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(54) **Title**: MUTATED LENTIVIRAL ENV PROTEINS AND THEIR USE AS DRUGS

(57) **Abstract**: The present invention relates to a pharmaceutical composition comprising, as active substance a mutated lentiviral ENV protein, substantially devoid of immunosuppressive properties or a variant of said mutated lentiviral ENV protein or a fragment of the above proteins, in association with a pharmaceutically acceptable carrier.

MUTATED LENTIVIRAL ENV PROTEINS AND THEIR USE AS DRUGS

The present invention relates to mutated lentiviral ENV proteins and their use as drugs.

Any discussion of the prior art throughout the specification should in no way be considered as an admission that such prior art is widely known or forms part of common general knowledge in the field.

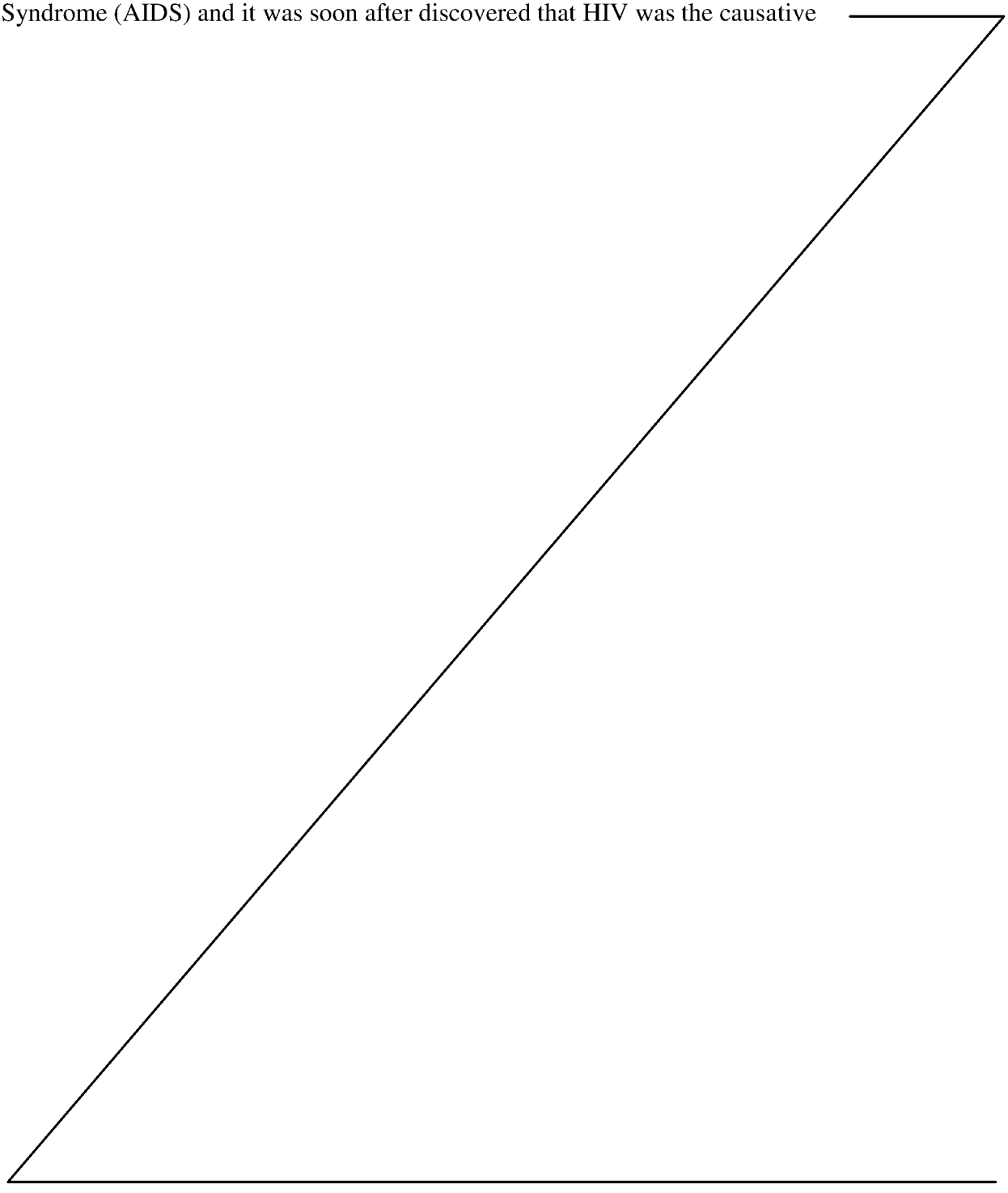
Lentivirus is a genus of slow viruses of the Retroviridae family, characterized by a long incubation period. Lentiviruses can deliver a significant amount of genetic information into the DNA of the host cell and have the unique ability among retroviruses of being able to replicate in non-dividing cells, so they are one of the most efficient methods of a gene delivery vector. HIV, SIV, and FIV are all examples of lentiviruses.

Human immunodeficiency virus (HIV) is according to WHO one of the most serious health crisis the world faces today. AIDS has killed more than 25 million people since 1981. In the most severely affected countries, the average life expectancy is now declining to 49 years of age - 13 years less than in the absence of AIDS. According to UNAIDS an estimated number of 39.5 million people were living with HIV virus in 2006 and 4.3 million were infected in 2006. In many regions new infections are heavily concentrated in the younger generations (15-24 years of age). Access to treatment and care has greatly increased in recent years. Determining real time trends to HIV incidence and in particular the impact of prevention programmes ideally requires long studies of a large number of people. Given the practical difficulties of conducting such studies focus has been placed on young women and their infants. Children living with HIV typically acquire infection through a mother-to-child-transmission (MTCT), which occur during pregnancy, delivery or during breastfeeding. Renewed efforts are urgently required to increase access to comprehensive and integrated programs to prevent HIV infection in infants and young children, which will indicate a route to HIV-free generations.

There are two known types of HIV; HIV-1 and HIV-2 that infect humans. They belong to a group of retroviruses called Lentiviruses and a virus similar to HIV has been found in African monkeys. Retroviruses transfer their genes from a producer cell to a target cell as a genomic

RNA transcript, which is reverse-transcribed after infection and integrated into the DNA genome of the target cell.

The first person with a documented HIV-infection died in 1959. In the early 1980s doctors in the US become aware, that more and more patients suffered from abnormal infections and showed signs of immune failure. The syndrome was named Acquired Immune Deficiency Syndrome (AIDS) and it was soon after discovered that HIV was the causative



agent for the observed destruction of the immune system. Initially patients were offered a treatment based solely on pain relief and almost all inevitably died. In mid 1990s there were two important breakthroughs in treatment. Firstly, a new group of antiretroviral agents were discovered and secondly it became possible to measure the amount of HIV virus in blood. These two advances made it possible to treat patients with a combination of different agents and doctors were able to check, whether the treatment actually worked. The result was that the immune system of infected patients gradually became normal and patients lived longer. Today infected people in Western countries are having the same level of quality of life as those not infected and they are able to have children, although the economical and psychological consequences of having HIV are huge. The situation is, however, even more severe in developing countries, where more than 95% of those people infected with HIV/AIDS are living. Worldwide more than 25 million people have died from AIDS in the last 25 years.

Approximately 95% of the people who get infected today live in the developing countries, where expensive antiviral drugs are not available. Therefore, there is an urgent need for an effective vaccine - the only effective solution to the uncontrolled HIV pandemic. During the last few years research has brought up new knowledge on the fundamental biology of HIV-virus which is leading to new antiviral drugs and strategies for vaccine design. In spite of these substantial advances, an effective vaccine does not yet exist. Only attenuated (that is live but weakened) HIV-strains has been able to provide immunity in primate studies even though they will never reach a required safety profile suitable for mass vaccination.

The replication process for HIV-1 has an error rate of about one per 10,000 base pairs.

Since the entire viral genome is just under 10,000 base pairs, it is estimated that on average one error is introduced into the HIV-1 genome at each viral replication cycle.

This high mutation rate contributes to extensive variability of the viruses inside any one person and an even wider variability across populations.

This variability has resulted in three HIV-1 variants being described, and the subspecies of virus called "clades." The distinctions are based on the structure of the envelope proteins, which are especially variable. The M (for major) variant is by far the most prevalent world wide. Within the M variant are clades A, B. C, D, E, F. G H. I, J and K, with clades A through E representing the vast majority of infections globally. Clades A, C and D are dominant in Africa, while clade B is the most prevalent in Europe, North and South

America and Southeast Asia. Clades E and C are dominant in Asia. These clades differ by as much as 35%. Another variant is clade O, which is observed in Cameroun isolates of HIV-1. The greatest variation in structure is seen in the envelope proteins gpl20 and gp41.

There are two important results from the very high mutation rate of HIV- 1 that have profound consequences for the epidemic. First, the high mutation rate is one of the mechanisms that allow the virus to escape from control by drug therapies. These new viruses represent resistant strains. The high mutation rate also allows the virus to escape the patient's immune system by altering the structures that are recognized by immune components. An added consequence of this extensive variability is that the virus can also escape from control by vaccines, and therefore makes it difficult to find vaccines based on envelope proteins which are effective.

Moreover, the virus produces proteins having immunosuppressive properties, allowing to escape the patient's immune system survey. Thus, cell expressing such proteins become “invisible” to the immune system.

Consequently for a vaccine, there is a need to provide proteins as antigens having lost, or substantially lost, their immunosuppressive functions, in order to generate an efficient response. This will enable the individuals once infected by the virus to allow the immune system to destroy the infected cells and prevent/cure the infection..

Prior art has already intended to provide such proteins.

For instance, the international application WO 2005/095,442 (Inventors : Renard, Mangeney & Heidmann) discloses mutations in the immunosuppressive domains of endogenous retroviruses (ERV) or onco retroviruses, such as HTLV or FeLV, ENV proteins. This document demonstrates that mutations at a specific position abolish the immunosuppressive properties of ENV proteins of ERV or onco retroviruses. However, the international application WO 2005/095, 442 never mentions or suggests that the mutations made in the immunosuppressive domain of ERV- or onco retroviruses ENV proteins can be transposable to lentiviral ENV proteins.

The international application WO 2010/022,740 discloses an extremely wide consensus sequence of a region of HIV ENV protein, described as follows:

$$X(1\text{-}22)\text{–}C(23)\text{–}X(24\text{-}28)\text{-}C(29)\text{-}(X30\text{-}50)$$

wherein the amino acid residues of the consensus sequence are selected from the groups of residues consisting of:

X(1): L, S, R, P, F, A, V, M, and I; and

X(2): Q, R, K, H, L, M, and P; and

X(3): A, T, V, H, S, R, Q, G, M, and E; and

X(4): R, K, G, E, T, S, C, M, and H; and

X(5): V, I, L, D, A, S, F, M, and G; and

X(6): L, Q, V, M, P, W, T, and I; and

X(7): A, S, T, V, L, G, F, D, M, and E; and

X(8): V, L, I, M, A, W, K, G, and E; and

X(9): E, K, G, D, A, V, M, and F; and

X(10): X; and

X(11): Y, L, F, H, C, I, T, M, and N; and

X(12): L, I, V, M, Q, P, T, Y, and A; and

X(13): K, R, Q, G, S, E, H, W, T, V, M, N, Z, Y, A, P, and C; and

X(14): D, N, G, E, Y, V, S, H, A, M, and I; and

X(15): Q, R, H, K, P, L, M, and N; and

X(16): Q, K, R, T, H, E, S, P, M, and L; and

X(17): L, F, I, R, V, P, S, M, and H, and

X(18): L, M, P, I, H, and S; and

X(19): X; and

X(20): I, L, M, V, S, F, T, D, A, R, P, and J; and

X(21): W, R, G, F, L, M, and T; and

X(22): G, D, A, R, M, and C; and

X(24): X; and

X(25): G, R, E, N, A, M, and D; and

X(26): K, R, N, E, Q, T, S, I, M, and G; and

X(27): L, H, I, T, V, F, R, Q, S, P, A, J, M, and Y; and

X(28): I, V, T, L, R, F and M; and

X(30): T, P, Y, A, N, S, I, V, R, L, M, and H; and

X(31): T, S, P, N, M and I; and

X(32): A, N, T, S, D, R, FQ, P, I, E, V, M, L, K, H, C, and B; and

X(33): V, A, L, M, G, R, and C; and

X(34): X; and

X(35): W, R, G, L, M, and P; and

X(36): N, S, D, B, K, E, R, Q, M, and G; and

X(37): S, T, A, N, D, V, I, E, Y, K, L, R, G, P, M, F, W, H, Q, B, and C; and

X(38): S, T, N, I, G, R, L, C, A, W, M and E; and

X(39): W, G, A, R, E, C, Y, V, S, M, and H; and

X(40): X; and

X(41): N, G, K, S, D, E, T, R, H, P, A, B, V, Q, Y, M, and I; and

X(42): K, R, N, D, S, T, G, E, I, V, Y, Q, P, H, A, W, M, and C, and

X(43): S, T, N, K, I, R, D, E, P, L, A, W, G, M, H, Y, F, V, and C,

X(44): L, Y, Q, F, E, H, S, V, K, M, T, I, W, N, D, R, P, A, and G; and

X(45): D, E, N, S, T, K, G, L, A, Q, H, I, Y, B, R, V, P, M, F, W, Z, and C; and

X(46): E, D, Q, Y, K, N, T, S, A, W, H, M, R, I, G, L, V, Z, F, B, and P ; and

X(47): I, D, E, M, G, T, Q, S, W, L, N, Y, K, V, R, F, A, P, and H, and

X(48): W, I, T, N, D, E, L, G, S, Y, R, V, K, H, A, Q, M, and F; and

X((49): D, N, E, G, W, Q, K, H, L, B, S, I, Y, T, A, R, M, Z, and V; and

X(50): N, D, T, K, S, H, L, G, E, W, I, Q, M, R, B, Y, P, and A;

This consensus sequence contains 50 amino acids, in which the specific amino acids in position 10, 19, 24, 34 and 40 are defined as affecting the immunogenic properties of a HIV-1 envelope polypeptide, and the 45 remaining positions are randomly defined including the most common amino acids of wild-type HIV ENV proteins.

In fact, the teaching of WO 2010/022,740 is a transposition from endogenous retroviruses (ERV) or onco retroviruses to lentivirus on the basis of the teaching of WO 2005/095,442 (Inventors : Renard, Mangeney & Heidmann), but said transposition is inappropriate in the case of lentivirus, as shown by the Inventor of the present invention.

Briefly speaking, Dr Heidmann is an Inventor in WO 2005/095,442 and in the present invention. As a matter of fact, the effects of the mutations described in WO 2005/095,442 were also tested in lentivirus by the Inventor of the present invention, but no effect was observed when the mutations identified in endogenous retroviruses or onco retroviruses were transposed into ENV protein of lentivirus.

Moreover, since any amino acid can be assigned to the positions 10, 19, 24, 34 or 40 in the consensus sequence, WO 2010/022,740 teaches that such mutations can be effective using

any amino acid residue. This teaching is in contradiction with the present invention, showing that the immunosuppressive properties of HIV-1 ENV protein are only affected by specific mutations that are defined not only by their position, but also by the nature of the substituted amino acid residues.

Furthermore, WO 2010/022,740 discloses experimental results for only one specific mutation within the immunosuppressive domain of HIV ENV protein, as defined by the 50 amino acids consensus sequence. The mutation, a substitution by R as the only one exemplified in the international application WO 2010/022,740, occurs at the amino acid in position 19, which again is equivalent to the position disclosed in the international application WO 2005/095,442 if one simply aligns ENV sequences (see Fig 3 in WO 2010/022,740, which is a copy of Figure 3 in *Benit et al. 2001, Journal of Virology, Vol. 75, No. 23, p.11709-11719*) (Of note not only the position of the amino acid, but also the nature of the substitution (by arginine) is similar to the one described in WO 2005/095,442).

More specifically, when aligning the ENV sequences respectively of an endogenous retrovirus or onco retrovirus and a lentivirus, according to Figure 3 of Benit et al. :

Endogenous or onco retrovirus :

L Q N R R G L D L L F L K (E) G G L C A A L (WO 2005/095,442)

Lentivirus:

L A V E R Y L K D Q Q L L (G) I W G C S G K (WO 2010/022,740)

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it appears that the position 19 in lentivirus corresponds to the position in WO 2005/095,442 where a specific substitution into arginine, E→R for endogenous or onco retrovirus, results in loss of immunosuppressive activity.

The international application WO 2010/022,740 discloses that said mutated HIV ENV protein inhibits proliferation of PBMC *ex vivo,* but such *ex vivo* result has no *in vivo* predictive value.

However, WO 2010/022,740 never discloses or suggests that mutants are efficient in vivo, i.e. that cell expressing mutants are detected by the immune system.

Moreover, as disclosed hereafter, such mutations are not efficient in vivo. Indeed, results disclosed hereafter in the example section relative to the present invention demonstrate that said substitution G19R does not inhibit in vivo the immunosuppressive properties of the ENV protein.

As a consequence, WO 2010/022,740 raises the same technical problem as the present invention, but does not offer an appropriate technical solution. This prior art reveals the difficulties to overcome the identification of the effective mutations affecting the immunosuppressive properties of the lentiviral ENV proteins.

Thus, the provision of in vivo effective non immunosuppressive lentiviral ENV proteins remains.

One aim of the invention is to provide new mutated ENV proteins devoid of immunosuppressive properties.

Another aim of the invention is to provide a new pharmaceutical composition efficient for treating lentiviral infection.

Another aim of the invention is to provide an efficient vaccine.

According to a first aspect, the invention provides a pharmaceutical composition comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein having at least 90% identity, to one sequence chosen from the group consisting of SEQ ID NO : 216, SEQ ID NO : 420 and SEQ ID NO : 421,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

in association with a pharmaceutically acceptable carrier,

said substantial absence of immunosuppressive activity of the above mentioned mutated human or simian lentiviral ENV protein or of the above defined fragment being liable to be assessed by the fact that in an in vivo assay involving engrafted tumor cells rejection,

said tumor cells being transduced either so as to express said mutated ENV protein or said fragment (mutated ENV tumor cells),

or said tumor cells being transduced so as to express said wild type ENV protein or a fragment thereof (wild type ENV tumor cells),

or said tumor cells being not transduced (normal tumor cells),

the following ratio :

immunosuppression index of said mutated ENV protein or of said fragment ($i_{mutated\ env}$) / immunosuppression index of wild type ENV protein ($i_{wild\ type\ env}$) is less than 0.5,

$i_{mutated\ env}$ being defined by : (maximum area reached by mutated ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells), and

$i_{wild\ type\ env}$ being defined by : (maximum area reached by wild type ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells).

According to a second aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention, consisting of modifying the immunosuppressive property of:

a wild-type human or simian lentiviral ENV protein,

or a fragment of said wild-type human or simian lentiviral ENV protein, said fragment comprising at least 40 amino acids,

said ENV protein or fragment thereof presenting a transmembrane subunit (TM) comprising an immunosuppressive domain (ISU) containing the following amino acid sequence :

A-[I/V]-E-[K/R]-X'$_a$-X'$_b$-X-D-Q (SEQ ID NO: 427),

wherein

X represents any amino acid,

X'$_a$ is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and

X'$_b$ is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

said method comprising a step of introduction of at least one mutation of X'$_a$ and/or X'$_b$,

to obtain:

an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein having at least 90% identity, to one sequence chosen from the group consisting of SEQ ID NO : 216, SEQ ID NO : 420 and SEQ ID NO : 421,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

said substantial absence of immunosuppressive activity of the above mentioned mutated human or simian lentiviral ENV protein or of the above defined fragment being liable to be assessed by the fact that in an in vivo assay involving engrafted tumor cells rejection,

said tumor cells being transduced either so as to express said mutated ENV protein or said fragment (mutated ENV tumor cells),

or said tumor cells being transduced so as to express said wild type ENV protein or a fragment thereof (wild type ENV tumor cells),

or said tumor cells being not transduced (normal tumor cells),

the following ratio :

immunosuppression index of said mutated ENV protein or of said fragment ($i_{mutated\ env}$) / immunosuppression index of wild type ENV protein ($i_{wild\ type\ env}$) is less than 0.5,

$i_{mutated\ env}$ being defined by : (maximum area reached by mutated ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells), and

$i_{wild\ type\ env}$ being defined by : (maximum area reached by wild type ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells).

According to a third aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention, consisting of modifying the immunosuppressive property of :

a wild-type human or simian lentiviral ENV protein,

or a fragment of said wild-type human or simian lentiviral ENV protein, said fragment comprising at least 40 amino acids,

said ENV protein or fragment thereof presenting a transmembrane subunit (TM) comprising an immunosuppressive domain (ISU) containing the following amino acid sequence :

A-[I/V]-E-[K/R]-Y-L-X-D-Q (SEQ ID NO : 1),

wherein

X represents any amino acid,

said method comprising a step of introduction of at least one mutation of Y in position 5 and/or L in position 6,

to obtain:

an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

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wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R.

According to a fourth aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R.

According to a fifth aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R, or

X_a is F or L, and X_b is F, G or R, or

X_a is A, G or R, and X_b is A.

According to a sixth aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is F, G or R, or

X_a is F or L, and X_b is F, G or R, or

X_a is A, G or R, and X_b is A, or

X_a is A, G or R, and X_b is F, G or R.

According to a seventh aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R.

According to an eighth aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is F, G or R.

According to a ninth aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

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wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is R, or

X_a is R, and X_b is R.

According to a tenth aspect, the invention provides a method to obtain the active substance of a pharmaceutical composition, as defined in the invention,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising an additional mutation in one at least of the amino acids at positions, 29, 36 and 37 of SEQ ID NO: X :

A[I/V]E[K/R]$X_aX_bX_1$DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VP$X_c$$X_{10}Z_1Z_2Z_3Z_4Z_5X_dX_e$[S/T] (SEQ ID NO: 426)

wherein

X_a and X_b are as defined in any one of claims 1 to 14,

X_1 to X_{10} represent any amino acid,

Z_1 to Z_5 represent no amino acid or any amino acid, independently from each other

such that

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- X_c is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V or Y, preferably A, D, or N,
- X_d is A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, Y or W, preferably A, G, S or Y,
- Xe is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, T, V, Y or W, preferably A, D or N.

According to an eleventh aspect, the invention provides the active substance when prepared according to method of the invention.

Unless the context clearly requires otherwise, throughout the description and the claims, the words "comprise", "comprising", and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of "including, but not limited to".

The invention relates to a pharmaceutical composition comprising as active substance:

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein having at least 70% identity, preferably at least 80% identity, to one sequence chosen from the group consisting of SEQ ID NO : 216, SEQ ID NO : 420 and SEQ ID NO : 421,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L, R or deleted, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G, R or deleted, or

X_a is A, F, G, L, R or deleted, and X_b is A, F, G, R or deleted,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L, R or deleted, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G, R or deleted, or

X_a is A, F, G, L, R or deleted, and X_b is A, F, G, R or deleted,

in association with a pharmaceutically acceptable carrier,

said substantial absence of immunosuppressive activity of the above mentioned mutated human or simian lentiviral ENV protein or of the above defined fragment being liable to be assessed by the fact that in an *in vivo* assay involving engrafted tumor cells rejection,

said tumor cells being transduced either so as to express said mutated ENV protein or said fragment ("mutated ENV tumor cells"),

or said tumor cells being transduced so as to express said wild type ENV protein or a fragment thereof ("wild type ENV tumor cells"),

or said tumor cells being not transduced ("normal tumor cells"),

the following ratio :

immunosuppression index of said mutated ENV protein or of said fragment ($i_{mutated\ env}$) / immunosuppression index of wild type ENV protein ($i_{wild\ type\ env}$) is less than 0.5,

$i_{mutated\ env}$ being defined by : (maximum area reached by mutated ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells), and

$i_{wild\ type\ env}$ being defined by : (maximum area reached by wild type ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells).

The present application is based on the unexpected observation made by the Inventors that some specific amino acids of the immunosuppressive domain of a lentiviral ENV protein can be mutated conferring to said lentiviral ENV protein essentially no immunosuppressive properties, or no immunosuppressive properties, while retaining its antigenicity, the three-dimentional structure of the immunosuppressive domain, and its expression at the plasma membrane. Moreover, the mutated lentiviral ENV protein according to the invention does not alter the infectivity of a virus expressing it.

In the invention, the "mutated simian or human lentiviral ENV proteins" means that the ENV proteins derive from the expression of an *env* gene of a lentivirus of human or simian.

Lentiviruses according to the invention encompassed by the invention are HIV-1 and 2 and Simian immunodeficiency virus (SIV).

Because of the high mutation rate of HIV-1, HIV-2 and SIV viruses, the "mutated ENV protein", as defined in the invention, encompasses two meanings.

According to the first meaning, the said "mutated ENV protein" is the unnatural result of the intervention of human beings.

According to the second meaning, the mutated ENV protein also encompasses naturally occurring variants for which up to now the non immunosuppressive properties remain unknown.

This second meaning takes into consideration the natural variability of HIV and SIV variants inside a same infected individual, wherein the said "mutated ENV protein" might be non immunosuppressive but its property is undetectable because an HIV infected patient always carries many HIV variants, the majority of which is immunosuppressive.

The three following proteins correspond to wild type sequences of the ENV protein of HIV-1, HIV-2 and SIV respectively. In the invention, they are considered as reference sequences of wild type ENV proteins.

SEQ ID NO: 417 wild type HIV-1	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCS GKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTS LIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYIK IFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGPD RPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRLR DLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVSL LNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 418 Wild type HIV-2	MCGRNQLFVASLLASACLIYCVQYVTVFYGVPVWRNASIPLFC ATKNRDTWGTIQCLPDNDDYQEIALNVTEAFDAWNNTVTEQA VEDVWSLFETSIKPCVKLTPLCVAMRCNSTTAKNTTSTPTTTTT ANTTIGENSSCIRTDNCTGLGEEEMVDCQFNMTGLERDKKKLY NETWYSKDVVCESNDTKKEKTCYMNHCNTSVITESCDKHYW DTMRFRYCAPPGFALLRCNDTNYSGFEPNCSKVVAATCTRMM ETQTSTWFGFNGTRAENRTYIYWHGRDNRTIISLNKFYNLTVH CKRPGNKTVVPITLMSGLVFHSQPINRRPRQAWCWFKGEWKE AMKEVKLTLAKHPRYKGTNDTEKIRFIAPGERSDPEVAYMWT NCRGEFLYCNMTWFLNWVENRTNQTQHNYVPCHIKQIINTWH KVGKNVYLPPREGQLTCNSTVTSIIANIDGGENQTNITFSAEVA

	ELYRLELGDYKLIEVTPIGFAPTPVKRYSSAPVRNKRGVFVLGF LGFLTTAGAAMGAASLTLSAQSRTLLAGIVQQQQQLLDVVKR QQEMLRLTVWGTKNLQARVTAIEKYLKDQAQLNSWGCAFRQ VCHTTVPWVNDTLTPDWNNMTWQEWEQRIRNLEANISESLEQ AQIQQEKNMYELQKLNSWDVFGNWFDLTSWIKYIQYGVYIVV GIIVLRIVIYVVQMLSRLRKGYRPVFSSPPAYFQQIHIHKDREQP AREETEEDVGNSVGDNWWPWPIRYIHFLIRQLIRLLNRLYNICR DLLSRSFQTLQLISQSLRRALTAVRDWLRFNTAYLQYGGEWIQ EAFRAFARATGETLTNAWRGFWGTLGQIGRGILAVPRRIRQGA EIALL
SEQ ID NO: 419 wild type SIV mac239	MGCLGNQLLIAILLLSVYGIYCTLYVTVFYGVPAWRNATIPLFC ATKNRDTWGTTQCLPDNGDYSEVALNVTESFDAWNNTVTEQ AIEDVWQLFETSIKPCVKLSPLCITMRCNKSETDRWGLTKSITT TASTTSTTASAKVDMVNETSSCIAQDNCTGLEQEQMISCKFNM TGLKRDKKKEYNETWYSADLVCEQGNNTGNESRCYMNHCNT SVIQESCDKHYWDAIRFRYCAPPGYALLRCNDTNYSGFMPKCS KVVVSSCTRMMETQTSTWFGFNGTRAENRTYIYWHGRDNRTI ISLNKYYNLTMKCRRPGNKTVLPVTIMSGLVFHSQPINDRPKQ AWCWFGGKWKDAIKEVKQTIVKHPRYTGTNNTDKINLTAPGG GDPEVTFMWTNCRGEFLYCKMNWFLNWVEDRNTANQKPKE QHKRNYVPCHIRQIINTWHKVGKNVYLPPREGDLTCNSTVTSLI ANIDWIDGNQTNITMSAEVAELYRLELGDYKLVEITPIGLAPTD VKRYTTGGTSRNKRGVFVLGFLGFLATAGSAMGAASLTLTAQ SRTLLAGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTA IEKYLKDQAQLNAWGCAFRQVCHTTVPWPNASLTPKWNNET WQEWERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF GNWFDLASWIKYIQYGVYIVVGVILLRIVIYIVQMLAKLRQGY RPVFSSPPSYFQQTHIQQDPALPTREGKERDGGEGGGNSSWPW QIEYIHFLIRQLIRLLTWLFSNCRTLLSRVYQILQPILQRLSATLQ RIREVLRTELTYLQYGWSYFHEAVQAVWRSATETLAGAWGDL WETLRRGGRWILAIPRRIRQGLELTLL

Variant in the invention encompasses SIV, HIV-1 and HIV-2 ENV proteins.

Variants of the HIV-1 mutated ENV proteins according to the invention have at least 70%, preferably at least 80%, more preferably at least 90% of identity with the wild type amino acid sequence of the HIV-1 ENV protein, and comprises the mutations as described above, and harbour no immunosuppressive activity.

Variants of the HIV-2 mutated ENV proteins according to the invention have at least 70%, preferably at least 80%, more preferably at least 90% of identity with the wild type amino acid sequence of the HIV-2 ENV protein, and comprises the mutations as described above, and harbour no immunosuppressive activity.

