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- (56) Related Art  
**US 20140065105 A1**  
**US 20140248305 A1**  
**LASARO M. O. et al., MOLECULAR THERAPY, 2009, vol. 17, no. 8, pages 1333 - 1339**  
**TATSIS N. et al., THE JOURNAL OF IMMUNOLOGY, 2009, vol. 182, no. 10, pages 6587 - 6599**



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(54) Title: COMPOSITIONS AND METHODS OF REPLICATION DEFICIENT ADENOVIRAL VECTORS FOR VACCINE APPLICATIONS

(57) Abstract: The invention includes compositions and methods of generating a chimpanzee-derived adenovirus AdC6 or AdC7 vector vaccine comprising a deletion of E1, a deletion of E3 ORF3, ORF4, ORF5, ORF6, and ORF7 and a sequence encoding HIV protein gp140, gp160 or Gag, methods of treating and/or preventing or immunizing against HIV and methods of inducing an effector T cell, memory T cell and B cell immune response in a mammal administered the composition produced thereby. Furthermore, the invention encompasses a pharmaceutical composition for vaccinating a mammal as well as a protein expression system.

## TITLE OF THE INVENTION

Compositions and Methods of Replication Deficient Adenoviral Vectors For Vaccine  
Applications

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## CROSS-REFERENCE TO RELATED APPLICATION

This application claims priority to U.S. Provisional Application Serial No.  
62/369,288, filed August 1, 2016, the contents of which are incorporated by reference herein  
in their entirety.

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STATEMENT REGARDING FEDERALLY SPONSORED  
RESEARCH OR DEVELOPMENT

This invention was made with government support under grants P01  
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has certain rights in the invention.

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## BACKGROUND OF THE INVENTION

Vaccination is widely recognized as the most effective method of preventing  
or ameliorating morbidity from infectious diseases. However, traditional methods of vaccine  
development using inactivation or attenuation of viruses have failed for some of the most  
deadly human pathogens, necessitating new approaches. Progresses in research have enabled  
the genetic manipulation of viruses allowing their attenuation as well as incorporation of  
other foreign sequences. Viral vectors have been studied as potential tools to deliver vaccines  
as they present advantages over traditional vaccines in that they stimulate a broad range of  
immune responses including antibody (B cell), T helper cell- (CD4<sup>+</sup> T cell), and cytotoxic T  
lymphocyte- (CTL, CD8<sup>+</sup> T cell) mediated immunity. These viral vector vaccines could be  
used against various infectious and malignant diseases (Small and Hildegund, Curr Opin  
Virol. 2011, October 1; 1(4): 241–245).

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Adenoviruses (Ad) vectors are commonly used as vaccine carriers because of  
their ability to induce insert-specific CD8<sup>+</sup> T cell responses, they have broad tropism, high  
transduction efficiency and relatively pose no to low risks. However, vaccination is less  
effective in the presence of neutralizing antibodies (nAb) and pre-existing Ad-specific  
immunity represents a major obstacle for Ad-based vaccines as it decreases gene transfer

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efficacy and increases vector-mediated toxicity. Until now, most Ad vectors are based on human serotype 5 (AdHu5). This virus is endemic in most human populations, and neutralizing antibodies specific to AdHu5 can be detected in up to 40–90% of humans. Seroprevalence of other known human Ads also fluctuate globally with the occurrence of natural infection.

To avoid the potential limitations imposed by preexisting immunity, vectors based on rare human Ad serotypes and Ad from other species are being explored. For instance, vectors based on alternative Ad serotypes are in development, including AdHu26, 35, 48, and the chimpanzee-derived AdC6, C7, and C68. Neutralizing titers to these various rare Ad serotypes are typically low in humans, with seroprevalence to AdC6 and AdC7 less than 5% of adults in the United States and less than 10% seropositive in equatorial Africa, the natural habitat for chimpanzees. However clinical proof of safety, tolerability and immunogenicity of these alternates Ad vectors remain lacking. Certain Adenovirus vectors are disclosed in U.S. Application No. 14/190,787.

Clearly, there is a need in the art for methods of producing more efficient adenovirus vector vaccine systems that circumvent the host's pre-existing immunity, support gene expression of large foreign inserts, while inducing a potent immune response and being stable and safe for the host. The present invention fulfills this need.

