Ser Pro Cys Leu Thr Asp Lys
        290                 295                 300

ggt tcg atc caa agt gac aaa cct ttt cag aat gta tca agg att gct      960
Gly Ser Ile Gln Ser Asp Lys Pro Phe Gln Asn Val Ser Arg Ile Ala
    305                 310                 315

ata gga aac tgc ccg aaa tat gta aag caa ggg tcc ctg atg tta gca     1008
Ile Gly Asn Cys Pro Lys Tyr Val Lys Gln Gly Ser Leu Met Leu Ala
320                 325                 330                 335

act gga atg cgc aac atc cct ggc aaa cag gca aag ggc tta ttt ggg     1056
Thr Gly Met Arg Asn Ile Pro Gly Lys Gln Ala Lys Gly Leu Phe Gly
                340                 345                 350

gca att gct gga ttc att gaa aat ggt tgg caa ggc ctg att gat ggg     1104
Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Gln Gly Leu Ile Asp Gly
            355                 360                 365

tgg tat gga ttc agg cac caa aat gct gaa gga aca gga act gct gca     1152
Trp Tyr Gly Phe Arg His Gln Asn Ala Glu Gly Thr Gly Thr Ala Ala
        370                 375                 380

gac ctg aag tca act cag gca gcc att gat cag ata aat ggc aag ctg     1200
Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys Leu
    385                 390                 395

aac aga ttg ata gag aag aca aat gaa aaa tat cac caa ata gaa aag     1248
Asn Arg Leu Ile Glu Lys Thr Asn Glu Lys Tyr His Gln Ile Glu Lys
400                 405                 410                 415

gaa ttc gaa cag gtg gaa gga aga ata caa gac ctt gag aag tac gtt     1296
Glu Phe Glu Gln Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val
                420                 425                 430

gag gac act aag att gat ttg tgg tca tac aat gct gaa ttg cta gta     1344
Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val
            435                 440                 445

gca cta gag aat cag cac aca ata gat gtc aca gac tcc gaa atg aac     1392
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```
Ala Leu Glu Asn Gln His Thr Ile Asp Val Thr Asp Ser Glu Met Asn
        450                 455                 460

aag ctt ttt gaa aga gta aga agg caa tta aga gag aat gca gaa gat     1440
Lys Leu Phe Glu Arg Val Arg Arg Gln Leu Arg Glu Asn Ala Glu Asp
    465                 470                 475

caa ggc aac ggt tgt ttc gag ata ttc cat cag tgt gac aac aat tgt     1488
Gln Gly Asn Gly Cys Phe Glu Ile Phe His Gln Cys Asp Asn Asn Cys
480                 485                 490                 495

ata gaa agc att aga aac gga act tat gac cac aac atc tac agg gat     1536
Ile Glu Ser Ile Arg Asn Gly Thr Tyr Asp His Asn Ile Tyr Arg Asp
                500                 505                 510

gaa gcc atc aac aat cga atc aaa ata aat cct gtc act ttg acg atg     1584
Glu Ala Ile Asn Asn Arg Ile Lys Ile Asn Pro Val Thr Leu Thr Met
            515                 520                 525

ggg tac aag gac ata atc ctg tgg att tct ttc tcc atg tca tgc ttt     1632
Gly Tyr Lys Asp Ile Ile Leu Trp Ile Ser Phe Ser Met Ser Cys Phe
        530                 535                 540

gtc ttc gtg gca ctg att ctg gga ttt gtt cta tgg gct tgt caa aac     1680
Val Phe Val Ala Leu Ile Leu Gly Phe Val Leu Trp Ala Cys Gln Asn
    545                 550                 555

ggg aat atc cga tgc caa atc tgt ata taa agaa                       1714
Gly Asn Ile Arg Cys Gln Ile Cys Ile
560                 565
```

<210> 32
<211> 568
<212> PRT
<213> Influenza A virus

<400> 32

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Met Ile Ala Leu Ile Leu Val Ala Leu Ala Leu Ser His Thr Ala Tyr
1               5                   10                  15

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

His His Ala Val Glu Asn Gly Thr Ser Val Lys Thr Leu Thr Asp Asn
        35                  40                  45

His Val Glu Val Val Ser Ala Lys Glu Leu Val Glu Thr Asn His Thr
    50                  55                  60

Asp Glu Leu Cys Pro Ser Pro Leu Lys Leu Val Asp Gly Gln Asp Cys
65                  70                  75                  80

Asp Leu Ile Asn Gly Ala Leu Gly Ser Pro Gly Cys Asp Arg Leu Gln
                85                  90                  95

Asp Thr Thr Trp Asp Val Phe Ile Glu Arg Pro Thr Ala Val Asp Thr
            100                 105                 110

Cys Tyr Pro Phe Asp Val Pro Asp Tyr Gln Ser Leu Arg Ser Ile Leu
```

115 120 125

Ala Ser Ser Gly Ser Leu Glu Phe Ile Ala Glu Gln Phe Thr Trp Asn
130 135 140

Gly Val Lys Val Asp Gly Ser Ser Ser Ala Cys Leu Arg Gly Gly Arg
145 150 155 160

Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu Thr Lys Glu Thr Asn Gly
165 170 175

Asn Tyr Gly Pro Ile Asn Val Thr Lys Glu Asn Thr Gly Ser Tyr Val
180 185 190

Arg Leu Tyr Leu Trp Gly Val His His Pro Ser Ser Asp Asn Glu Gln
195 200 205

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

Ser Asp Gln Ile Ser Ile Val Pro Asn Ile Gly Ser Arg Pro Arg Val
225 230 235 240

Arg Asn Gln Ser Gly Arg Ile Ser Ile Tyr Trp Thr Leu Val Asn Pro
245 250 255

Gly Asp Ser Ile Ile Phe Asn Ser Ile Gly Asn Leu Ile Ala Pro Arg
260 265 270

Gly His Tyr Lys Ile Ser Lys Ser Thr Lys Ser Thr Val Leu Lys Ser
275 280 285

Asp Lys Arg Ile Gly Ser Cys Thr Ser Pro Cys Leu Thr Asp Lys Gly
290 295 300

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

Gly Asn Cys Pro Lys Tyr Val Lys Gln Gly Ser Leu Met Leu Ala Thr
325 330 335

Gly Met Arg Asn Ile Pro Gly Lys Gln Ala Lys Gly Leu Phe Gly Ala
340 345 350

Ile Ala Gly Phe Ile Glu Asn Gly Trp Gln Gly Leu Ile Asp Gly Trp
355 360 365

Tyr Gly Phe Arg His Gln Asn Ala Glu Gly Thr Gly Thr Ala Ala Asp
370 375 380

Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys Leu Asn

385 390 395 400

Arg Leu Ile Glu Lys Thr Asn Glu Lys Tyr His Gln Ile Glu Lys Glu
405 410 415

Phe Glu Gln Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val Glu
420 425 430

Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala
435 440 445

Leu Glu Asn Gln His Thr Ile Asp Val Thr Asp Ser Glu Met Asn Lys
450 455 460

Leu Phe Glu Arg Val Arg Arg Gln Leu Arg Glu Asn Ala Glu Asp Gln
465 470 475 480

Gly Asn Gly Cys Phe Glu Ile Phe His Gln Cys Asp Asn Asn Cys Ile
485 490 495

Glu Ser Ile Arg Asn Gly Thr Tyr Asp His Asn Ile Tyr Arg Asp Glu
500 505 510

Ala Ile Asn Asn Arg Ile Lys Ile Asn Pro Val Thr Leu Thr Met Gly
515 520 525

Tyr Lys Asp Ile Ile Leu Trp Ile Ser Phe Ser Met Ser Cys Phe Val
530 535 540

Phe Val Ala Leu Ile Leu Gly Phe Val Leu Trp Ala Cys Gln Asn Gly
545 550 555 560

Asn Ile Arg Cys Gln Ile Cys Ile
565

<210> 33
<211> 1728
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (8)..(1720)
<223>

<400> 33
aaacaaa atg aac act caa atc atc gtc att cta gtc ctc gga ctg tcg 49
Met Asn Thr Gln Ile Ile Val Ile Leu Val Leu Gly Leu Ser
1 5 10

atg gtg aga tct gac aag att tgt ctc ggg cac cat gcc gta gca aat 97
Met Val Arg Ser Asp Lys Ile Cys Leu Gly His His Ala Val Ala Asn
15 20 25 30

ggg aca aaa gtc aac aca cta act gag aaa gga gtg gaa gtg gtc aat 145
Gly Thr Lys Val Asn Thr Leu Thr Glu Lys Gly Val Glu Val Val Asn