Variants of the SIV mutated ENV proteins according to the invention have at least 70%, preferably at least 80%, more preferably at least 90% of identity with the wild type amino acid sequence of the SIV ENV protein, and comprises the mutations as described above, and harbour no immunosuppressive activity.

The three following proteins (SEQ ID NO : 216, 420 and 421) correspond to three mutated sequences of the ENV protein of HIV-1, HIV-2 and SIV respectively. In the invention, they are considered as reference sequences of the mutated ENV proteins.

More specifically, SEQ ID NO : 216 corresponds to the SEQ ID NO : 417 in which the amino acid residue Y in position 5 (X_a) of the sequence A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q has been substituted by R.

SEQ ID NO : 420 corresponds to the SEQ ID NO : 418 in which the amino acid residue Y in position 5 (X_a) of the sequence A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q has been substituted by R.

SEQ ID NO : 421 corresponds to the SEQ ID NO : 419 in which the amino acid residue Y in position 5 (X_a) of the sequence A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q has been substituted by R.

SEQ ID NO: 216 mutated HIV-1	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARILAVER**R**LKDQQLLGIWGCS GKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTS LIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYIK IFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGPD RPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRLR DLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVSL LNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 420 mutated HIV-2	MCGRNQLFVASLLASACLIYCVQYVTVFYGVPVWRNASIPLFC ATKNRDTWGTIQCLPDNDDYQEIALNVTEAFDAWNNTVTEQA

	VEDVWSLFETSIKPCVKLTPLCVAMRCNSTTAKNTTSTPTTTTT ANTTIGENSSCIRTDNCTGLGEEEMVDCQFNMTGLERDKKKLY NETWYSKDVVCESNDTKKEKTCYMNHCNTSVITESCDKHYW DTMRFRYCAPPGFALLRCNDTNYSGFEPNCSKVVAATCTRMM ETQTSTWFGFNGTRAENRTYIYWHGRDNRTIISLNKFYNLTVH CKRPGNKTVVPITLMSGLVFHSQPINRRPRQAWCWFKGEWKE AMKEVKLTLAKHPRYKGTNDTEKIRFIAPGERSDPEVAYMWT NCRGEFLYCNMTWFLNWVENRTNQTQHNYVPCHIKQIINTWH KVGKNVYLPPREGQLTCNSTVTSIIANIDGGENQTNITFSAEVA ELYRLELGDYKLIEVTPIGFAPTPVKRYSSAPVRNKRGVFVLGF LGFLTTAGAAMGAASLTLSAQSRTLLAGIVQQQQQLLDVVKR QQEMLRLTVWGTKNLQARVTAIEK**R**LKDQAQLNSWGCAFRQ VCHTTVPWVNDTLTPDWNNMTWQEWEQRIRNLEANISESLEQ AQIQQEKNMYELQKLNSWDVFGNWFDLTSWIKYIQYGVYIVV GIIVLRIVIYVVQMLSRLRKGYRPVFSSPPAYFQQIHIHKDREQP AREETEEDVGNSVGDNWWPWPIRYIHFLIRQLIRLLNRLYNICR DLLSRSFQTLQLISQSLRRALTAVRDWLRFNTAYLQYGGEWIQ EAFRAFARATGETLTNAWRGFWGTLGQIGRGILAVPRRIRQGA EIALL
SEQ ID NO: 421 mutated SIV mac239	MGCLGNQLLIAILLLSVYGIYCTLYVTVFYGVPAWRNATIPLFC ATKNRDTWGTTQCLPDNGDYSEVALNVTESFDAWNNTVTEQ AIEDVWQLFETSIKPCVKLSPLCITMRCNKSETDRWGLTKSITT TASTTSTTASAKVDMVNETSSCIAQDNCTGLEQEQMISCKFNM TGLKRDKKKEYNETWYSADLVCEQGNNTGNESRCYMNHCNT SVIQESCDKHYWDAIRFRYCAPPGYALLRCNDTNYSGFMPKCS KVVVSSCTRMMETQTSTWFGFNGTRAENRTYIYWHGRDNRTI ISLNKYYNLTMKCRRPGNKTVLPVTIMSGLVFHSQPINDRPKQ AWCWFGGKWKDAIKEVKQTIVKHPRYTGTNNTDKINLTAPGG GDPEVTFMWTNCRGEFLYCKMNWFLNWVEDRNTANQKPKE QHKRNYVPCHIRQIINTWHKVGKNVYLPPREGDLTCNSTVTSLI ANIDWIDGNQTNITMSAEVAELYRLELGDYKLVEITPIGLAPTD VKRYTTGGTSRNKRGVFVLGFLGFLATAGSAMGAASLTLTAQ SRTLLAGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTA IEK**R**LKDQAQLNAWGCAFRQVCHTTVPWPNASLTPKWNNET WQEWERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF GNWFDLASWIKYIQYGVYIVVGVILLRIVIYIVQMLAKLRQGY RPVFSSPPSYFQQTHIQQDPALPTREGKERDGGEGGGNSSWPW QIEYIHFLIRQLIRLLTWLFSNCRTLLSRVYQILQPILQRLSATLQ RIREVLRTELTYLQYGWSYFHEAVQAVWRSATETLAGAWGDL WETLRRGGRWILAIPRRIRQGLELTLL

The invention also encompasses the variants of the ‘‘mutated simian or human lentiviral ENV protein’’, harbouring the above mentioned mutations, and conferring a lack of immunosuppressive properties to said variant.

Variants of the HIV-1 mutated ENV proteins according to the invention have at least 70%, preferably at least 80%, more preferably at least 90% of identity with the reference

mutated sequence of HIV-1 ENV protein (SEQ ID NO : 216), and comprises the mutations as described above, and harbour no immunosuppressive activity.

Variants of the HIV-2 mutated ENV proteins according to the invention have at least 70%, preferably at least 80%, more preferably at least 90% of identity with the reference mutated sequence of the HIV-2 ENV protein (SEQ ID NO : 420), and comprises the mutations as described above, and harbour no immunosuppressive activity.

Variants of the SIV mutated ENV proteins according to the invention have at least 70%, preferably at least 80%, more preferably at least 90% of identity with the reference mutated sequence of the SIV ENV protein (SEQ ID NO : 421), and comprises the mutations as described above, and harbour no immunosuppressive activity.

The immunosuppressive domain (ISU) of the lentivirus according to the invention can be delimited by the sequence SEQ ID NO: 6,

xGIVQQQxxLLxxxxxxQxxLxLxxWGxKxLQxRxxA[I/V]E[K/R]YLxDQxxLx (SEQ ID NO: 6)

in which x represents any amino acid.

SEQ ID NO: 6 corresponds to the non mutated ISU domain.

In this SEQ ID NO : 6, "x" (in small letters) is to be considered independently from "X" (in capital letters) used for the first time in SEQ ID NO : 416 of the present invention.

SEQ ID NO: 6 comprises SEQ ID NO: 1.

The most advantageous immunosuppressive domains of the wild type ENV proteins according to the invention comprise the following sequences:

HIV-1 ENV protein comprises the amino acid sequence AVERYLKDQ (SEQ ID NO: 7),

HIV-2 ENV protein comprises the amino acid sequence AIEKYLKDQ (SEQ ID NO: 8), and

SIV ENV protein comprises the amino acid sequence SEQ ID NO: 7 or 8.

When applying the mutations as defined above, the ISU domain looses its immunosuppressive properties.

In said SEQ ID NO: 6, the underlined amino acids are the essential amino acids.

In the invention, the ISU domain, as defined by SEQ ID NO: 6, is the minimal essential domain of the ENV protein according to the invention which harbours an immunosuppressive activity.

Examples of wild type ISU domains:

HIV-1

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLG (SEQ ID NO : 366)

SGIVQQQNNLLRAIEAQQHLLKLTVWGIKQLQARILAVERYLKDQQLLG (SEQ ID NO : 367)

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARVLAVERYLKDQQLLG (SEQ ID NO : 368)

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLG (SEQ ID NO : 369)

SGIVQQQNNLLRAIEAQQQMLQLTVWGIKQLRARVLAVERYLRDQQLLG (SEQ ID NO : 370)

SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERYLRDQQLLG (SEQ ID NO : 371)

SIV

SGIVQQQNNLLKAIEAQQHLLQLSIWGVKQLQARLLAVERYLQDQQILG (SEQ ID NO : 372)

SGIVQQQNNLLRAIEAQQHLLQLSVWGIKQLQARVLAIERYLRDQQILG (SEQ ID NO : 373)

AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVSAIEKYLKDQAQLN (SEQ ID NO : 374)

AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQAQLN (SEQ ID NO : 375)

HIV2

AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKYLKDQAQLN (SEQ ID NO : 376)

AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQALLN (SEQ ID NO : 377)

The localization of an ISU domain can be determined in all ENV proteins of viruses as described in *Benit et al. 2001, Journal of Virology, Vol. 75, No. 23, p.11709-11719*. In a broad meaning, the ISU domain is defined by its structure and its localization, irrespective of the fact that it possesses or not an immunosuppressive activity.

In the invention, the ISU domain refers to a specific domain in which a mutation can affect the immunosuppressive property of the ENV protein.

The immunosuppressive property of the ENV protein is preferably measured using *in vivo* procedures, which are representative of the physiological environment.

The immunosuppressive properties of the mutated ENV proteins according to the invention are measured according to an *in vivo* procedure to assay the immunosuppressive activity of a ENV protein disclosed previously [*Mangeney and Heidmann Proc Natl Acad Sci USA 1998;95: 14920-14925; Mangeney et al. Proc Natl Acad Sci USA, 2007, 104(51):20534-9*].

As a physiological test, this *in vivo* procedure is performed using ENV proteins, or fragment thereof, which are not associated to another component or carrier proteins, such as BSA.

Briefly, a wild-type (wild type lentiviral ENV protein) or modified nucleic acid expressing the protein to be tested (mutated lentiviral ENV protein) is transfected in tumour cell lines such as MCA 205 or Cl8.1 cell lines by known transfection methods. The tumour cells expressing the protein to be tested are then injected especially subcutaneous (s.c.) injection to a host, generally mice. Following said injection, the establishment of tumour or, to the contrary, its rejection, is determined and the tumour area is measured. Tumor establishment was determined by palpation and tumor area (mm^2) was determined by measuring perpendicular tumor diameters. Immunosuppression index is defined as $i= (S_{env}-S_{none})/S_{none}$, wherein S_{env} is the maximum area reached by a tumour expressing an envelope protein and S_{none} is the maximum area reached by a tumour not expressing ENV protein (negative control).

According to an embodiment of the invention, the above defined ratio relative to the immunosuppressive index can be less than 0.2, and can even have a negative value (see Figures 2 and 3).

In vitro assay could be carried out, using high doses of synthetic peptides but they are indirect and less convincing, since the expression "immunosuppressive" is relevant when applied to animals possessing a complete immune system and not to cell lines.

An additional difficulty for the functional characterization of an ISU domain relies on the fact that the ISU carried by the retroviral ENV proteins is a highly structured proteic domain, with trimer formation within the complete ENV proteins (Caffrey M., *Biochimica et Biophysica Acta, 1536:116-122, 2001*; Caffrey et al., *The EMBO Journal, Vol. 17, No. 16, p.4572-4584, 1998*). Such structures are not naturally formed with ISU peptides of limited length, and this is most probably why most studies carried out with peptides provide irrelevant results and/or are dependent on specific coupling of the peptides to carrier proteins (such as BSA, e.g. *Denner et al., Current Science, AIDS 1994, 8:1063-1072*).

As mentioned above, the ENV proteins according to the invention are mutated. This mutation is made *in vitro*. Thus, the mutated ENV proteins according to the invention are isolated, and does not correspond to naturally occurring counterpart.

As mentioned above, the lentiviral mutated ENV proteins are substantially devoid of immunosuppressive properties. This means that the mutated ENV proteins according to the invention have no, or have reduced immunosuppressive properties with respect to the natural non mutated ENV protein from a virus of the same species. For instance, a mutated HIV ENV protein according to the invention has reduced immunosuppressive properties with respect to the wild type HIV ENV protein.

In the invention, the terms "substantially devoid of immunosuppressive properties" means that the mutated ENV proteins according to the invention have an immunosuppressive index less than about 0.2 [*Mangeney and Heidmann Proc Natl Acad Sci USA 1998;95: 14920-14925; Mangeney et al. Proc Natl Acad Sci USA, 2007, 104(51):20534-9*].

In the invention, structures responsible for the antigenicity of the mutated lentiviral ENV protein are essentially preserved.

As intended herein, the expression "structures responsible for antigenicity" relates to structures of the protein which are liable to interact with components of the immune system such as antibodies or membrane receptors of immune cells, in particular T cells.

The mutation(s) within the immunosuppressive domain of the lentiviral ENV proteins is (are) sufficient to decrease the immunosuppressive activity of the mutated lentiviral ENV

protein with respect to the corresponding wild type ENV. However, it might be advantageous that another amino acid be also mutated because it ensures that the structure of the mutated ENV protein is essentially conserved with respect to the corresponding wild type ENV protein.

The mutated lentiviral ENV protein has substantially retained the structure, especially the antigenic structure, e.g., immunogenic determinants, of the original determined lentiviral ENV protein, i.e. the wild type non mutated lentiviral ENV protein.

These properties can be evaluated by measuring the fusion and/or infectious properties of said mutated lentiviral ENV with respect to the same properties in the wild type non mutated lentiviral ENV protein (see example).

Generally speaking, the mutated ENV protein involved in the present invention has an average length of about 700 to about 950 amino acids.

The invention encompasses fragments of the mutated ENV protein as defined above, provided that said fragment:

- comprises at least the sequence SEQ ID NO: 2, as defined above,
- comprises at least 40 amino acids, preferably comprises at least 50 amino acids,
- is substantially devoid of immunosuppressive properties, as defined above,
- preferably, comprises the extracellular parts of the ENV protein,
- retains the structure of the ENV protein from which it derives,
- harbours the same epitopes as the corresponding fragment in the wild type ENV protein.

According to a particular embodiment, the fragment of the mutated ENV protein of the invention can comprise about 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650 or 700 amino acids. These values are given only in an illustrative way, as the man skilled in the art will understand that the fragment can comprise any number of amino acids comprised between 40 and 700.

Advantageously, the fragments according to the invention are such that, while retaining the antigenic structure of the full length mutated ENV protein, and thus of the wild type ENV

protein, they have lost major antigenic regions that are responsible for antigenicity in another region than the region corresponding to the immunosuppressive domain.

The invention also relates to a pharmaceutical composition wherein the active substance is an isolated non naturally occurring mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, as above defined, or fragments thereof.

In a particular embodiment, the invention relates to a pharmaceutical composition as defined above comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

in association with a pharmaceutically acceptable carrier.

The invention relates to a pharmaceutical composition as defined above comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

in association with a pharmaceutically acceptable carrier.

According to a particular embodiment, the invention relates to a pharmaceutical composition as defined above comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G, R,

in association with a pharmaceutically acceptable carrier.

According to a particular embodiment, the invention relates to a pharmaceutical composition as defined above comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G or R,

in association with a pharmaceutically acceptable carrier.

According to another particular embodiment, the invention also relates to a pharmaceutical composition as defined above comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

in association with a pharmaceutically acceptable carrier.

According to another particular embodiment, the invention relates to a pharmaceutical composition as defined above, comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

in association with a pharmaceutically acceptable carrier.

According to another particular embodiment, the invention relates to a pharmaceutical composition as defined above,

wherein

X_a is R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is R, or

X_a is R, and X_b is R.

According to another particular embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the following amino acid sequences :

A-I-E-K-X_a-X_b-X-DQ (SEQ ID NO: 422),

A-I-E-R-X_a-X_b-X-DQ (SEQ ID NO: 423),

A-V-E-K-X_a-X_b-X-DQ (SEQ ID NO: 424),

A-V-E-R-X_a-X_b-X-DQ (SEQ ID NO: 425).

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein the resulting immunosuppressive domain, contained in the mutated lentiviral protein, comprises the amino acid sequence of the list consisting of: SEQ ID NO :9 to SEQ ID NO :37.

In the invention "SEQ ID NO : 9 to SEQ ID NO :37" encompass SEQ ID NO : 9, SEQ ID NO : 10, SEQ ID NO : 11, SEQ ID NO : 12, SEQ ID NO : 13, SEQ ID NO : 14, SEQ ID NO : 15, SEQ ID NO : 16, SEQ ID NO : 17, SEQ ID NO : 18, SEQ ID NO : 19, SEQ ID NO : 20, SEQ ID NO : 21, SEQ ID NO : 22, SEQ ID NO : 23, SEQ ID NO : 24, SEQ ID NO : 25, SEQ ID NO : 26, SEQ ID NO : 27, SEQ ID NO : 28, SEQ ID NO : 29, SEQ ID NO : 30, SEQ ID NO : 31, SEQ ID NO : 32, SEQ ID NO : 33, SEQ ID NO : 34, SEQ ID NO : 35, SEQ ID NO : 36 and SEQ ID NO : 37.

The correspondence is the following one:

AVERALKD	SEQ ID NO : 9
AVERFLKD	SEQ ID NO : 10
AVERGLKD	SEQ ID NO : 11
AVERLLKD	SEQ ID NO : 12
AVERRLKD	SEQ ID NO : 13

AVERYAKD	SEQ ID NO : 14
AVERYFKD	SEQ ID NO : 15
AVERYGKD	SEQ ID NO : 16
AVERYRKD	SEQ ID NO : 17
AVERAAKD	SEQ ID NO : 18

AVERAFKD	SEQ ID NO : 19
AVERAGKD	SEQ ID NO : 20
AVERARKD	SEQ ID NO : 21
AVERFAKD	SEQ ID NO : 22
AVERFFKD	SEQ ID NO : 23
AVERFGKD	SEQ ID NO : 24
AVERFRKD	SEQ ID NO : 25
AVERGAKD	SEQ ID NO : 26
AVERGFKD	SEQ ID NO : 27
AVERGGKD	SEQ ID NO : 28

AVERGRKD	SEQ ID NO : 29
AVERLAKD	SEQ ID NO : 30
AVERLFKD	SEQ ID NO : 31
AVERLGKD	SEQ ID NO : 32
AVERLRKD	SEQ ID NO : 33
AVERRAKD	SEQ ID NO : 34
AVERRFKD	SEQ ID NO : 35
AVERRGKD	SEQ ID NO : 36
AVERRRKD	SEQ ID NO : 37

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein the resulting immunosuppressive domain, contained in the mutated lentiviral protein, comprises the amino acid sequence of the list consisting of: SEQ ID NO :38 to SEQ ID NO :66.

In the invention "SEQ ID NO : 38 to SEQ ID NO :66" encompass SEQ ID NO : 38, SEQ ID NO : 39, SEQ ID NO : 40, SEQ ID NO : 41, SEQ ID NO : 42, SEQ ID NO : 43, SEQ ID NO : 44, SEQ ID NO : 45, SEQ ID NO : 46, SEQ ID NO : 47, SEQ ID NO : 48, SEQ ID NO : 49, SEQ ID NO : 50, SEQ ID NO : 51, SEQ ID NO : 52, SEQ ID NO : 53, SEQ ID NO : 54, SEQ ID NO : 55, SEQ ID NO : 56, SEQ ID NO : 57, SEQ ID NO : 58, SEQ ID NO : 59, SEQ ID NO : 60, SEQ ID NO : 61, SEQ ID NO : 62, SEQ ID NO : 63, SEQ ID NO : 64, SEQ ID NO : 65 and SEQ ID NO : 66.

The correspondence is the following one:

AIEKALKD	SEQ ID NO : 38
AIEKFLKD	SEQ ID NO : 39
AIEKGLKD	SEQ ID NO : 40
AIEKLLKD	SEQ ID NO : 41
AIEKRLKD	SEQ ID NO : 42

AIEKYAKD	SEQ ID NO : 43
AIEKYFKD	SEQ ID NO : 44
AIEKYGKD	SEQ ID NO : 45
AIEKYRKD	SEQ ID NO : 46
AIEKAAKD	SEQ ID NO : 47
AIEKAFKD	SEQ ID NO : 48

AIEKAGKD	SEQ ID NO : 49
AIEKARKD	SEQ ID NO : 50
AIEKFAKD	SEQ ID NO : 51
AIEKFFKD	SEQ ID NO : 52
AIEKFGKD	SEQ ID NO : 53
AIEKFRKD	SEQ ID NO : 54
AIEKGAKD	SEQ ID NO : 55
AIEKGFKD	SEQ ID NO : 56
AIEKGGKD	SEQ ID NO : 57

AIEKGRKD	SEQ ID NO : 58
AIEKLAKD	SEQ ID NO : 59
AIEKLFKD	SEQ ID NO : 60
AIEKLGKD	SEQ ID NO : 61
AIEKLRKD	SEQ ID NO : 62
AIEKRAKD	SEQ ID NO : 63
AIEKRFKD	SEQ ID NO : 64
AIEKRGKD	SEQ ID NO : 65
AIEKRRKD	SEQ ID NO : 66

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein the resulting immunosuppressive domain, contained in the mutated lentiviral protein, comprises the amino acid sequence of the list consisting of: SEQ ID NO : 67 to SEQ ID NO : 95.

In the invention "SEQ ID NO : 67 to SEQ ID NO :95" encompass SEQ ID NO : 67, SEQ ID NO : 68, SEQ ID NO : 69, SEQ ID NO : 70, SEQ ID NO : 71, SEQ ID NO : 72, SEQ ID NO : 73, SEQ ID NO : 74, SEQ ID NO : 75, SEQ ID NO : 76, SEQ ID NO : 77, SEQ ID NO : 78, SEQ ID NO : 79, SEQ ID NO : 80, SEQ ID NO : 81, SEQ ID NO : 82, SEQ ID NO : 83, SEQ ID NO : 84, SEQ ID NO : 85, SEQ ID NO : 86, SEQ ID NO : 87, SEQ ID NO : 88, SEQ ID NO : 89, SEQ ID NO : 90, SEQ ID NO : 91, SEQ ID NO : 92, SEQ ID NO : 93, SEQ ID NO : 94 and SEQ ID NO : 95.

The correspondence is the following one:

AIERALKD	SEQ ID NO : 67
AIERFLKD	SEQ ID NO : 68
AIERGLKD	SEQ ID NO : 69
AIERLLKD	SEQ ID NO : 70
AIERRLKD	SEQ ID NO : 71
AIERYAKD	SEQ ID NO : 72
AIERYFKD	SEQ ID NO : 73
AIERYGKD	SEQ ID NO : 74
AIERYRKD	SEQ ID NO : 75

AIERAAKD	SEQ ID NO : 76
AIERAFKD	SEQ ID NO : 77
AIERAGKD	SEQ ID NO : 78
AIERARKD	SEQ ID NO : 79
AIERFAKD	SEQ ID NO : 80
AIERFFKD	SEQ ID NO : 81
AIERFGKD	SEQ ID NO : 82

AIERFRKD	SEQ ID NO : 83
AIERGAKD	SEQ ID NO : 84
AIERGFKD	SEQ ID NO : 85
AIERGGKD	SEQ ID NO : 86
AIERGRKD	SEQ ID NO : 87
AIERLAKD	SEQ ID NO : 88
AIERLFKD	SEQ ID NO : 89

AIERLGKD	SEQ ID NO : 90
AIERLRKD	SEQ ID NO : 91
AIERRAKD	SEQ ID NO : 92
AIERRFKD	SEQ ID NO : 93
AIERRGKD	SEQ ID NO : 94
AIERRRKD	SEQ ID NO : 95

As mentioned above, the previous ENV proteins having their ISU comprising the above sequence are devoid of immunosuppressive properties.
Thus, in other words, any ENV protein of human or simian lentivirus having in their ISU an amino acid sequence comprising of the sequences SEQ ID NO: 9 to 95, is devoid of immunosuppressive properties.
In other words, a simian or human lentiviral ENV protein comprising, within its ISU domain, an amino acid sequence selected from SEQ ID NO: 9 to 95 is devoid of immunosuppressive properties.

In particular, the invention relates to a pharmaceutical composition as defined above, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences :

SEQ ID NO : 13, SEQ ID NO : 42, SEQ ID NO : 71,
SEQ ID NO : 9 to 12,
SEQ ID NO : 14 to 41,
SEQ ID NO : 43 to 70, and
SEQ ID NO : 72 to 95.

In particular, the invention relates to a pharmaceutical composition as defined above, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences :

SEQ ID NO : 13, SEQ ID NO : 42, SEQ ID NO : 71,
SEQ ID NO : 9, 11, 15 to 21, 23 to 29, 31 to 38, 40, 44 to 50, 52 to 58, 60 to 67, 69, 73 to 79, 81 to 87, 89 to 95.

In the invention, the fragments of the mutated ENV proteins according to the invention comprise or consist of the following sequences: SEQ ID NO: 67 to 211.
These fragments are also devoid of immunosuppressive properties.

However, these fragments retain the structure and the antigenicity of the corresponding immunosuppressive domain that is not mutated, i.e. the wild type immunosuppressive domain.

In the invention, the fragments of the mutated ENV proteins according to the invention comprise or consist of the following sequences: SEQ ID NO: 96 to 211.

The correspondences are as follows

SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERALKDQQLLG	SEQ ID NO : 96
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERFLKDQQLLG	SEQ ID NO : 97
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERGLKDQQLLG	SEQ ID NO : 98
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERLLKDQQLLG	SEQ ID NO : 99
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERRLKDQQLLG	SEQ ID NO : 100
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERYAKDQQLLG	SEQ ID NO : 101
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERYFKDQQLLG	SEQ ID NO : 102
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERYGKDQQLLG	SEQ ID NO : 103
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERYRKDQQLLG	SEQ ID NO : 104
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERAAKDQQLLG	SEQ ID NO : 105
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERAFKDQQLLG	SEQ ID NO : 106
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERAGKDQQLLG	SEQ ID NO : 107
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERARKDQQLLG	SEQ ID NO : 108
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERFAKDQQLLG	SEQ ID NO : 109
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERFFKDQQLLG	SEQ ID NO : 110
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERFGKDQQLLG	SEQ ID NO : 111
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERFRKDQQLLG	SEQ ID NO : 112
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERGAKDQQLLG	SEQ ID NO : 113

SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERGF KDQQLLG	SEQ ID NO : 114
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERGG KDQQLLG	SEQ ID NO : 115
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERGR KDQQLLG	SEQ ID NO : 116
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERLA KDQQLLG	SEQ ID NO : 117
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERLF KDQQLLG	SEQ ID NO : 118
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERLG KDQQLLG	SEQ ID NO : 119
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERLR KDQQLLG	SEQ ID NO : 120
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERRA KDQQLLG	SEQ ID NO : 121
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERRF KDQQLLG	SEQ ID NO : 122
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERRG KDQQLLG	SEQ ID NO : 123
SGIVQQQSNLLRAIQARQHMLQLTVWGIKQLQARVLAVERRR KDQQLLG	SEQ ID NO : 124

AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKA LKDQAQLNSWGCAFRQ	SEQ ID NO : 125
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKF LKDQAQLNSWGCAFRQ	SEQ ID NO : 126
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKG LKDQAQLNSWGCAFRQ	SEQ ID NO : 127
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKL LKDQAQLNSWGCAFRQ	SEQ ID NO : 128
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKR LKDQAQLNSWGCAFRQ	SEQ ID NO : 129
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKY AKDQAQLNSWGCAFRQ	SEQ ID NO : 130
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKY FKDQAQLNSWGCAFRQ	SEQ ID NO : 131
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKY GKDQAQLNSWGCAFRQ	SEQ ID NO : 132
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKY RKDQAQLNSWGCAFRQ	SEQ ID NO : 133
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKA AKDQAQLNSWGCAFRQ	SEQ ID NO : 134
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKA FKDQAQLNSWGCAFRQ	SEQ ID NO : 135
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKA GKDQAQLNSWGCAFRQ	SEQ ID NO : 136

AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKA RKDQAQLNSWGCAFRQ	SEQ ID NO : 137
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKF AKDQAQLNSWGCAFRQ	SEQ ID NO : 138
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKF FKDQAQLNSWGCAFRQ	SEQ ID NO : 139
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKF GKDQAQLNSWGCAFRQ	SEQ ID NO : 140
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKF RKDQAQLNSWGCAFRQ	SEQ ID NO : 141
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKG AKDQAQLNSWGCAFRQ	SEQ ID NO : 142
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKG FKDQAQLNSWGCAFRQ	SEQ ID NO : 143
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKG GKDQAQLNSWGCAFRQ	SEQ ID NO : 144
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKG RKDQAQLNSWGCAFRQ	SEQ ID NO : 145
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKL AKDQAQLNSWGCAFRQ	SEQ ID NO : 146
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKL FKDQAQLNSWGCAFRQ	SEQ ID NO : 147
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKL GKDQAQLNSWGCAFRQ	SEQ ID NO : 148
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKL RKDQAQLNSWGCAFRQ	SEQ ID NO : 149
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKR AKDQAQLNSWGCAFRQ	SEQ ID NO : 150
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKR FKDQAQLNSWGCAFRQ	SEQ ID NO : 151
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKR GKDQAQLNSWGCAFRQ	SEQ ID NO : 152
AGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKR RKDQAQLNSWGCAFRQ	SEQ ID NO : 153

AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKA LQDQARLNSWGCAFRQ	SEQ ID NO : 154
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKF LQDQARLNSWGCAFRQ	SEQ ID NO : 155
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKG LQDQARLNSWGCAFRQ	SEQ ID NO : 156
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKL LQDQARLNSWGCAFRQ	SEQ ID NO : 157
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKR LQDQARLNSWGCAFRQ	SEQ ID NO : 158
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKY AQDQARLNSWGCAFRQ	SEQ ID NO : 159

AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKY FQDQARLNSWGCAFRQ	SEQ ID NO : 160
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKY GQDQARLNSWGCAFRQ	SEQ ID NO : 161
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKY RQDQARLNSWGCAFRQ	SEQ ID NO : 162
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKA AQDQARLNSWGCAFRQ	SEQ ID NO : 163
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKA FQDQARLNSWGCAFRQ	SEQ ID NO : 164
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKA GQDQARLNSWGCAFRQ	SEQ ID NO : 165
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKA RQDQARLNSWGCAFRQ	SEQ ID NO : 166
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKF AQDQARLNSWGCAFRQ	SEQ ID NO : 167
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKF FQDQARLNSWGCAFRQ	SEQ ID NO : 168
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKF GQDQARLNSWGCAFRQ	SEQ ID NO : 169
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKF RQDQARLNSWGCAFRQ	SEQ ID NO : 170
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKG AQDQARLNSWGCAFRQ	SEQ ID NO : 171
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKG FQDQARLNSWGCAFRQ	SEQ ID NO : 172
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKG GQDQARLNSWGCAFRQ	SEQ ID NO : 173
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKG RQDQARLNSWGCAFRQ	SEQ ID NO : 174
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKL AQDQARLNSWGCAFRQ	SEQ ID NO : 175
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKL FQDQARLNSWGCAFRQ	SEQ ID NO : 176
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKL GQDQARLNSWGCAFRQ	SEQ ID NO : 177
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKL RQDQARLNSWGCAFRQ	SEQ ID NO : 178
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKR AQDQARLNSWGCAFRQ	SEQ ID NO : 179
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKR FQDQARLNSWGCAFRQ	SEQ ID NO : 180
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKR GQDQARLNSWGCAFRQ	SEQ ID NO : 181
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQARVTAIEKR RQDQARLNSWGCAFRQ	SEQ ID NO : 182

AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKA LKDQAQLNAWGCAFRQ	SEQ ID NO : 183
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKF LKDQAQLNAWGCAFRQ	SEQ ID NO : 184
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKG LKDQAQLNAWGCAFRQ	SEQ ID NO : 185
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKL LKDQAQLNAWGCAFRQ	SEQ ID NO : 186
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKR LKDQAQLNAWGCAFRQ	SEQ ID NO : 187
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKY AKDQAQLNAWGCAFRQ	SEQ ID NO : 188
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKY FKDQAQLNAWGCAFRQ	SEQ ID NO : 189
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKY GKDQAQLNAWGCAFRQ	SEQ ID NO : 190
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKY RKDQAQLNAWGCAFRQ	SEQ ID NO : 191
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKA AKDQAQLNAWGCAFRQ	SEQ ID NO : 192
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKA FKDQAQLNAWGCAFRQ	SEQ ID NO : 193
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKA GKDQAQLNAWGCAFRQ	SEQ ID NO : 194
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKA RKDQAQLNAWGCAFRQ	SEQ ID NO : 195
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKF AKDQAQLNAWGCAFRQ	SEQ ID NO : 196
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKF FKDQAQLNAWGCAFRQ	SEQ ID NO : 197
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKF GKDQAQLNAWGCAFRQ	SEQ ID NO : 198
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKF RKDQAQLNAWGCAFRQ	SEQ ID NO : 199
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKG AKDQAQLNAWGCAFRQ	SEQ ID NO : 200
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKG FKDQAQLNAWGCAFRQ	SEQ ID NO : 201
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKG GKDQAQLNAWGCAFRQ	SEQ ID NO : 202
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKG RKDQAQLNAWGCAFRQ	SEQ ID NO : 203
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKL AKDQAQLNAWGCAFRQ	SEQ ID NO : 204
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKL FKDQAQLNAWGCAFRQ	SEQ ID NO : 205
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKL	SEQ ID NO : 206

GKDQAQLNAWGCAFRQ	
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKL RKDQAQLNAWGCAFRQ	SEQ ID NO : 207
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKR AKDQAQLNAWGCAFRQ	SEQ ID NO : 208
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKR FKDQAQLNAWGCAFRQ	SEQ ID NO : 209
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKR GKDQAQLNAWGCAFRQ	SEQ ID NO : 210
AGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKR RKDQAQLNAWGCAFRQ	SEQ ID NO : 211

In particular, the invention relates to a pharmaceutical composition as defined above, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences : SEQ ID NO : 96, 98, 100, 102 to 108, 110 to 116, 118 to 125, 127, 129, 131 to 137, 139 to 145, 147 to 154, 156, 158, 160 to 166, 168 to 174, 176 to 183, 185, 187, 189 to 195, 197 to 203, 205 to 211.