## SUMMARY OF THE INVENTION

The invention provides a composition comprising a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, wherein the early gene E1 is deleted, the ORF3, ORF4, ORF5, ORF6, and ORF7 from the early gene E3 are deleted, and wherein the nucleic acid sequence further comprises a promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag.

In one embodiment, the promoter is a constitutive promoter. In another embodiment, the promoter is a cytomegalovirus immediate early promoter (CMV). In yet another embodiment, the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 1-8.

In another aspect, the invention provides a protein expression system comprising the composition listed above herein which comprises a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, wherein the early gene E1



is deleted, the ORF3, ORF4, ORF5, ORF6, and ORF7 from the early gene E3 are deleted, wherein the nucleic acid sequence further comprises a promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag, and further  
5 wherein the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 1-8.

The invention also provides a protein expression system comprising the composition listed above herein which comprises a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, wherein the early gene E1 is deleted, the ORF3, ORF4, ORF5, ORF6, and ORF7 from the early gene E3 are deleted, wherein the  
10 nucleic acid sequence further comprises a promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag, and further wherein the nucleic acid sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 9-16.

The invention further provides a method of eliciting an immune response in a mammal against a heterologous protein. The method of the invention comprises administering to the mammal a composition comprising a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, wherein the early gene E1 is deleted, the ORF3, ORF4, ORF5, ORF6, and ORF7 from the early gene E3 are deleted,  
20 and wherein the nucleic acid sequence further comprises a promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag.

In one embodiment, the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 1-8.

In another aspect, the invention provides a method of treating and/or preventing HIV in a mammal. The method of the invention comprises administering a therapeutically effective amount of a composition encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-8.

In yet another aspect, the invention provides method of vaccinating a mammal  
30 against HIV infection. The method of the invention comprises administering to the mammal a pharmaceutically acceptable amount of the composition listed above herein, which comprises a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, wherein the early gene E1 is deleted, the ORF3, ORF4, ORF5, ORF6, and ORF7 from the early gene E3 are deleted, wherein the nucleic acid sequence further comprises a

promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag, and further wherein administration of the composition elicits an immune response in the mammal.

5 In one embodiment, the composition is administered prophylactically to the mammal. In another embodiment, the composition is administered therapeutically to the mammal. In yet another embodiment, composition is administered in combination with an adjuvant.

10 In a further aspect, the invention includes a method of generating a effector and memory T cell immune response to a heterologous protein in a mammal. The method of the invention comprises the steps of: (a) administering the composition of the invention listed above herein to a mammal in an amount effective to elicit an immune response in the mammal; (b) administering a second effective amount of the chimpanzee-derived adenovirus vector of the composition of the invention listed above herein at a second, subsequent time  
15 period, wherein T memory cells directed against the heterologous protein are reactivated in the mammal.

In one embodiment, the composition administered first in (a) and second in (b) comprises a same or a different HIV heterologous protein selected from the group consisting of gp140, gp160 and Gag. In another embodiment, the composition administered first in (a)  
20 and in (b) has a same or a different serotype selected from the group consisting of AdC6 and AdC7.

In yet a further aspect, the invention includes a method of generating an adaptive B cell immune response to a heterologous protein in a mammal. The method of the invention comprises the steps of: (a) administering the composition of the invention listed  
25 above herein to a mammal in an amount effective to elicit an immune response in the mammal; (b) administering a second effective amount of the composition of the invention listed above herein at a second, subsequent time period, wherein B memory cells directed against the heterologous protein are reactivated in the mammal.

In some embodiments, the mammal is a human.

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#### BRIEF DESCRIPTION OF THE DRAWINGS

For the purpose of illustrating the invention, there are depicted in the drawings certain embodiments of the invention. However, the invention is not limited to the precise arrangements and instrumentalities of the embodiments depicted in the drawings.

5 Figs. 1A-1D are series of graphs illustrating the neutralizing antibody titers to MW965 PV compared to non-specific neutralization of MuLV PV. Figs. 1A-1C (groups 1-6, upper and lower graphs): sera of mice were tested after the last immunization at a 1:40 dilution for neutralization of the indicated pseudotyped lentiviruses. Data show % neutralization of each individual samples from the 6 groups. Median and IQR are indicated  
 10 by lines. Differences to neutralization of the control were determined by Friedman test with Dunn correction. \* indicates p-values below 0.05. Fig. 1D: titers of neutralizing antibodies against MW965 PV.