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                35                  40                  45

gcc acg gag aca gtg gag att aca gga ata aat aaa gtg tgc aca aaa      193
Ala Thr Glu Thr Val Glu Ile Thr Gly Ile Asn Lys Val Cys Thr Lys
            50                  55                  60

ggg aag aaa gcg gtg gac ttg gga tct tgt gga ata ctg gga act atc      241
Gly Lys Lys Ala Val Asp Leu Gly Ser Cys Gly Ile Leu Gly Thr Ile
        65                  70                  75

att ggg cct cca caa tgt gac tct cat ctt aaa ttc aaa gct gat ctg      289
Ile Gly Pro Pro Gln Cys Asp Ser His Leu Lys Phe Lys Ala Asp Leu
    80                  85                  90

ata ata gaa aga aga aat tca agt gac atc tgt tac cca ggg aaa ttc      337
Ile Ile Glu Arg Arg Asn Ser Ser Asp Ile Cys Tyr Pro Gly Lys Phe
95                  100                 105                 110

act aat gag gaa gca ctg aga caa ata atc aga gaa tct ggt gga att      385
Thr Asn Glu Glu Ala Leu Arg Gln Ile Ile Arg Glu Ser Gly Gly Ile
                115                 120                 125

gac aaa gag cca atg gga ttt aga tat tca gga ata aaa aca gac ggg      433
Asp Lys Glu Pro Met Gly Phe Arg Tyr Ser Gly Ile Lys Thr Asp Gly
            130                 135                 140

gca acc agt gcg tgt aag aga aca gtg tcc tct ttc tac tca gaa atg      481
Ala Thr Ser Ala Cys Lys Arg Thr Val Ser Ser Phe Tyr Ser Glu Met
        145                 150                 155

aaa tgg ctt tta tcc agc aag gat aac cag gtg ttc cca caa ctg aat      529
Lys Trp Leu Leu Ser Ser Lys Asp Asn Gln Val Phe Pro Gln Leu Asn
    160                 165                 170

cag aca tac agg aac aac aga aaa gaa cca gcc cta att gtt tgg gga      577
Gln Thr Tyr Arg Asn Asn Arg Lys Glu Pro Ala Leu Ile Val Trp Gly
175                 180                 185                 190

gta cat cat tca agc tcc ttg gat gag caa aat aag cta tat gga gct      625
Val His His Ser Ser Ser Leu Asp Glu Gln Asn Lys Leu Tyr Gly Ala
                195                 200                 205

ggg aac aag ctg ata aca gta gga agc tca aaa tac caa caa tcg ttt      673
Gly Asn Lys Leu Ile Thr Val Gly Ser Ser Lys Tyr Gln Gln Ser Phe
            210                 215                 220

tca cca agt cca ggg gac agg ccc aaa gtg aat ggt cag gcc ggg agg      721
Ser Pro Ser Pro Gly Asp Arg Pro Lys Val Asn Gly Gln Ala Gly Arg
        225                 230                 235

atc gac ttt cat tgg atg cta ttg gac cca ggg gat aca gtc act ttt      769
Ile Asp Phe His Trp Met Leu Leu Asp Pro Gly Asp Thr Val Thr Phe
    240                 245                 250

acc ttc aat ggt gca ttc ata gcc cca gat aga gcc acc ttt ctc cgc      817
Thr Phe Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Thr Phe Leu Arg
255                 260                 265                 270

tct aat gcc cca tcg gga gtt gag tac aat ggg aag tca ctg gga ata      865
Ser Asn Ala Pro Ser Gly Val Glu Tyr Asn Gly Lys Ser Leu Gly Ile
                275                 280                 285

cag agt gat gca caa att gat gaa tca tgt gaa ggg gaa tgc ttc tac      913
Gln Ser Asp Ala Gln Ile Asp Glu Ser Cys Glu Gly Glu Cys Phe Tyr
            290                 295                 300

agt gga ggg aca ata aac agc cct ttg cca ttt caa aac atc gat agt      961
Ser Gly Gly Thr Ile Asn Ser Pro Leu Pro Phe Gln Asn Ile Asp Ser
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        305                 310                 315

tgg gct gtc gga agg tgc ccc aga tat gta aag caa tca agc ctg ccg     1009
Trp Ala Val Gly Arg Cys Pro Arg Tyr Val Lys Gln Ser Ser Leu Pro
    320                 325                 330

ctg gcc tta gga atg aaa aat gta cca gag aaa ata cat act agg gga     1057
Leu Ala Leu Gly Met Lys Asn Val Pro Glu Lys Ile His Thr Arg Gly
335                 340                 345                 350

ctg ttc ggt gca att gca gga ttc atc gag aat gga tgg gaa gga ctc     1105
Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Leu
                355                 360                 365

att gat gga tgg tat gga ttt agg cat cag aat gca cag ggg cag gga     1153
Ile Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ala Gln Gly Gln Gly
            370                 375                 380

aca gct gct gac tac aag agt act cag gct gca att gac cag ata aca     1201
Thr Ala Ala Asp Tyr Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Thr
        385                 390                 395

ggg aaa ctt aat aga tta att gaa aaa acc aac aca cag ttt gaa ctc     1249
Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr Asn Thr Gln Phe Glu Leu
    400                 405                 410

ata gac aat gag ttc act gaa gtg gag cag cag ata ggc aat gta ata     1297
Ile Asp Asn Glu Phe Thr Glu Val Glu Gln Gln Ile Gly Asn Val Ile
415                 420                 425                 430

aac tgg aca agg gac tcc ttg act gag atc tgg tca tac aat gct gaa     1345
Asn Trp Thr Arg Asp Ser Leu Thr Glu Ile Trp Ser Tyr Asn Ala Glu
                435                 440                 445

ctt cta gta gca atg gaa aat cag cat aca att gac ctt gca gat tct     1393
Leu Leu Val Ala Met Glu Asn Gln His Thr Ile Asp Leu Ala Asp Ser
            450                 455                 460

gaa atg aac aaa ctc tat gag aga gtg aga aga cag cta agg gag aat     1441
Glu Met Asn Lys Leu Tyr Glu Arg Val Arg Arg Gln Leu Arg Glu Asn
        465                 470                 475

gcc gag gag gat gga act gga tgt ttt gag att ttc cac cga tgt gac     1489
Ala Glu Glu Asp Gly Thr Gly Cys Phe Glu Ile Phe His Arg Cys Asp
    480                 485                 490

gat caa tgt atg gag agc ata cga aat aat act tac aat cac act gaa     1537
Asp Gln Cys Met Glu Ser Ile Arg Asn Asn Thr Tyr Asn His Thr Glu
495                 500                 505                 510

tat cga cag gaa gcc tta cag aat agg ata atg atc aat ccg gta aag     1585
Tyr Arg Gln Glu Ala Leu Gln Asn Arg Ile Met Ile Asn Pro Val Lys
                515                 520                 525

ctt agt ggt ggg tac aaa gat gtg ata cta tgg ttt agc ttc ggg gca     1633
Leu Ser Gly Gly Tyr Lys Asp Val Ile Leu Trp Phe Ser Phe Gly Ala
            530                 535                 540

tca tgt gta atg ctt cta gcc att gct atg ggt ctt att ttc atg tgt     1681
Ser Cys Val Met Leu Leu Ala Ile Ala Met Gly Leu Ile Phe Met Cys
        545                 550                 555

gtg aaa aac ggg aat ctg cgg tgc act atc tgt ata taa ttatttga       1728
Val Lys Asn Gly Asn Leu Arg Cys Thr Ile Cys Ile
    560                 565                 570
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<210> 34