Advantageously, the invention relates to the pharmaceutical composition as defined above, wherein said mutated protein consists of one of the following sequences SEQ ID NO : 212 to 269

HIV-1 LAI

MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERALKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW	SEQ ID NO : 212

EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERFLKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 213
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERGLKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 214
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK	SEQ ID NO : 215

NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERLLKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERRLKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 216
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT	SEQ ID NO : 217

LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERYAKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERYFKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 218
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERYGKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL	SEQ ID NO : 219

DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERYR**KDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 220
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERAA**KDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 221
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY	SEQ ID NO : 222

YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERAFKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERAGKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 223
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV	SEQ ID NO : 224

QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERARKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERFAKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 225
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV	SEQ ID NO : 226

QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERFFKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERFGKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 227
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERFRKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW	SEQ ID NO : 228

EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERGAKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 229
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERGFKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 230
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK	SEQ ID NO : 231

NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERGGKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERGRKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 232
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT	SEQ ID NO : 233

LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERLAKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERLFKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 234
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERLGKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL	SEQ ID NO : 235

DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERLRKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 236
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERRAKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 237
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY	SEQ ID NO : 238

YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERRFKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERRGKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	SEQ ID NO : 239
MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVY YGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDP NPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPC VKLTPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIK NCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTS VITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVS TVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIV	SEQ ID NO : 240

QLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQA HCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIV THSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTIT LPCRIKQFINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDG GNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGARSMTLTV QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL **AVERRRKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQI WNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLEL DKWASLWNWFNITNWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRL VNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGW EALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIE VVQGACRAIRHIPRRIRQGLERILL	

HIV-BH10

MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERA** **LKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 241
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI	SEQ ID NO : 242

KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERF** **LKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERG** **LKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 243
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERL** **LKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS	SEQ ID NO : 244

LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERR** **LKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 245
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERY** **AKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 246
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV	SEQ ID NO : 247

YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERY** **FKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMT WMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASL WNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVRQ GYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSLA LIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYW WNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAY RAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERY** **GKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 248
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS	SEQ ID NO : 249

VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERY** **RKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERA** **AKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 250
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL	SEQ ID NO : 251

LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERA** **FKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMT WMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASL WNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVRQ GYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSLA LIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYW WNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAY RAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERA** **GKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 252
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERA** **RKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY	SEQ ID NO : 253

WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERF** **AKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 254
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERF** **FKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMT WMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASL WNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVRQ GYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSLA LIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYW WNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAY RAIRHIPRRIRQGLERILL	SEQ ID NO : 255
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI	SEQ ID NO : 256

STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERF** **GKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERF** **RKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 257
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI	SEQ ID NO : 258

KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERG** **AKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERG** **FKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMT WMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASL WNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVRQ GYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSLA LIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYW WNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAY RAIRHIPRRIRQGLERILL	SEQ ID NO : 259
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERG** **GKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS	SEQ ID NO : 260

LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERG** **RKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 261
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERL** **AKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 262
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV	SEQ ID NO : 263

YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERL** **FKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMT WMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASL WNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVRQ GYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSLA LIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYW WNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAY RAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERL** **GKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 264
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS	SEQ ID NO : 265

VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERL** **RKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERR** **AKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 266
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL	SEQ ID NO : 267

LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERR** **FKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMT WMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASL WNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVRQ GYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSLA LIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYW WNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAY RAIRHIPRRIRQGLERILL	
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERR** **GKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	SEQ ID NO : 268
MRVKEKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTV YYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD PNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP CVKLTPLCVSLKCTDLKNDTNTNSSSGRMIMEKGEIKNCSFNI STSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQAC PKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCT HGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQS VEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS RAKWNNTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFN CGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRI KQIINMWQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSN NESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR RVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQL LSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**AVERR** **RKDQ**QLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM TWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWAS LWNWFNITNWLWYIKLFIMIVGGLVGLRIVFAVLSVVNRVR QGYSPLSFQTHLPIPRGPDRPEGIEEEGGERDRDRSIRLVNGSL ALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKY	SEQ ID NO : 269

WWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG AYRAIRHIPRRIRQGLERILL	

The invention also encompasses the variants of the above sequences, harbouring the above mentioned mutations, and conferring to said variant a lack of immunosuppressive properties.

In particular, the invention relates to a pharmaceutical composition as defined above, wherein said isolated mutated human or simian lentiviral ENV protein consists of one of the amino acid sequences : SEQ ID NO : 212, 214, 216, 218 to 224, 226 to 232, 234 to 241, 243, 245, 247 to 253, 255 to 261, 263 to 269.

The invention also relates to a pharmaceutical composition as defined above, wherein said mutated protein comprises additional mutations either downstream the C-terminal end of the sequence SEQ ID NO : 416 or upstream the N-terminal end of SEQ ID NO : 416.
These additional mutations can be advantageous to maintain the three-dimensional structure of the immunosuppressive domain and of the ENV protein (see details concerning the membrane expression of the ENV protein [see figure 4 and example] and concerning infectivity [see figure 5 and example]).

In a particular embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said mutated protein comprises an additional mutation in one at least of the amino acids at positions 29, 36 and 37 of SEQ ID NO: 426 :
A[I/V]E[K/R]$X_aX_bX_1$DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VP$X_cX_{10}Z_1Z_2Z_3Z_4Z_5$ X_dX_e[S/T] (SEQ ID NO: 426)
wherein

X_a and X_b are as defined above,

X_1 to X_{10} represent any amino acid,

Z_1 to Z_5 represent no amino acid or any amino acid, independently from each other such that

- X_c is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y, or deleted, preferably A, D, or N,

- X_d is A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, Y, W, or deleted, preferably A, G, S or Y,
- X_e is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, T, V, Y, W, or deleted, preferably A, D or N.

This sequence contains the following amino acid sequence A[I/V]E[K/R]$X_aX_bX_1$DQ (SEQ ID NO : 416) elongated on its C-terminal end in which additional mutations are present.
It is to be noted that "X_1" in the above mentioned sequence SEQ ID NO : 426 has the same meaning as "X" in SEQ ID NO : 416.

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, said mutated protein comprising the amino acid sequences of the group consisting of SEQ ID NO: 271 to SEQ ID NO: 283.

SEQ ID NO: 271, contains the mutations Y41R, K72A:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPWNASWSNASLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 272, contains the mutations Y41R, K72G:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPWNASWSNGSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 273, contains the mutations Y41R, K72S:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPWNASWSNSSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 274, contains the mutations Y41R, W65D:

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPDNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 275, contains the mutations Y41R, W65A:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPANASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 276, contains the mutations Y41R, W65N:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPNNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 277, contains the mutations Y41R, S73D:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPWNASWSNKDLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 278, contains the mutations Y41R, S73A:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPWNASWSNKALEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 279, contains the mutations Y41R, S73N:
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG
KLICTTAVPWNASWSNKNLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK
NEQEL.

SEQ ID NO: 280, contains the mutations Y41R, K72Y:

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG KLICTTAVPWNASWSNYSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK NEQEL.

SEQ ID NO: 281, contains the mutations R40A, Y41R, K72A: SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVEARLKDQQLLGIWGCSG KLICTTAVPWNASWSNASLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK NEQEL.

SEQ ID NO: 282, contains the mutations Y41R, K72A, S73A: SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG KLICTTAVPWNASWSNAALEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK NEQEL.

SEQ ID NO: 283, contains the mutations Y41R, W65A, K72A, S73A: SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSG KLICTTAVPANASWSNAALEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEK NEQEL.

The mutations in the above mutated peptides are indicated by the amino acid residues which are bolded and underlined.

In another aspect, the invention relates to a pharmaceutical composition as defined above, comprising an additional mutation of one at least of the amino acids X_{11}, X_{12}, X_{13} and X_{14} in the following sequence (containing the above defined SEQ ID NO: 416 sequence) :

$X_{11}X_{12}$ $X_{13}X_{14}$I LA[I/V]E[K/R]$X_aX_bX_1$DQ (SEQ ID NO: 428),

wherein

X_1 represents any amino acid,

Xa and Xb are as defined above,

X_{11} is :

- either deleted,
- or A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, Y or W, in particular A, G or R,

and/or

X_{12} is :

- either deleted,
- or A, C, D, E, F, G, H, I, K, L, M, N, P, R, S, T, V, Y or W, in particular A, G or R,

and/or

X_{13} is :

- either deleted,
- or C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y or W, in particular R or G,

and/or

X_{14} is :

- either deleted,
- or A, C, D, E, F, G, H, I, K, L, M, N, P, Q, S, T, V, Y or W, in particular A or G.

This sequence contains the following amino acid sequence A[I/V]E[K/R]$X_aX_bX_1$DQ (SEQ ID NO : 416) elongated on its N-terminal end in which additional mutations are present.
It is to be noted that "X_1" in SEQ ID NO : 428 has exactly the same meaning as "X" in SEQ ID NO : 416.

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said mutated lentiviral protein, said variant or said fragment harbour a three-dimensional structure similar to the structure of the natural non mutated lentiviral ENV protein, non mutated lentiviral ENV variant or non mutated lentiviral ENV fragment thereof.
The skilled person knows how to measure the antigenicity, by using standard proceedings.

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said mutated lentiviral protein, said variant or said fragment are expressed at the plasma membrane at a level substantially identical to the expression at the plasma membrane of the natural non mutated lentiviral ENV protein, non mutated lentiviral ENV variant or non mutated lentiviral ENV fragment thereof.
The membrane expression of the lentiviral ENV protein according to the invention can be measured by any techniques allowing determination of a plasma membrane protein. For instance, cells can be transfected with an expression vector allowing the expression of the

mutated lentiviral ENV protein according to the invention. Cells are then incubated with an antibody recognizing specifically the extracellular part of said lentiviral mutated ENV protein. The complex (antibody/ENV protein) is detected by another antibody, and the complex can be quantified by flow cytometry (see for instance figure 4, and example).
If no complex is detected, the mutated ENV protein is not expressed at the plasma membrane. On the contrary, if the protein is expressed, this means that the mutated ENV protein is expressed at the plasma membrane.

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said mutated lentiviral ENV protein is such that a lentivirus, or a pseudotype, expressing said mutated lentiviral ENV protein, instead of the non mutated ENV protein, has a viral titer similar to the viral titer of said lentivirus, or pseudotype, expressing the non mutated lentiviral protein.
Viral titer is measured according to a commonly used protocol, and as described in the example (see figure 5).

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said mutated lentiviral ENV protein is a HIV-1 lentiviral protein consisting of the amino acid sequences SEQ ID NO: 284 to SEQ ID NO: 292.

SEQ ID NO: 284 Y41R	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERRLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP

	DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 285 Y41R, K72A	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERRLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNASLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 286 Y41R, K72G	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERRLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNGSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 287 Y41R, K72S	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP

	KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERRLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNSSLEQIWNNMTWMEWDREINNYTS LIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYIK IFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGPD RPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRLR DLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVSL LNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 288 Y41G	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERGLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 289 Y41L	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL

	RAIEAQQHLLQLTVWGIKQLQARIL**AVERLLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 290 Y41A	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERALKDQ**QLLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 291 Y41F	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERFLKDQ**QLLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL
SEQ ID NO: 292	MRVKEKYQHLWRWGWKWGTMLLGILMICSATEKLWVTVYY

L42R	GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNP QEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKL TPLCVSLKCTDLGNATNTNSSNTNSSSGEMMMEKGEIKNCSFN ISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQACP KVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGI RPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINC TRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWN ATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFY CNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQ EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGG GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV GIGALFLGFLGAAGSTMGARSMTLTVQARQLLSGIVQQQNNLL RAIEAQQHLLQLTVWGIKQLQARIL**AVERYRKDQ**QLLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYT SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYI KIFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRL RDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS LLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQGLERILL

Also, the following proteins are advantageous in the invention:

SEQ ID NO: 293 SIV MM251 L42R	MGCLGNQLLIAILLLSVYGIYCTQYVTVFYGVPAWRNATIPLFC ATKNRDTWGTTQCLPDNGDYSELALNVTESFDAWENTVTEQA IEDVWQLFETSIKPCVKLSPLCITMRCNKSETDRWGLTKSSTTIT TAAPTSAPVSEKIDMVNETSSCIAQNNCTGLEQEQMISCKFTMT GLKRDKTKEYNETWYSTDLVCEQGNSTDNESRCYMNHCNTS VIQESCDKHYWDTIRFRYCAPPGYALLRCNDTNYSGFMPKCSK VVVSSCTRMMETQTSTWFGFNGTRAENRTYIYWHGRDNRTIIS LNKYYNLTMKCRRPGNKTVLPVTIMSGLVFHSQPINDRPKQA WCWFGGKWKDAIKEVKQTIVKHPRYTGTNNTDKINLTAPGGG DPEVTFMWTNCRGEFLYCKMNWFLNWVEDRDVTTQRPKERH RRNYVPCHIRQIINTWHKVGKNVYLPPREGDLTCNSTVTSLIAN IDWTDGNQTSITMSAEVAELYRLELGDYKLVEITPIGLAPTDVK RYTTGGTSRNKRGVFVLGFLGFLATAGSAMGAASLTLTAQSR TLLAGIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT**AIE** **KYRKDQ**AQLNAWGCAFRQVCHTTVPWPNASLTPDWNNDTW QEWERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDVFG NWFDLASWIKYIQYGIYVVVGVILLRIVIYIVQMLAKLRQGYRP VFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWPWQI EYIHFLIRQLIRLLTWLFSNCRTLLSRAYQILQPILQRLSATLRRV REVLRTELTYLQYGWSYFHEAVQAGWRSATETLAGAWRDLW ETLRRGGRWILAIPRRIRQGLELTLL

SEQ ID NO: 294 HIV2 L42R	MEPGRNQLFVVILLTSACLVYCSQYVTVFYGIPAWKNASIPLFC ATKNRDTWGTIQCLPDNDDYQEIILNVTEAFDAWNNTVTEQA VEDVWHLFETSIKPCVKLTPLCVAMNCSRVQGNTTTPNPRTSS STTSRPPTSAASIINETSNCIENNTCAGLGYEEMMQCEFNMKGL

	EQDKKRRYKDTWYLEDVVCDNTTAGTCYMRHCNTSIIKESCD KHYWDAMRFRYCAPPGFALLRCNDTNYSGFEPKCTKVVAASC TRMMETQTSTWFGFNGTRAENRTYIYWHGRDNRTIISLNKYY NLTMRCKRPGNKTVLPITLMSGLVFHSQPINTRPRQAWCRFGG RWREAMQEVKQTLVQHPRYKGINDTGKINFTKPGAGSDPEVA FMWTNCRGEFLYCNMTWFLNWVEDKNQTRRNYCHIKQIINT WHKVGKNVYLPPREGELACESTVTSIIANIDIDKNRTHTNITFS AEVAELYRLELGDYKLIEITPIGFAPTDQRRYSSTPVRNKRGVF VLGFLGFLATAGSAMGARSLTLSAQSRTLLAGIVQQQQQLLDV VKRQQEMLRLTVWGTKNLQARVT**AIEKYRKHQ**AQLNSWGC AFRQVCHTTVPWVNDSLSPDWKNMTWQEWEKQVRYLEANIS QSLEEAQIQQEKNMYELQKLNSWDILGNWFDLTSWVKYIQYG VHIVVGIIALRIAIYVVQLLSRFRKGYRPVFSSPPGYLQQIHIHK DRGQPANEGTEEDVGGDSGYDLWPWPINYVQFLIHLLTRLLIG LYNICRDLLSKNSPTRRLISQSLTAIRDWLRLKAAQLQYGCEWI QEAFQAFARTTRETLAGAWGWLWEAARRIGRGILAVPRRIRQ GAELALL

Advantageously: the mutated lentiviral proteins are

1 - SEQ ID NO: 284 to 294; these mutated ENV proteins having substantially no immunosuppressive properties

advantageously,

2- SEQ ID NO: 284 to SEQ ID NO: 292; these mutated ENV proteins having substantially no immunosuppressive properties and being highly expressed at the plasma membrane,

more advantageously,

3- SEQ ID NO: 284 to SEQ ID NO: 291; these mutated ENV proteins having substantially no immunosuppressive properties, being highly expressed at the plasma membrane and conferring to a virus expressing them a medium or high viral titer,

in particular

4- Y41F (SEQ ID NO: 291), Y41L (SEQ ID NO: 289), Y41A (SEQ ID NO: 290); these mutated ENV proteins having substantially no immunosuppressive properties, being highly expressed at the plasma membrane and confers to a virus expressing them a high viral titer.

As mentioned above “confering to a virus expressing them a medium or high viral titer” means that, when the sequence of the wild type ENV protein is substituted by the sequence of the mutated ENV in the lentiviral or pseudotype retrovirus, the virus thus expresses a mutated lentiviral ENV protein, along with other wild type viral proteins (GAG, PRO, POL), said mutated ENV protein conferring to the virus the ability to enter in its target cell:

- either at a level comparable or higher to the ability of the wild type virus, i.e. high ability
- or at a lower level compared to the ability of the wild type virus, i.e. medium or low ability.

The ability to enter in the target cell can be measured by the viral load. Viral load is a measure of the amount of target cells that can be infected by a given amount (1 mL) of virus (see figure 5 and example).

The invention also relates to a pharmaceutical composition comprising a nucleic acid molecule coding for a mutated lentiviral ENV protein, or variant of said protein, or fragments thereof, as defined above, in association with a pharmaceutically acceptable carrier.

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said nucleic acid is comprised in a vector, said vector comprising means allowing the expression of said mutated lentiviral ENV protein, or variant of said protein, or fragments thereof.

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said nucleic acid is comprised in a vector, said nucleic acid being placed under the control of sequences that allow the expression of said mutated lentiviral ENV protein, or variant of said protein, or fragments thereof.

In another embodiment, the invention relates to a pharmaceutical composition, as defined above, in particular as a vaccine, comprising a DNA molecule coding for said mutated lentiviral ENV protein, or variant of said protein, or fragments thereof.

DNA vaccines expressing ENV proteins can be produced as described in Bellier et al., (DNA vaccines expressing retrovirus-like particles are efficient immunogens to induce neutralizing antibodies, *Vaccine*, 27(42):5772-80, 2009).

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, said vector being chosen among an eukaryotic or

prokaryotic expression vector , in particular an eukaryotic vector which is a viral vector, in particular a pox vector, such as a fowlpox, a canarypox, or a MVA (modified vaccinia virus Ankara) vector, an adenoviral vector, a lentiviral vector, a measles vector, a Sendaï virus or a CMV (cytomegalovirus) vector.

In another advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, further comprising at least one nucleotide molecule coding for a GAG and/or a PRO and/or a POL protein and/or a mutated NEF protein substantially devoid of immunosuppressive properties, of a lentivirus, preferably a lentivirus of the same origin as the mutated lentiviral ENV protein.
The advantageous mutated Nef protein contains a substitution at position 93, as described in the international application WO 2006/018289 (Inventors : Renard M., Mangeney M. and Heidmann T.) and a deletion of the N-terminus of the protein involved in its myristoylation.
GAG expression will produce virus like particles (VLPs) which are particularly advantageous for a vaccine, in particular if the ENV protein is associated with the VLP (Guerbois et al., *Virology,* 388:191-203, 2009).

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains said at least one nucleic acid molecule coding for a GAG protein and/or a PRO protein and/or a POL protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains all said at least one nucleic acid molecule coding for a GAG protein and/or a PRO protein and/or a POL

protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in a vector which is different from the at least one vector containing said at least one nucleic acid molecule coding for a GAG protein and/or a PRO protein and/or a POL protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, said nucleic acid molecule coding for a GAG protein, said nucleic acid molecule coding for a PRO protein, said nucleic acid molecule coding for a POL protein and said nucleic acid molecule coding for a mutated NEF protein substantially devoid of immunosuppressive properties, are all contained in vectors which are different from each other.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, comprising at least one nucleic acid molecule coding for a GAG protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties,

of a human or simian lentivirus, said lentivirus being preferably of the same origin as the mutated lentiviral ENV protein.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains said at least one nucleic acid molecule coding for a GAG protein and/or a mutated NEF protein,

wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains a nucleic acid molecule coding for a GAG protein and for a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains a nucleic acid molecule coding for a GAG protein and for a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties,
said vector being preferably a measles vector (Guerbois et al., *Virology,* 388:191-203, 2009) or a canary pox vector (Poulet et al., *Veterinary Record*, 153(5):141-145, 2003 ; Vaccari et al., *Expert Review of Vaccines*, Vol. 9, No 9, pages 997-1005, 2010).

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in a vector which is different from the at least one vector containing said at least one nucleic acid molecule coding for a GAG protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

In another particular embodiment, the invention relates to a pharmaceutical composition, as defined above, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, said nucleic acid molecule coding for a GAG protein and said nucleic acid

molecule coding for a mutated NEF protein substantially devoid of immunosuppressive properties, are all contained in vectors which are different from each other.

The invention also relates to a pharmaceutical composition according the above definition, for its use as vaccine, for the treatment or the prevention of lentiviral infection, in particular HIV-1 infection, HIV-2 infection and SIV infection.
As mentioned above the pharmaceutical composition according to the invention encompasses a vaccine, comprising as active substance, a protein as defined above, or a nucleic acid as defined above, or a vector as defined above, or a combination thereof.

In a particular embodiment, the pharmaceutical composition according to the invention encompasses a vaccine, comprising a nucleic acid coding for a GAG protein as defined above, a nucleic acid coding for a mutated ENV protein as defined above and a nucleic acid coding for a mutated NEF protein as defined above.

In a particular embodiment, the pharmaceutical composition according to the invention encompasses a vaccine as defined above, comprising a nucleic acid coding for a GAG protein as defined above, a nucleic acid coding for a mutated ENV protein as defined above and a nucleic acid coding for a mutated NEF protein as defined above, which are contained in a same vector, said same vector being preferably a canary pox vector or a measles vector, more preferably a measles vector.

In a particular embodiment, the pharmaceutical composition according to the invention encompasses a vaccine, comprising a GAG protein as defined above, a mutated ENV protein as defined above and a mutated NEF protein as defined above.

In a particular embodiment, the pharmaceutical composition according to the invention encompasses a vaccine, comprising a GAG protein as defined above, a mutated ENV protein as defined above and a mutated NEF protein as defined above which are associated to at least one adjuvant.

A comprehensive list of adjuvants that can be used in HIV vaccines is indicated in the FRANKLIN PIERCE LAW CENTER EDUCATIONAL REPORT: PATENT LANDSCAPE OF ADJUVANT FOR HIV VACCINES which is incorporated herein by reference. This list includes:

- Aluminum-based compounds such as aluminum phosphate and aluminum hydroxide.

- Immunostimulatory adjuvants like CpG, MPL and QS21 orMF59 which is a squalene oil-in water emulsions.

- Freunds incomplete adjuvant (FIA) or Freund's complete adjuvant (FCA), can also be used.

- Calcium phosphate in particular orthophosphates, metaphosphates or pyrophosphates and occasionally hydrogen or hydroxide ions.

- Muramyl dipeptide (*N*-Acetyl muramyl-L-alanine-D-isoglutamine, MDP) and its synthetic analogs such as muramyl tripeptide phosphatidylethanolamine MTPPTdEtn),

- Trehalose-6,6'-dimycolate,

- Saponins (Triterpenoid glycosides) like QS-21

- Stearyl Tyrosine (octadecyl ester hydrochloride salt of tyrosine)

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Immunostimulatory adjuvants can include the following classes of compounds:

- Polysaccharides like:
    - *Chitosan*:
    - *Inulin*:

- *Beta – Glucans*
- *Lipo-Polysaccharides or endotoxin*
- *MGN-3Actinidia eriantha (AEPS)*:
- *Eldexomer*:
- *CpG ODN*

- Liposomes like
  - *Dehydration-rehydration liposome vesicles (DRVs)*
  - *Cytotoxic T lymphocyte (CTL)*
  - *CAF01*
  - *Liposomes containing lipid A (LA)*

- Lipid Polysine Core Peptides (LCP)

- Cytokine like GM-CSF, IL-2,IL-12 or IL-15

- Lipid A and Monophosphoryl Lipid A (MPL)

- Lipopeptide which are molecules consisting of lipid connected to a peptide. They are derived from the lipoprotein of bacterial cell wall.
- Exogenous Immunostimulatory Adjuvants which are compounds, or proteins that are not found in the human body like:
  - Proteosomes in particular Multiple Antigenic Peptides (MAP) or Exogenous Toxins

Suitably, the total amount mutated lentiviral ENV protein in a single dose of the immunogenic composition is l0μg and/or the total amount of unfused polypeptide in a single dose of the immunogenic composition is 20μg. In one embodiment, the total amount of all antigens in a single dose of the immunogenic composition is 0.5-50μg, 2-40μg, 5-30μg, 10μ-20μg or around 30μg, around 20μg or around l0μg.

The amount of mutated lentiviral ENV protein in a dose of the immunogenic composition is selected as an amount which induces an immune response without significant, adverse side effects in typical recipients. Such amount will vary depending upon which specific immunogen is employed and the dosing or vaccination regimen that is selected. An optimal amount for a particular immunogenic composition can be ascertained by standard studies involving observation of relevant immune responses in subjects.

Administration of the pharmaceutical composition can take the form of one or of more than one individual dose, for example as repeat doses of the same polypeptide containing composition, or in a heterologous "prime-boost" vaccination regime, including proteins and vectors. In one embodiment, the immunogenic composition of the invention is initially administered to a subject as two or three doses, wherein the doses are separated by a period of two weeks to three months, preferably one month.

Conveniently, the composition is administered to a subject (for instance as a booster) every 6-24, or 9-18 months, for instance annually. For instance, the composition is administered to a subject (for instance as a booster) at six month or 1 year intervals. Suitably in this respect, subsequent administrations of the composition to the subject boost the immune response of earlier administrations of the composition to the same subject.