Figs. 2A-2B are series of graphs and histograms illustrating sera binding studies from study mice. Fig. 2A displays results from sera of the same mice shown in Figs.  
 15 1A-1D tested 4 weeks after each immunization at serial dilutions for binding to HIV-1 clade C gp140. Fig. 2A shows the results for median adsorbance  $\pm$  interquartile range (IQR) for data obtained with sera from individual mice tested at a 1:2000 dilution. Background data obtained with pre-bleeds were subtracted (OD < 0.1). The bars below indicate the timing of priming (P) and boosting (B) for each group shown to the right. Fig. 2B shows samples from  
 20 the 1<sup>st</sup> bleeds after the last boost that were also tested for binding to a peptide expressing the sequence of the V2 loop of HIV-1 clade C. Results show adsorbance after subtraction of pre-bleed results for the 1:100 dilution of sera. Dots show results for individual mice, bars the medians and error bars the IQR.

Fig. 3 is a table depicting the characteristics of the Rhesus Macaques (RM)  
 25 tested in the present invention. Animals were distributed with high or low nAb responses to AdHu5 and AdHu26 equally into three groups of twelve RMs each. Each group had eight Mamu-A\*01<sup>+</sup> RMs and groups 1 and 3 each had one Mamu-B\*17<sup>+</sup> animal

Figs. 4A-4C are series of graphs illustrating virus acquisition, viral loads over time and levels of SIV genome integration. Fig. 4A shows viral titers over time in 12 control  
 30 animals and 12 animals each vaccinated with AdC or AdHu vectors. Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> animals are highlighted in dark grey. The bottom graph to the right shows median titers for the three groups (Controls, "Co"; AdC7/AdC6, "AdC"; AdHu26/AdHu5, "AdH"). Differences in viral loads (area under the curve) and set point viral loads were determined by Kruskal-Wallis test with Dunn correction. Fig. 4B shows as Kaplan-Meier curves infection

according to weeks after 1<sup>st</sup> challenge in Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> (left, n=3 for AdC and controls, n=4 for AdHu5) and Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> RMs (right, n=9 for AdC and controls, n=8 for AdHu). Differences were calculated by Log-rank (Mantel Cox) test. Fig. 4C shows to the left relative levels of integrated SIV genome at 2 (light grey symbol) and 12 (dark grey symbol) weeks after infection of subcohorts of the animals (n = 7 for AdC, n = 11 for AdHu5, n = 4 for controls). Each samples was tested by qPCR using 40-60 replicates. Outliers were excluded by median absolute deviation tests. Differences within one group between weeks 2 and 12 were determined by multiple t-tests. Differences between the three groups were calculated by 2-way Anova. The right graph shows number of challenges required till infection for AdC- and AdHu-vaccinated animals maintained stable levels of SIV integration (change <100, light grey symbol) or showed pronounced increases (change >100, dark grey symbol). Differences between animals of one group with high vs. low integration were calculated by multiple t-tests with Sidak-Holms correction.

Figs. 5A-5C are series of graphs depicting the titers of Env-specific Abs. Env-specific Abs of individual animals were measured by ELISA. Graphs show median Ab titers  $\pm$  IQR for serial dilutions of sera from for AdC (closed squares) and AdHu (open squares) vaccinated MamuA\*01<sup>-</sup>/B17<sup>-</sup> (Fig. 5A, n = 3 for AdC- and 4 for AdHu-vaccinated animals) and Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> RMs (Fig. 5B, n = 9 for AdC and 8 for AdHu-vaccinated animals). Fig. 5C shows titers of individual animals of the 3 groups after challenges (n = 12 per group). Connecting lines indicate significant differences \*  $p \leq 0.05$ , \*\*  $p \leq 0.01$  by Mann-Whitney tests.