<211> 570
<212> PRT
<213> Influenza A virus

<400> 34

```
Met Asn Thr Gln Ile Ile Val Ile Leu Val Leu Gly Leu Ser Met Val
1               5                  10                  15

Arg Ser Asp Lys Ile Cys Leu Gly His His Ala Val Ala Asn Gly Thr
            20                  25                  30

Lys Val Asn Thr Leu Thr Glu Lys Gly Val Glu Val Val Asn Ala Thr
        35                  40                  45

Glu Thr Val Glu Ile Thr Gly Ile Asn Lys Val Cys Thr Lys Gly Lys
    50                  55                  60

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

Pro Pro Gln Cys Asp Ser His Leu Lys Phe Lys Ala Asp Leu Ile Ile
                85                  90                  95

Glu Arg Arg Asn Ser Ser Asp Ile Cys Tyr Pro Gly Lys Phe Thr Asn
            100                 105                 110

Glu Glu Ala Leu Arg Gln Ile Ile Arg Glu Ser Gly Gly Ile Asp Lys
        115                 120                 125

Glu Pro Met Gly Phe Arg Tyr Ser Gly Ile Lys Thr Asp Gly Ala Thr
    130                 135                 140

Ser Ala Cys Lys Arg Thr Val Ser Ser Phe Tyr Ser Glu Met Lys Trp
145                 150                 155                 160

Leu Leu Ser Ser Lys Asp Asn Gln Val Phe Pro Gln Leu Asn Gln Thr
                165                 170                 175

Tyr Arg Asn Asn Arg Lys Glu Pro Ala Leu Ile Val Trp Gly Val His
            180                 185                 190

His Ser Ser Ser Leu Asp Glu Gln Asn Lys Leu Tyr Gly Ala Gly Asn
        195                 200                 205

Lys Leu Ile Thr Val Gly Ser Ser Lys Tyr Gln Gln Ser Phe Ser Pro
    210                 215                 220

Ser Pro Gly Asp Arg Pro Lys Val Asn Gly Gln Ala Gly Arg Ile Asp
225                 230                 235                 240

Phe His Trp Met Leu Leu Asp Pro Gly Asp Thr Val Thr Phe Thr Phe
                245                 250                 255
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Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Thr Phe Leu Arg Ser Asn
            260                 265                 270

Ala Pro Ser Gly Val Glu Tyr Asn Gly Lys Ser Leu Gly Ile Gln Ser
        275                 280                 285

Asp Ala Gln Ile Asp Glu Ser Cys Glu Gly Glu Cys Phe Tyr Ser Gly
    290                 295                 300

Gly Thr Ile Asn Ser Pro Leu Pro Phe Gln Asn Ile Asp Ser Trp Ala
305                 310                 315                 320

Val Gly Arg Cys Pro Arg Tyr Val Lys Gln Ser Ser Leu Pro Leu Ala
                325                 330                 335

Leu Gly Met Lys Asn Val Pro Glu Lys Ile His Thr Arg Gly Leu Phe
            340                 345                 350

Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Leu Ile Asp
        355                 360                 365

Gly Trp Tyr Gly Phe Arg His Gln Asn Ala Gln Gly Gln Gly Thr Ala
    370                 375                 380

Ala Asp Tyr Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Thr Gly Lys
385                 390                 395                 400

Leu Asn Arg Leu Ile Glu Lys Thr Asn Thr Gln Phe Glu Leu Ile Asp
                405                 410                 415

Asn Glu Phe Thr Glu Val Glu Gln Gln Ile Gly Asn Val Ile Asn Trp
            420                 425                 430

Thr Arg Asp Ser Leu Thr Glu Ile Trp Ser Tyr Asn Ala Glu Leu Leu
        435                 440                 445

Val Ala Met Glu Asn Gln His Thr Ile Asp Leu Ala Asp Ser Glu Met
    450                 455                 460

Asn Lys Leu Tyr Glu Arg Val Arg Arg Gln Leu Arg Glu Asn Ala Glu
465                 470                 475                 480

Glu Asp Gly Thr Gly Cys Phe Glu Ile Phe His Arg Cys Asp Asp Gln
                485                 490                 495

Cys Met Glu Ser Ile Arg Asn Asn Thr Tyr Asn His Thr Glu Tyr Arg
            500                 505                 510

Gln Glu Ala Leu Gln Asn Arg Ile Met Ile Asn Pro Val Lys Leu Ser
        515                 520                 525
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Gly Gly Tyr Lys Asp Val Ile Leu Trp Phe Ser Phe Gly Ala Ser Cys
    530                 535                 540

Val Met Leu Leu Ala Ile Ala Met Gly Leu Ile Phe Met Cys Val Lys
545                 550                 555                 560

Asn Gly Asn Leu Arg Cys Thr Ile Cys Ile
                565                 570

<210>  35
<211>  1779
<212>  DNA
<213>  Influenza A virus

<220>
<221>  CDS
<222>  (29)..(1735)
<223>

<400>  35
agcaaaagca ggggtctaat ctattaaa atg gag aga ata gtg ctt ttt ctt       52
                                  Met Glu Arg Ile Val Leu Phe Leu
                                  1               5

gca ata gtc agt ctt gtc aaa agt gac cag att tgc att ggt tat cat      100
Ala Ile Val Ser Leu Val Lys Ser Asp Gln Ile Cys Ile Gly Tyr His
    10                  15                  20

gca aat aac tcg aca gaa cag gtt gac aca ata atg gag aag aat gtg      148
Ala Asn Asn Ser Thr Glu Gln Val Asp Thr Ile Met Glu Lys Asn Val
25                  30                  35                  40

act gtc aca cat gcc caa gac ata ctc gaa aag aca cac aac ggg aag      196
Thr Val Thr His Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys
                45                  50                  55

ctc tgc agt cta aat gga gtg aag cct ctc atc ttg agg gat tgt agt      244
Leu Cys Ser Leu Asn Gly Val Lys Pro Leu Ile Leu Arg Asp Cys Ser
            60                  65                  70

gta gct gga tgg ctc ctt gga aat ccc atg tgt gac gag ttc ctt aat      292
Val Ala Gly Trp Leu Leu Gly Asn Pro Met Cys Asp Glu Phe Leu Asn
        75                  80                  85

gtg cca gaa tgg tct tac ata gtg gag aag gac aat cca atc aac agc      340
Val Pro Glu Trp Ser Tyr Ile Val Glu Lys Asp Asn Pro Ile Asn Ser
    90                  95                  100

ctt tgc tac cca ggg gac ttt aat gac tac gaa gaa ttg aaa cac cta      388
Leu Cys Tyr Pro Gly Asp Phe Asn Asp Tyr Glu Glu Leu Lys His Leu
105                 110                 115                 120

ttg agc agt aca aac cac ttt gag aaa att caa atc atc ccc agg agt      436
Leu Ser Ser Thr Asn His Phe Glu Lys Ile Gln Ile Ile Pro Arg Ser
                125                 130                 135

tct tgg tcc aat cat gat gcc tca tca gga gta agc tct gca tgt cca      484
Ser Trp Ser Asn His Asp Ala Ser Ser Gly Val Ser Ser Ala Cys Pro
            140                 145                 150

tac aat ggg agg tcc tcc ttt ttt aga aat gtg gta tgg ctt atc gaa      532
Tyr Asn Gly Arg Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Glu
        155                 160                 165
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aag aac aat gca tac cca aca ata aag agg agt tac aac aat acc aac      580
Lys Asn Asn Ala Tyr Pro Thr Ile Lys Arg Ser Tyr Asn Asn Thr Asn
    170                 175                 180

caa gag gat ctt cta ata ttg tgg ggg att cac cat cct aat gac gca      628
Gln Glu Asp Leu Leu Ile Leu Trp Gly Ile His His Pro Asn Asp Ala
185                 190                 195                 200

gca gaa cag aca aag ctc tat caa aat cca acc act tat gtc tct gtc      676
Ala Glu Gln Thr Lys Leu Tyr Gln Asn Pro Thr Thr Tyr Val Ser Val
                205                 210                 215

ggg aca tca aca ctg aat cag aga tca att cca gaa ata gcc acc agg      724
Gly Thr Ser Thr Leu Asn Gln Arg Ser Ile Pro Glu Ile Ala Thr Arg
            220                 225                 230

ccc aaa gta aat gga cag agc gga aga gtg gaa ttc ttt tgg aca att      772
Pro Lys Val Asn Gly Gln Ser Gly Arg Val Glu Phe Phe Trp Thr Ile
        235                 240                 245

tta aag ccc aat gat gca att aat ttt gag agt aat ggg aac ttc ata      820
Leu Lys Pro Asn Asp Ala Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile
    250                 255                 260

gct cca gaa tat gca tac aaa att gtc aag aag ggg gac tct gca atc      868
Ala Pro Glu Tyr Ala Tyr Lys Ile Val Lys Lys Gly Asp Ser Ala Ile
265                 270                 275                 280

atg aaa agc gat ttg gaa tat ggt aac tgt aat gct aag tgt caa act      916
Met Lys Ser Asp Leu Glu Tyr Gly Asn Cys Asn Ala Lys Cys Gln Thr
                285                 290                 295

cca gtg ggt gcg ata aac tcc agc atg ccc ttc cac aat ata cac cct      964
Pro Val Gly Ala Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro
            300                 305                 310

ctc acc atc ggg gaa tgc ccc aaa tac gta aaa tca gat agg ttg gtc     1012
Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val Lys Ser Asp Arg Leu Val
        315                 320                 325

ctt gca act ggg ctc agg aac gtc cct cag agg gag acg cgc agg cag     1060
Leu Ala Thr Gly Leu Arg Asn Val Pro Gln Arg Glu Thr Arg Arg Gln
    330                 335                 340

aaa aga ggt cta ttt ggg gct ata gca ggt ttt ata gaa ggg gga tgg     1108
Lys Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp
345                 350                 355                 360

cag gga atg gta gac ggt tgg tat gga tac cat cat agc aac gag cag     1156
Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn Glu Gln
                365                 370                 375

ggg agc ggg tat gct gcg gac aaa gag tcc act caa aag gca att gat     1204
Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp
            380                 385                 390

ggg atc acc aat aag gtc aac tca atc att gac aaa atg aac act caa     1252
Gly Ile Thr Asn Lys Val Asn Ser Ile Ile Asp Lys Met Asn Thr Gln
        395                 400                 405

ttt gag acc gtt gga aag gaa ttt aat aat ttg gag agg agg ata gag     1300
Phe Glu Thr Val Gly Lys Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu
    410                 415                 420

aat ttg aac aag aaa atg gaa gac ggg ttt cta gat gtc tgg act tac     1348
Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr
425                 430                 435                 440
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aat gcc gaa ctt cta gtt ctc atg gaa aat gaa agg act ctg gat ttt     1396
Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe
                445                 450                 455

cat gac tca aac gtc aaa aac ctt tat gat aaa gtc cga cta cag ctt     1444
His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu
            460                 465                 470

aag gat aat gct aag gaa ctg ggt aat ggt tgt ttc gag ttc tac cat     1492
Lys Asp Asn Ala Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His
        475                 480                 485

aaa tgt gac aat gaa tgt atg gaa agc gtg aga aac ggg aca tat gac     1540
Lys Cys Asp Asn Glu Cys Met Glu Ser Val Arg Asn Gly Thr Tyr Asp
    490                 495                 500

tac cca cag tat tca gaa gaa gca aga ctg aac aga gag gaa ata agt     1588
Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Asn Arg Glu Glu Ile Ser
505                 510                 515                 520

ggg gtt aaa ttg gaa tta atg gga gtt tac caa ata ctg tca att tat     1636
Gly Val Lys Leu Glu Leu Met Gly Val Tyr Gln Ile Leu Ser Ile Tyr
                525                 530                 535

tca aca gtg gca agt tcc cta gca ctg gca atc atg ata gct ggt cta     1684
Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met Ile Ala Gly Leu
            540                 545                 550

tct ttt tgg atg tgt tcc aat gga tca ttg cag tgc aga att tgc att     1732
Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
        555                 560                 565

taa atttatgagt tcagattgta gttaaaaaca cccttgtttc tact               1779
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<210> 36
<211> 568
<212> PRT
<213> Influenza A virus

<400> 36

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Met Glu Arg Ile Val Leu Phe Leu Ala Ile Val Ser Leu Val Lys Ser
1               5                   10                  15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asn Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Asp Asn Pro Ile Asn Ser Leu Cys Tyr Pro Gly Asp Phe Asn
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100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Thr Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Arg Ser Ser Trp Ser Asn His Asp Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Asn Gly Arg Ser Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Glu Lys Asn Asn Ala Tyr Pro Thr Ile
165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
180 185 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
195 200 205

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

Ser Ile Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly
225 230 235 240

Arg Val Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
245 250 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
260 265 270

Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Asp Leu Glu Tyr Gly
275 280 285

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

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305 310 315 320

Tyr Val Lys Ser Asp Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Val
325 330 335

Pro Gln Arg Glu Thr Arg Arg Gln Lys Arg Gly Leu Phe Gly Ala Ile
340 345 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
355 360 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys

370 375 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser
385 390 395 400

Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Thr Val Gly Lys Glu Phe
405 410 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
420 425 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
435 440 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
450 455 460

Tyr Asp Lys Val Arg Leu Gln Leu Lys Asp Asn Ala Lys Glu Leu Gly
465 470 475 480

Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
485 490 495

Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
500 505 510

Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Leu Met Gly
515 520 525

Val Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
530 535 540

Leu Ala Ile Met Ile Ala Gly Leu Ser Phe Trp Met Cys Ser Asn Gly
545 550 555 560

Ser Leu Gln Cys Arg Ile Cys Ile
565

<210> 37
<211> 1665
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (1)..(1665)
<223>

<400> 37
atg gag aaa ata gtg ctt ctt ctt gca aca gtc agt ctt gtt aaa agt 48
Met Glu Lys Ile Val Leu Leu Leu Ala Thr Val Ser Leu Val Lys Ser
1 5 10 15

gac cag att tgc att ggt tac cat gca aac aac tcg aca gag cag gtt 96
Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val

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            20                  25                  30

gac aca ata atg gaa aag aat gtt act gtt aca cat gcc caa gac ata      144
Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

ctg gaa agg aca cac aac ggg aag ctc tgc gat cta aat gga gtg aag      192
Leu Glu Arg Thr His Asn Gly Lys Leu Cys Asp Leu Asn Gly Val Lys
    50                  55                  60

cct ctg att ttg agg gat tgt agt gta gct gga tgg ctc ctc gga aac      240
Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

cct atg tgt gac gaa ttc atc aat gtg ccg gaa tgg tct tac ata gtg      288
Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

gag aag gcc agt cca gcc aat gac ctc tgt tat cca ggg aat ttc aac      336
Glu Lys Ala Ser Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
            100                 105                 110

gac tat gaa gaa ctg aaa cac cta ttg agc aga ata aac cat ttt gag      384
Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

aaa att cag atc atc ccc aaa agt tct tgg tcc aat cat gat gcc tca      432
Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asn His Asp Ala Ser
    130                 135                 140

tca ggg gta agc tca gca tgt cca tac ctt ggg aag tcc tcc ttt ttc      480
Ser Gly Val Ser Ser Ala Cys Pro Tyr Leu Gly Lys Ser Ser Phe Phe
145                 150                 155                 160

aga aat gtg gta tgg ctt atc aaa aag aac agt aca tac cca aca ata      528
Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile
                165                 170                 175

aag agg agc tac aat aat acc aac caa gaa gat ctt ttg gta ctg tgg      576
Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190

ggg att cac cat cct aat gat gcg gca gag cag aca aag ctc tat caa      624
Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

aac cca acc acc tac att tcc gtt gga aca tca aca ctg aac cag aga      672
Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
    210                 215                 220

ttg gtt cca gaa ata gct act aga ccc aaa gta aac ggg caa agt gga      720
Leu Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

aga ata gag ttc ttc tgg aca att tta aag ccg aat gat gcc atc aat      768
Arg Ile Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

ttc gag agt aat gga aat ttc att gct cca gaa tat gca tac aaa att      816
Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

gtc aag aaa ggg gac tca aca att atg aaa agt gaa ttg gaa tat ggt      864
Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

aac tgc aac acc aag tgt caa act cca atg ggg gcg ata aac tct agt      912
Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
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    290                 295                 300

atg cca ttc cac aac ata cac ccc ctc acc atc ggg gaa tgc ccc aaa      960
Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

tat gtg aaa tca aac aga tta gtc ctt gcg act gga ctc aga aat gcc     1008
Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ala
                325                 330                 335

cct caa aga gag aga aga aga aaa aag aga gga cta ttt gga gct ata     1056
Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

gca ggt ttt ata gag gga gga tgg cag gga atg gta gat ggt tgg tat     1104
Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

ggg tac cac cat agc aat gag cag ggg agt gga tac gct gca gac caa     1152
Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Gln
    370                 375                 380

gaa tcc act caa aag gca ata gat gga gtc acc aat aag gtc aac tcg     1200
Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400

atc att aac aaa atg aac act cag ttt gag gcc gtt gga agg gaa ttt     1248
Ile Ile Asn Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

aat aac ttg gaa agg agg ata gag aat tta aac aag aag atg gaa gac     1296
Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

gga ttc cta gat gtc tgg act tac aat gcc gaa ctt ctg gtt ctc atg     1344
Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
        435                 440                 445

gaa aat gag aga act cta gac ttt cat gac tca aat gtc aag aac ctt     1392
Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460

tac gac aag gtc cga cta cag ctt agg gat aat gca aag gag ctg ggt     1440
Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

aat ggt tgt ttc gaa ttc tat cac aaa tgt gat aac gaa tgt atg gaa     1488
Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

agt gta aaa aac gga acg tat gac tac ccg cag tat tca gaa gaa gca     1536
Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510

aga cta aac aga gag gaa ata agt gga gta aaa ttg gaa tca atg gga     1584
Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Met Gly
        515                 520                 525

act tac caa ata ctg tca ctt tat tca aca gtg gcg agt tcc cta gca     1632
Thr Tyr Gln Ile Leu Ser Leu Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

ctg gca atc atg gta gct ggt cta tct tta tgg                         1665
Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp
545                 550                 555
```