In an embodiment, the immunogenic composition of the invention is used as part of a prime -boost regimen for use in the treatment or prevention of disease or infection by HIV-1 strains from one or more clades different from the one or more HIV-1 clades in the immunogenic composition. Conveniently, the composition is the priming dose. Alternatively, the composition is the boosting dose.

Suitably, two or more priming and/ or boosting doses are administered. A heterologous prime-boost regime uses administration of different forms of immunogenic composition or vaccine in the prime and the boost, each of which can itself include two or more administrations. The priming composition and the boosting composition will have at least one antigen in common, although it is not necessarily an identical form of the antigen, it can be a different form of the same antigen.

Prime boost immunisations according to the invention can be homologous prime-boost regimes or heterologous prime-boost regimes. Homologous prime-boost regimes utilize the same composition for prime and boost, for instance the immunogenic composition of the

invention. Heterologous prime-boost regimes can be performed with a combination of protein and DNA- based formulations. Such a strategy is considered to be effective in inducing broad immune responses. Adjuvanted protein vaccines induce mainly antibodies and CD4+ T cell immune responses, while delivery of DNA as a plasmid or a recombinant vector induces strong CD8+ T cell responses. Thus, the combination of protein and DNA vaccination can provide for a wide variety of immune responses. This is particularly relevant in the context of HIV, since neutralizing antibodies, CD4+ T cells and CD8+ T cells are thought to be important for the immune defense against HIV-1.

The invention also relates to a pharmaceutical composition according the above definition, for its use for the treatment of lentiviral infection.

The invention also relates to a method for treating patient afflicted by pathologies related to lentiviral infection, comprising the administration to a patient in a need thereof of a pharmaceutically efficient amount of the pharmaceutical composition as defined above.
The invention also relates to a method for inducing an immune response against a lentivirus that has infected an individual, said method comprising the administration to a patient in a need thereof of a pharmaceutically efficient amount of the pharmaceutical composition as defined above.

The invention also relates to a pharmaceutical composition as defined above, further comprising an antiviral agent.

The composition according to the invention can also be used in combination with the antiviral compositions listed in Table 1 below:

Intelence® (TMC 125/etravirine) Tibotec -	Non-nucleoside reverse transcriptase inhibitor
Agenerase®(APV/amprenavir) GSK -	Protease inhibitor
Aptivus®(TPV/tipranavir) Boehringer -	Protease inhibitor
Crixivan®(IDV/indinavir) MSD -	Protease inhibitor
Invirase®(SQV/saquinavir) Roche -	Protease inhibitor
Kaletra®(LPV.r/lopinavir + ritonavir) Abbott	Protease inhibitor
Norvir®(ritonavir) Abbott -	Protease inhibitor
Prezista®(TMC 114/darunavir)	Protease inhibitor

Tibotec/Janssen-Cilag -	
Reyataz®(ATZ/atazanavir) BMS -	Protease inhibitor
Telzir®(APV/fosamprenavir) GSK -	Protease inhibitor
Viracept®(nelfinavir) Roche -	Protease inhibitor
Fuzeon®(T20/enfuvirtide) Roche -	Fusion inhibitor
Celsentri®(maraviroc) Pfizer -	Entry inhibitor
Isentress®(MK 0518/raltegravir) Merck -	Integrase inhibitor
Rescriptor®(delavirdine) Agouron -	Non-nucleoside reverse transcriptase inhibitor
Sustiva®(EFV/efavirenz) BMS -	Non-nucleoside reverse transcriptase inhibitor
Viramune®(nevirapine) Boehringer -	Non-nucleoside reverse transcriptase inhibitor
Combivir®(Retrovir®+Epivir®) GSK -	Nucleoside reverse transcriptase inhibitor
Emtriva®(FTC, emtricitabine) Gilead -	Nucleoside reverse transcriptase inhibitor
Epivir®(3TC, lamivudine) GSK -	Nucleoside reverse transcriptase inhibitor
Kivexa®(Ziagen®+ Epivir®) GSK -	Nucleoside reverse transcriptase inhibitor
Retrovir®(AZT/zidovudine) QSK -	Nucleoside reverse transcriptase inhibitor
Trizivir®(Retrovir®+ Epivir®+ Ziagen®) GSK -	Nucleoside reverse transcriptase inhibitor
Videx®(ddI/didanosine) BMS -	Nucleoside reverse transcriptase inhibitor
Viread®(TDF/tenofovir) Gilead -	Nucleoside reverse transcriptase inhibitor
Zerit®(d4T/stavudine) BMS -	Nucleoside reverse transcriptase inhibitor
Ziagen®(ABC/abacavir) GSK -	Nucleoside reverse transcriptase inhibitor
Truvada®(Emtriva® + Viread®) Gilead -	Nucleoside reverse transcriptase inhibitor
Atripla®(Sustiva®+ Emtriva®+ Viread®) BMS / GILEAD	Nucleoside and non-nucleoside reverse transcriptase inhibitor

Table 1: Trade names of the different antivirals used for HIV treatment, as well as their specificity of action.

The invention also relates to a pharmaceutical composition as defined above, for simultaneous, separate or sequential use.

The invention relates to a pharmaceutical composition as defined above for its use for stimulating an immune response in a host organism.

The invention relates to a pharmaceutical composition as defined above for its use for inducing a specific immune response against the HIV ENV protein.

The invention relates to a pharmaceutical composition as defined above for its use for the prevention or the treatment of HIV infection, or pathologies related to AIDS.

The invention relates to a pharmaceutical composition as defined above, as a vaccine, for its use for inducing a specific immune response against the HIV ENV protein.

The invention relates to a pharmaceutical composition as defined above, as a vaccine, for its use for the prevention or the treatment of HIV infection, or pathologies related to AIDS.

In another aspect, the invention also relates to a method to obtain the active substance of a pharmaceutical composition, as defined above, consisting of modifying the immunosuppressive property of:
a wild-type human or simian lentiviral ENV protein,
or a fragment of said wild-type human or simian lentiviral ENV protein, said fragment comprising at least 40 amino acids,
said ENV protein or fragment thereof presenting a transmembrane subunit (TM) comprising an immunosuppressive domain (ISU) containing the following amino acid sequence :

A-[I/V]-E-[K/R]-X'$_a$-X'$_b$-X-D-Q (SEQ ID NO: 427),

wherein
X represents any amino acid,
X'$_a$ is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and
X'$_b$ is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

said method comprising a step of introduction of at least one mutation of X'$_a$ and/or X'$_b$,

to obtain:
an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
said mutated human or simian lentiviral ENV protein having at least 70% identity, preferably at least 80% identity, to one sequence chosen from the group consisting of SEQ ID NO : 216, SEQ ID NO : 420 and SEQ ID NO : 421,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L, R or deleted, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G, R or deleted, or

X_a is A, F, G, L, R or deleted, and X_b is A, F, G, R or deleted,

said substantial absence of immunosuppressive activity of the above mentioned mutated human or simian lentiviral ENV protein or of the above defined fragment being liable to be assessed by the fact that in an *in vivo* assay involving engrafted tumor cells rejection,

said tumor cells being transduced either so as to express said mutated ENV protein or said fragment (mutated ENV tumor cells),

or said tumor cells being transduced so as to express said wild type ENV protein or a fragment thereof (wild type ENV tumor cells),

or said tumor cells being not transduced (normal tumor cells),

the following ratio :

immunosuppression index of said mutated ENV protein or of said fragment ($i_{mutated\ env}$) / immunosuppression index of wild type ENV protein ($i_{wild\ type\ env}$) is less than 0.5,

$i_{mutated\ env}$ being defined by : (maximum area reached by mutated ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells), and

$i_{wild\ type\ env}$ being defined by : (maximum area reached by wild type ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells).

The invention also relates to a method to obtain the active substance of a pharmaceutical composition, according to the above defined method, consisting of modifying the immunosuppressive property of :

a wild-type human or simian lentiviral ENV protein,

or a fragment of said wild-type human or simian lentiviral ENV protein, said fragment comprising at least 40 amino acids,

said ENV protein or fragment thereof presenting a transmembrane subunit (TM) comprising an immunosuppressive domain (ISU) containing the following amino acid sequence :

A-[I/V]-E-[K/R]-Y-L-X-D-Q (SEQ ID NO : 1),

wherein

X represents any amino acid,

said method comprising a step of introduction of at least one mutation of Y in position 5 and/or L in position 6,

to obtain:

an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L, R or deleted, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G, R or deleted, or

X_a is A, F, G, L, R or deleted, and X_b is A, F, G, R or deleted.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein
X represents any amino acid,
and either
X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or
X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or
X_a is A, F, G, L or R, and X_b is A, F, G or R.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition, ,
wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein
X represents any amino acid,
and either
X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or
X_a is Y, I, H, C or T, and X_b is A, F, G or R, or
X_a is A, F, G, L or R, and X_b is A, F, G or R.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein
X represents any amino acid,
and either
X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or
X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R, or
X_a is F or L, and X_b is F, G or R, or
X_a is A, G or R, and X_b is A.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,
wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein
X represents any amino acid,
and either
X_a is A, G, or R, and X_b is L, I, V, M or P, or
X_a is Y, I, H, C or T, and X_b is F, G or R, or
X_a is F or L, and X_b is F, G or R, or

X_a is A, G or R, and X_b is A, or
X_a is A, G or R, and X_b is F, G or R.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,
wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,
X represents any amino acid,
and either
X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or
X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,
wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,
X represents any amino acid,
and either

X_a is A, G, or R, and X_b is L, I, V, M or P, or
X_a is Y, I, H, C or T, and X_b is F, G or R.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,
wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,
X represents any amino acid,
and either
X_a is R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or
X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is R, or
X_a is R, and X_b is R.

The invention also relates to a method as defined above to obtain the active substance of a pharmaceutical composition,
wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,
said mutated ENV protein and fragment thereof comprising a mutation in one at least of the amino acids at positions, 29, 36 and 37 of SEQ ID NO: 426 :

A[I/V]E[K/R]$X_aX_bX_1$DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VP$X_cX_{10}Z_1Z_2Z_3Z_4Z_5$
X_dX_e[S/T] (SEQ ID NO: 426)

wherein

X_a and X_b are as defined in anyone of claims 1 to 15,

X_1 to X_{10} represent any amino acid,

Z_1 to Z_5 represent no amino acid or any amino acid, independently from each other

such that

- X_c is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y, or deleted, preferably A, D, or N,
- X_d is A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, Y, W, or deleted, preferably A, G, S or Y,
- X_e is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, T, V, Y, W, or deleted, preferably A, D or N.

The present invention relates to a pharmaceutical composition comprising as active substance :

a) an isolated non naturally occurring mutated human or simian lentiviral ENV having substantially no immunosuppressive activity, said mutated human or simian lentiviral ENV resulting from mutation of the transmembrane subunit (TM) of a wild type human or simian lentiviral ENV protein, the transmembrane subunit comprising an immunosuppressive domain (ISU) comprising the following amino acid sequence:

A-[I/V]-E-[K/R]-Y-L-X-D-Q (SEQ ID NO: 1),

said sequence encompassing

AIEKYLXDQ (SEQ ID NO: 2), AIERYLXDQ (SEQ ID NO: 3), AVEKYLXDQ (SEQ ID NO: 4) and AVERYLXDQ (SEQ ID NO: 5), wherein X represents any natural amino acid,

wherein the amino acids at the positions chosen among

- the position 4 of SEQ ID NO: 1,

- the position 5 of SEQ ID NO: 1,

- the position 6 of SEQ ID NO: 1,

- the positions 4 and 5 of SEQ ID NO: 1,

- the position 4 and 6 of SEQ ID NO: 1,

- the position 5 and 6 of SEQ ID NO: 1, and

- the position 4, 5 and 6 of SEQ ID NO: 1,

are :

- *either deleted,*
- *or substituted by another amino acid such that*
    - *when the immunosuppressive domain comprises SEQ ID NO : 2 or 4*
        - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, W or Y, and/or*
        - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
        - *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*
    - *when the immunosuppressive domain comprises SEQ ID NO : 3 or 5,*
        - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, L, M, N, P, Q, S, T, V, W or Y, and/or*
        - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
        - *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*

or

b) a fragment of said mutated human or simian lentiviral ENV, said fragment comprising at least the immunosuppressive domain (ISU) of said wild type human or simian lentiviral ENV comprising the following amino acid sequence:

A-[I/V]-E-[K/R]-Y-L-X-D-Q (SEQ ID NO: 1),

wherein the amino acids at the positions chosen among

- the position 4 of SEQ ID NO: 1,

- the position 5 of SEQ ID NO: 1,

- the position 6 of SEQ ID NO: 1,

- the positions 4 and 5of SEQ ID NO: 1,

- the position 4 and 6 of SEQ ID NO: 1,

- the position 5 and 6 of SEQ ID NO: 1, and

- the position 4, 5 and 6 of SEQ ID NO: 1,

are :

- *either deleted,*
- *or substituted by another amino acid such that*
    - *when the immunosuppressive domain comprises SEQ ID NO : 2 or 4*
        - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, W or Y, and/or*
        - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
        - *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*
    - *when the immunosuppressive domain comprises SEQ ID NO : 3 or 5,*
        - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, L, M, N, P, Q, S, T, V, W or Y, and/or*
        - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
        - *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*

said fragment having substantially no immunosuppressive properties,
in association of a pharmaceutically acceptable carrier.

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein the amino acids at the positions of the group consisting of
- the position 4 of SEQ ID NO: 1,
- the position 5 of SEQ ID NO: 1,
- the position 6 of SEQ ID NO: 1,
- the positions 4 and 5 of SEQ ID NO: 1,
- the position 4 and 6 of SEQ ID NO: 1,
- the position 5 and 6 of SEQ ID NO: 1, and
- the position 4, 5 and 6 of SEQ ID NO: 1,

- *are substituted by another amino acid such that*
    - *when the immunosuppressive domain comprises SEQ ID NO : 2 or 4*
        - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, W or Y, and/or*

- *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
- *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*

o *when the immunosuppressive domain comprises SEQ ID NO : 3 or 5,*

- *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, L, M, N, P, Q, S, T, V, W or Y, and/or*
- *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
- *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y.*

Advantageously, the mutated lentiviral protein according to the invention, comprised in the above defined composition, comprises the amino acid sequence of the list consisting of: SEQ ID NO: 407 to SEQ ID NO: 414.

The correspondence is the following one:

AVEAALKD	*SEQ ID NO : 407*	*AIEAALKD*	*SEQ ID NO : 411*
AVEEALKD	*SEQ ID NO : 408*	*AIEEALKD*	*SEQ ID NO : 412*
AVESALKD	*SEQ ID NO : 409*	*AIESALKD*	*SEQ ID NO : 413*
AVETALKD	*SEQ ID NO : 410*	*AIETALKD*	*SEQ ID NO : 414*

These proteins have been mutated at position 4 of SEQ ID NO: 1, by substitution, and the amino acid at position 5 has been substituted by A.

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein the amino acids at the positions of the group consisting of

- the position 5 of SEQ ID NO: 1,

- the position 6 of SEQ ID NO: 1, and

- the position 5 and 6 of SEQ ID NO: 1,

- *are substituted by another amino acid such that*
  - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*

- *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y.*

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said immunosuppressive domain (ISU) comprises the amino acid sequence of the group consisting of: SEQ ID NO : 4 or 5.

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said immunosuppressive domain (ISU) comprises the amino acid sequence SEQ ID NO : 5, and wherein

- *the amino acid residue at position 5 of SEQ ID NO: 5 is substituted by A, F, G, L or R, or*
- *the amino acid residue at position 6 of SEQ ID NO: 5 is substituted by A, F, G or R, or*
- *the amino acid residues at position 5 and 6 of SEQ ID NO: 5 are substituted by A, F, G, or R.*

This is the case when said ENV protein is the ENV protein of HIV 1 virus.

The invention also relates to a pharmaceutical composition as defined above, wherein said immunosuppressive domain (ISU) comprises the amino acid sequence SEQ ID NO : 2, and wherein

- *the amino acid residue at position 5 of SEQ ID NO: 2 is substituted by A, F, G, L or R, or*
- *the amino acid residue at position 6 of SEQ ID NO: 2 is substituted by A, F, G or R, or*
- *the amino acid residues at position 5 and 6 of SEQ ID NO: 2 are substituted by A, F, G, or R.*

The invention also relates to a pharmaceutical composition as defined above, wherein said immunosuppressive domain (ISU) comprises the amino acid sequence SEQ ID NO : 3, and wherein

- *the amino acid residue at position 5 of SEQ ID NO: 3 is substituted by A, F, G, L or R, or*
- *the amino acid residue at position 6 of SEQ ID NO: 3 is substituted by A, F, G or R, or*
- *the amino acid residues at position 5 and 6 of SEQ ID NO: 3 are substituted by A, F, G, or R.*

In one advantageous embodiment, the invention relates to a pharmaceutical composition as defined above, wherein said mutated protein further comprises the wild type amino acid sequence SEQ ID NO: 270,

$X_1DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VPWX_{10}Z_1Z_2Z_3Z_4Z_5[N/S][E/D/N/A][S/T]$ (SEQ ID NO: 270)

wherein X_1-X_{10} represents any amino acid,

wherein Z_1 to Z_5 represent no amino acid or any natural amino acid, independently from each other,

said mutated lentiviral protein further comprising a mutation in one at least of the amino acids at positions 23, 30 and 31 of SEQ ID NO: 270

said mutation being :

- *either a deletion,*
- *or a substitution such that*
  - *the amino acid at position 25 of SEQ ID NO: 270 is substituted by A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y,*
  - *the amino acid at position 32 of SEQ ID NO: 270 is substituted by A, C, D, E, F, G, H, I, K, L, M, P, Q, R, T, V, Y, W,*
  - *the amino acid at position 33 of SEQ ID NO: 270 is substituted by C, F, G, H, I, K, L, M, P, Q, R, S, T, V, Y, W.*

In one advantageous embodiment, the invention relates to a pharmaceutical composition comprising as active substance :

an isolated non naturally occurring mutated human or simian lentiviral ENV having substantially no immunosuppressive activity, said mutated human or simian lentiviral ENV resulting from mutation of a wild type human or simian lentiviral ENV protein, said wild

type human or simian lentiviral ENV protein comprising the following amino acid sequence:

A[I/V]E[K/R]YLX$_1$DQX$_2$X$_3$LX$_4$X$_5$WGC[A/S][F/G]X$_6$X$_7$CVX$_8$TX$_9$VPWX$_{10}$Z$_1$Z$_2$Z$_3$Z$_4$Z$_5$[N/S][E/D/N/A][S/T] (SEQ ID NO: 415),

wherein X$_1$-X$_{10}$ represents any amino acid,

wherein Z$_1$ to Z$_5$ represent no amino acid or any natural amino acid, independently from each other,

wherein the amino acids at the positions chosen among

- the position 4 of SEQ ID NO: 1,

- the position 5 of SEQ ID NO: 1,

- the position 6 of SEQ ID NO: 1,

- the positions 4 and 5 of SEQ ID NO: 1,

- the position 4 and 6 of SEQ ID NO: 1,

- the position 5 and 6 of SEQ ID NO: 1, and

- the position 4, 5 and 6 of SEQ ID NO: 1,

are :

- *either deleted,*
- *or substituted by another amino acid such that*
    - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W or Y, and/or*
    - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
    - *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*

and further wherein

one at least of the amino acids at positions 29, 36 and 37 of the amino acid sequence SEQ ID NO : 415 are mutated, by

- *either a deletion,*
- *or a substitution such that*
    - *the amino acid at position 29 of SEQ ID NO: 415 is substituted by A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y,*

- *the amino acid at position 36 of SEQ ID NO: 415 is substituted by A, C, D, E, F, G, H, I, K, L, M, P, Q, R, T, V, Y, W,*
- *the amino acid at position 37 of SEQ ID NO: 415 is substituted by C, F, G, H, I, K, L, M, P, Q, R, S, T, V, Y, W.*

In another aspect, the invention relates to a pharmaceutical composition as defined above, further comprising a mutation at the position X_4
$X_1DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VPWX_{10}Z_1Z_2Z_3Z_4Z_5[N/S][E/D/N/A][S/T]$ *(SEQ ID NO: 270)*
wherein X_1-X_3 *and* X_5-X_{10} *represents any amino acid,*
Z_1 *to* Z_5 *represent no amino acid or any amino acid, independently from each other*
said mutation being :
- *either a deletion,*
- *or a substitution by A, C, D, E, F, H, I, K, L, M, P, Q, R, S, T, V, Y or W.*

In one advantageous embodiment, the invention relates to a pharmaceutical composition comprising as active substance :
an isolated non naturally occurring mutated human or simian lentiviral ENV having substantially no immunosuppressive activity, said mutated human or simian lentiviral ENV resulting from mutation of a wild type human or simian lentiviral ENV protein, said wild type human or simian lentiviral ENV protein comprising the following amino acid sequence:
$A[I/V]E[K/R]YLX_1DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VPWX_{10}Z_1Z_2Z_3Z_4Z_5[N/S][E/D/N/A][S/T]$ *(SEQ ID NO: 415),*
wherein X_1-X_{10} *represents any amino acid,*
wherein Z_1 *to* Z_5 *represent no amino acid or any natural amino acid, independently from each other,*
wherein the amino acids at the positions chosen among
- the position 4 of SEQ ID NO: 1,
- the position 5 of SEQ ID NO: 1,
- the position 6 of SEQ ID NO: 1,
- the positions 4 and 5 of SEQ ID NO: 1,

- the position 4 and 6 of SEQ ID NO: 1,

- the position 5 and 6 of SEQ ID NO: 1, and

- the position 4, 5 and 6 of SEQ ID NO: 1,

are :

- *either deleted,*
- *or substituted by another amino acid such that*
    - *the amino acid residue at position 4 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W or Y, and/or*
    - *the amino acid residue at position 5 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, I, L, M, N, P, Q, R, S, T, V or W, and/or*
    - *the amino acid residue at position 6 of SEQ ID NO: 1 is substituted by A, C, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W or Y,*

and possibly, further wherein

one at least of the amino acids at positions 29, 36 and 37 of the amino acid sequence SEQ ID NO : 415 are mutated, by

- *either a deletion,*
- *or a substitution such that*
    - *the amino acid at position 29 of SEQ ID NO: 415 is substituted by A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, Y,*
    - *the amino acid at position 36 of SEQ ID NO: 415 is substituted by A, C, D, E, F, G, H, I, K, L, M, P, Q, R, T, V, Y, W,*
    - *the amino acid at position 37 of SEQ ID NO: 415 is substituted by C, F, G, H, I, K, L, M, P, Q, R, S, T, V, Y, W,*

and/or possibly further wherein the amino acid at position X_4 is either deleted or substituted by A, C, D, E, F, H, I, K, L, M, P, Q, R, S, T, V, Y or W, preferably by R or H.

LEGEND TO THE FIGURES

Figure 1 :

Amino acid sequences of the HIV ectodomain deletants, with the indicated length, and of single mutant (substitution are underlined) ectodomains.

Figure 2:
Functional delineation of the immunosuppressive domain of the HIV envelope. The immunosuppressive activity of 115aa-long and truncated HIV envelope ectodomains (see structures on the left) was tested using the MCA205 tumor rejection *in vivo* assay. Immunosuppression indexes are given as histograms on the right (mean values +/- SD).

Figure 3 :
Functional identification of the aminoacid in the HIV envelope ectodomain directly involved in immunosuppressive activity, and search for aminoacid substitutions inhibiting this activity. Immunosuppresive activity was tested in vivo as in Figure 2.

Figure 4 :
Expression profile of mutated HIV envelopes using full-length HIVenv-expressing vectors and an anti-SU HIVenv(110H) monoclonal antibody (FACS). The data are expressed as percentages of the control HIVenv WT.

Figure 5 :
Infectivity of HIVenv-pseudotyped viral particles showing functionality of the full-length WT and of specifically mutated HIV envelopes. The results are expressed as viral titers (number of infected target cells/mL of virus supernatant).

Figure 6 :
Functional identification of the amino acid in the SIV envelope ectodomain directly involved in immunosuppressive activity, and search for aminoacid substitutions inhibiting this activity. Immunosuppressive activity was tested using the in vivo MCA205 tumor rejection assay. Immunosuppression indexes are represented as histograms (mean values +/- SD).

EXAMPLE
Immunosuppressive domains have been identified on the envelope proteins of oncoretroviruses, of either the gamma- (murine MLV) or the delta (e.g. human HTLV) type, as well as of some endogenous retroviruses (e.g. HERV-FRD). These domains have a

highly conserved crystallographic structure, although their primary sequences are quite diverse, and an amino-acid (either Q, E, or K) at a definite position has previously been demonstrated to be essential for the immunosuppresive activity of the corresponding envelope protein. Mutation of this amino acid to an Arginine (R) was further demonstrated to result in inhibition of the immunosuppressive activity of the mutated envelope protein, with in some cases complete conservation of the other functional properties of the envelope protein, including its ability to be normally expressed at the cell membrane, to be captured by a nascent retroviral particle, and finally to confer infectivity of the mutant virus in vitro. Such mutants allowed an unambiguous demonstration of the essential role of the immunosuppressive activity for viremia in vivo, with the mutant IS- virus being unable to escape the host immune system and propagate in an immunocompetent animal [*Schlecht-Louf et al., Proc Natl Acad Sci U S A. 2010;107(8):3782-7*].

On the basis of the identification of an IS domain and on the ability of the IS function to be inhibited by specific mutations within the IS domain that do not disrupt the antigenic structure of the corresponding viral protein, vaccinal approaches are being developed with vaccines containing mutated « optimized » IS-negative viral antigens, which demonstrate an increased immunognicity as compared to those using the native viral antigens. Search for similar IS domains and appropriate mutations in the case of non-oncogenic–but still pathogenic- retroviruses such as HIV is therefore of interest to tentatively develop improved vaccines.

Actually, in the case of the other major class of retroviruses, namely the lentiviruses (among which the human HIV1 and HIV2, and the SIV simian homologues), the crystallographic structure of the envelope protein discloses some similarities but also very important differences, especially in the domain corresponding to the IS domain of oncoretroviruses, with evidence in HIV and SIV for a severely extended helix-loop-helix domain, and no evidence for sequence similarities with the IS domain of oncoretroviruses. Furthermore, an IS domain with strong amino-acid similarities with the IS domain of oncoretroviruses was identified within an accessory protein of HIV and SIV, namely within the Nef protein. This protein is specifically produced by these complex retroviruses and is not encoded by oncoretroviruses. The Nef protein is essential for viremia in vivo, and it possesses several domains responsible for immune escape, among which the identified IS domain, thus strongly suggesting that lentiviruses had transferred the

immunosuppressive activity found in oncoretroviruses within their envelope protein, to the accessory Nef protein. In agreement with this hypothesis, Nef-deleted or Nef-mutated retroviruses have a severely attenuated pathogenicity in in vivo macaque animal models.
Here, the Inventors report on the identification of an IS activity carried by the HIV and SIV envelope proteins, and on specific mutations that inhibit this activity without major disrupt ion of the overall structure of the corresponding envelope proteins.

Results

Delination of the immunosuppressive domain of the HIV Envelope

Delineation of the immunosuppressive domain of the HIV envelope was achieved using an *in vivo* tumor rejection assay, that the Inventors had previously used to demonstrate the immunosuppressive activity of the Env protein of oncoretroviruses (murine MoMLV and simian MPMV). The rationale of the assay can be summarized as follows: while injection of MCA205 tumor cells (H-2^b) into allogeneic Balb/c mice (H-2^d) leads to the formation of no tumor or transient tumors that are rapidly rejected, injection of the same cells, but stably expressing an immunosuppressive retroviral Env protein, leads to the growth of larger tumors that persist for a longer time –in spite of the expression of the new exogenous antigen. This difference is not associated with a difference in intrinsic cell growth rate since it is not observed in syngeneic C57BL/6 mice, and is immune system-dependent. The extent of "immunosuppression" can be quantified by an index based on tumor size: $(A_{env}-A_{none})/A_{none}$, where A_{env} and A_{none} are the mean areas at the peak of growth of tumors from Balb/c mice injected with *env*-expressing or control cells, respectively. A positive index indicates that *env* expression facilitates tumor growth, as a consequence of its immunosuppressive activity; a null or negative index points to no effect or even an inhibitory effect, respectively. The latter may be explained by a stimulation of the immune response of the host against the new foreign antigen, represented by a non-immunosuppressive Env protein, expressed at the surface of tumor cells.
To first delineate a minimal immunosuppressive domain (ISD) active *in vivo*, the Inventors analyzed the effect of a series of truncations/deletions within the HIV *env* gene. Assay of the series of C-term truncations in Fig. 1&2 identified a 49 residue-long domain with IS activity, with the 6 aa shorter HIV43 fragment and subsequent C-term truncated HIV37 and HIV30 fragments being IS-negative. HIV49 is embedded into the so-called

ectodomain, which corresponds to a soluble part of the extracellular domain of the TM subunit, and consists in the a-helical domain involved in HIV TM trimerization, and the N-term part of the loop containing the 2 well-conserved, 6 aa-distant, cysteine residues found in most retroviral envelopes. Refine delineation of the amino acis responsible for IS activity was then performed by arginine-scanning between aa 36 and 51, i.e. in the domain associated with the transition from IS positive to negative Env subdomains. As illustrated in Fig. 3, all the X-to-Arg substitutions resulted in no significant change in the IS activity of HIV115, with one exception for Y41 and L42, which resulted in loss of IS activity of the mutant peptide.

Mutations at position 41

The Inventors then checked that the Y41R substitution did not alter the overall capacity of the HIV envelope to be expressed by an eucaryotic cell and to be exported at the cell membrane, by introducing the Y41R substitution into an expression vector for the HIV envelope. A FACS analysis of cell transfected with both the wild-type and the Y41R mutant using an anti-SU specific monoclonal antibody actually demonstrated quantitative expression of the mutant envelope at the cell surface, thus indicating that the Y41R mutation does not significantly alter the HIV Env structure and SU-TM interaction (figure 4).