Figs. 6A-6B are series of dot plots demonstrating the role of Abs in preventing SIV acquisition. The graphs show Spearman's correlations between antibody titers at wk 32 and number of challenges need to achieve infection for AdC (Fig. 6A, n = 10) and AdHu (Fig. 6B, n = 11) vaccinated RMs. R- (correlation coefficient) and unadjusted p-values are shown within the graphs. Animals that were not infected after 10 challenges were excluded.

Figs. 7A-7L are series of graphs depicting the kinetics of Gag-specific T cell responses. The graphs show frequencies of Gag-specific total CD8<sup>+</sup> (Fig. 7A, Fig. 7G) and CD4<sup>+</sup> (Fig. 7D, Fig. 7J), CD8<sub>CM</sub> (Fig. 7B, Fig. 7H), CD4<sub>CM</sub> (Fig. 7E, Fig. 7K), CD8<sub>EM</sub> (Fig. 7C, Fig. 7I) and CD4<sub>EM</sub> (Fig. 7F, Fig. 7L) T cells of AdC- (Figs. 7A-7F) and AdHu- (Figs. 7G-7L) vaccinated animals (n = 12 per group) as the sum of all possible functionally distinct responses calculated from Boolean gating after subtraction of background responses. Each graph shows median responses  $\pm$  IQR of Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> (closed squares, n = 3 for AdC- and n = 4 for AdHu-vaccinated animals) and Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> (open squares, n = 9 for

AdC- and  $n = 8$  for AdHu-vaccinated animals) RMs. (\*) indicates significant differences between the two subcohorts by Mann-Whitney tests.

Fig. 8. is a series of graphs showing the effect of CD8 depletion on serum viral loads. The graphs show relative viral loads of subcohorts of AdC (right, black squares,  $n = 5$ ) and AdHu (left, grey circles,  $n = 4$ ) animals that were treated 28 weeks after the last challenge with antibodies to CD8. Of note the one animal that had detectable titers before depletion also maintained titers by 65 days after antibody treatment had been initiated.

Fig. 9 is a dot plot showing the cross-reactivity of Ad binding Abs. Pre-immunization sera and sera harvested 4 weeks after the 2<sup>nd</sup> intra-tracheal administration of AdHu vectors from 16 RMs of groups 1 and 2 were tested for antibodies to the Ad vectors by ELISA on plates coated with Ad vectors expressing an irrelevant transgene. Adsorbance values of pre-bleeds were subtracted from those of immune sera before calculating titers. Graphs show titers of individual sera with lines indicating median titer  $\pm$  IQR.

Figs. 10A-10D are series of graphs depicting the role of viral loads and peak viral loads in increasing Ab titers after challenge. The graphs show correlations by Spearman between Ab titers at week 62 and viral loads (Fig. 10A, Fig. 10C) or peak viral loads (Fig. 10B, Fig. 10D) for AdC- (Fig. 10A, Fig. 10B,  $n = 12$ ) and AdHu- (Fig. 10C, Fig. 10D,  $n = 12$ ) vaccinated RMs. R- and unadjusted p-values are shown within the graphs.

Fig. 11 is a series of graphs illustrating Gag and Env-specific T cell responses of control animals. Six of the control animals were tested the day of first challenge and shortly after challenges for frequencies of Gag and Env specific CD4<sup>+</sup> (closed black squares) and CD8<sup>+</sup> (open white squares) T cells. Graphs show median frequencies  $\pm$  IQR of individual animals before and after challenge  $\pm$  IQR.

Figs. 12A-12F are series of dot plots depicting the effect of CD8<sup>+</sup> T cell subsets on viral loads and peak viral loads. The graphs show correlations by Spearman between CD8<sub>EM</sub> (Fig. 12A, Fig. 12C, Fig. 12D, Fig. 12F) and CD8<sub>CM</sub> (Fig. 12B, Fig. 12E) frequencies after the boost and peak viral loads (Fig. 12A, Fig. 12B, Fig. 12D, Fig. 12E) or set viral loads over time (Fig. 12C, Fig. 12F) in AdC- (Figs. 12A-12C,  $n = 12$ ) and AdHu- (Figs. 12D-12F,  $n = 12$ ) vaccinated RMs. R- and unadjusted p-values are shown within the graphs.