<210> 38

<211> 555
<212> PRT
<213> Influenza A virus

<400> 38

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Met Glu Lys Ile Val Leu Leu Leu Ala Thr Val Ser Leu Val Lys Ser
1               5                  10                  15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Arg Thr His Asn Gly Lys Leu Cys Asp Leu Asn Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Ala Ser Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
            100                 105                 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asn His Asp Ala Ser
    130                 135                 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Leu Gly Lys Ser Ser Phe Phe
145                 150                 155                 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile
                165                 170                 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

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

Leu Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

Arg Ile Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255
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Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ala
                325                 330                 335

Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Gln
    370                 375                 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400

Ile Ile Asn Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
        435                 440                 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510

Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Met Gly
        515                 520                 525
```

```
Thr Tyr Gln Ile Leu Ser Leu Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp
545                 550                 555
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<210> 39
<211> 1707
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (1)..(1707)
<223>

<400> 39

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atg gag aaa ata gtg ctt ctt ctt gca ata gtc agt ctt gtt aaa agt       48
Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1               5                  10                  15

gat cag att tgc atc ggt tac cat gca aac aac tcg aca gag cag gtt       96
Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

gac aca ata atg gaa aag aac gtt act gtt aca cat acc caa gac ata      144
Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Thr Gln Asp Ile
        35                  40                  45

ctg gaa aag aaa cac aac ggg aag ctc tgc gat cta gat gga gtg aag      192
Leu Glu Lys Lys His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

cct cta att ttg aga gat tgt agt gta gct gga tgg ctc ctc gga aac      240
Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

cca atg tgt gac gaa ttc atc aat gta ccc gaa tgg tct tac ata gtg      288
Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

gag aag gcc agt cca gca aat ggt ctc tgt tac cca gga gat ttc aac      336
Glu Lys Ala Ser Pro Ala Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn
            100                 105                 110

gac tat gaa gaa ctg aaa cac cta ttg agc aga ata aac cat ttt gag      384
Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

aaa att cag atc atc ccc aaa agt tct tgg tcc aat cat gaa gcc tcg      432
Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asn His Glu Ala Ser
    130                 135                 140

tca ggg gtg agc tca gca tgt cca tac cag ggg agg tcc tcc ttt ttc      480
Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg Ser Ser Phe Phe
145                 150                 155                 160

aga aat gtg gta tgg ctc atc aaa aag aac ggt gca tac cca aca ata      528
Arg Asn Val Val Trp Leu Ile Lys Lys Asn Gly Ala Tyr Pro Thr Ile
                165                 170                 175

aag agg agc tac aat aat acc aat caa gaa gat ctt ttg gta ctg tgg      576
Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190
```