A series of distinct substitutions at the Y41 position were finally performed to tentatively identify whether other amino acids could be substituted to generate IS-negative variants: the amino acid assayed included the positively charged K and H (in addition to R), the small A and G, and the hydrophobic L and F residues. Again it was checked that these substitutions did not alter the overall structure of the HIV Env with the corresponding mutations.

Among them, substitution of Y41 by A, G, L and F resulted in loss of IS (figure 3), and did not alter the overall structure of the HIV Env with the corresponding mutations (figure 4 and 5).

Further mutation outside of the ISU domain

The effects of a set of second mutations at positions that are structurally close to Y41 position within the ENV ectodomain three-dimensional structure were also tested. Two of them (Y41R-K72A and Y41R-K78G) maintain a high level expression at cell membrane and confer infectivity (figure 5).

Mutations at position 42

Interestingly, the adjacent position to the position Y41, position L42, also resulted in loss of IS activity of the mutant peptide when the mutation L42R is introduced. This mutation maintains a high level expression at cell membrane of the mutated HIV ENV protein (figure 4).

Mutations within the SIV ENV protein

Interestingly, mutation at the homologous position in SIV ENV (L42) of the position L42 in HIV-1 ENV ectodoamin also resulted in specific loss of IS activities (Figure 6).

Accordingly, the present investigation has clearly identified a definite location and a definite substitution(s) within the HIV env resulting in the loss of its IS activity. Being compatible with the conservation of the overall structure of the human and simian lentiviral Env proteins, these substitutions should be introduced in all pharmaceutical preparations which include the Env protein as a vaccine antigen.

Materials and Methods

Mice and cell lines: C57Bl/6 and Balb/c mice, 6-10 weeks old, were obtained from CER Janvier (Laval, France). Mice were maintained in the animal facility of the Gustave Roussy Institute in accordance with institutional regulations. 293T (ATCC CRL11268), and MCA205 cells were cultured in DMEM supplemented with 10% fetal calf serum (Invitrogen), streptomycin (100 µg/ml) and penicillin (100 units/ml).

Plasmid construction: The PCEL/E160 encoding the envelope protein of the BRU/LAI HIV-1 isolate is a gift from Dr Marc Sitbon. To generate the pDFG plasmids encoding the various fragments of HIV-1 envelope ectodomain, PCR fragments generated using PCEL/E160 as a template and primer pairs 1-2 (pDFG-HIV115), 1-3 (pDFG-HIV81), 1-4 (pDFG-HIV67), 1-5 (pDFG-HIV55), 1-6 (pDFG-HIV49), 1-7 (pDFG-HIV43), 1-8 (pDFG-HIV37), 1-9 (pDFG-HIV30) were digested with SfiI and MluI and inserted into pDFG-ectoSyncytin-1 (Mangeney et al, 2007) opened with the same enzymes.

Mutated pDFG-HIV115 were obtained by successive PCR using appropriate primers. A first series of PCR was performed with pDFG HIV115 as template using primers 1-11 and 10-2, 1-13 and 12-2, 1-15 and 14-2 or 1-17 and 16-2 to introduce the E39R, Y41R, K43R or D44R mutations respectively, and primers 1-18 and 19-2, 1-20 and 21-2, 1-22 and 23-2,

1-24 and 25-2, 1-26 and 27-2, 1-28 and 29-2, 1-30 and 31-2, 1-32 and 33-2, 1-34 and 35-2, or 1-36 and 37-2 to introduce the L36R, A37R, V38R, L42R, Q45R, Q46R, L47R, L48R, G49R, or I50R mutations respectively. The PCR products were then used as templates in subsequent PCR using primers 1-2. These PCR fragments were digested with SfiI and MluI and inserted into pDFG-ectoSyncytin-1 (Mangeney et al, 2007) opened with the same enzymes.

All the constructions were sequenced before use.

Table 1. Primer list

N°	Name	Primer sequence (5'-3')	SEQ ID
1	TM HIV Sfi-Sens	ACATggcccagccggccTCTGGTATAGTGCAGCAGC	SEQ ID NO: 295
2	TM HIV115 Mlu-AS	GTATacgcgtTTATAATTCTTGTTCATTCTTTTC	SEQ ID NO: 296
3	TM HIV81 Mlu AS	GTATacgcgtTTACATGTTATTCCAAATCTGTTCC	SEQ ID NO: 297
4	TM HIV67 Mlu AS	GTATacgcgtTTAAGCATTCCAAGGCACAGC	SEQ ID NO: 298
5	TM HIV55 Mlu AS	GTATacgcgtTTATCCAGAGCAACCCCAAATCC	SEQ ID NO: 299
6	TMHIV49 Mlu AS	GTATacgcgtTTACCCCAGGAGCTGTTGATCC	SEQ ID NO: 300
7	TMHIV43 Mlu AS	GTATacgcgtTTACTTTAGGTATCTTTCCACAGC	SEQ ID NO: 301
8	TMHIV37 Mlu AS	GTATacgcgtTTAAGCCAGGATTCTTGCCTGGAG	SEQ ID NO: 302
9	TMHIV30 Mlu AS	GTATacgcgtTTACTGCTTGATGCCCCAGAC	SEQ ID NO: 303
18	TMHIV115 L36R as	CTTTCCACAGCCcGGATTCTTGCCTG	SEQ ID NO: 304
19	TMHIV115 L36R s	CAGGCAAGAATCCgGGCTGTGGAAAG	SEQ ID NO: 305
20	TMHIV115 A37R as	GTATCTTTCCACAcgCAGGATTCTTGCC	SEQ ID NO: 306
21	TMHIV115 A37R s	GGCAAGAATCCTGcgTGTGGAAAGATAC	SEQ ID NO: 307
22	TMHIV115 V38R as	CTTTAGGTATCTTTCCctAGCCAGGATTCTTGCC	SEQ ID NO: 308
23	TMHIV115 V38R s	GGCAAGAATCCTGGCTagGGAAAGATACCTAAAG	SEQ ID NO: 309
11	TMHIV115 E39R AS	CCTTTAGGTATCTTctCACAGCCAGGATTC	SEQ ID NO: 310
10	TMHIV115 E39R S	GAATCCTGGCTGTGagAAGATACCTAAAGG	SEQ ID NO: 311
13	TMHIV115 Y41R AS	GTTGATCCTTTAGGcgTCTTTCCACAGCCAG	SEQ ID NO: 312
12	TMHIV115 Y41R S	CTGGCTGTGGAAAGAcgCCTAAAGGATCAAC	SEQ ID NO: 313
24	TMHIV115 L42R as	GGAGCTGTTGATCCTTTcGGTATCTTTCCACAGCC	SEQ ID NO: 314
25	TMHIV115 L42R s	GGCTGTGGAAAGATACCgAAAGGATCAACAGCTCC	SEQ ID NO: 315
15	TMHIV115 K43R AS	GAGCTGTTGATCCcTTAGGTATCTTTCCAC	SEQ ID NO: 316
14	TMHIV115 K43R S	GTGGAAAGATACCTAAgGGATCAACAGCTC	SEQ ID NO: 317
17	TMHIV115 D44R AS	AGGAGCTGTTGAcgCTTTAGGTATCTTT	SEQ ID NO: 318
16	TMHIV115 D44R S	AAAGATACCTAAAGcgTCAACAGCTCCT	SEQ ID NO: 319
26	TMHIV115 Q45R as	CCCAGGAGCTGTcGATCCTTTAGGTATC	SEQ ID NO: 320
27	TMHIV115 Q45R s	GATACCTAAAGGATCgACAGCTCCTGGG	SEQ ID NO: 321

N°	Name	Primer sequence (5'-3')	SEQ ID
28	TMHIV115 Q46R as	CAAATCCCCAGGAGCcGTTGATCCTTTAG	SEQ ID NO: 322
29	TMHIV115 Q46R s	CTAAAGGATCAACgGCTCCTGGGGATTTG	SEQ ID NO: 323
30	TMHIV115 L47R as	CAAATCCCCAGGcGCTGTTGATCCTTTAG	SEQ ID NO: 324
31	TMHIV115 L47R s	CTAAAGGATCAACAGCgCCTGGGGATTTG	SEQ ID NO: 325
32	TMHIV115 L48R as	CCCAAATCCCCcGGAGCTGTTG	SEQ ID NO: 326
33	TMHIV115 L48R s	CAACAGCTCCgGGGGATTTGGG	SEQ ID NO: 327
34	TMHIV115 G49R as	CCCCAAATCCgCAGGAGCTGTTG	SEQ ID NO: 328
35	TMHIV115 G49R s	CAACAGCTCCTGcGGATTTGGGG	SEQ ID NO: 329
36	TMHIV115 I50R as	GCAACCCCAtcTCCCCAGGAGCTG	SEQ ID NO: 330
37	TMHIV115 I50R s	CAGCTCCTGGGGAgaTGGGGTTGC	SEQ ID NO: 331
38	TMHIV115 W51R as	GCAACCCCAtcTCCCCAGGAGCTG	SEQ ID NO: 332
39	TMHIV115 W51R s	CAGCTCCTGGGGAgaTGGGGTTGC	SEQ ID NO: 333

HIV115 Y41 mutant construction: To explore the amino acid sequence necessary for the loss of immunosuppression, HIV115 Y41 mutants were produced by PCR using the pDFG HIV115 WT plasmid as template and pairs of primers 1-42 and 43-2, 1-44 and 45-2, 1-46 and 47-2, 1-48 and 49-2, 1-50 and 51-2, or 1-52 and 53-2, to introduce the Y41K, Y41H, Y41A, Y41G, Y41F, or Y41L mutations respectively. The PCR products were then used as templates in subsequent PCR using primers 1-2. These PCR fragments were digested with SfiI and MluI and inserted into pDFG-ectoSyncytin-1 (Mangeney et al, 2007) opened with the same enzymes

All the constructions were sequenced before use.

N°	Name	Primer sequence (5'-3')	SEQ ID NO
42	TMHIV115 Y41K as	GTTGATCCTTTAGtTtTCTTTCCACAGCCAG	SEQ ID NO: 334
43	TMHIV115 Y41K s	CTGGCTGTGGAAAGAaAaCTAAAGGATCAAC	SEQ ID NO: 335
44	TMHIV115 Y41H as	GTTGATCCTTTAGGTgTCTTTCCACAGCCAG	SEQ ID NO: 336
45	TMHIV115 Y41H s	CTGGCTGTGGAAAGAcACCTAAAGGATCAAC	SEQ ID NO: 337
46	TMHIV115 Y41A as	GTTGATCCTTTAGGgcTCTTTCCACAGCCAG	SEQ ID NO: 338
47	TMHIV115 Y41A s	CTGGCTGTGGAAAGAgcCCTAAAGGATCAAC	SEQ ID NO: 339
48	TMHIV115 Y41G as	GTTGATCCTTTAGGccTCTTTCCACAGCCAG	SEQ ID NO: 340
49	TMHIV115 Y41G s	CTGGCTGTGGAAAGAggCCTAAAGGATCAAC	SEQ ID NO: 341
50	TMHIV115 Y41F as	GTTGATCCTTTAGGaATCTTTCCACAGCCAG	SEQ ID NO: 342

51	TMHIV115 Y41F s	CTGGCTGTGGAAAGATtCCTAAAGGATCAAC	SEQ ID NO: 343
52	TMHIV115 Y41L as	GTTGATCCTTTAGGagTCTTTCCACAGCCAG	SEQ ID NO: 344
53	TMHIV115 Y41L s	CTGGCTGTGGAAAGActCCTAAAGGATCAAC	SEQ ID NO: 345

HIV115 Y41 double mutants construction: HIV115 Y41R K72A, G or S double mutants were produced by PCR using the pDFG HIV115 Y41R plasmid as template and pairs of primers 1-94 and 93-2, 1-96 and 95-2, or 1-98 and 97-2. The PCR products were then used as templates in subsequent PCR using primers 1-2. These PCR fragments were digested with SfiI and MluI and inserted into pDFG-ectoSyncytin-1 (Mangeney et al, 2007) opened with the same enzymes. HIV115 R40X Y41R double-mutants were produced by PCR using the pDFG HIV115 Y41R as template and pairs of primers 1-54 and 55-2, 1-56 and 57-2 to introduce the R40A and R40E mutations respectively. HIV115 R40X Y41A double-mutants were produced by PCR using the pDFG HIV115 Y41A as template and pairs of primers 1-58 and 59-2, 1-60 and 61-2, 1-62 and 63-2, 1-64 and 65-2 to introduce the R40A, R40E, R40S, R40T mutations respectively. HIV115 R40X simple mutants were also generated using pDFG HIV115 WT as template and pairs of primers 1-66 and 67-2, 1-68 and 69-2, 1-70 and 71-2, 1-72 and 73-2.

The PCR products were then used as templates in subsequent PCR using primers 1-2. These PCR fragments were digested with SfiI and MluI and inserted into pDFG-ectoSyncytin-1 (Mangeney et al, 2007) opened with the same enzyme.

N°	Name	Primer sequence (5'-3')	SEQ ID
54	TM HIV115 R40AY41R-S	CTGGCTGTGGAAgcAcgCCTAAAGGATCAAC	SEQ ID NO: 378
55	TM HIV115 R40AY41R-AS	GTTGATCCTTTAGGcgTgcTTCCACAGCCAG	SEQ ID NO: 379
56	TM HIV115 R40EY41R-S	CTGGCTGTGGAAgaAcgCCTAAAGGATCAAC	SEQ ID NO: 380

N°	Name	Primer sequence (5'-3')	SEQ ID
57	TM HIV115 R40EY41R-AS	GTTGATCCTTTAGGcgTtcTTCCACAGCCAG	SEQ ID NO: 381
58	TM HIV115 R40AY41A-S	CTGGCTGTGGAAgctgcCCTAAAGGATCAAC	SEQ ID NO: 382
59	TM HIV115 R40AY41A-AS	GTTGATCCTTTAGGgcagcTTCCACAGCCAG	SEQ ID NO: 383
60	TM HIV115 R40EY41A-S	CTGGCTGTGGAAgaagcCCTAAAGGATCAAC	SEQ ID NO: 384
61	TM HIV115 R40EY41A-AS	GTTGATCCTTTAGGgcttcTTCCACAGCCAG	SEQ ID NO: 385
62	TM HIV115 R40SY41A-S	CTGGCTGTGGAAagcgcCCTAAAGGATCAAC	SEQ ID NO: 386
63	TM HIV115 R40SY41A-AS	GTTGATCCTTTAGGgcgctTTCCACAGCCAG	SEQ ID NO: 387
64	TM HIV115 R40TY41A-S	CTGGCTGTGGAAacagcCCTAAAGGATCAAC	SEQ ID NO: 388
65	TM HIV115 R40TY41A-AS	GTTGATCCTTTAGGgctgtTTCCACAGCCAG	SEQ ID NO: 389
66	TM HIV115 R40A-S	CTGGCTGTGGAAgctTACCTAAAGGATCAAC	SEQ ID NO: 390
67	TM HIV115 R40A-AS	GTTGATCCTTTAGGTAagcTTCCACAGCCAG	SEQ ID NO: 391

N°	Name	Primer sequence (5'-3')	SEQ ID
68	TM HIV115 R40E-S	CTGGCTGTGGAAgaaTACCTAAAGGATCAAC	SEQ ID NO: 392
69	TM HIV115 R40E-AS	GTTGATCCTTTAGGTAttcTTCCACAGCCAG	SEQ ID NO: 393
70	TM HIV115 R40S-S	CTGGCTGTGGAAagcTACCTAAAGGATCAAC	SEQ ID NO: 394
71	TM HIV115 R40S-AS	GTTGATCCTTTAGGTAgctTTCCACAGCCAG	SEQ ID NO: 395
72	TM HIV115 R40T-S	CTGGCTGTGGAAacaTACCTAAAGGATCAAC	SEQ ID NO: 396
73	TM HIV115 R40T-AS	GTTGATCCTTTAGGTAtgtTTCCACAGCCAG	SEQ ID NO: 397
93	TMHIV115 K72A s	GCTAGTTGGAGTAATgcATCTCTGGAACAGATTTGG	SEQ ID NO: 398
94	TMHIV115 K72A as	CCAAATCTGTTCCAGAGATgcATTACTCCAACTAGC	SEQ ID NO: 399
95	TMHIV115 K72G s	GCTAGTTGGAGTAATggATCTCTGGAACAGATTTGG	SEQ ID NO: 400
96	TMHIV115 K72G as	CCAAATCTGTTCCAGAGATccATTACTCCAACTAGC	SEQ ID NO: 401
97	TMHIV115 K72S s	GCTAGTTGGAGTAATtcATCTCTGGAACAGATTTGG	SEQ ID NO: 402
98	TMHIV115 K72S as	CCAAATCTGTTCCAGAGATgaATTACTCCAACTAGC	SEQ ID NO: 403

Introduction of HIV115 mutations into an HIV Env expression vector: To introduce these HIV envelope mutations into the HIVenv pTr712 expression vector (Schnierle et al PNAS 1997), a silent mutation was first generated to create an SfiI insertion site. PCR fragments were generated using pTr712as a template and primer pairs 38-39 and 40-41. The PCR products were then used as templates in subsequent PCR using primers 38-41.

The resulting PCR fragment was then digested with BsaBI and HindIII and inserted into the pTr712 plasmid opened with the same enzymes resulting in the pTr712-Sfi plasmid.
PCR fragments of each HIV115 mutation were then generated by using primers 40-41 and the pDFG HIV115 mutant plasmids as templates, digestion with SfiI and HindIII and then insertion into the pTr712-Sfi plasmid opened with the same enzymes.
All the constructions were sequenced before use.

N°	Name	Primer sequence (5'-3')	SEQ ID NO
38	HIV BH10 BsaBI s	acaaattagatgttcatcaaatattacaggg	SEQ ID NO: 346
39	HIV BH10 SfiI mutsil as	GCAACAGATGCTGTTGgGCCTCA ATgGCCCTCAGCAAATTGTTC	SEQ ID NO: 347
40	HIV BH10 SfiI mutsil s	GAACAATTTGCTGAGGGCcATTG AGGCcCAACAGCATCTGTTGC	SEQ ID NO: 348
41	HIV BH10 HindIII as	gtgtattaagcttgtgtaattgttaatttctc	SEQ ID NO: 349
74	EnvHIVTr712-Xho-Age-Kozak-S	NNNNNCTCGAGACCGGTccaactaga accATGAGAGTGAAGGAGAAATA TCAGC	SEQ ID NO : 404
75	EnvHIVTr712-Mlu-AS	NNNNNACGCGTTCAATATCCCTG CCTAACTC	SEQ ID NO : 405
76	EnvHIVWT-Mlu-AS	NNNNNACGCGTTTATAGCAAAAT CCTTTCCAAGC	SEQ ID NO : 406

Establishment of *env*-expressing tumor cells and MCA205 tumor-rejection assay: 7.5 x 10^5 293T cells were cotransfected with the *env*-expressing pDFG retroviral vector to be tested (1.75 µg) and expression vectors for the MLV proteins (0.55 µg for the amphotropic MLV *env* vector and 1.75 µg for the MLV *gag* and *pol* vector). 36 hours post-transfection, supernatants were harvested for infection of MCA205 tumor cells (2.5 ml of supernatant per 5 x 10^5 cells with 8 µg/ml polybrene). Cells were maintained in selective medium (400 units/ml hygromycin) for 3 weeks, and then washed with PBS, trypsinized and inoculated subcutaneously in the shaved area of each mouse right flank as in Mangeney et al (1998, 2007). Tumor growth was monitored by palpation twice or thrice weekly and tumor area (mm^2) determined by measuring perpendicular tumor diameters. The extent of

"immunosuppression" was quantified by an index based on tumor size: $(A_{env}-A_{none})/A_{none}$, where A_{env} and A_{none} are the mean areas at the peak of growth of tumors from Balb/c mice injected with *env*-expressing or control cells, respectively.

Analysis of HIVenv expression : 293T cells were transfected with 4mg of the expression vector for the HIV-1 envelope (pTr712) either wild-type or mutated at the indicated positions, by Calcium Phosphate precipitation. Cells are washed 16h later and then harvested 2 days post-transfection using PBS-EDTA 5mM. The 110-H monoclonal antibody (anti-V3 loop, gift from Hybridolab, Pasteur Institute) was used (1/200 dilution) to stain the HIV envelope. As a secondary antibody, the Inventors used the goat anti mouse IgG Alexa 488 (1/400) (Invitrogen). For intracellular HIVenv staining, 293T cells were fixed with a formaldehyde buffer and then permeabilized (BD cytofix /cytoperm, BD Biosciences). The isotype mouse anti IgG1Kappa (BD Biosciences) was used to control non-specific staining. Fluorescence was acquired by flow cytometry using a FACS Calibur (BD Biosciences), and data analysed by the CellQuest software (BD Biosciences).

Mutated Env pseudotyping and measure of viral titer:293T cells are triple transfected with 3mg of a reporter MLV vector carrying GFP (CNCG), 1.75mg Mo-MLV gag-pol vector and 0.55mg phCMV vector encoding HIV-1 envelope wt or mutated at the indicated positions. The infectivity of Mo-MLV virions pseudotyped with HIV-1 Env, harvested 48 hours post-transfection, is measured using U87 cells ($CD4^+$, $CXCR4^+$) as target cells. The infectivity of the enveloppes is analysed after 72h exposure diluted 0.45mm-filtered supernatant in presence of 4mg/mL polybrene. The fluorescence (GFP) is acquired by flow cytometry using a FACS Calibur (BD Biosciences). The results are analysed by the CellQuest software (BD Biosciences). The resulting titers (number of infected cells/mL) are calculated as the following : (% GFP^+cells (infected) x plated cell number)/volume of supernatant x 1000.

Env SIV mutants construction : PCR fragments were generated using p239 SPE3' (the plasmid encoding the SIV half virus containing the envelope protein) as a template and primer pairs 77-79 and 78-80, 77-81 and 78-82, 77-83 and 78-84, 77-85 and 78-86, 77-87 and 78-88, 77-89 and 78-90 to introduce the E39R, K40R, Y41R, L42R, K43R, D44R

mutations respectively. The PCR products were the used as templates in subsequent PCR using primers 77-78. The resulting PCR fragment was then digested with BmgBI and NheI and inserted into the p239 SPE3' plasmid opened with the same enzymes.
All the constructions were sequenced before use.

Introduction of SIV mutants ectodomain into pDFG : To generate the pDFG plasmids encoding the fragment of SIV envelope ectodomain-55, PCR fragments generated using p239 SPE3' WT and mutants as a template and primer pairs 91-92, were digested with SfiI and MluI and inserted into pDFG opened with the same enzymes.

77	Env SIV S	ccgctcagtcccgaactttattggc	SEQ ID NO: 350
78	Env SIV AS	ggtggggaagagaacactggcc	SEQ ID NO: 351
79	SIV env E39R s	cagactagggtcactgccatcCGCaagtacttaaaggaccaggcg	SEQ ID NO: 352
80	SIV env E39R as	cgcctggtcctttaagtacttGCGgatggcagtgaccctagtctg	SEQ ID NO: 353
81	SIV env K40R s	actagggtcactgccatcgagCGCtacttaaaggaccaggcgcag	SEQ ID NO: 354
82	SIV env K40R as	ctgcgcctggtcctttaagtaGCGctcgatggcagtgaccctagt	SEQ ID NO: 355
83	SIV env Y41R s	GCCATCGAGAAGcgCTTAAAGGACCAGGCG	SEQ ID NO: 356
84	SIV env Y41R as	CGCCTGGTCCTTTAAGcgCTTCTCGATGGC	SEQ ID NO: 357
85	SIV env L42R s	gtcactgccatcgagaagtacCGCaaggaccaggcgcagctg	SEQ ID NO: 358
86	SIV env L42R as	cagctgcgcctggtccttGCGgtacttctcgatggcagtgac	SEQ ID NO: 359
87	SIV env K43R s	gccatcgagaagtacttaCGCgaccaggcgcagctgaatgcttgg	SEQ ID NO: 360
88	SIV env K43R as	ccaagcattcagctgcgcctggtcGCGtaagtacttctcgatggc	SEQ ID NO: 361
89	SIV env D44R s	gagaagtacttaaagCGCcaggcgcagctgaatgcttgg	SEQ ID NO: 362
90	SIV env D44R as	attcagctgcgcctgGCGctttaagtacttctcgatggc	SEQ ID NO: 363
91	TMSIV55 Sfi S	ACATggcccagccggccgctgggatagtgcagcaac	SEQ ID NO: 364
92	TMSIV55 Mlu AS	GTATacgcgtTTAaaacgcacatccccaagcattc	SEQ ID NO: 365

Comparative example: test of the *in vivo* effect of the mutation G49R, which corresponds to the mutation "*G19R*" in the international application WO 2010/022,740.

WO 2010/022,740 discloses a consensus sequence of 50 amino acid of the HIV ENV protein. In this sequence, it is suggested that substitution of amino acids in positions 10, 19, 24, 34 and 40 affect the immunosuppressive properties of the HIV ENV protein.

These mutations are a transposition in lentivirus of the teaching of WO 2005/095,442 limited to endogenous or onco retroviruses. The authors of WO 2005/095,442 are also the

authors of the present application and they early observed that such a transposition is not effective.

Despite the fact that any amino acids can be assigned to the positions 10, 19, 24, 34 or 40 in the consensus sequence of WO 2010/022,740, only one substitution (one residue for one position) was tested by *ex vivo* experiments in WO 2010/022,740. It is the mutation *''G19R''*, which corresponds to the mutation G49R in the present figures 1 and 3.

Because the immune response of an individual involves different organs and different cellular and non-cellular components, *ex vivo* results have no predictive value concerning the *in vivo* immunosuppressive properties of a viral protein.

To determine if the mutations previously disclosed in WO 2010/022,740 are suitable for a medical use, the mutation G49R has been tested using the MCA205 tumor rejection *in vivo* assay, as defined in the section ''*Establishment of env-expressing tumor cells and MCA205 tumor-rejection assay''* of the Example.

As shown in Figure 3, the peptide G49R remains almost as immunosuppressive *in vivo* as the wild type HIV 115 peptide, with an immunosuppression index which is higher than 0,5. Thus, the mutation G49R does not induce a significant decrease of the *in vivo* immunosuppressive properties of the HIV ENV protein, with a ratio of immunosuppression index of G49R mutated ENV HIV 115 peptide ($i_{\text{mutated env}}$) / immunosuppression index of wild type ENV HIV 115 peptide ($i_{\text{wild type env}}$), which is 0,7 (*i.e.* higher than 0,5).

This result demonstrates the insufficiently described teaching of WO 2010/022740 since the only one mutation tested in WO 2010/022,740, using an *ex vivo* test, does not significantly affect the *in vivo* immunosuppressive properties of the HIV ENV protein.

As a consequence, WO 2010/022,740 raises the same technical problem as the present invention but does not offer a technical solution.

2012350258 25 Jan 2017

CLAIMS

1. Pharmaceutical composition comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein having at least 90% identity, to one sequence chosen from the group consisting of SEQ ID NO : 216, SEQ ID NO : 420 and SEQ ID NO : 421,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

in association with a pharmaceutically acceptable carrier,

said substantial absence of immunosuppressive activity of the above mentioned mutated human or simian lentiviral ENV protein or of the above defined fragment being liable to be assessed by the fact that in an in vivo assay involving engrafted tumor cells rejection, said tumor cells being transduced either so as to express said mutated ENV protein or said fragment (mutated ENV tumor cells),
or said tumor cells being transduced so as to express said wild type ENV protein or a fragment thereof (wild type ENV tumor cells),
or said tumor cells being not transduced (normal tumor cells),
the following ratio :
immunosuppression index of said mutated ENV protein or of said fragment ($i_{mutated\ env}$) / immunosuppression index of wild type ENV protein ($i_{wild\ type\ env}$) is less than 0.5,
$i_{mutated\ env}$ being defined by : (maximum area reached by mutated ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells), and
$i_{wild\ type\ env}$ being defined by : (maximum area reached by wild type ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells).

2. Pharmaceutical composition according to claim 1 comprising as active substance :
a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,
said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein
X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

in association with a pharmaceutically acceptable carrier.

3. Pharmaceutical composition according to claim 1 comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G, R,

in association with a pharmaceutically acceptable carrier.

4. Pharmaceutical composition according to any one of claims 1 to 3 comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

or

X_a is F or L, and X_b is F, G or R,

or

X_a is A, G or R, and X_b is A,

or

X_a is A, G or R, and X_b is F, G or R,

in association with a pharmaceutically acceptable carrier.

5. Pharmaceutical composition according to claim 1 or claim 3, comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R,

in association with a pharmaceutically acceptable carrier.

6. Pharmaceutical composition according to any one of claims 1 to 5 comprising as active substance :

a) an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said mutated human or simian lentiviral ENV protein resulting from mutation of the transmembrane (TM) subunit of a wild type human or simian lentiviral ENV protein,

said mutated human or simian lentiviral ENV protein comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

or

b) at least one fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

said fragment comprising at least 40 amino acids,

said fragment comprising a mutated immunosuppressive domain (ISU) containing the following amino acid sequence:

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P,

or

X_a is Y, I, H, C or T, and X_b is F, G or R,

in association with a pharmaceutically acceptable carrier.

7. Pharmaceutical composition according to any one of claims 1, 3 or 5,

wherein

X_a is R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is R, or

X_a is R, and X_b is R.

8. Pharmaceutical composition according to any one of claims 1 to 7, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the following amino acid sequences :

A-I-E-K-X_a-X_b-X-DQ (SEQ ID NO: 422),

A-I-E-R-X_a-X_b-X-DQ (SEQ ID NO: 423),

A-V-E-K-X_a-X_b-X-DQ (SEQ ID NO: 424),

A-V-E-R-X_a-X_b-X-DQ (SEQ ID NO: 425).

9. Pharmaceutical composition according to any one of claims 1 to 8, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences :

SEQ ID NO : 13, SEQ ID NO : 42, SEQ ID NO : 71,

SEQ ID NO : 9 to 12,

SEQ ID NO : 14 to 41,

SEQ ID NO : 43 to 70, and
SEQ ID NO : 72 to 95.