Figs. 13A-13D are series of dot plots depicting the effect of peak viral loads on CD4<sup>+</sup> T cell subsets. The graphs show correlations by Spearman between total CD4<sup>+</sup> T (Fig. 13A, Fig. 13C) and CD4<sub>EM</sub> (Fig. 13B, Fig. 13D) frequencies after challenges and peak

viral loads for AdC- (Fig. 13A, Fig. 13B, n = 12) and AdHu- (Fig. 13C, Fig. 13D, n = 12) vaccinated RMs. R- and unadjusted p-values are shown within the graphs.

Fig. 14 is a series of graphs depicting the effect of Gag-specific CD8<sup>+</sup> T cells on levels of SIV integration. The graph on the right shows frequencies of Gag-specific CD8<sub>EM</sub> T cells before challenge in animals with low levels of SIV integration by 2 weeks after infection (<50,000, dark grey symbol, AdC: n = 4, AdHu: n = 5) as compared to animals with high levels of integration (>50,000, light grey symbols, AdC: n = 3, AdHu: n = 6). Differences were determined by multiple t-tests with Sidak-Holms correction. The graphs in the middle and to the right show frequencies of Gag-specific CD8<sub>CM</sub> (middle) and CD8<sub>EM</sub> T cells (right) before challenge in animals with low levels of SIV integration by 12 weeks after infection (<10<sup>6</sup>, dark grey symbol, AdC: n = 4, AdHu: n = 5) as compared to animals with high levels of integration (>10<sup>6</sup>, light grey symbols, AdC: n = 3, AdHu: n = 6). Differences were determined by multiple t-tests with Sidak-Holms correction. Lines with star above indicate significant differences.

Figs. 15A-15L are series of graphs illustrating Env-specific T Cell responses in vaccinated RMs. Frequencies of Env-specific total CD8<sup>+</sup>, CD8<sub>CM</sub> and CD8<sub>EM</sub>, total CD4<sub>CM</sub> and CD4<sub>EM</sub> T cells tested before and after challenges in 6 randomly selected control RMs are shown. Organization and symbols of the graph are identical to those of Figs. 7A-7L.

Fig. 16 is a series of histograms demonstrating the functions of Gag-specific total CD8<sup>+</sup> T cells over time. The graphs show median frequencies ± IQR of Gag-specific CD8<sup>+</sup> T cells from AdC- (left graphs) and AdHu- (right graphs) vaccinated Mamu-A\*01<sup>-</sup>/B17<sup>-</sup> (white bars; AdC: n = 3, AdHu: n = 4) and Mamu-A\*01<sup>+</sup>/B17<sup>+</sup> RMs (grey bars; AdC: n = 9, AdHu: n = 8) exhibiting either of the possible 15 combinations of functions. Cells were tested at different times after vaccination. (#) indicates significant differences by Wilcoxon Rank test calculated by Spice software.

Fig. 17 is a series of histograms demonstrating the functions of Gag-specific total CD4<sup>+</sup> T cells over time. The graphs show frequencies of functionally distinct Gag-specific CD4<sup>+</sup> T cells mirroring the design of Fig. 16. with Mamu-A\*01<sup>-</sup>/B17<sup>-</sup> (white bars AdC: n = 3, AdHu: n = 4) and Mamu-A\*01<sup>+</sup>/B17<sup>+</sup> RMs (grey bars AdC: n = 9, AdHu: n = 8). (#) indicates significant differences by Wilcoxon Rank test calculated by Spice software.

Fig. 18 is a series of histograms demonstrating the functions of CD8<sup>+</sup> and CD4<sup>+</sup> T cell subsets. The graphs show median frequencies ± IQR of Gag-specific CD8<sub>CM</sub>, CD8<sub>EM</sub>, CD4<sub>CM</sub> and CD4<sub>EM</sub> from AdC- (left graphs) and AdHu- (right graphs) vaccinated

Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> (white bars; AdC: n = 3, AdHu: n = 4) and Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> RMs (grey bars; AdC: n = 9, AdHu: n = 8) exhibiting either of the possible 15 combination of functions. Cells were tested 48 weeks after priming, i.e., shortly before the 1<sup>st</sup> SIV challenge. (#) indicates significant differences by Wilcoxon Rank test calculated by Spice software.