```
ggg att cac cat cct aat gat gcg gca gag cag aca aag ctc tat caa      624
Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

aac cca acc acc tat att tcc gtt gga aca tca aca cta aat cag aga      672
Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
    210                 215                 220

ttg gta cca aaa ata gct act aga tcc aaa gta aac ggg caa agt gga      720
Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

aga atg gag ttc ttc tgg aca att tta aag ccg aat gat gct atc aac      768
Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

ttc gag agt aat gga aat ttc att gct cca gaa tat gca tac aaa att      816
Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

gtc aag aaa ggg gac tca gca att atg aaa agt gaa ttg gaa tat ggt      864
Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

aac tgc aac acc aag tgt caa act cca atg ggg gcg ata aac tct agt      912
Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

atg cca ttc cac aac ata cac cct ctc acc atc ggg gaa tgc ccc aaa      960
Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

tat gtg aaa tca aac aga tta gtc ctt gcg aca ggg ctc aga aat agc     1008
Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

cct caa aga gag aga agg aga aaa aag aga gga ctg ttt gga gct ata     1056
Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

gca ggt ttt ata gag gga gga tgg cag gga atg gta gat ggt tgg tat     1104
Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

ggg tac cac cat agc aat gag cag ggg agt gga tac gct gca gac aaa     1152
Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
    370                 375                 380

gaa tcc act caa aag gca ata gat gga gtc acc aat aag gtc aac tcg     1200
Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400

atc att gac aaa atg aac act cag ttt gag gca gtt gga agg gaa ttt     1248
Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

aat aac tta gaa agg aga ata gag aat tta aac aag aag atg gaa gac     1296
Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

gga ttc cta gat gtc tgg act tat aat gct gaa ctt ctg gtt ctc atg     1344
Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
        435                 440                 445

gaa aat gag aga act cta gac ttt cat gac tca aat gtc aag aac ctt     1392
Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460
```

```
tac gac aag gtc cga cta caa ctt agg gat aat gca aag gag ctg ggt     1440
Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

aac ggt tgt ttc gag ttc tat cac aaa tgt gat aat gaa tgt atg gaa     1488
Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

agt gta aga aac gga acg tat gac tac ccg cag tat tca gaa gaa gca     1536
Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510

aga cta aac aga gag gaa ata agt gga gta aaa ttg gaa tca ata gga     1584
Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
        515                 520                 525

act tac caa ata ctg tca att tat tca aca gtg gcg agt tcc cta gca     1632
Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

ctg gca atc atg gta gct ggt cta tct tta tgg atg tgc tcc aat gga     1680
Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545                 550                 555                 560

tcg tta caa tgc aga att tgc att taa                                1707
Ser Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 40
<211> 568
<212> PRT
<213> Influenza A virus

<400> 40

```
Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1               5                   10                  15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Thr Gln Asp Ile
        35                  40                  45

Leu Glu Lys Lys His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Ala Ser Pro Ala Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn
            100                 105                 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125
```

```
Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asn His Glu Ala Ser
    130                 135                 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg Ser Ser Phe Phe
145                 150                 155                 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Gly Ala Tyr Pro Thr Ile
                165                 170                 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

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

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
    370                 375                 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400
```

```
Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
        435                 440                 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510

Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
        515                 520                 525

Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545                 550                 555                 560

Ser Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 41
<211> 1741
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (9)..(1715)
<223>

<400> 41

```
ctgtcaaa atg gag aaa ata gtg ctt ctt ttt gca ata gtc agt ctt gtt      50
         Met Glu Lys Ile Val Leu Leu Phe Ala Ile Val Ser Leu Val
         1               5                   10

aaa agt gat cag att tgc att ggt tac cat gca aac aac tcg aca gag      98
Lys Ser Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu
15                  20                  25                  30

cag gtt gac aca ata atg gaa aag aac gtt act gtt aca cat gcc caa     146
Gln Val Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln
                35                  40                  45
```

```
gac ata ctg gaa aag aca cac aat ggg aag ctc tgc gat cta gat gga      194
Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly
            50                  55                  60

gtg aag cct cta att ttg aga gat tgt agt gta gct gga tgg ctc ctc      242
Val Lys Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu
        65                  70                  75

gga aac cca atg tgt gac gaa ttc atc aat gtg ccg gaa tgg tct tac      290
Gly Asn Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr
    80                  85                  90

ata gtg gag aag gcc aat cca gtc aat gac ctc tgt tac cca ggg gat      338
Ile Val Glu Lys Ala Asn Pro Val Asn Asp Leu Cys Tyr Pro Gly Asp
95                  100                 105                 110

ttc aat gac tat gaa gaa ttg aaa cac cta ttg agc aga ata aac cat      386
Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His
                115                 120                 125

ttt gag aaa att cag atc atc ccc aaa agt tct tgg tcc agt cat gaa      434
Phe Glu Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Ser His Glu
            130                 135                 140

gcc tca ttg ggg gtg agc tca gca tgt cca tac cag gga aag tcc tcc      482
Ala Ser Leu Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Lys Ser Ser
        145                 150                 155

ttt ttc aga aat gtg gta tgg ctt atc aaa aag aac agt aca tac cca      530
Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro
    160                 165                 170

aca ata aag agg agc tac aat aat acc aac caa gaa gat ctt ttg gta      578
Thr Ile Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val
175                 180                 185                 190

ctg tgg ggg att cac cat cct aat gat gcg gca gag cag aca aag ctc      626
Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu
                195                 200                 205

tat caa aac cca acc acc tat att tcc gtt ggg aca tct aca cta aac      674
Tyr Gln Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn
            210                 215                 220

cag aga ttg gta cca aga ata gct act aga tcc aaa gta aac ggg caa      722
Gln Arg Leu Val Pro Arg Ile Ala Thr Arg Ser Lys Val Asn Gly Gln
        225                 230                 235

agt gga agg atg gag ttc ttc tgg aca att tta aaa ccg aat gat gca      770
Ser Gly Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala
    240                 245                 250

atc aac ttc gag agt aat gga aat ttc att gct cca gaa tat gca tac      818
Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr
255                 260                 265                 270

aaa att gtc aag aaa ggg gac tca aca att atg aaa agt gaa ttg gaa      866
Lys Ile Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu
                275                 280                 285

tat ggt aac tgc aac acc aag tgt caa act cca atg ggg gcg ata aac      914
Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn
            290                 295                 300

tct agc atg cca ttc cac aat ata cac cct ctc acc atc ggg gaa tgc      962
Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys
        305                 310                 315
```

```
ccc aaa tat gtg aaa tca aac aga tta gtc ctt gcg act ggg ctc aga      1010
Pro Lys Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg
    320                 325                 330

aat agc cct caa aga gag aga aga aga aaa aag aga gga tta ttt gga      1058
Asn Ser Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly
335                 340                 345                 350

gct ata gca ggt ttt ata gag gga gga tgg cag gga atg gta gat ggt      1106
Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly
                355                 360                 365

tgg tat ggg tac cac cat agc aac gag cag ggg agt ggg tac gct gca      1154
Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala
            370                 375                 380

gac aaa gaa tcc act caa aag gca ata gat gga gtc acc aat aag gtc      1202
Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val
        385                 390                 395

aac tcg att att gac aaa atg aac act cag ttt gag gcc gtt gga agg      1250
Asn Ser Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg
    400                 405                 410

gaa ttt aac aac tta gaa agg aga ata gag aat tta aac aag aag atg      1298
Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met
415                 420                 425                 430

gaa gac ggg ttc cta gat gtc tgg act tat aat gct gaa ctt cta gtt      1346
Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val
                435                 440                 445

ctc atg gaa aac gag aga act cta gac ttt cat gac tca aat gtc aag      1394
Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys
            450                 455                 460

aac ctt tac gac aag gtc cga cta cag ctt agg gat aat gca aag gag      1442
Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu
        465                 470                 475

ctg ggt aac ggt tgt ttc gag ttc tat cat aaa tgt gat aat gaa tgt      1490
Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys
    480                 485                 490

atg gaa agt gta aga aac gga acg tat gac tac ccg cag tat tca gaa      1538
Met Glu Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu
495                 500                 505                 510

gaa gca aga cta aaa aga gag gaa ata agt gga gta aaa ttg gaa tca      1586
Glu Ala Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser
                515                 520                 525

ata gga att tac caa ata ttg tca att tat tct aca gtg gcg agc tcc      1634
Ile Gly Ile Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser
            530                 535                 540

cta gca ctg gca atc atg gta gct ggt cta tcc tta tgg atg tgc tcc      1682
Leu Ala Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser
        545                 550                 555

aat ggg tcg tta caa tgc aga att tgc att taa atttgtgagt tcagattgta    1735
Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
    560                 565