10. Pharmaceutical composition according to any one of claims 1 to 8, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences :
SEQ ID NO : 13, SEQ ID NO : 42, SEQ ID NO : 71,
SEQ ID NO : 9, 11, 15 to 21, 23 to 29, 31 to 38, 40, 44 to 50, 52 to 58, 60 to 67, 69, 73 to 79, 81 to 87, 89 to 95.

11. Pharmaceutical composition according to any one of claims 1 to 8, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences : SEQ ID NO : 96 to 211.

12. Pharmaceutical composition according to any one of claims 1 to 8, wherein said isolated mutated human or simian lentiviral ENV protein or said fragment of said isolated mutated human or simian lentiviral ENV protein comprises one of the amino acid sequences : SEQ ID NO : 96, 98, 100, 102 to 108, 110 to 116, 118 to 125, 127, 129, 131 to 137, 139 to 145, 147 to 154, 156, 158, 160 to 166, 168 to 174, 176 to 183, 185, 187, 189 to 195, 197 to 203, 205 to 211.

13. Pharmaceutical composition according to any one of claims 1 to 8, wherein said isolated mutated human or simian lentiviral ENV protein consists of one of the amino acid sequences : SEQ ID NO : 212 to 269.

14. Pharmaceutical composition according to any one of claims 1 to 8, wherein said isolated mutated human or simian lentiviral ENV protein consists of one of the amino acid sequences : SEQ ID NO : 212, 214, 216, 218 to 224, 226 to 232, 234 to 241, 243, 245, 247 to 253, 255 to 261, 263 to 269.

15. Pharmaceutical composition according to any one of claims 1 to 14, wherein said isolated mutated human or simian lentiviral ENV protein comprises an additional mutation in one at least of the amino acids at positions 29, 36 and 37 of SEQ ID NO: 426 :

A[I/V]E[K/R]$X_aX_bX_1$DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VP$X_cX_{10}Z_1Z_2Z_3Z_4Z_5X_dX_e$[S/T] (SEQ ID NO: 426)

wherein

X_a and X_b are as defined in any one of claims 1 to 14,

X_1 to X_{10} represent any amino acid,

Z_1 to Z_5 represent no amino acid or any amino acid, independently from each other

such that

- X_c is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V or Y, preferably A, D, or N,
- X_d is A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, Y or W,preferably A, G, S or Y,
- X_e is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, T, V, Y or W, preferably A, D or N.

16. Pharmaceutical composition according to any one of claims 1 to 15, wherein said mutated protein consists of one of the amino acid sequences of the group consisting of SEQ ID NO : 271 to 283.

17. Pharmaceutical composition comprising as active substance a nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, as defined in any one of claims 1 to 16.

18. Pharmaceutical composition according to claim 18, wherein said nucleic acid molecule being contained in a vector, said vector comprising means allowing the expression of the mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, as defined in any one of claims 1 to 16.

19. Pharmaceutical composition according to claim 18, wherein said vector being chosen among a measles vector, a canarypox vector, a pox vector, a fowlpox, an adenoviral vector, a lentiviral vector, a Sendaï virus, a Cytomegalovirus vector or a Modified Vaccinia Ankara vector.

20. Pharmaceutical composition, according to any one of claims 17 to 19, comprising at least one nucleic acid molecule coding for a GAG protein and/or a PRO protein and/or a POL protein and/or a mutated NEF protein, wherein
said mutated NEF protein is substantially devoid of immunosuppressive properties,
of a human or simian lentivirus, said lentivirus being preferably of the same origin as the mutated lentiviral ENV protein.

21. Pharmaceutical composition, according to any one of claims 18 to 20, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains said at least one nucleic acid molecule coding for a GAG protein and/or a PRO protein and/or a POL protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

22. Pharmaceutical composition, according to claim 20 or claim 21, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains all said at least one nucleic acid molecule coding for a GAG protein and/or a PRO protein and/or a POL protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

23. Pharmaceutical composition, according to claim 20 or claim 21, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in a vector which is different from the at least one vector containing said at least one nucleic

acid molecule coding for a GAG protein and/or a PRO protein and/or a POL protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

24. Pharmaceutical composition, according to claim 20 or claim 23, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, said nucleic acid molecule coding for a GAG protein, said nucleic acid molecule coding for a PRO protein, said nucleic acid molecule coding for a POL protein and said nucleic acid molecule coding for a mutated NEF protein substantially devoid of immunosuppressive properties, are all contained in vectors which are different from each other.

25. Pharmaceutical composition, according to any one of claims 17 to 20, comprising at least one nucleic acid molecule coding for a GAG protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties,
of a human or simian lentivirus, said lentivirus being preferably of the same origin as the mutated lentiviral ENV protein.

26. Pharmaceutical composition, according to claims 20 or claim 25, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains said at least one nucleic acid molecule coding for a GAG protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

27. Pharmaceutical composition, according to any one of claims 20, 25 or 26, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains a nucleic acid molecule coding for a GAG protein and for a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

28. Pharmaceutical composition, according to any one of claims 20, or 25 to 27, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in the same vector as the one which also contains a nucleic acid molecule coding for a GAG protein and for a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties,
said vector being a measles vector or a canary pox vector.

29. Pharmaceutical composition, according to claim 20 or claim 25, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, is contained in a vector which is different from the at least one vector containing said at least one nucleic acid molecule coding for a GAG protein and/or a mutated NEF protein, wherein said mutated NEF protein is substantially devoid of immunosuppressive properties.

30. Pharmaceutical composition, according to any one of claims 20, 25 or 29, wherein said nucleic acid molecule coding for a mutated human or simian lentiviral ENV protein, or a fragment of said mutated human or simian lentiviral ENV protein, said nucleic acid molecule coding for a GAG protein and said nucleic acid molecule coding for a mutated NEF protein substantially devoid of immunosuppressive properties, are all contained in vectors which are different from each other.

31. Pharmaceutical composition according to any one of claims 1 to 30, in association with at least one antiviral compound, preferably for a simultaneous, separated or sequential use.

32. Pharmaceutical composition according to any one of claims 1 to 31, for its use for stimulating an immune response in a host organism.

33. Pharmaceutical composition according to any one of claims 1 to 32, for its use for the prevention or the treatment of lentiviral infection, preferably HIV-1 infection, HIV-2 infection or SIV infection.

34. Pharmaceutical composition according to any one of claims 1 to 33, for its use as a vaccine, in particular against HIV-1 infection, HIV-2 infection or SIV infection.

35. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, consisting of modifying the immunosuppressive property of:
a wild-type human or simian lentiviral ENV protein,
or a fragment of said wild-type human or simian lentiviral ENV protein, said fragment comprising at least 40 amino acids,
said ENV protein or fragment thereof presenting a transmembrane subunit (TM) comprising an immunosuppressive domain (ISU) containing the following amino acid sequence :

A-[I/V]-E-[K/R]-X'$_a$-X'$_b$-X-D-Q (SEQ ID NO: 427),

wherein
X represents any amino acid,
X'$_a$ is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and
X'$_b$ is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y,

said method comprising a step of introduction of at least one mutation of X'$_a$ and/or X'$_b$,

to obtain:
an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,
said mutated human or simian lentiviral ENV protein having at least 90% identity, to one sequence chosen from the group consisting of SEQ ID NO : 216, SEQ ID NO : 420 and SEQ ID NO : 421,
or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R,

said substantial absence of immunosuppressive activity of the above mentioned mutated human or simian lentiviral ENV protein or of the above defined fragment being liable to be assessed by the fact that in an in vivo assay involving engrafted tumor cells rejection, said tumor cells being transduced either so as to express said mutated ENV protein or said fragment (mutated ENV tumor cells),

or said tumor cells being transduced so as to express said wild type ENV protein or a fragment thereof (wild type ENV tumor cells),

or said tumor cells being not transduced (normal tumor cells),

the following ratio :

immunosuppression index of said mutated ENV protein or of said fragment ($i_{mutated\ env}$) / immunosuppression index of wild type ENV protein ($i_{wild\ type\ env}$) is less than 0.5,

$i_{mutated\ env}$ being defined by : (maximum area reached by mutated ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells), and

$i_{wild\ type\ env}$ being defined by : (maximum area reached by wild type ENV tumor cells - maximum area reached by normal tumor cells) / (maximum area reached by normal tumor cells).

36. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35, consisting of modifying the immunosuppressive property of :

a wild-type human or simian lentiviral ENV protein,

or a fragment of said wild-type human or simian lentiviral ENV protein, said fragment comprising at least 40 amino acids,

said ENV protein or fragment thereof presenting a transmembrane subunit (TM) comprising an immunosuppressive domain (ISU) containing the following amino acid sequence :

A-[I/V]-E-[K/R]-Y-L-X-D-Q (SEQ ID NO : 1),

wherein

X represents any amino acid,

said method comprising a step of introduction of at least one mutation of Y in position 5 and/or L in position 6,

to obtain:

an isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R.

37. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, F, G, L or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is A, F, G or R, or

X_a is A, F, G, L or R, and X_b is A, F, G or R.

38. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R, or

X_a is F or L, and X_b is F, G or R, or

X_a is A, G or R, and X_b is A.

39. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is F, G or R, or

X_a is F or L, and X_b is F, G or R, or

X_a is A, G or R, and X_b is A, or

X_a is A, G or R, and X_b is F, G or R.

40. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is F, G or R.

41. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is A, G, or R, and X_b is L, I, V, M or P, or

X_a is Y, I, H, C or T, and X_b is F, G or R.

42. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to any one of claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising a mutated immunosuppressive domain (ISU) containing the following amino sequence :

A-[I/V]-E-[K/R]-X_a-X_b-X-D-Q (SEQ ID NO: 416),

wherein,

X represents any amino acid,

and either

X_a is R, and X_b is C, D, E, H, I, K, L, M, N, P, Q, S, T, V, W or Y, or

X_a is C, D, E, H, I, K, M, N, P, Q, S, T, V, W or Y, and X_b is R, or

X_a is R, and X_b is R.

43. A method to obtain the active substance of a pharmaceutical composition, as defined in any one of claims 1 to 31, according to claim 35,

wherein said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity,

or a fragment of said isolated mutated human or simian lentiviral ENV protein having substantially no immunosuppressive activity, said fragment comprising at least 40 amino acids,

said mutated ENV protein and fragment thereof comprising an additional mutation in one at least of the amino acids at positions, 29, 36 and 37 of SEQ ID NO: X :

A[I/V]E[K/R]$X_aX_bX_1$DQX_2X_3LX_4X_5WGC[A/S][F/G]X_6X_7CVX_8TX_9VP$X_cX_{10}Z_1Z_2Z_3Z_4Z_5X_dX_e$[S/T] (SEQ ID NO: 426)

wherein

X_a and X_b are as defined in any one of claims 1 to 14,

X_1 to X_{10} represent any amino acid,

Z_1 to Z_5 represent no amino acid or any amino acid, independently from each other

such that

- X_c is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V or Y, preferably A, D, or N,
- X_d is A, C, D, E, F, G, H, I, L, M, N, P, Q, R, S, T, V, Y or W, preferably A, G, S or Y,
- X_e is A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, T, V, Y or W, preferably A, D or N.

44. The active substance when prepared according to method of any one of claims 35 to 43.

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQ **HIV30**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILA **HIV37**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLK **HIV43**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLG **HIV49**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSG **HIV55**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNA **HIV67**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM **HIV81**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **HIV115**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIRAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 L36R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILRVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 A37R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILARERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 V38R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVRRYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 E39R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 Y41R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYRKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 L42R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLRDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 K43R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKRQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 D44R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDRQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 Q45R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQRLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 Q46R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQRLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 L47R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLRGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 L48R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLRIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 G49R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGRWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNE
QEL **115 I50R**
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIRGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL **115 W51R**

Figure 1(first part)

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **HIV115**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERRLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41R**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERHLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41H**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERKLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41K**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERGLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41G**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERLLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41L**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERALKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41A**

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERFLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ

EL **115 Y41F**

Figure 1 (end)

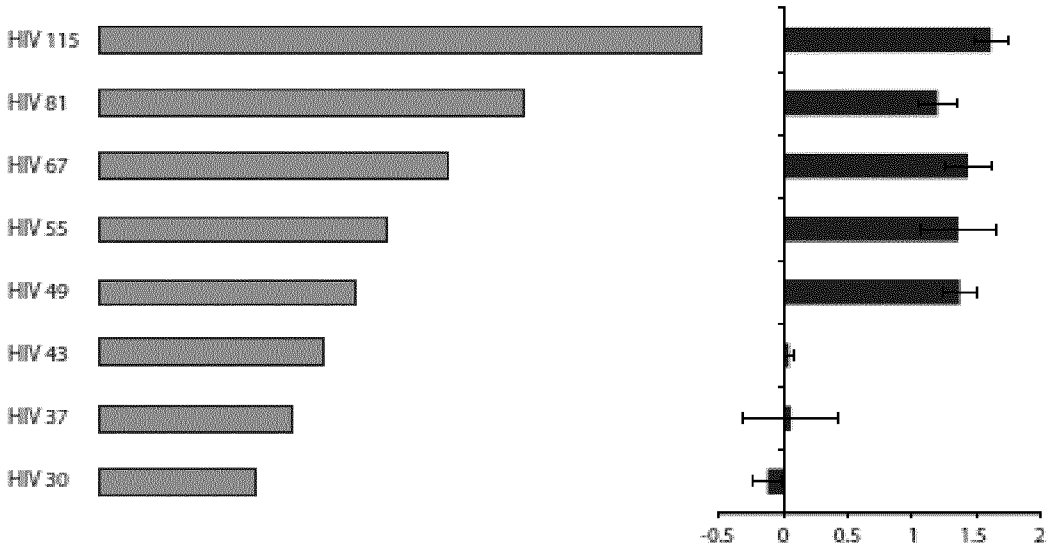
HIV 115
HIV 81
HIV 67
HIV 55
HIV 49
HIV 43
HIV 37
HIV 30
-0.5
0
0.5
1
1.5
2

Figure 2

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQ - HIV 30
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILA - HIV 37
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLK - HIV 43
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLG - HIV 49
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSG - HIV 55
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNA - HIV 67
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM - HIV 81
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDREINNYTSLIHSLIEESQNQQEKNEQ
EL - HIV 115

SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGC...KNEQEL - HIV 115
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARI**R**AVERYLKDQQLLGIWGC...KNEQEL - HIV 115 L36R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL**R**VERYLKDQQLLGIWGC...KNEQEL - HIV 115 A37R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILA**R**ERYLKDQQLLGIWGC...KNEQEL - HIV 115 V38R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAV**R**RYLKDQQLLGIWGC...KNEQEL - HIV 115 E39R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**R**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**R**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41R K72A
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**R**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41R K72G
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**R**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41R K72S
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**H**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41H
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**K**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41K
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**G**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41G
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**L**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41L
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**A**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41A
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVER**F**LKDQQLLGIWGC...KNEQEL - HIV 115 Y41F
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERY**R**KDQQLLGIWGC...KNEQEL - HIV 115 L42R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYL**R**DQQLLGIWGC...KNEQEL - HIV 115 K43R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLK**R**QQLLGIWGC...KNEQEL - HIV 115 D44R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKD**R**QLLGIWGC...KNEQEL - HIV 115 Q45R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ**R**LLGIWGC...KNEQEL - HIV 115 Q46R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ**R**LGIWGC...KNEQEL - HIV 115 L47R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQL**R**GIWGC...KNEQEL - HIV 115 L48R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLL**R**IWGC...KNEQEL - HIV 115 G49R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLG**R**WGC...KNEQEL - HIV 115 I50R
SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGI**R**GC...KNEQEL - HIV 115 W51R

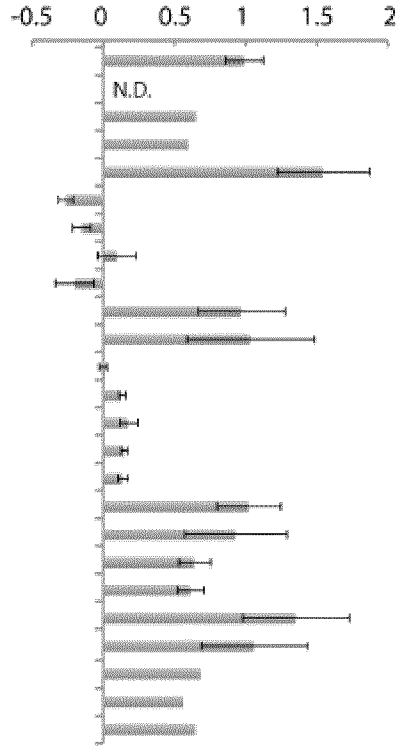

Figure 3

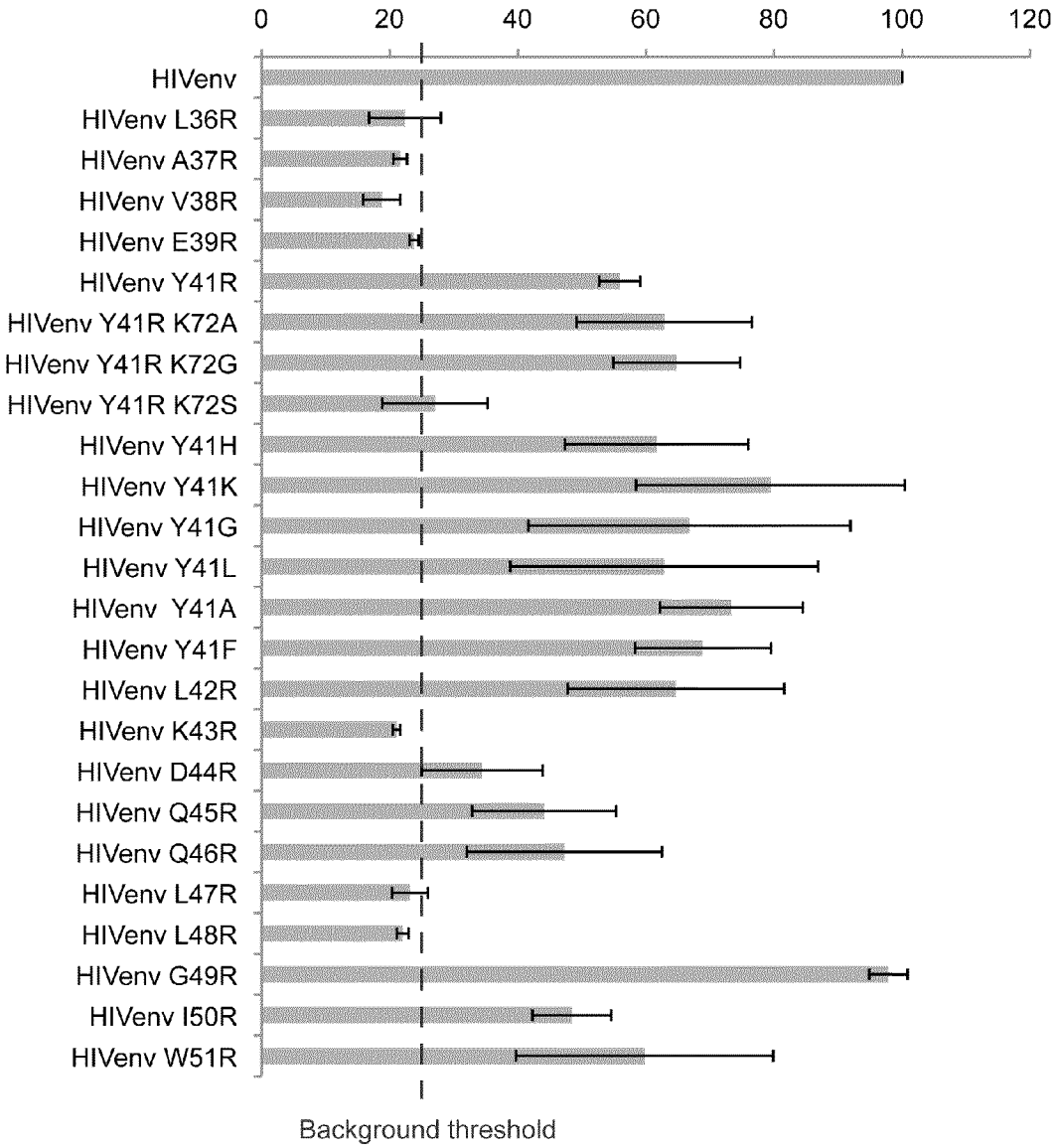
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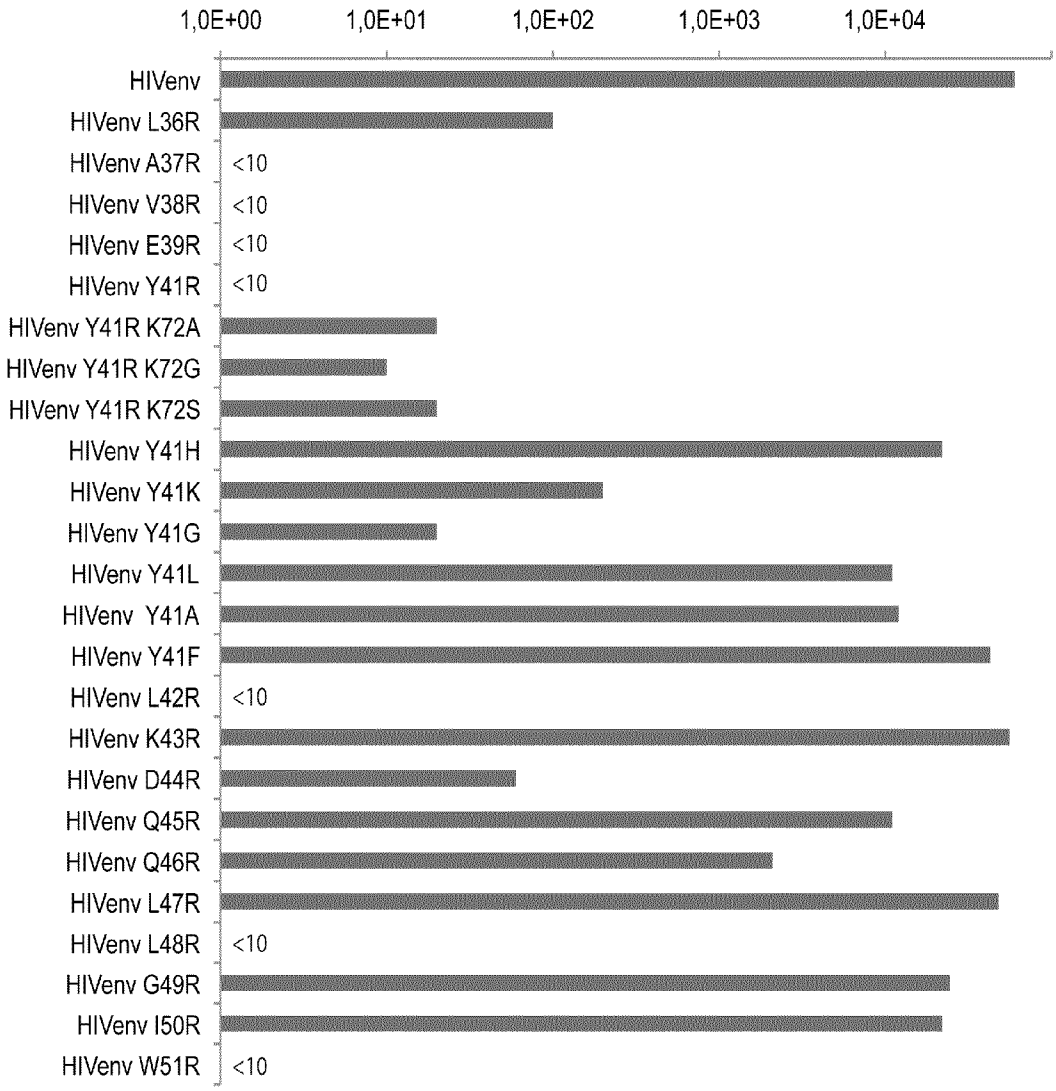
Figure 4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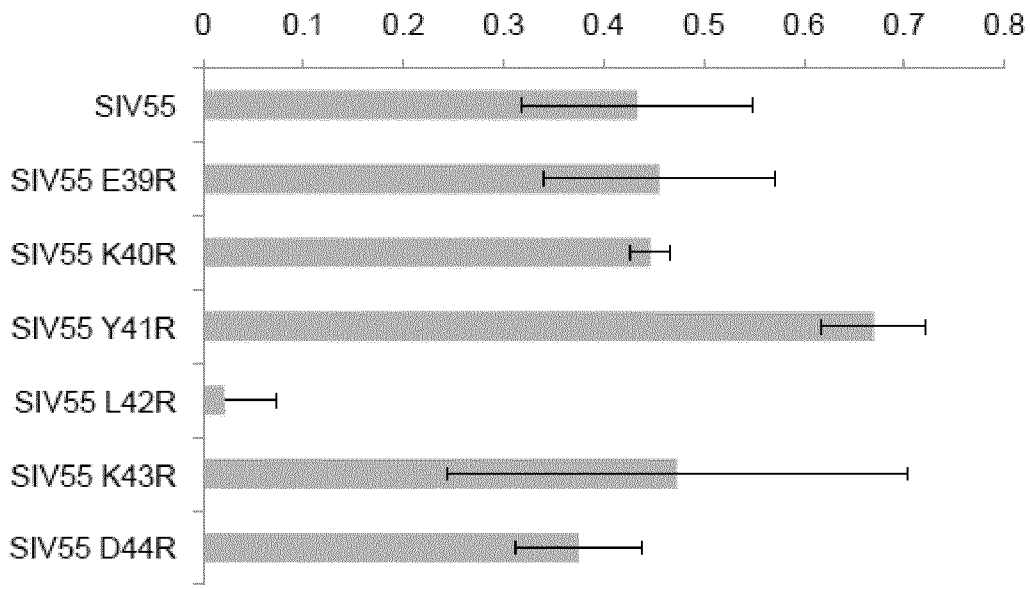
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Figure 6

SEQUENCE LISTING

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INSTITUT GUSTAVE ROUSSY
UNIVERSITE PARIS SUD XI
VIROXIS SAS

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<220>
<223> fragement of lentiviral ENV ISU

<400> 89

Ala Ile Glu Arg Leu Phe Lys Asp
1 5

<210> 90
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> fragement of lentiviral ENV ISU

<400> 90

Ala Ile Glu Arg Leu Gly Lys Asp
1 5

<210> 91
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> fragement of lentiviral ENV ISU

<400> 91

Ala Ile Glu Arg Leu Arg Lys Asp
1 5

<210> 92
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> fragement of lentiviral ENV ISU

<400> 92

Ala Ile Glu Arg Arg Ala Lys Asp

1 5

<210> 93
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> fragement of lentiviral ENV ISU

<400> 93

Ala Ile Glu Arg Arg Phe Lys Asp
1 5

<210> 94
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> fragement of lentiviral ENV ISU

<400> 94

Ala Ile Glu Arg Arg Gly Lys Asp
1 5

<210> 95
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> fragement of lentiviral ENV ISU

<400> 95

Ala Ile Glu Arg Arg Arg Lys Asp
1 5

<210> 96
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 96

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Ala Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 97
<211> 49
<212> PRT
<213> Artificial sequence

<220>
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<400> 97

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Phe Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 98
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 98

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Gly Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 99
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 99

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

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Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Val Leu Ala Val Glu Arg Leu Leu Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly
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<210> 100
<211> 49
<212> PRT
<213> Artificial sequence

<220>
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<400> 100

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Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Val Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly
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<210> 101
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 101

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Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Val Leu Ala Val Glu Arg Tyr Ala Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly
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<210> 102
<211> 49
<212> PRT

<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 102

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Tyr Phe Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 103
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 103

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Tyr Gly Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 104
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 104

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Tyr Arg Lys Asp Gln Gln Leu Leu

35 40 45

Gly

<210> 105
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 105

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Ala Ala Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 106
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 106

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Ala Phe Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 107
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 107

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Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Val Leu Ala Val Glu Arg Ala Gly Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly
```

<210> 108
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 108

```
Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Val Leu Ala Val Glu Arg Ala Arg Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly
```

<210> 109
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 109

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Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Val Leu Ala Val Glu Arg Phe Ala Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly
```

<210> 110
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 110

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Phe Phe Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 111
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 111

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Phe Gly Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 112
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 112

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln

20 25 30

Ala Arg Val Leu Ala Val Glu Arg Phe Arg Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 113
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 113

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Gly Ala Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 114
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 114

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Gly Phe Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 115
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 115

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1   5   10   15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Val Leu Ala Val Glu Arg Gly Gly Lys Asp Gln Gln Leu Leu
        35   40   45

Gly

<210> 116
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 116

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1   5   10   15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Val Leu Ala Val Glu Arg Gly Arg Lys Asp Gln Gln Leu Leu
        35   40   45

Gly

<210> 117
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 117

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1   5   10   15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Val Leu Ala Val Glu Arg Leu Ala Lys Asp Gln Gln Leu Leu
        35   40   45

Gly

<210> 118
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 118

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Leu Phe Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 119
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 119

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Leu Gly Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 120
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 120

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala

1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Leu Arg Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 121
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 121

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Arg Ala Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 122
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 122

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Arg Phe Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 123

<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 123

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Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15


Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30


Ala Arg Val Leu Ala Val Glu Arg Arg Gly Lys Asp Gln Gln Leu Leu
        35                  40                  45


Gly
```

<210> 124
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV1 ENV ISU

<400> 124

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Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1               5                   10                  15


Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30


Ala Arg Val Leu Ala Val Glu Arg Arg Arg Lys Asp Gln Gln Leu Leu
        35                  40                  45


Gly
```

<210> 125
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 125

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Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30
```

```
Ala Arg Val Thr Ala Ile Glu Lys Ala Leu Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  126
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  126

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Ala Arg Val Thr Ala Ile Glu Lys Phe Leu Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  127
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  127

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  128
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU
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<400> 128

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 129
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 129

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 130
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 130

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Ala Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln

50 55

<210> 131
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 131

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Phe Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 132
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 132

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Gly Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 133
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 133

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

```
Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Arg Lys Asp Gln Ala Gln Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 134
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 134

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Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 135
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 135

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Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Ala Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 136
<211> 57
<212> PRT

<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 136

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 137
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 137

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 138
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 138

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Phe Ala Lys Asp Gln Ala Gln Leu