5 Figs. 19A-19D are series of images depicting various maps and sequences of AdC6 and AdC7. Figs. 19A-19B : Maps of AdC6 and AdC7 vectors expressing Env. Fig. 19C: Maps of pShuttle plasmids containing gp140 (DU172 and DU422).

10 Figs. 20A-20K are a list of the nucleotide (Figs. 20A-20H) and amino acid (Figs. 20I-20K) sequences of the AdC6 vector expressing gp140 (SEQ ID NOs: 1 and 9 respectively).

Figs. 21A-21J are a list of the nucleotide (Figs. 21A-21G) and amino acid (Figs. 21H-21J) sequences of the AdC6 vector expressing Gag (SEQ ID NOs: 2 and 10 respectively).

15 Figs. 22A-22K are a list of the nucleotide (Figs. 22A-22H) and amino acid (Figs. 22I-22K) sequences of the AdC7 vector expressing gp140 (SEQ ID NOs: 3 and 11 respectively).

Figs. 23A- 23K are a list of the nucleotide (Figs. 23A-23H) and amino acid sequences (Figs. 23I-23K) of the AdC7 vector expressing Gag (SEQ ID NOs: 4 and 12 respectively).

20 Figs. 24A-24K are a list of the nucleotide (Figs. 24A-24H) and amino acid sequences (Figs. 24I-43K) of the AdC6 vector expressing gp160, construct DU172 (SEQ ID NOs: 5 and 13 respectively).

25 Figs. 25A-25K are a list of the nucleotide (Figs. 25A-25H) and amino acid (Figs. 25I-25K) sequences of the AdC6 vector expressing gp160, construct DU422 (SEQ ID NOs: 6 and 14 respectively).

Figs. 26A-26K are a list of the nucleotide (Figs. 26A-26H) and amino acid (Figs. 26I-26K) sequences of the AdC7 vector expressing gp160, construct DU172 (SEQ ID NOs: 7 and 15 respectively).

30 Figs. 27A-27K are a list of the nucleotide (Figs. 27A-27H) and amino acid (Figs. 27I-27K) sequences of the AdC7 vector expressing gp160, construct DU422 (SEQ ID NOs: 8 and 16 respectively).

## DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to compositions and methods for generating a chimpanzee-derived adenovirus vector comprising a nucleic acid sequence comprising a deletion in some of the adenovirus early genes (i.e. deletion of E1 and a partial deletion E3) and a promoter sequence linked to a sequence encoding a heterologous protein comprising, in certain embodiments, an HIV gp140, gp160, or HIV Gag protein or other potentially toxic proteins such as the rabies virus glycoprotein. Additionally, the current invention includes compositions and methods of treating of and/or preventing or immunizing against, a specific disease or disorder, and methods of inducing an effector and memory T and B cell immune response in a mammal administered the chimpanzee-derived adenovirus vector the invention.

### Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although any methods and materials similar or equivalent to those described herein may be used in the practice for testing of the present invention, the preferred materials and methods are described herein. In describing and claiming the present invention, the following terminology will be used.

It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

As used herein, the articles “a” and “an” are used to refer to one or to more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

The term “antibody” or “Ab” as used herein, refers to a protein, or polypeptide sequence derived from an immunoglobulin molecule, which specifically binds to a specific epitope on an antigen. Antibodies can be intact immunoglobulins derived from natural sources or from recombinant sources and can be immunoreactive portions of intact immunoglobulins. The antibodies useful in the present invention may exist in a variety of forms including, for example, polyclonal antibodies, monoclonal antibodies, intracellular antibodies (“intrabodies”), Fv, Fab and F(ab)<sub>2</sub>, as well as single chain antibodies (scFv) and humanized antibodies (Harlow et al., 1998, Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, Antibodies: A Laboratory Manual, Cold Spring Harbor, New York; Houston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; Bird et al., 1988, Science 242:423-426). An antibody may be derived from natural



sources or from recombinant sources. Antibodies are typically tetramers of immunoglobulin molecules.

The term “ameliorating” or “treating” means that the clinical signs and/or the symptoms associated with a disease are lessened as a result of the actions performed. The signs or symptoms to be monitored will be well known to the skilled clinician.