gttaaa                                                              1741
```

<210> 42

<211> 568
<212> PRT
<213> Influenza A virus

<400> 42

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

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Ala Asn Pro Val Asn Asp Leu Cys Tyr Pro Gly Asp Phe Asn
            100                 105                 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Ser His Glu Ala Ser
    130                 135                 140

Leu Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Lys Ser Ser Phe Phe
145                 150                 155                 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile
                165                 170                 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

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

Leu Val Pro Arg Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255
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Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
    370                 375                 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400

Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
        435                 440                 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510

Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
        515                 520                 525
```

```
Ile Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545                 550                 555                 560

Ser Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 43
<211> 1704
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (1)..(1704)
<223>

<400> 43

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atg gag aaa ata gtg ctt ctt ctt gca ata gtc agt ctt gtt aaa agt       48
Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1               5                   10                  15

gat cag att tgc att ggt tac cat gca aac aac tcg aca gag cag gtt       96
Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

gac aca ata atg gaa aag aac gtc act gtt aca cat gcc caa gac ata      144
Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

ctg gaa aag aca cac aac ggg aag ctc tgc gat cta gat gga gtg aag      192
Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

cct cta att tta aga gat tgt agt gta gct gga tgg ctc ctc ggg aac      240
Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

cca atg tgt gac gaa ttc atc aat gtg ccg gaa tgg tct tac ata gtg      288
Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

gag aag gcc aat cca tcc aat gac ctc tgt tac cca ggg aat ttc aac      336
Glu Lys Ala Asn Pro Ser Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
            100                 105                 110

gac tat gaa gaa ctg aaa cac cta ttg agc aga ata aac cat ttt gaa      384
Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

aaa att cag atc atc ccc aaa agt tct tgg tcc gat cat gaa gcc tca      432
Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
    130                 135                 140

tca ggg gtg agc tca gca tgt cca tac cag gga agg tcc tcc ttt ttc      480
Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg Ser Ser Phe Phe
145                 150                 155                 160

aga aat gtg gta tgg ctt atc aaa aag aac agt gca tac cca aca ata      528
Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Ala Tyr Pro Thr Ile
                165                 170                 175
```

```
aag aga agc tac aat aat acc aac caa gaa gat ctt ttg gta ctg tgg      576
Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190

ggg att cac cat cca aat gat gcg gca gag cag aca aga ctc tat caa      624
Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
        195                 200                 205

aac cca acc aca tat att tcc gtt ggg aca tca aca cta aac cag aga      672
Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
    210                 215                 220

ttg gta cca aaa ata gct act aga tcc aaa ata aac ggg caa agt gga      720
Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Ile Asn Gly Gln Ser Gly
225                 230                 235                 240

agg atg gag ttc ttc tgg aca att tta aaa ccg aat gat gca atc agc      768
Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Ser
                245                 250                 255

ttt gag agt aat gga aat ttc att gct cca gaa tat gca tac aaa att      816
Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

gtc aag aaa ggg gac tca gca att atg aaa agt gaa ttg gaa tat ggt      864
Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

aac tgc aac acc aag tgt caa act cca atg ggg gcg ata aac tct agt      912
Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

atg cca ttc cac aac ata cac cct ctc acc atc gga gaa tgc ccc aaa      960
Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

tat gtg aaa tca agc aga tta gtc ctt gcg act ggg ctc aga aat agc     1008
Tyr Val Lys Ser Ser Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

cct caa aga gag aga aga aaa aag aga gga cta ttt gga gct ata gca     1056
Pro Gln Arg Glu Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile Ala
            340                 345                 350

ggt ttt ata gag gga gga tgg cag ggg atg gta gat ggt tgg tat ggg     1104
Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
        355                 360                 365

tac cac cat agc aat gag cag ggg agt ggg tac gct gca gac aaa gaa     1152
Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
    370                 375                 380

tcc act caa aag gca ata gat gga gtc acc aat aag gtc aac tcg atc     1200
Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
385                 390                 395                 400

att gac aaa atg aac act cag ttt gag gcc gtt gga agg gaa ttt aat     1248
Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
                405                 410                 415

aac tta gaa agg aga ata gaa aat tta aac aag aag atg gaa gac gga     1296
Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
            420                 425                 430

ttc cta gat gtc tgg act tat aat gct gaa ctt ctg gtt ctc atg gaa     1344
Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
        435                 440                 445
```

```
aat gag aga act cta gac ttt cat gac tca aat gtc aag aac ctt tac     1392
Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
    450                 455                 460

gac aag gtc cga cta cag ctt agg gat aat gca aag gag ctg ggt aac     1440
Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
465                 470                 475                 480

ggt tgt ttc gag ttc tat cac aga tgt gat aat gaa tgt ata gaa agt     1488
Gly Cys Phe Glu Phe Tyr His Arg Cys Asp Asn Glu Cys Ile Glu Ser
                485                 490                 495

gta aga aac gga acg tat gac tac ccg cag tat tca gaa gaa gca aga     1536
Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
            500                 505                 510

tta aaa aga gag gaa ata agt gga gta aaa ttg gaa tca ata gga act     1584
Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
        515                 520                 525

tac caa ata ctg tca att tat tca aca gtg gca agt tcc cta gca ctg     1632
Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
    530                 535                 540

gca atc atg gtg gct ggt cta tct tta tgg atg tgc tcc aat gga tcg     1680
Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
545                 550                 555                 560

tta caa tgc aga att tgc att taa                                    1704
Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 44
<211> 567
<212> PRT
<213> Influenza A virus

<400> 44

```
Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1               5                   10                  15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Ala Asn Pro Ser Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
            100                 105                 110
```

```
Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
    130                 135                 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg Ser Ser Phe Phe
145                 150                 155                 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Ala Tyr Pro Thr Ile
                165                 170                 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
            180                 185                 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
        195                 200                 205

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

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Ile Asn Gly Gln Ser Gly
225                 230                 235                 240

Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Ser
                245                 250                 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Ser Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

Pro Gln Arg Glu Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile Ala
            340                 345                 350

Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
        355                 360                 365

Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
    370                 375                 380
```

```
Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
385                 390                 395                 400

Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
                405                 410                 415

Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
            420                 425                 430

Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
        435                 440                 445

Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
    450                 455                 460

Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
465                 470                 475                 480

Gly Cys Phe Glu Phe Tyr His Arg Cys Asp Asn Glu Cys Ile Glu Ser
                485                 490                 495

Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
            500                 505                 510

Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
        515                 520                 525

Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
    530                 535                 540

Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
545                 550                 555                 560

Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 45
<211> 1737
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (15)..(1721)
<223>

<400> 45

```
ttcaatctgt caaa atg gag aaa ata gtg ctt ctt ctt gca ata gtc agt      50
                Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser
                1               5                   10

ctt gtt aaa agt gat cag att tgc att ggt tac cat gca aac aac tca      98
Leu Val Lys Ser Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser
        15                  20                  25
```

```
aca gag cag gtt gac aca ata atg gaa aag aac gtc act gtt aca cac      146
Thr Glu Gln Val Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His
    30                  35                  40

gcc caa gac ata ctg gag aag aca cac aac ggg aaa ctc tgc gat cta      194
Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu
45                  50                  55                  60

gat gga gtg aag cct cta att tta aga gat tgt agt gta gct gga tgg      242
Asp Gly Val Lys Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp
                65                  70                  75

ctc ctc ggg aac cca atg tgt gac gaa ttc ctc aat gtg ccg gaa tgg      290
Leu Leu Gly Asn Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp
            80                  85                  90

tct tac ata gtg gag aag atc aat cca gcc aat gac ctc tgt tac cca      338
Ser Tyr Ile Val Glu Lys Ile Asn Pro Ala Asn Asp Leu Cys Tyr Pro
        95                  100                 105

ggg aat ttc aac gac tat gaa gaa ctg aaa cac cta ttg agc aga ata      386
Gly Asn Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile
    110                 115                 120

aac cat ttt gag aaa ata cag atc atc ccc aaa agt tct tgg tca gat      434
Asn His Phe Glu Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp
125                 130                 135                 140

cat gaa gcc tca tca ggg gtg agc tca gca tgt cca tac cag gga agg      482
His Glu Ala Ser Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg
                145                 150                 155

tcc tcc ttt ttt aga aat gtg gta tgg ctt atc aaa aag gac aat gca      530
Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asp Asn Ala
            160                 165                 170

tac cca aca ata aag aga agt tac aat aat acc aac caa gaa gat ctt      578
Tyr Pro Thr Ile Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu
        175                 180                 185

ttg gta ctg tgg ggg att cac cat cca aat gat gcg gca gag cag aca      626
Leu Val Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr
    190                 195                 200

agg ctc tat caa aac cca acc acc tat att tcc gtt ggt aca tca aca      674
Arg Leu Tyr Gln Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr
205                 210                 215                 220

cta aac cag aga ctg gta cca aaa ata gct act aga tcc aag gta aac      722
Leu Asn Gln Arg Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn
                225                 230                 235

ggg caa agt gga agg atg gag ttc ttt tgg aca att tta aaa ccg aat      770
Gly Gln Ser Gly Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn
            240                 245                 250

gat gca ata aac ttt gag agt aat gga aat ttc att gct cca gaa aat      818
Asp Ala Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Asn
        255                 260                 265

gca tac aaa att gtc aag aaa ggg gac tca aca att atg aaa agt gaa      866
Ala Tyr Lys Ile Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu
    270                 275                 280

ttg gaa tat ggt aac tgc aac acc aag tgt caa act cca ata ggg gcg      914
Leu Glu Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala
285                 290                 295                 300
```

```
ata aac tct agt atg cca ttc cac aac atc cac cct ctc acc atc ggg      962
Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly
                305                 310                 315

gaa tgc ccc aaa tat gtg aaa tca aac aga tta gtc ctt gcg act ggg     1010
Glu Cys Pro Lys Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly
            320                 325                 330

ctc aga aat agc cct caa gga gag aga aga aga aga aag aga gga cta     1058
Leu Arg Asn Ser Pro Gln Gly Glu Arg Arg Arg Arg Lys Arg Gly Leu
        335                 340                 345

ttt gga gct ata gca ggt ttt ata gag gga gga tgg cag gga atg gta     1106
Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val
    350                 355                 360

gat ggt tgg tat ggg tac cac cat agc aac gag cag ggg agt ggg tac     1154
Asp Gly Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr
365                 370                 375                 380

gct gca gac aaa gaa tcc act caa aag gca ata gat gga gtc acc aat     1202
Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn
                385                 390                 395

aag gtc aac tcg atc att gac aaa atg aac act cag ttt gag gct gtt     1250
Lys Val Asn Ser Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val
            400                 405                 410

gga agg gaa ttt aat aac tta gaa agg aga ata gaa aat tta aac aag     1298
Gly Arg Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys
        415                 420                 425

aag atg gaa gac gga ttc cta gat gtc tgg act tat aat gct gaa ctt     1346
Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu
    430                 435                 440

ctg gtt ctc atg gaa aat gag aga act cta gac ttt cat gac tca aat     1394
Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn
445                 450                 455                 460

gtc aag aac ctt tac gac aag gtc cga cta cag ctt agg gat aat gca     1442
Val Lys Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala
                465                 470                 475

aag gag ctt ggt aac ggt tgt ttc gag ttc tat cat aga tgt gat aat     1490
Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Arg Cys Asp Asn
            480                 485                 490

gaa tgt atg gaa agt gta aga aac gga acg tat gac tac ccg cag tat     1538
Glu Cys Met Glu Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr
        495                 500                 505

tca gaa gaa gca aga tta aaa aga gag gaa ata agt gga gta aaa ttg     1586
Ser Glu Glu Ala Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu
    510                 515                 520

gaa tca ata gga act tac caa ata ctg tca att tat tca aca gtg gcg     1634
Glu Ser Ile Gly Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala
525                 530                 535                 540

agc tcc cta gca ctg gca atc atg gtg gct ggt cta tct tta tgg atg     1682
Ser Ser Leu Ala Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met
                545                 550                 555

tgc tcc aat gga tcg tta caa tgc aga att tgc att taa atttgtgagt      1731
Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
            560                 565
```