```
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  139
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  139

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Ala Arg Val Thr Ala Ile Glu Lys Phe Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  140
<211>  57
<212>  PRT
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<220>
<223>  fragment of HIV2 ENV ISU

<400>  140

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Ala Arg Val Thr Ala Ile Glu Lys Phe Gly Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  141
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  141
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```
Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Ala Arg Val Thr Ala Ile Glu Lys Phe Arg Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  142
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  142

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  143
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  143

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Ala Arg Val Thr Ala Ile Glu Lys Gly Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
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<210> 144
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 144

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 145
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 145

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 146
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 146

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln

20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 147
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 147

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Leu Phe Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 148
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 148

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 149
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 149

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50   55

<210> 150
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 150

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50   55

<210> 151
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 151

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

Ala Arg Val Thr Ala Ile Glu Lys Arg Phe Lys Asp Gln Ala Gln Leu
        35   40   45

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Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  152
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  152

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  153
<211>  57
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  153

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  154
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  154

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
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1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  155
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  155

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Phe Leu Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  156
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  156

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  157
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<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 157

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 158
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 158

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 159
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 159

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30
```

```
Ala Arg Val Thr Ala Ile Glu Lys Tyr Ala Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55

<210>  160
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  160

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Phe Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55

<210>  161
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  161

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Gly Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55

<210>  162
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU
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<400> 162

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Arg Gln Asp Gln Ala Arg Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 163
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 163

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 164
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 164

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Ala Phe Gln Asp Gln Ala Arg Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln

50 55

<210> 165
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 165

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 166
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 166

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 167
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 167

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

```
Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Phe Ala Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55

<210>  168
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  168

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Phe Phe Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55

<210>  169
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of HIV2 ENV ISU

<400>  169

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Phe Gly Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55

<210>  170
<211>  57
<212>  PRT
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<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 170

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Phe Arg Gln Asp Gln Ala Arg Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 171
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 171

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 172
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 172

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Gly Phe Gln Asp Gln Ala Arg Leu

35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 173
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 173

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 174
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 174

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 175
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 175

```
Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 176
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 176

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Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Ala Arg Val Thr Ala Ile Glu Lys Leu Phe Gln Asp Gln Ala Arg Leu
        35                  40                  45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 177
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 177

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Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 178
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 178

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 179
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 179

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 180
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 180

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln

20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Arg Phe Gln Asp Gln Ala Arg Leu
35 40 45

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 181
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 181

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 182
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of HIV2 ENV ISU

<400> 182

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ser Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 183
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 183

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

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

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50   55

<210> 184
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 184

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

Thr Arg Val Thr Ala Ile Glu Lys Phe Leu Lys Asp Gln Ala Gln Leu
        35   40   45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50   55

<210> 185
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 185

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

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

```
Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  186
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  186

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  187
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  187

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  188
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  188

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
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1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Tyr Ala Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 189
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 189

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Tyr Phe Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 190
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 190

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Tyr Gly Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 191

<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 191

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Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Thr Arg Val Thr Ala Ile Glu Lys Tyr Arg Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
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<210> 192
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 192

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 193
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 193

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30
```

```
Thr Arg Val Thr Ala Ile Glu Lys Ala Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  194
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  194

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  195
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  195

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  196
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU
```

<400> 196

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Phe Ala Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 197
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 197

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Phe Phe Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 198
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 198

Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Phe Gly Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln

50 55

<210> 199
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 199

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Phe Arg Lys Asp Gln Ala Gln Leu
35 40 45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 200
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 200

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

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

Asn Ala Trp Gly Cys Ala Phe Arg Gln
50 55

<210> 201
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 201

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

```
Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Thr Arg Val Thr Ala Ile Glu Lys Gly Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 202
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 202

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 203
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 203

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 204
<211> 57
<212> PRT

<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 204

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 205
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 205

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Thr Arg Val Thr Ala Ile Glu Lys Leu Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 206
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 206

```
Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


Thr Arg Val Thr Ala Ile Glu Lys Leu Gly Lys Asp Gln Ala Gln Leu
```

```
        35                  40                  45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  207
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  207

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  208
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  208

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15


Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30


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


Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55


<210>  209
<211>  57
<212>  PRT
<213>  Artificial sequence

<220>
<223>  fragment of SIV ENV ISU

<400>  209
```

```
Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

Thr Arg Val Thr Ala Ile Glu Lys Arg Phe Lys Asp Gln Ala Gln Leu
        35                  40                  45

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 210
<211> 57
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of SIV ENV ISU

<400> 210

```
Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 211
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> fragment of SIV ENV ISU

<400> 211

```
Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1               5                   10                  15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20                  25                  30

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

Asn Ala Trp Gly Cys Ala Phe Arg Gln
    50                  55
```

<210> 212
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 212

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240
```

```
Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510
```

```
Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780
```

```
Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  213
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  213

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
```

165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile

435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Leu
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu

705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 214
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 214

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

```
Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365
```

```
Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640
```

```
Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  215
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  215

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15
```

```
Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285
```

```
Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560
```

```
Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830
```

```
Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860
```

<210> 216
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 216

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205
```

```
Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480
```

```
Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750
```

```
Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  217
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  217

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
```

130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser

405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Ala
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys

675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 218
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 218

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

```
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335
```

```
Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Phe
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605
```

```
Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860
```

<210> 219
<211> 861

<212> PRT
<213> Human immunodeficiency virus type 1

<400> 219

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255
```

```
Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525
```

```
Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Gly
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800
```

```
Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  220
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  220

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175
```

```
Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445
```

```
Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Arg
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720
```

```
Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  221
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  221

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
```

```
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
```

370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Ala
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn

645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 222
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 222

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

```
Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300
```

```
Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg
305                 310                 315                 320

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575
```

```
Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Phe
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845
```

```
Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  223
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  223

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125


Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140


Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160


Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175


Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190


Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205


Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220
```

```
Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495
```

```
Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Gly
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765
```

```
Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  224
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  224

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140
```

```
Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415
```

```
Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Arg
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685
```

```
Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  225
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  225

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
```

65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser

```
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Ala
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
```

610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 226
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 226

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270
```

```
Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540
```

```
Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Phe
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815
```

```
Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  227
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  227

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190
```

```
Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460
```

```
Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Gly
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735
```

```
Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  228
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  228

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110
```

```
Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380
```

```
Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Arg
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655
```

```
Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  229
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  229

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
```

35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg

305 310 315 320

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Ala

580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu

850 855 860

<210> 230
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 230

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

```
Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510
```

```
Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Phe
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780
```

```
Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800


Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815


Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830


Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845


Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  231
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  231

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125


Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140


Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160
```

```
Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430
```

```
Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Gly
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700
```

```
Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720


Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735


Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750


Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765


Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780


Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800


Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815


Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830


Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845


Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  232
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  232

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80
```

```
Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350
```

```
Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Arg
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620
```

```
Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  233
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  233

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
```

```
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
```

275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu

```
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Ala
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
```

820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 234
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 234

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

```
Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480
```

```
Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Phe
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750
```

```
Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  235
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  235

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125
```

```
Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400
```

```
Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Gly
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670
```

```
Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  236
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  236

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45
```

```
Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg
305                 310                 315                 320
```

```
Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Arg
            580                 585                 590
```

```
Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860
```

<210> 237
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 237

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
```

245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu

515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Ala
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr

785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 238
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 238

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

```
Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445
```

```
Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Phe
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720
```

```
Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  239
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  239

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95
```

```
Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365
```

```
Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Gly
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640
```

```
Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  240
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  240

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15
```

```
Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285
```

```
Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560
```

```
Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Arg
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830
```

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 241
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 241

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala

210 215 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
260 265 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val

485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Leu Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr

755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 242
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 242

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

```
Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415
```

```
Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Leu Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685
```

```
Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  243
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  243

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60
```

```
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335
```

```
Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln
            340                 345                 350

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Leu Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605
```

```
Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855
```

<210> 244
<211> 856
<212> PRT

<213> Human immunodeficiency virus type 1

<400> 244

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255
```

```
Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525
```

```
Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Leu Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800
```

```
Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  245
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  245

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
```

180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
260 265 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu

```
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
```

725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 246
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 246

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

```
Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380
```

```
Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Ala Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655
```

```
Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  247
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  247

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30
```

```
Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300
```

```
Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
305                 310                 315                 320

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575
```

```
Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Phe Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845
```

```
Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  248
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  248

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125


Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140


Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160


Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175


Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190


Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205


Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220
```

```
Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495
```

```
Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Gly Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765
```

```
His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855

<210>  249
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  249

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
```

```
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
```

420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Arg Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val

690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 250
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 250

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

```
Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln
            340                 345                 350
```

```
Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Ala Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620
```

```
Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855
```

<210> 251
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 251

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270
```

```
Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540
```

```
Leu Ser Gly Ile Val Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Phe Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815
```

```
Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855
```

<210> 252
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 252

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190
```

```
Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460
```

```
Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Gly Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735
```

```
Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  253
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  253

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
```

115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
260 265 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp

385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Arg Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp

660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 254
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 254

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

```
Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
305                 310                 315                 320
```

```
Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Ala Lys Asp Gln Gln Leu
            580                 585                 590
```

```
Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855
```

<210> 255
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 255

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240
```

```
Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510
```

```
Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Phe Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780
```

```
Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800


Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815


Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830


Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845


Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  256
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  256

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125


Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140


Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160
```

```
Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430
```

```
Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Gly Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700
```

```
Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  257
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  257

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
```

85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
260 265 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp

355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Arg Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser

625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 258
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 258

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

```
Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285
```

```
Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560
```

```
Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Ala Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830
```

```
Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845


Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  259
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  259

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125


Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140


Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160


Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175


Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190


Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205
```

```
Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480
```

```
Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Phe Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750
```

```
Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855
```

<210> 260
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 260

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125
```

```
Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400
```

```
Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Gly Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670
```

```
Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  261
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  261

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
```

50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
260 265 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala

325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Arg Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val

595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 262

<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 262

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255
```

```
Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525
```

```
Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Ala Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800
```

```
Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  263
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  263

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175
```

```
Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445
```

```
Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Phe Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720
```

```
Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  264
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  264

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95
```

```
Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365
```

```
Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Gly Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640
```

```
Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  265
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  265

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
```

```
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
```

290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu

565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Arg Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg

835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 266
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 266

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

```
Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495
```

```
Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Ala Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765
```

```
His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  267
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  267

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140
```

```
Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415
```

```
Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Phe Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685
```

```
Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855


<210>  268
<211>  856
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  268

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60
```

```
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
            260                 265                 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
        275                 280                 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
    290                 295                 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
                325                 330                 335
```

```
Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln
            340                 345                 350

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
        355                 360                 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
    370                 375                 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385                 390                 395                 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
                405                 410                 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
            420                 425                 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
        435                 440                 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
    450                 455                 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465                 470                 475                 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
                485                 490                 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
            500                 505                 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
        515                 520                 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu
    530                 535                 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545                 550                 555                 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
                565                 570                 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Gly Lys Asp Gln Gln Leu
            580                 585                 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
        595                 600                 605
```

```
Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
    610                 615                 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625                 630                 635                 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
                645                 650                 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
            660                 665                 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
        675                 680                 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
    690                 695                 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705                 710                 715                 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
                725                 730                 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
            740                 745                 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
        755                 760                 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
    770                 775                 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785                 790                 795                 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
                805                 810                 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
            820                 825                 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
        835                 840                 845

Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855
```

<210> 269
<211> 856
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 269

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Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
    130                 135                 140

Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
145                 150                 155                 160

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
                165                 170                 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Thr
            180                 185                 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
        195                 200                 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
    210                 215                 220

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
225                 230                 235                 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
                245                 250                 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
```

260 265 270

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

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

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Lys Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu
450 455 460

Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg
465 470 475 480

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
500 505 510

Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
515 520 525

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu

530 535 540

Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu
545 550 555 560

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu
565 570 575

Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Arg Lys Asp Gln Gln Leu
580 585 590

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
595 600 605

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
660 665 670

Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
675 680 685

Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val
690 695 700

Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
705 710 715 720

Leu Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
740 745 750

Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
755 760 765

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn

805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Tyr Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 270
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> fragemnt of lentiviral ENV protein

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

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<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa = A or S

<220>
<221> misc_feature
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<221> misc_feature
<222> (20)..(20)
<223> Xaa can be any naturally occurring amino acid

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<221> misc_feature
<222> (24)..(24)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(29)
<223> Xaa = no or any amino acid

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> Xaa = N or S

<220>
<221> MISC_FEATURE
<222> (31)..(31)
<223> Xaa = E, D, N or A

<220>
<221> MISC_FEATURE
<222> (32)..(32)
<223> Xaa = S or T

<400> 270

Xaa Asp Gln Xaa Xaa Leu Xaa Xaa Trp Gly Cys Xaa Xaa Xaa Xaa Cys
1   5   10   15

Val Xaa Thr Xaa Val Pro Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

<210> 271
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 271

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35   40   45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50   55   60

Trp Asn Ala Ser Trp Ser Asn Ala Ser Leu Glu Gln Ile Trp Asn Asn
65   70   75   80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85   90   95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100   105   110

Gln Glu Leu
        115

<210> 272
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 272

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
50 55 60

Trp Asn Ala Ser Trp Ser Asn Gly Ser Leu Glu Gln Ile Trp Asn Asn
65 70 75 80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
85 90 95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
100 105 110

Gln Glu Leu
115

<210> 273
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 273

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
50 55 60

Trp Asn Ala Ser Trp Ser Asn Ser Ser Leu Glu Gln Ile Trp Asn Asn
65 70 75 80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
85 90 95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
100 105 110

Gln Glu Leu
115

<210> 274
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 274

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
50 55 60

Asp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn
65 70 75 80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
85 90 95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
100 105 110

Gln Glu Leu
115

<210> 275
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 275

```
Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala
1               5                   10                  15

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50                  55                  60

Ala Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn
65                  70                  75                  80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85                  90                  95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100                 105                 110

Gln Glu Leu
        115


<210>  276
<211>  115
<212>  PRT
<213>  Artificial sequence

<220>
<223>  derived from lentiviral ENV ISU

<400>  276

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50                  55                  60

Asn Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn
65                  70                  75                  80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85                  90                  95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100                 105                 110
```

Gln Glu Leu
115

<210> 277
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 277

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
50 55 60

Trp Asn Ala Ser Trp Ser Asn Lys Asp Leu Glu Gln Ile Trp Asn Asn
65 70 75 80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
85 90 95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
100 105 110

Gln Glu Leu
115

<210> 278
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 278

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
35 40 45

```
Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50                  55                  60

Trp Asn Ala Ser Trp Ser Asn Lys Ala Leu Glu Gln Ile Trp Asn Asn
65                  70                  75                  80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85                  90                  95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100                 105                 110

Gln Glu Leu
        115
```

<210> 279
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 279

```
Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala
1               5                   10                  15

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50                  55                  60

Trp Asn Ala Ser Trp Ser Asn Lys Asn Leu Glu Gln Ile Trp Asn Asn
65                  70                  75                  80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85                  90                  95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100                 105                 110

Gln Glu Leu
        115
```

<210> 280
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 280

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35   40   45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50   55   60

Trp Asn Ala Ser Trp Ser Asn Tyr Ser Leu Glu Gln Ile Trp Asn Asn
65   70   75   80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85   90   95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100   105   110

Gln Glu Leu
        115

<210> 281
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 281

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Ile Leu Ala Val Glu Ala Arg Leu Lys Asp Gln Gln Leu Leu
        35   40   45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50   55   60

Trp Asn Ala Ser Trp Ser Asn Ala Ser Leu Glu Gln Ile Trp Asn Asn
65   70   75   80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
85 90 95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
100 105 110

Gln Glu Leu
115

<210> 282
<211> 115
<212> PRT
<213> Artificial sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 282

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
50 55 60

Trp Asn Ala Ser Trp Ser Asn Ala Ala Leu Glu Gln Ile Trp Asn Asn
65 70 75 80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
85 90 95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
100 105 110

Gln Glu Leu
115

<210> 283
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> derived from lentiviral ENV ISU

<400> 283

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

```
Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
            20                  25                  30

Ala Arg Ile Leu Ala Val Glu Arg Arg Leu Lys Asp Gln Gln Leu Leu
        35                  40                  45

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
    50                  55                  60

Ala Asn Ala Ser Trp Ser Asn Ala Ala Leu Glu Gln Ile Trp Asn Asn
65                  70                  75                  80

Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu
                85                  90                  95

Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
            100                 105                 110

Gln Glu Leu
        115


<210>  284
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  284

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
```

130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser

405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Leu
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys

675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 285
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 285

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

```
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335
```

```
Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605
```

```
Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Ala Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860
```

<210> 286
<211> 861

<212> PRT
<213> Human immunodeficiency virus type 1

<400> 286

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255
```

```
Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525
```

```
Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Gly Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800
```

```
Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860
```

<210> 287
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 287

```
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175
```

```
Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445
```

```
Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Arg Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Ser Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720
```

```
Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  288
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  288

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
```

100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly

370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Gly Leu
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn

645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 289
<211> 861
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 289

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

```
Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300
```

```
Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg
305                 310                 315                 320

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575
```

```
Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Leu Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845
```

```
Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  290
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  290

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15


Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30


Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45


Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60


Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80


Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95


Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110


Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125


Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140


Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160


Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175


Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190


Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205


Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220
```

```
Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495
```

```
Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Ala Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765
```

```
Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  291
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  291

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140
```

```
Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415
```

```
Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Phe Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685
```

```
Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  292
<211>  861
<212>  PRT
<213>  Human immunodeficiency virus type 1

<400>  292

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                   10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
```

65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser

340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Arg
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu

610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

<210> 293
<211> 881
<212> PRT
<213> Simian immunodeficiency virus

<220>
<221> misc_feature
<222> (736)..(736)
<223> Xaa can be any naturally occurring amino acid

<400> 293

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

Val Tyr Gly Ile Tyr Cys Thr Gln Tyr Val Thr Val Phe Tyr Gly Val
            20                  25                  30

Pro Ala Trp Arg Asn Ala Thr Ile Pro Leu Phe Cys Ala Thr Lys Asn
        35                  40                  45

Arg Asp Thr Trp Gly Thr Thr Gln Cys Leu Pro Asp Asn Gly Asp Tyr
    50                  55                  60

Ser Glu Leu Ala Leu Asn Val Thr Glu Ser Phe Asp Ala Trp Glu Asn
65                  70                  75                  80

Thr Val Thr Glu Gln Ala Ile Glu Asp Val Trp Gln Leu Phe Glu Thr
                85                  90                  95

Ser Ile Lys Pro Cys Val Lys Leu Ser Pro Leu Cys Ile Thr Met Arg
            100                 105                 110

Cys Asn Lys Ser Glu Thr Asp Arg Trp Gly Leu Thr Lys Ser Ser Thr
        115                 120                 125

Thr Ile Thr Thr Ala Ala Pro Thr Ser Ala Pro Val Ser Glu Lys Ile
    130                 135                 140

Asp Met Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asn Asn Cys Thr
145                 150                 155                 160

Gly Leu Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Thr Met Thr Gly
                165                 170                 175

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

Asp Leu Val Cys Glu Gln Gly Asn Ser Thr Asp Asn Glu Ser Arg Cys
        195                 200                 205

Tyr Met Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys
    210                 215                 220

His Tyr Trp Asp Thr Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr
225                 230                 235                 240
```

```
Ala Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys
                245                 250                 255

Cys Ser Lys Val Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln
            260                 265                 270

Thr Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr
        275                 280                 285

Tyr Ile Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn
    290                 295                 300

Lys Tyr Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr
305                 310                 315                 320

Val Leu Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro
                325                 330                 335

Ile Asn Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp
            340                 345                 350

Lys Asp Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg
        355                 360                 365

Tyr Thr Gly Thr Asn Asn Thr Asp Lys Ile Asn Leu Thr Ala Pro Gly
    370                 375                 380

Gly Gly Asp Pro Glu Val Thr Phe Met Trp Thr Asn Cys Arg Gly Glu
385                 390                 395                 400

Phe Leu Tyr Cys Lys Met Asn Trp Phe Leu Asn Trp Val Glu Asp Arg
                405                 410                 415

Asp Val Thr Thr Gln Arg Pro Lys Glu Arg His Arg Arg Asn Tyr Val
            420                 425                 430

Pro Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys
        435                 440                 445

Asn Val Tyr Leu Pro Pro Arg Glu Gly Asp Leu Thr Cys Asn Ser Thr
    450                 455                 460

Val Thr Ser Leu Ile Ala Asn Ile Asp Trp Thr Asp Gly Asn Gln Thr
465                 470                 475                 480

Ser Ile Thr Met Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu
                485                 490                 495

Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile Gly Leu Ala Pro Thr
            500                 505                 510
```

```
Asp Val Lys Arg Tyr Thr Thr Gly Gly Thr Ser Arg Asn Lys Arg Gly
        515                 520                 525

Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala
    530                 535                 540

Met Gly Ala Ala Ser Leu Thr Leu Thr Ala Gln Ser Arg Thr Leu Leu
545                 550                 555                 560

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
                565                 570                 575

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            580                 585                 590

Thr Arg Val Thr Ala Ile Glu Lys Tyr Arg Lys Asp Gln Ala Gln Leu
        595                 600                 605

Asn Ala Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro
    610                 615                 620

Trp Pro Asn Ala Ser Leu Thr Pro Asp Trp Asn Asn Asp Thr Trp Gln
625                 630                 635                 640

Glu Trp Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu
                645                 650                 655

Leu Glu Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln
            660                 665                 670

Lys Leu Asn Ser Trp Asp Val Phe Gly Asn Trp Phe Asp Leu Ala Ser
        675                 680                 685

Trp Ile Lys Tyr Ile Gln Tyr Gly Ile Tyr Val Val Val Gly Val Ile
    690                 695                 700

Leu Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ala Lys Leu Arg
705                 710                 715                 720

Gln Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Ser Tyr Phe Gln Xaa
                725                 730                 735

Thr His Thr Gln Gln Asp Pro Ala Leu Pro Thr Arg Glu Gly Lys Glu
            740                 745                 750

Gly Asp Gly Gly Glu Gly Gly Gly Asn Ser Ser Trp Pro Trp Gln Ile
        755                 760                 765

Glu Tyr Ile His Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Trp
    770                 775                 780
```

```
Leu Phe Ser Asn Cys Arg Thr Leu Leu Ser Arg Ala Tyr Gln Ile Leu
785                 790                 795                 800

Gln Pro Ile Leu Gln Arg Leu Ser Ala Thr Leu Arg Arg Val Arg Glu
                805                 810                 815

Val Leu Arg Thr Glu Leu Thr Tyr Leu Gln Tyr Gly Trp Ser Tyr Phe
            820                 825                 830

His Glu Ala Val Gln Ala Gly Trp Arg Ser Ala Thr Glu Thr Leu Ala
        835                 840                 845

Gly Ala Trp Arg Asp Leu Trp Glu Thr Leu Arg Arg Gly Gly Arg Trp
    850                 855                 860

Ile Leu Ala Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Leu Thr Leu
865                 870                 875                 880

Leu
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<210> 294
<211> 860
<212> PRT
<213> Human immunodeficiency virus type 2

<400> 294

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Met Glu Pro Gly Arg Asn Gln Leu Phe Val Val Ile Leu Leu Thr Ser
1               5                   10                  15

Ala Cys Leu Val Tyr Cys Ser Gln Tyr Val Thr Val Phe Tyr Gly Ile
            20                  25                  30

Pro Ala Trp Lys Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
        35                  40                  45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
    50                  55                  60

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

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp His Leu Phe Glu Thr
                85                  90                  95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
            100                 105                 110

Cys Ser Arg Val Gln Gly Asn Thr Thr Thr Pro Asn Pro Arg Thr Ser
        115                 120                 125

Ser Ser Thr Thr Ser Arg Pro Pro Thr Ser Ala Ala Ser Ile Ile Asn
```

130 135 140

Glu Thr Ser Asn Cys Ile Glu Asn Asn Thr Cys Ala Gly Leu Gly Tyr
145 150 155 160

Glu Glu Met Met Gln Cys Glu Phe Asn Met Lys Gly Leu Glu Gln Asp
165 170 175

Lys Lys Arg Arg Tyr Lys Asp Thr Trp Tyr Leu Glu Asp Val Val Cys
180 185 190

Asp Asn Thr Thr Ala Gly Thr Cys Tyr Met Arg His Cys Asn Thr Ser
195 200 205

Ile Ile Lys Glu Ser Cys Asp Lys His Tyr Trp Asp Ala Met Arg Phe
210 215 220

Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu Arg Cys Asn Asp Thr
225 230 235 240

Asn Tyr Ser Gly Phe Glu Pro Lys Cys Thr Lys Val Val Ala Ala Ser
245 250 255

Cys Thr Arg Met Met Glu Thr Gln Thr Ser Thr Trp Phe Gly Phe Asn
260 265 270

Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr Trp His Gly Arg Asp
275 280 285

Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr Tyr Asn Leu Thr Met Arg
290 295 300

Cys Lys Arg Pro Gly Asn Lys Thr Val Leu Pro Ile Thr Leu Met Ser
305 310 315 320

Gly Leu Val Phe His Ser Gln Pro Ile Asn Thr Arg Pro Arg Gln Ala
325 330 335

Trp Cys Arg Phe Gly Gly Arg Trp Arg Glu Ala Met Gln Glu Val Lys
340 345 350

Gln Thr Leu Val Gln His Pro Arg Tyr Lys Gly Ile Asn Asp Thr Gly
355 360 365

Lys Ile Asn Phe Thr Lys Pro Gly Ala Gly Ser Asp Pro Glu Val Ala
370 375 380

Phe Met Trp Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Thr
385 390 395 400

Trp Phe Leu Asn Trp Val Glu Asp Lys Asn Gln Thr Arg Arg Asn Tyr

405 410 415

Cys His Ile Lys Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn
420 425 430

Val Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Glu Ser Thr Val
435 440 445

Thr Ser Ile Ile Ala Asn Ile Asp Ile Asp Lys Asn Arg Thr His Thr
450 455 460

Asn Ile Thr Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu
465 470 475 480

Gly Asp Tyr Lys Leu Ile Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr
485 490 495

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

Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met
515 520 525

Gly Ala Arg Ser Leu Thr Leu Ser Ala Gln Ser Arg Thr Leu Leu Ala
530 535 540

Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln
545 550 555 560

Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Ala
565 570 575

Arg Val Thr Ala Ile Glu Lys Tyr Arg Lys His Gln Ala Gln Leu Asn
580 585 590

Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp
595 600 605

Val Asn Asp Ser Leu Ser Pro Asp Trp Lys Asn Met Thr Trp Gln Glu
610 615 620

Trp Glu Lys Gln Val Arg Tyr Leu Glu Ala Asn Ile Ser Gln Ser Leu
625 630 635 640

Glu Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys
645 650 655

Leu Asn Ser Trp Asp Ile Leu Gly Asn Trp Phe Asp Leu Thr Ser Trp
660 665 670

Val Lys Tyr Ile Gln Tyr Gly Val His Ile Val Val Gly Ile Ile Ala

675 680 685

Leu Arg Ile Ala Ile Tyr Val Val Gln Leu Leu Ser Arg Phe Arg Lys
690 695 700

Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Leu Gln Gln Ile
705 710 715 720

His Ile His Lys Asp Arg Gly Gln Pro Ala Asn Glu Gly Thr Glu Glu
725 730 735

Asp Val Gly Gly Asp Ser Gly Tyr Asp Leu Trp Pro Trp Pro Ile Asn
740 745 750

Tyr Val Gln Phe Leu Ile His Leu Leu Thr Arg Leu Leu Ile Gly Leu
755 760 765

Tyr Asn Ile Cys Arg Asp Leu Leu Ser Lys Asn Ser Pro Thr Arg Arg
770 775 780

Leu Ile Ser Gln Ser Leu Thr Ala Ile Arg Asp Trp Leu Arg Leu Lys
785 790 795 800

Ala Ala Gln Leu Gln Tyr Gly Cys Glu Trp Ile Gln Glu Ala Phe Gln
805 810 815

Ala Phe Ala Arg Thr Thr Arg Glu Thr Leu Ala Gly Ala Trp Gly Trp
820 825 830

Leu Trp Glu Ala Ala Arg Arg Ile Gly Arg Gly Ile Leu Ala Val Pro
835 840 845

Arg Arg Ile Arg Gln Gly Ala Glu Leu Ala Leu Leu
850 855 860

<210> 295
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 295
acatggccca gccggcctct ggtatagtgc agcagc 36

<210> 296
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 296
gtatacgcgt ttataattct tgttcattct tttc 34

<210> 297
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 297
gtatacgcgt ttacatgtta ttccaaatct gttcc 35

<210> 298
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 298
gtatacgcgt ttaagcattc caaggcacag c 31

<210> 299
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 299
gtatacgcgt ttatccagag caacccccaaa tcc 33

<210> 300
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 300
gtatacgcgt ttaccccagg agctgttgat cc 32

<210> 301
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 301
gtatacgcgt ttactttagg tatctttcca cagc 34

<210> 302
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 302
gtatacgcgt ttaagccagg attcttgcct ggag 34

<210> 303
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 303
gtatacgcgt ttactgcttg atgccccaga c 31

<210> 304
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 304
ctttccacag cccggattct tgcctg 26

<210> 305
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 305
caggcaagaa tccgggctgt ggaaag 26

<210> 306
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 306
gtatctttcc acacgcagga ttcttgcc 28

<210> 307

<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 307
ggcaagaatc ctgcgtgtgg aaagatac 28

<210> 308
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 308
ctttaggtat ctttccctag ccaggattct tgcc 34

<210> 309
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 309
ggcaagaatc ctggctaggg aaagatacct aaag 34

<210> 310
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 310
cctttaggta tcttctcaca gccaggattc 30

<210> 311
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 311
gaatcctggc tgtgagaaga tacctaaagg 30

<210> 312
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 312
gttgatcctt taggcgtctt tccacagcca g 31

<210> 313
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 313
ctggctgtgg aaagacgcct aaaggatcaa c 31

<210> 314
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 314
ggagctgttg atcctttcgg tatctttcca cagcc 35

<210> 315
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 315
ggctgtggaa agataccgaa aggatcaaca gctcc 35

<210> 316
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of lentiviral ENV protein

<400> 316
gagctgttga tcccttaggt atctttccac 30

<210> 317
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for introducing mutation within the ISU of

lentiviral ENV protein

<400> 317
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<210> 346
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<220>
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<211> 44
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<220>
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<210> 348
<211> 44
<212> DNA
<213> Artificial sequence

<220>
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<400> 348
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<210> 349
<211> 32
<212> DNA
<213> Artificial sequence

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<400> 349
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<400> 350
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<220>
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<400> 351
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<220>
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<400> 352
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<212> DNA
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<400> 354
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<212> DNA
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<400> 356
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<210> 357
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<400> 357
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<400> 358
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<210> 359
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<220>
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<400> 359
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<210> 360
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<210> 361
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<400> 361
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<212> DNA
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<220>
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<400> 362
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<220>
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<400> 363
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<210> 364
<211> 36
<212> DNA
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<220>
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<400> 364
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<210> 365
<211> 35
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<220>
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<400> 365
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<210> 366
<211> 49
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<220>
<223> derived from the ISU domain of HIV1

<400> 366

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 367
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> derived from the ISU domain of HIV1

<400> 367

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

Gln Gln His Leu Leu Lys Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 368
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> derived from the ISU domain of HIV1

<400> 368

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 369
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> derived from the ISU domain of HIV1

<400> 369

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

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 370
<211> 49
<212> PRT
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<220>
<223> derived from the ISU domain of HIV1

<400> 370

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

Gln Gln Gln Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Arg
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 371
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> derived from the ISU domain of HIV1

<400> 371

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Gln Ala
1 5 10 15

Arg Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
20 25 30

Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu
35 40 45

Gly

<210> 372
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<220>
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<400> 372

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

Gln Gln His Leu Leu Gln Leu Ser Ile Trp Gly Val Lys Gln Leu Gln
20 25 30

Ala Arg Leu Leu Ala Val Glu Arg Tyr Leu Gln Asp Gln Gln Ile Leu
35 40 45

Gly

<210> 373
<211> 49
<212> PRT
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<220>
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<400> 373

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

Gln Gln His Leu Leu Gln Leu Ser Val Trp Gly Ile Lys Gln Leu Gln
            20   25   30

Ala Arg Val Leu Ala Ile Glu Arg Tyr Leu Arg Asp Gln Gln Ile Leu
        35   40   45

Gly

<210> 374
<211> 49
<212> PRT
<213> Artificial sequence

<220>
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<400> 374

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

Thr Arg Val Ser Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu
        35   40   45

Asn

<210> 375
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<400> 375

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1   5   10   15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
            20   25   30

Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu
        35   40   45

Asn

<210> 376
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> derived from the ISU domain of HIV2

<400> 376

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu
35 40 45

Asn

<210> 377
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> derived from the ISU domain of HIV2

<400> 377

Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg
1 5 10 15

Gln Gln Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln
20 25 30

Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Leu Leu
35 40 45

Asn

<210> 378
<211> 31
<212> DNA
<213> Artificial sequence

<220>
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<400> 378
ctggctgtgg aagcacgcct aaaggatcaa c 31

<210> 379
<211> 31
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<220>
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<400> 379
gttgatcctt taggcgtgct tccacagcca g 31

<210> 380
<211> 31
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<400> 380
ctggctgtgg aagaacgcct aaaggatcaa c 31

<210> 381
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<220>
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<400> 381
gttgatcctt taggcgttct tccacagcca g 31

<210> 382
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<220>
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<400> 383
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<210> 385
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<220>
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<400> 385
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<210> 386
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<220>
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<400> 386
ctggctgtgg aaagcgccct aaaggatcaa c 31

<210> 387
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<220>
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<400> 387
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<210> 388
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<400> 388
ctggctgtgg aaacagccct aaaggatcaa c 31

<210> 389
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<220>
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<400> 389
gttgatcctt tagggctgtt tccacagcca g 31

<210> 390
<211> 31

<212> DNA
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<220>
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<400> 390
ctggctgtgg aagcttacct aaaggatcaa c 31

<210> 391
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<400> 391
gttgatcctt taggtaagct tccacagcca g 31

<210> 392
<211> 31
<212> DNA
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<400> 392
ctggctgtgg aagaatacct aaaggatcaa c 31

<210> 393
<211> 31
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<213> Artificial sequence

<220>
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<400> 393
gttgatcctt taggtattct tccacagcca g 31

<210> 394
<211> 31
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<220>
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<400> 394
ctggctgtgg aaagctacct aaaggatcaa c 31

<210> 395
<211> 31
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<220>
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<400> 395
gttgatcctt taggtagctt tccacagcca g 31

<210> 396
<211> 31
<212> DNA
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<220>
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<400> 396
ctggctgtgg aaacatacct aaaggatcaa c 31

<210> 397
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide used for introducing a second mutation

<400> 397
gttgatcctt taggtatgtt tccacagcca g 31

<210> 398
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide used for introducing a second mutation

<400> 398
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<210> 399
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide used for introducing a second mutation

<400> 399
ccaaatctgt tccagagatg cattactcca actagc 36

<210> 400
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide used for introducing a second mutation

<400> 400
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<210> 401
<211> 36
<212> DNA
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<220>

<223> Oligonucleotide used for introducing a second mutation

<400> 401
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<210> 402
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide used for introducing a second mutation

<400> 402
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<210> 403
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 403
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<210> 404
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<220>
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<223> n is a, c, g, or t

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<210> 405
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<220>
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<400> 405
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<210> 406
<211> 34
<212> DNA
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<220>
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<400> 406
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<211> 8
<212> PRT
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<220>
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<400> 407

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1 5

<210> 408
<211> 8
<212> PRT
<213> Artificial sequence

<220>
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<400> 408

Ala Val Glu Glu Ala Leu Lys Asp
1 5

<210> 409
<211> 8
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<213> Artificial sequence

<220>
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<400> 409

Ala Val Glu Ser Ala Leu Lys Asp
1 5

<210> 410
<211> 8
<212> PRT
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<220>
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<400> 410

Ala Val Glu Thr Ala Leu Lys Asp
1 5

<210> 411
<211> 8
<212> PRT
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<220>
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<400> 411

Ala Ile Glu Ala Ala Leu Lys Asp
1 5

<210> 412
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> fragment of lentiviral ENV ISU

<400> 412

Ala Ile Glu Glu Ala Leu Lys Asp
1 5

<210> 413
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<220>
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<400> 413

Ala Ile Glu Ser Ala Leu Lys Asp
1 5

<210> 414
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<400> 414

Ala Ile Glu Thr Ala Leu Lys Asp
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<210> 415
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Ala Xaa Glu Xaa Tyr Leu Xaa Asp Gln Xaa Xaa Leu Xaa Xaa Trp Gly
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Cys Xaa Xaa Xaa Xaa Cys Val Xaa Thr Xaa Val Pro Trp Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa
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<210> 416
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<400> 416

Ala Xaa Glu Xaa Xaa Xaa Xaa Asp Gln
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<213> Human immunodeficiency virus type 1

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Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1               5                  10                  15

Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
            20                  25                  30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
        35                  40                  45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
    50                  55                  60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65                  70                  75                  80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
                85                  90                  95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
        115                 120                 125

Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
    130                 135                 140

Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145                 150                 155                 160

Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
                165                 170                 175

Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
            180                 185                 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
        195                 200                 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
    210                 215                 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225                 230                 235                 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
                245                 250                 255
```

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Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
            260                 265                 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
        275                 280                 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
    290                 295                 300

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

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
                325                 330                 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
            340                 345                 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
        355                 360                 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
    370                 375                 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385                 390                 395                 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
                405                 410                 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
            420                 425                 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
        435                 440                 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
    450                 455                 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465                 470                 475                 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
                485                 490                 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
            500                 505                 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
        515                 520                 525
```

```
Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
    530                 535                 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu
545                 550                 555                 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
                565                 570                 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
            580                 585                 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
        595                 600                 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
    610                 615                 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625                 630                 635                 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
                645                 650                 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
            660                 665                 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
        675                 680                 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
    690                 695                 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705                 710                 715                 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
                725                 730                 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
            740                 745                 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
        755                 760                 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
    770                 775                 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785                 790                 795                 800
```

```
Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
                805                 810                 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
            820                 825                 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
        835                 840                 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
    850                 855                 860


<210>  418
<211>  859
<212>  PRT
<213>  Human immunodeficiency virus type 2

<400>  418

Met Cys Gly Arg Asn Gln Leu Phe Val Ala Ser Leu Leu Ala Ser Ala
1               5                   10                  15

Cys Leu Ile Tyr Cys Val Gln Tyr Val Thr Val Phe Tyr Gly Val Pro
            20                  25                  30

Val Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn Arg
        35                  40                  45

Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr Gln
    50                  55                  60

Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn Thr
65                  70                  75                  80

Val Thr Glu Gln Ala Val Glu Asp Val Trp Ser Leu Phe Glu Thr Ser
                85                  90                  95

Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Arg Cys
            100                 105                 110

Asn Ser Thr Thr Ala Lys Asn Thr Thr Ser Thr Pro Thr Thr Thr Thr
        115                 120                 125

Thr Ala Asn Thr Thr Ile Gly Glu Asn Ser Ser Cys Ile Arg Thr Asp
    130                 135                 140

Asn Cys Thr Gly Leu Gly Glu Glu Glu Met Val Asp Cys Gln Phe Asn
145                 150                 155                 160

Met Thr Gly Leu Glu Arg Asp Lys Lys Lys Leu Tyr Asn Glu Thr Trp
                165                 170                 175

Tyr Ser Lys Asp Val Val Cys Glu Ser Asn Asp Thr Lys Lys Glu Lys
```

```
            180                 185                 190

Thr Cys Tyr Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys
        195                 200                 205

Asp Lys His Tyr Trp Asp Thr Met Arg Phe Arg Tyr Cys Ala Pro Pro
    210                 215                 220

Gly Phe Ala Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Glu
225                 230                 235                 240

Pro Asn Cys Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu
                245                 250                 255

Thr Gln Thr Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn
            260                 265                 270

Arg Thr Tyr Ile Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser
        275                 280                 285

Leu Asn Lys Phe Tyr Asn Leu Thr Val His Cys Lys Arg Pro Gly Asn
    290                 295                 300

Lys Thr Val Val Pro Ile Thr Leu Met Ser Gly Leu Val Phe His Ser
305                 310                 315                 320

Gln Pro Ile Asn Arg Arg Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly
                325                 330                 335

Glu Trp Lys Glu Ala Met Lys Glu Val Lys Leu Thr Leu Ala Lys His
            340                 345                 350

Pro Arg Tyr Lys Gly Thr Asn Asp Thr Glu Lys Ile Arg Phe Ile Ala
        355                 360                 365

Pro Gly Glu Arg Ser Asp Pro Glu Val Ala Tyr Met Trp Thr Asn Cys
    370                 375                 380

Arg Gly Glu Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val
385                 390                 395                 400

Glu Asn Arg Thr Asn Gln Thr Gln His Asn Tyr Val Pro Cys His Ile
                405                 410                 415

Lys Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val Tyr Leu
            420                 425                 430

Pro Pro Arg Glu Gly Gln Leu Thr Cys Asn Ser Thr Val Thr Ser Ile
        435                 440                 445

Ile Ala Asn Ile Asp Gly Gly Glu Asn Gln Thr Asn Ile Thr Phe Ser
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450 455 460

Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu
465 470 475 480

Ile Glu Val Thr Pro Ile Gly Phe Ala Pro Thr Pro Val Lys Arg Tyr
485 490 495

Ser Ser Ala Pro Val Arg Asn Lys Arg Gly Val Phe Val Leu Gly Phe
500 505 510

Leu Gly Phe Leu Thr Thr Ala Gly Ala Ala Met Gly Ala Ala Ser Leu
515 520 525

Thr Leu Ser Ala Gln Ser Arg Thr Leu Leu Ala Gly Ile Val Gln Gln
530 535 540

Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln Glu Met Leu Arg
545 550 555 560

Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala Ile
565 570 575

Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala
580 585 590

Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Val Asn Asp Thr Leu
595 600 605

Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Arg Ile
610 615 620

Arg Asn Leu Glu Ala Asn Ile Ser Glu Ser Leu Glu Gln Ala Gln Ile
625 630 635 640

Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp Asp
645 650 655

Val Phe Gly Asn Trp Phe Asp Leu Thr Ser Trp Ile Lys Tyr Ile Gln
660 665 670

Tyr Gly Val Tyr Ile Val Val Gly Ile Ile Val Leu Arg Ile Val Ile
675 680 685

Tyr Val Val Gln Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val
690 695 700

Phe Ser Ser Pro Pro Ala Tyr Phe Gln Gln Ile His Ile His Lys Asp
705 710 715 720

Arg Glu Gln Pro Ala Arg Glu Glu Thr Glu Glu Asp Val Gly Asn Ser

725 730 735

Val Gly Asp Asn Trp Trp Pro Trp Pro Ile Arg Tyr Ile His Phe Leu
740 745 750

Ile Arg Gln Leu Ile Arg Leu Leu Asn Arg Leu Tyr Asn Ile Cys Arg
755 760 765

Asp Leu Leu Ser Arg Ser Phe Gln Thr Leu Gln Leu Ile Ser Gln Ser
770 775 780

Leu Arg Arg Ala Leu Thr Ala Val Arg Asp Trp Leu Arg Phe Asn Thr
785 790 795 800

Ala Tyr Leu Gln Tyr Gly Gly Glu Trp Ile Gln Glu Ala Phe Arg Ala
805 810 815

Phe Ala Arg Ala Thr Gly Glu Thr Leu Thr Asn Ala Trp Arg Gly Phe
820 825 830

Trp Gly Thr Leu Gly Gln Ile Gly Arg Gly Ile Leu Ala Val Pro Arg
835 840 845

Arg Ile Arg Gln Gly Ala Glu Ile Ala Leu Leu
850 855

<210> 419
<211> 879
<212> PRT
<213> Simian immunodeficiency virus

<400> 419

Met Gly Cys Leu Gly Asn Gln Leu Leu Ile Ala Ile Leu Leu Leu Ser
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Val Tyr Gly Ile Tyr Cys Thr Leu Tyr Val Thr Val Phe Tyr Gly Val
20 25 30

Pro Ala Trp Arg Asn Ala Thr Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Thr Gln Cys Leu Pro Asp Asn Gly Asp Tyr
50 55 60

Ser Glu Val Ala Leu Asn Val Thr Glu Ser Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Ile Glu Asp Val Trp Gln Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Ser Pro Leu Cys Ile Thr Met Arg
100 105 110

```
Cys Asn Lys Ser Glu Thr Asp Arg Trp Gly Leu Thr Lys Ser Ile Thr
        115                 120                 125

Thr Thr Ala Ser Thr Thr Ser Thr Thr Ala Ser Ala Lys Val Asp Met
    130                 135                 140

Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asp Asn Cys Thr Gly Leu
145                 150                 155                 160

Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Asn Met Thr Gly Leu Lys
                165                 170                 175

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

Val Cys Glu Gln Gly Asn Asn Thr Gly Asn Glu Ser Arg Cys Tyr Met
        195                 200                 205

Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys His Tyr
    210                 215                 220

Trp Asp Ala Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr Ala Leu
225                 230                 235                 240

Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys Cys Ser
                245                 250                 255

Lys Val Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln Thr Ser
            260                 265                 270

Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile
        275                 280                 285

Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr
    290                 295                 300

Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr Val Leu
305                 310                 315                 320

Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro Ile Asn
                325                 330                 335

Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp Lys Asp
            340                 345                 350

Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg Tyr Thr
        355                 360                 365

Gly Thr Asn Asn Thr Asp Lys Ile Asn Leu Thr Ala Pro Gly Gly Gly
    370                 375                 380
```

```
Asp Pro Glu Val Thr Phe Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
385                 390                 395                 400

Tyr Cys Lys Met Asn Trp Phe Leu Asn Trp Val Glu Asp Arg Asn Thr
                405                 410                 415

Ala Asn Gln Lys Pro Lys Glu Gln His Lys Arg Asn Tyr Val Pro Cys
            420                 425                 430

His Ile Arg Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val
        435                 440                 445

Tyr Leu Pro Pro Arg Glu Gly Asp Leu Thr Cys Asn Ser Thr Val Thr
    450                 455                 460

Ser Leu Ile Ala Asn Ile Asp Trp Ile Asp Gly Asn Gln Thr Asn Ile
465                 470                 475                 480

Thr Met Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp
                485                 490                 495

Tyr Lys Leu Val Glu Ile Thr Pro Ile Gly Leu Ala Pro Thr Asp Val
            500                 505                 510

Lys Arg Tyr Thr Thr Gly Gly Thr Ser Arg Asn Lys Arg Gly Val Phe
        515                 520                 525

Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly
    530                 535                 540

Ala Ala Ser Leu Thr Leu Thr Ala Gln Ser Arg Thr Leu Leu Ala Gly
545                 550                 555                 560

Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln
                565                 570                 575

Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg
            580                 585                 590

Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ala
        595                 600                 605

Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Pro
    610                 615                 620

Asn Ala Ser Leu Thr Pro Lys Trp Asn Asn Glu Thr Trp Gln Glu Trp
625                 630                 635                 640

Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu
                645                 650                 655
```

```
Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu
            660                 665                 670

Asn Ser Trp Asp Val Phe Gly Asn Trp Phe Asp Leu Ala Ser Trp Ile
        675                 680                 685

Lys Tyr Ile Gln Tyr Gly Val Tyr Ile Val Val Gly Val Ile Leu Leu
    690                 695                 700

Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ala Lys Leu Arg Gln Gly
705                 710                 715                 720

Tyr Arg Pro Val Phe Ser Ser Pro Pro Ser Tyr Phe Gln Gln Thr His
                725                 730                 735

Ile Gln Gln Asp Pro Ala Leu Pro Thr Arg Glu Gly Lys Glu Arg Asp
            740                 745                 750

Gly Gly Glu Gly Gly Gly Asn Ser Ser Trp Pro Trp Gln Ile Glu Tyr
        755                 760                 765

Ile His Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Trp Leu Phe
    770                 775                 780

Ser Asn Cys Arg Thr Leu Leu Ser Arg Val Tyr Gln Ile Leu Gln Pro
785                 790                 795                 800

Ile Leu Gln Arg Leu Ser Ala Thr Leu Gln Arg Ile Arg Glu Val Leu
                805                 810                 815

Arg Thr Glu Leu Thr Tyr Leu Gln Tyr Gly Trp Ser Tyr Phe His Glu
            820                 825                 830

Ala Val Gln Ala Val Trp Arg Ser Ala Thr Glu Thr Leu Ala Gly Ala
        835                 840                 845

Trp Gly Asp Leu Trp Glu Thr Leu Arg Arg Gly Gly Arg Trp Ile Leu
    850                 855                 860

Ala Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Leu Thr Leu Leu
865                 870                 875


<210>  420
<211>  859
<212>  PRT
<213>  Human immunodeficiency virus type 2

<400>  420

Met Cys Gly Arg Asn Gln Leu Phe Val Ala Ser Leu Leu Ala Ser Ala
1               5                   10                  15
```

```
Cys Leu Ile Tyr Cys Val Gln Tyr Val Thr Val Phe Tyr Gly Val Pro
            20                  25                  30

Val Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn Arg
        35                  40                  45

Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr Gln
    50                  55                  60

Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn Thr
65                  70                  75                  80

Val Thr Glu Gln Ala Val Glu Asp Val Trp Ser Leu Phe Glu Thr Ser
                85                  90                  95

Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Arg Cys
            100                 105                 110

Asn Ser Thr Thr Ala Lys Asn Thr Thr Ser Thr Pro Thr Thr Thr Thr
        115                 120                 125

Thr Ala Asn Thr Thr Ile Gly Glu Asn Ser Ser Cys Ile Arg Thr Asp
    130                 135                 140

Asn Cys Thr Gly Leu Gly Glu Glu Glu Met Val Asp Cys Gln Phe Asn
145                 150                 155                 160

Met Thr Gly Leu Glu Arg Asp Lys Lys Lys Leu Tyr Asn Glu Thr Trp
                165                 170                 175

Tyr Ser Lys Asp Val Val Cys Glu Ser Asn Asp Thr Lys Lys Glu Lys
            180                 185                 190

Thr Cys Tyr Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys
        195                 200                 205

Asp Lys His Tyr Trp Asp Thr Met Arg Phe Arg Tyr Cys Ala Pro Pro
    210                 215                 220

Gly Phe Ala Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Glu
225                 230                 235                 240

Pro Asn Cys Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu
                245                 250                 255

Thr Gln Thr Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn
            260                 265                 270

Arg Thr Tyr Ile Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser
        275                 280                 285
```

```
Leu Asn Lys Phe Tyr Asn Leu Thr Val His Cys Lys Arg Pro Gly Asn
    290                 295                 300

Lys Thr Val Val Pro Ile Thr Leu Met Ser Gly Leu Val Phe His Ser
305                 310                 315                 320

Gln Pro Ile Asn Arg Arg Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly
                325                 330                 335

Glu Trp Lys Glu Ala Met Lys Glu Val Lys Leu Thr Leu Ala Lys His
            340                 345                 350

Pro Arg Tyr Lys Gly Thr Asn Asp Thr Glu Lys Ile Arg Phe Ile Ala
        355                 360                 365

Pro Gly Glu Arg Ser Asp Pro Glu Val Ala Tyr Met Trp Thr Asn Cys
    370                 375                 380

Arg Gly Glu Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val
385                 390                 395                 400

Glu Asn Arg Thr Asn Gln Thr Gln His Asn Tyr Val Pro Cys His Ile
                405                 410                 415

Lys Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val Tyr Leu
            420                 425                 430

Pro Pro Arg Glu Gly Gln Leu Thr Cys Asn Ser Thr Val Thr Ser Ile
        435                 440                 445

Ile Ala Asn Ile Asp Gly Gly Glu Asn Gln Thr Asn Ile Thr Phe Ser
    450                 455                 460

Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu
465                 470                 475                 480

Ile Glu Val Thr Pro Ile Gly Phe Ala Pro Thr Pro Val Lys Arg Tyr
                485                 490                 495

Ser Ser Ala Pro Val Arg Asn Lys Arg Gly Val Phe Val Leu Gly Phe
            500                 505                 510

Leu Gly Phe Leu Thr Thr Ala Gly Ala Ala Met Gly Ala Ala Ser Leu
        515                 520                 525

Thr Leu Ser Ala Gln Ser Arg Thr Leu Leu Ala Gly Ile Val Gln Gln
    530                 535                 540

Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln Glu Met Leu Arg
545                 550                 555                 560
```

```
Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala Ile
                565                 570                 575

Glu Lys Arg Leu Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala
            580                 585                 590

Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Val Asn Asp Thr Leu
        595                 600                 605

Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Arg Ile
    610                 615                 620

Arg Asn Leu Glu Ala Asn Ile Ser Glu Ser Leu Glu Gln Ala Gln Ile
625                 630                 635                 640

Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp Asp
                645                 650                 655

Val Phe Gly Asn Trp Phe Asp Leu Thr Ser Trp Ile Lys Tyr Ile Gln
            660                 665                 670

Tyr Gly Val Tyr Ile Val Val Gly Ile Ile Val Leu Arg Ile Val Ile
        675                 680                 685

Tyr Val Val Gln Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val
    690                 695                 700

Phe Ser Ser Pro Pro Ala Tyr Phe Gln Gln Ile His Ile His Lys Asp
705                 710                 715                 720

Arg Glu Gln Pro Ala Arg Glu Glu Thr Glu Glu Asp Val Gly Asn Ser
                725                 730                 735

Val Gly Asp Asn Trp Trp Pro Trp Pro Ile Arg Tyr Ile His Phe Leu
            740                 745                 750

Ile Arg Gln Leu Ile Arg Leu Leu Asn Arg Leu Tyr Asn Ile Cys Arg
        755                 760                 765

Asp Leu Leu Ser Arg Ser Phe Gln Thr Leu Gln Leu Ile Ser Gln Ser
    770                 775                 780

Leu Arg Arg Ala Leu Thr Ala Val Arg Asp Trp Leu Arg Phe Asn Thr
785                 790                 795                 800

Ala Tyr Leu Gln Tyr Gly Gly Glu Trp Ile Gln Glu Ala Phe Arg Ala
                805                 810                 815

Phe Ala Arg Ala Thr Gly Glu Thr Leu Thr Asn Ala Trp Arg Gly Phe
            820                 825                 830
```

```
Trp Gly Thr Leu Gly Gln Ile Gly Arg Gly Ile Leu Ala Val Pro Arg
        835                 840                 845


Arg Ile Arg Gln Gly Ala Glu Ile Ala Leu Leu
    850                 855


<210>  421
<211>  879
<212>  PRT
<213>  Simian immunodeficiency virus

<400>  421

Met Gly Cys Leu Gly Asn Gln Leu Leu Ile Ala Ile Leu Leu Leu Ser
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Val Tyr Gly Ile Tyr Cys Thr Leu Tyr Val Thr Val Phe Tyr Gly Val
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Pro Ala Trp Arg Asn Ala Thr Ile Pro Leu Phe Cys Ala Thr Lys Asn
        35                  40                  45


Arg Asp Thr Trp Gly Thr Thr Gln Cys Leu Pro Asp Asn Gly Asp Tyr
    50                  55                  60


Ser Glu Val Ala Leu Asn Val Thr Glu Ser Phe Asp Ala Trp Asn Asn
65                  70                  75                  80


Thr Val Thr Glu Gln Ala Ile Glu Asp Val Trp Gln Leu Phe Glu Thr
                85                  90                  95


Ser Ile Lys Pro Cys Val Lys Leu Ser Pro Leu Cys Ile Thr Met Arg
            100                 105                 110


Cys Asn Lys Ser Glu Thr Asp Arg Trp Gly Leu Thr Lys Ser Ile Thr
        115                 120                 125


Thr Thr Ala Ser Thr Thr Ser Thr Thr Ala Ser Ala Lys Val Asp Met
    130                 135                 140


Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asp Asn Cys Thr Gly Leu
145                 150                 155                 160


Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Asn Met Thr Gly Leu Lys
                165                 170                 175


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


Val Cys Glu Gln Gly Asn Asn Thr Gly Asn Glu Ser Arg Cys Tyr Met
        195                 200                 205
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Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys His Tyr
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Trp Asp Ala Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr Ala Leu
225                 230                 235                 240

Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys Cys Ser
                245                 250                 255

Lys Val Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln Thr Ser
            260                 265                 270

Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile
        275                 280                 285

Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr
    290                 295                 300

Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr Val Leu
305                 310                 315                 320

Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro Ile Asn
                325                 330                 335

Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp Lys Asp
            340                 345                 350

Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg Tyr Thr
        355                 360                 365

Gly Thr Asn Asn Thr Asp Lys Ile Asn Leu Thr Ala Pro Gly Gly Gly
    370                 375                 380

Asp Pro Glu Val Thr Phe Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
385                 390                 395                 400

Tyr Cys Lys Met Asn Trp Phe Leu Asn Trp Val Glu Asp Arg Asn Thr
                405                 410                 415

Ala Asn Gln Lys Pro Lys Glu Gln His Lys Arg Asn Tyr Val Pro Cys
            420                 425                 430

His Ile Arg Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val
        435                 440                 445

Tyr Leu Pro Pro Arg Glu Gly Asp Leu Thr Cys Asn Ser Thr Val Thr
    450                 455                 460

Ser Leu Ile Ala Asn Ile Asp Trp Ile Asp Gly Asn Gln Thr Asn Ile
465                 470                 475                 480
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Thr Met Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp
                485                 490                 495

Tyr Lys Leu Val Glu Ile Thr Pro Ile Gly Leu Ala Pro Thr Asp Val
            500                 505                 510

Lys Arg Tyr Thr Thr Gly Gly Thr Ser Arg Asn Lys Arg Gly Val Phe
        515                 520                 525

Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly
    530                 535                 540

Ala Ala Ser Leu Thr Leu Thr Ala Gln Ser Arg Thr Leu Leu Ala Gly
545                 550                 555                 560

Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln
                565                 570                 575

Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg
            580                 585                 590

Val Thr Ala Ile Glu Lys Arg Leu Lys Asp Gln Ala Gln Leu Asn Ala
        595                 600                 605

Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Pro
    610                 615                 620

Asn Ala Ser Leu Thr Pro Lys Trp Asn Asn Glu Thr Trp Gln Glu Trp
625                 630                 635                 640

Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu
                645                 650                 655

Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu
            660                 665                 670

Asn Ser Trp Asp Val Phe Gly Asn Trp Phe Asp Leu Ala Ser Trp Ile
        675                 680                 685

Lys Tyr Ile Gln Tyr Gly Val Tyr Ile Val Val Gly Val Ile Leu Leu
    690                 695                 700

Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ala Lys Leu Arg Gln Gly
705                 710                 715                 720

Tyr Arg Pro Val Phe Ser Ser Pro Pro Ser Tyr Phe Gln Gln Thr His
                725                 730                 735

Ile Gln Gln Asp Pro Ala Leu Pro Thr Arg Glu Gly Lys Glu Arg Asp
            740                 745                 750
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Gly Gly Glu Gly Gly Gly Asn Ser Ser Trp Pro Trp Gln Ile Glu Tyr
        755                 760                 765

Ile His Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Trp Leu Phe
    770                 775                 780

Ser Asn Cys Arg Thr Leu Leu Ser Arg Val Tyr Gln Ile Leu Gln Pro
785                 790                 795                 800

Ile Leu Gln Arg Leu Ser Ala Thr Leu Gln Arg Ile Arg Glu Val Leu
                805                 810                 815

Arg Thr Glu Leu Thr Tyr Leu Gln Tyr Gly Trp Ser Tyr Phe His Glu
            820                 825                 830

Ala Val Gln Ala Val Trp Arg Ser Ala Thr Glu Thr Leu Ala Gly Ala
        835                 840                 845

Trp Gly Asp Leu Trp Glu Thr Leu Arg Arg Gly Gly Arg Trp Ile Leu
    850                 855                 860

Ala Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Leu Thr Leu Leu
865                 870                 875


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<400>  422

Ala Ile Glu Lys Xaa Xaa Xaa Asp Gln
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<210>  423
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Ala Ile Glu Arg Xaa Xaa Xaa Asp Gln
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<400> 424

Ala Val Glu Lys Xaa Xaa Xaa Asp Gln
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<400> 425

Ala Val Glu Arg Xaa Xaa Xaa Asp Gln
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<210> 426
<211> 38
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Cys Xaa Xaa Xaa Xaa Cys Val Xaa Thr Xaa Val Pro Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa
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Ala Xaa Glu Xaa Xaa Xaa Xaa Asp Gln
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Xaa Xaa Xaa Xaa Ile Leu Ala Xaa Glu Xaa Xaa Xaa Xaa Asp Gln
1 5 10 15