tcagat 1737

<210> 46
<211> 568
<212> PRT
<213> Influenza A virus

<400> 46

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
20 25 30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
35 40 45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
50 55 60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65 70 75 80

Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
85 90 95

Glu Lys Ile Asn Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg Ser Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asp Asn Ala Tyr Pro Thr Ile
165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
180 185 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
195 200 205

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

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225 230 235 240

```
Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Asn Ala Tyr Lys Ile
            260                 265                 270

Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

Pro Gln Gly Glu Arg Arg Arg Arg Lys Arg Gly Leu Phe Gly Ala Ile
            340                 345                 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
        355                 360                 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
    370                 375                 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385                 390                 395                 400

Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
                405                 410                 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
            420                 425                 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
        435                 440                 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
    450                 455                 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465                 470                 475                 480

Asn Gly Cys Phe Glu Phe Tyr His Arg Cys Asp Asn Glu Cys Met Glu
                485                 490                 495

Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
            500                 505                 510
```

```
Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
        515                 520                 525

Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
    530                 535                 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545                 550                 555                 560

Ser Leu Gln Cys Arg Ile Cys Ile
                565
```

<210> 47
<211> 1745
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (15)..(1721)
<223>

<400> 47

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ttcaatctgt caaa atg gag aaa ata gtg ctt ctt gca ata atc agt        50
                 Met Glu Lys Ile Val Leu Leu Ala Ile Ile Ser
                 1               5                  10

ctt gtt aaa agt gat cag att tgc att ggt tac cat gca aac aac tcg        98
Leu Val Lys Ser Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser
        15                  20                  25

aca gag cag gtt gac aca ata atg gaa aag aac gtc act gtt aca cac       146
Thr Glu Gln Val Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His
    30                  35                  40

gcc caa gac ata ctg gaa aag aca cac aac ggg aag ctc tgc gat cta       194
Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu
45                  50                  55                  60

gac gga gtg aag cct cta att tta aga gat tgt agt gta gct gga tgg       242
Asp Gly Val Lys Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp
                65                  70                  75

ctc ctc ggg aat cca atg tgt gac gaa ttc ctc aat gtg ccg gaa tgg       290
Leu Leu Gly Asn Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp
            80                  85                  90

tct tac ata gtg gag aag atc aat cca gcc aat gac ctc tgt tac cca       338
Ser Tyr Ile Val Glu Lys Ile Asn Pro Ala Asn Asp Leu Cys Tyr Pro
        95                  100                 105

ggg aat ttc aac gac tat gaa gaa ctg aaa cac cta ttg agc aga ata       386
Gly Asn Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile
    110                 115                 120

aac cat ttt gag aaa att cag atc atc ccc aaa agt tct tgg tca gat       434
Asn His Phe Glu Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp
125                 130                 135                 140

cat gaa gcc tca tca ggg gtg agc tca gca tgt cca tac cag gga agg       482
His Glu Ala Ser Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg
                145                 150                 155
```

```
tcc tcc ttt ttt aga aat gtg gta tgg ctt atc aaa aag aac gat gca      530
Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asp Ala
            160                 165                 170

tac cca aca ata aag aga agt tac aat aat acc aac caa gaa gat ctt      578
Tyr Pro Thr Ile Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu
        175                 180                 185

ttg gta ctg tgg ggg att cac cat cca aat gat gcg gca gag cag aca      626
Leu Val Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr
    190                 195                 200

agg ctc tat caa aac cca acc acc tat att tcc gtt ggg aca tca aca      674
Arg Leu Tyr Gln Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr
205                 210                 215                 220

cta aac cag aga ttg gta cca aaa ata gct act aga tcc aag gta aac      722
Leu Asn Gln Arg Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn
                225                 230                 235

ggg caa agt gga agg atg gag ttc ttt tgg aca att tta aaa ccg aat      770
Gly Gln Ser Gly Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn
            240                 245                 250

gat gca ata aat ttt gag agt aat gga aat ttc att gct cca gaa aat      818
Asp Ala Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Asn
        255                 260                 265

gca tac aaa att gtc aag aaa ggg gac tca aca atc atg aaa agt gaa      866
Ala Tyr Lys Ile Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu
    270                 275                 280

ttg gaa tat ggt aac tgc aac acc aag tgt caa act cca ata ggg gcg      914
Leu Glu Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala
285                 290                 295                 300

ata aac tct agt atg cca ttc cac aac atc cac cct ctc acc atc ggg      962
Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly
                305                 310                 315

gaa tgc ccc aaa tat gtg aaa tca aac aga tta gtc ctt gcg act ggg     1010
Glu Cys Pro Lys Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly
            320                 325                 330

ctc aga aat agc cct caa gga gag aga aga aga aaa aag aga gga cta     1058
Leu Arg Asn Ser Pro Gln Gly Glu Arg Arg Arg Lys Lys Arg Gly Leu
        335                 340                 345

ttt gga gct ata gca ggt ttt ata gag gga gga tgg cag gga atg gta     1106
Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val
    350                 355                 360

gat ggt tgg tat ggg tac cac cat agc aac gag cag ggg agt ggg tac     1154
Asp Gly Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr
365                 370                 375                 380

gct gca gac aaa gaa tcc act caa aag gca ata gat gga gtc acc aat     1202
Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn
                385                 390                 395

aag gtc aac tcg atc att gac aaa atg aac act cag ttt gag gcc gtt     1250
Lys Val Asn Ser Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val
            400                 405                 410

gga agg gaa ttt aat aac tta gaa agg aga ata gag aat tta aac aag     1298
Gly Arg Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys
        415                 420                 425
```

```
aag atg gaa gac gga ttt cta gat gtc tgg act tat aat gct gaa ctt     1346
Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu
    430                 435                 440

ctg gtt ctc atg gaa aat gag aga act cta gac ttt cat gac tca aat     1394
Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn
445                 450                 455                 460

gtc aag aac ctt tac gac aag gtc cga cta cag ctt agg gat aat gca     1442
Val Lys Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala
                465                 470                 475

aag gag ctt ggt aac ggt tgt ttc gag ttc tat cac aga tgt gat aat     1490
Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Arg Cys Asp Asn
            480                 485                 490

gaa tgt atg gaa agt gta aga aac gga acg tat gac tac ccg cag tat     1538
Glu Cys Met Glu Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr
        495                 500                 505

tca gaa gaa tca aga tta aaa aga gag gaa ata agt gga gta aaa ttg     1586
Ser Glu Glu Ser Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu
    510                 515                 520

gaa tca ata gga act tat caa ata ctg tca att tat tca aca gtg gcg     1634
Glu Ser Ile Gly Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala
525                 530                 535                 540

agc tcc cta gca ctg gca atc atg gtg gct ggt cta tct tta tgg atg     1682
Ser Ser Leu Ala Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met
                545                 550                 555

tgc tcc aat gga tcg tta caa tgc aga att tgc att taa atttgtgagt     1731
Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
            560                 565

tcagattgta gtta                                                   1745
```

<210> 48
<211> 568
<212> PRT
<213> Influenza A virus

<400> 48

```
Met Glu Lys Ile Val Leu Leu Leu Ala Ile Ile Ser Leu Val Lys Ser
1               5                   10                  15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
```

85 90 95

Glu Lys Ile Asn Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Arg Ser Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asp Ala Tyr Pro Thr Ile
165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
180 185 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
195 200 205

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

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225 230 235 240

Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
245 250 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Asn Ala Tyr Lys Ile
260 265 270

Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
290 295 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305 310 315 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

Pro Gln Gly Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
340 345 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr

355 360 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
370 375 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
385 390 395 400

Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
405 410 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
420 425 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
435 440 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
450 455 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
465 470 475 480

Asn Gly Cys Phe Glu Phe Tyr His Arg Cys Asp Asn Glu Cys Met Glu
485 490 495

Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ser
500 505 510

Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
515 520 525

Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
530 535 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545 550 555 560

Ser Leu Gln Cys Arg Ile Cys Ile
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<212> DNA
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ctt gtc aaa agt gac caa att tgc att ggt tac cat gca aac aac tca      98
Leu Val Lys Ser Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser
        15                  20                  25

aca gag cag gtt gac aca ata atg gaa aag aat gtt act gtc acg cat     146
Thr Glu Gln Val Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His
    30                  35                  40

gcc caa gac ata ctg gaa aag aca cac aat ggg aag ctc tgc agt cta     194
Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu
45                  50                  55                  60

aat gga gtt aag cct ctc att ttg agg gat tgt agt gta gct gga tgg     242
Asn Gly Val Lys Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp
                65                  70                  75

ctc ctc gga aac ccc atg tgt gat gaa ttc ctc aat gtg ccg gaa tgg     290
Leu Leu Gly Asn Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp
            80                  85                  90

tct tac ata gtg gag aag gac agc cca atc aat ggc ctc tgc tac cca     338
Ser Tyr Ile Val Glu Lys Asp Ser Pro Ile Asn Gly Leu Cys Tyr Pro
        95                  100                 105

ggg gat ttc aac gac tat gaa gag ctg aaa cac ctg ttg agc agt aca     386
Gly Asp Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Thr
    110                 115                 120

aac cat ttt gag aaa att caa atc atc ccc agg agt tct tgg tcc gat     434
Asn His Phe Glu Lys Ile Gln Ile Ile Pro Arg Ser Ser Trp Ser Asp
125                 130                 135                 140

cat gat gcc tca tca gga gtg agc tcc gca tgt cca tat aat ggg agg     482
His Asp Ala Ser Ser Gly Val Ser Ser Ala Cys Pro Tyr Asn Gly Arg
                145                 150                 155

tcc tcc ttt ttc aga aat gta gtg tgg ctc atc aaa aag aac aat gca     530
Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Ala
            160                 165                 170

tac cca aca ata aaa agg aat tac aat aat act aac caa gaa gat ctt     578
Tyr Pro Thr Ile Lys Arg Asn Tyr Asn Asn Thr Asn Gln Glu Asp Leu
        175                 180                 185

ttg gta ctg tgg ggg att cac cat cct aat gat gca aca gag cag aca     626
Leu Val Leu Trp Gly Ile His His Pro Asn Asp Ala Thr Glu Gln Thr
    190                 195                 200

aag ctc tat caa aac cca acc acc tat gtt tct gtt gga aca tca aca     674
Lys Leu Tyr Gln Asn Pro Thr Thr Tyr Val Ser Val Gly Thr Ser Thr
205                 210                 215                 220

ctg aac cag aga tcg gtc cca gaa ata gct acc agg ccc aaa gta aat     722
Leu Asn Gln Arg Ser Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn
                225                 230                 235

ggg caa agt gga aga ata gag ttt ttc tgg aca atc tta aag cca aat     770
Gly Gln Ser Gly Arg Ile Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn
            240                 245                 250

gat gcc atc aat ttc gag agt aat gga aat ttt att gct cca gaa tat     818
Asp Ala Ile Asn Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr
        255                 260                 265

gca tac aaa att gcc aag aaa gga gac tca gca atc atg gaa agt gga     866
Ala Tyr Lys Ile Ala Lys Lys Gly Asp Ser Ala Ile Met Glu Ser Gly
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    270                 275                 280

ttg gag tat ggt aac tgc aac acc aag tgt caa act cca atg ggt gca      914
Leu Glu Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala
285                 290                 295                 300

ata aac tcc agc atg cca ttt cac aac ata cac cct ctc acc att ggg      962
Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly
                305                 310                 315

gaa tgc ccc aga tac gtg aag tca gat aga tta gtc ctt gca aca ggg     1010
Glu Cys Pro Arg Tyr Val Lys Ser Asp Arg Leu Val Leu Ala Thr Gly
            320                 325                 330

ctc agg aat gtc cct caa aga gaa aca aga gga cta ttt ggg gcc ata     1058
Leu Arg Asn Val Pro Gln Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile
        335                 340                 345

gca ggc ttc ata gaa gga ggg tgg caa gga atg gta gac ggt tgg tat     1106
Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
    350                 355                 360

gga tac cac cat agc aac aag caa ggg agt gga tac gct gca gac aaa     1154
Gly Tyr His His Ser Asn Lys Gln Gly Ser Gly Tyr Ala Ala Asp Lys
365                 370                 375                 380

gag tcc act caa aag gca ata gat gga atc act aat aag gtc aac tca     1202
Glu Ser Thr Gln Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser
                385                 390                 395

atc att gac aaa atg aac act cag ttt gag gcc gtt gga aag gaa ttt     1250
Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Lys Glu Phe
            400                 405                 410

aat aac tta gaa agg agg ata gag aat ttg aac aag aaa atg gaa gac     1298
Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
        415                 420                 425

gga ttc cta gat gtc tgg act tat aat gct gaa ctt ctg gtt ctc atg     1346
Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
    430                 435                 440

gaa aat gag aga acc cta gac ttt cat gac tca aat gtc aag aac ctt     1394
Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
445                 450                 455                 460

tac gac aag gtt cga cta cag ctt agg gat aat gca aag gag ctg ggt     1442
Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
                465                 470                 475

aat ggt tgt ttc gag ttc tat cac aaa tgt gat gat gaa tgt atg gca     1490
Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asp Glu Cys Met Ala
            480                 485                 490

agt gta aga aac gga acg tat gac tac ccg cag tat tca gaa gag gca     1538
Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
        495                 500                 505

aga cta aac aga gag gaa ata agt gga gta aaa ttg gaa tca ata gga     1586
Arg Leu Asn Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
    510                 515                 520

act tac caa ata ttg tca att tat tca aca gtg gcg agt tcc tta gca     1634
Thr Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
525                 530                 535                 540

ctg gca atc atg gta gct ggt cta tct ttc tgg atg tgc tcc aat gga     1682
Leu Ala Ile Met Val Ala Gly Leu Ser Phe Trp Met Cys Ser Asn Gly
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545 550 555

tca ttg caa tgc aga att tgc att taa acttgtgagt tcagattgta gtt 1732
Ser Leu Gln Cys Arg Ile Cys Ile
560

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Met Glu Lys Ile Val Leu Leu Phe Ala Ile Val Ser Leu Val Lys Ser
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Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
20 25 30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
35 40 45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Ser Leu Asn Gly Val Lys
50 55 60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65 70 75 80

Pro Met Cys Asp Glu Phe Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
85 90 95

Glu Lys Asp Ser Pro Ile Asn Gly Leu Cys Tyr Pro Gly Asp Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Thr Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Arg Ser Ser Trp Ser Asp His Asp Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Asn Gly Arg Ser Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Ala Tyr Pro Thr Ile
165 170 175

Lys Arg Asn Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
180 185 190

Gly Ile His His Pro Asn Asp Ala Thr Glu Gln Thr Lys Leu Tyr Gln
195 200 205

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

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Ser Val Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

Arg Ile Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

Ala Lys Lys Gly Asp Ser Ala Ile Met Glu Ser Gly Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
    290                 295                 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Arg
305                 310                 315                 320

Tyr Val Lys Ser Asp Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Val
                325                 330                 335

Pro Gln Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile
            340                 345                 350

Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His
        355                 360                 365

Ser Asn Lys Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln
    370                 375                 380

Lys Ala Ile Asp Gly Ile Thr Asn Lys Val Asn Ser Ile Ile Asp Lys
385                 390                 395                 400

Met Asn Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Asn Asn Leu Glu
                405                 410                 415

Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp
            420                 425                 430

Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg
        435                 440                 445

Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val
    450                 455                 460

Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn Gly Cys Phe
465                 470                 475                 480

Glu Phe Tyr His Lys Cys Asp Asp Glu Cys Met Ala Ser Val Arg Asn
                485                 490                 495
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Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Asn Arg
            500                 505                 510

Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr Tyr Gln Ile
        515                 520                 525

Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met
    530                 535                 540

Val Ala Gly Leu Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys
545                 550                 555                 560

Arg Ile Cys Ile
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