As used herein when referring to a measurable value such as an amount, a temporal duration, and the like, the term “about” is meant to encompass variations of  $\pm 20\%$  or  $\pm 10\%$ , more preferably  $\pm 5\%$ , even more preferably  $\pm 1\%$ , and still more preferably  $\pm 0.1\%$  from the specified value, as such variations are appropriate to perform the disclosed methods.

The term “biological” or “biological sample” refers to a sample obtained from an organism or from components (e.g., cells) of an organism. The sample may be of any biological tissue or fluid. Frequently the sample will be a “clinical sample” which is a sample derived from a patient. Such samples include, but are not limited to, bone marrow, cardiac tissue, sputum, blood, lymphatic fluid, blood cells (e.g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes.

As used herein, “greater” refers to expression levels which are at least 10% or more, for example, 20%, 30%, 40%, or 50%, 60%, 70%, 80%, 90% higher or more, and/or 1.1 fold, 1.2 fold, 1.4 fold, 1.6 fold, 1.8 fold, 2.0 fold higher or more, and any and all whole or partial increments therebetween, than a control.

As used herein, the terms “control,” or “reference” are used interchangeably and refer to a value that is used as a standard of comparison.

The term “immunogenicity” as used herein, refers to the innate ability of an antigen or organism to elicit an immune response in an animal when the antigen or organism is administered to the animal. Thus, “enhancing the immunogenicity” refers to increasing the ability of an antigen or organism to elicit an immune response in an animal when the antigen or organism is administered to an animal. The increased ability of an antigen or organism to elicit an immune response can be measured by, among other things, a greater number of antibodies that bind to an antigen or organism, a greater diversity of antibodies to an antigen or organism, a greater number of T-cells specific for an antigen or organism, a greater cytotoxic or helper T-cell response to an antigen or organism, a greater expression of cytokines in response to an antigen, and the like.

As used herein, the terms “eliciting an immune response” or “immunizing” refer to the process of generating a B cell and/or a T cell response against a heterologous protein.

5 The term “activation”, as used herein, refers to the state of a cell following sufficient cell surface moiety ligation to induce a noticeable biochemical or morphological change. Within the context of T cells, such activation refers to the state of a T cell that has been sufficiently stimulated to induce cellular proliferation. Activation of a T cell may also induce cytokine production and performance of regulatory or cytolytic effector functions. Within the context of other cells, this term infers either up or down regulation of a particular  
10 physico-chemical process.

The term “activated T cell” means a T cell that is currently undergoing cell division, cytokine production, performance of regulatory or cytolytic effector functions, and/or has recently undergone the process of “activation.”

The term “antigen” or “Ag” as used herein is defined as a molecule that  
15 provokes an immune response. This immune response may involve either antibody production, or the activation of specific immunologically-competent cells, or both. The skilled artisan will understand that any macromolecule, including virtually all proteins or peptides, can serve as an antigen. Furthermore, antigens can be derived from recombinant or genomic DNA. A skilled artisan will understand that any DNA, which comprises a  
20 nucleotide sequences or a partial nucleotide sequence encoding a protein that elicits an immune response therefore encodes an “antigen” as that term is used herein. Furthermore, one skilled in the art will understand that an antigen need not be encoded solely by a full-length nucleotide sequence of a gene. It is readily apparent that the present invention includes, but is not limited to, the use of partial nucleotide sequences of more than one gene  
25 and that these nucleotide sequences are arranged in various combinations to elicit the desired immune response. Moreover, a skilled artisan will understand that an antigen need not be encoded by a “gene” at all. It is readily apparent that an antigen can be generated synthesized or can be derived from a biological sample. Such a biological sample can include, but is not limited to a tissue sample, a tumor sample, a cell or a biological fluid.

30 “Heterologous antigens” used herein to refer to an antigen that is not endogenous to the organism comprising or expressing an antigen. As an example, a virus vaccine vector comprising or expressing a viral or tumor antigen comprises a heterologous antigen. The term “Heterologous protein” as used herein refers to a protein that elicits a beneficial immune response in a subject (i.e. mammal), irrespective of its source.

By the terms "Human Immunodeficiency Virus" or HIV" as used herein is meant any HIV strain or variant that is known in the art or that is heretofore unknown, including without limitation, HIV-1 and HIV-2. HIV-1 is exemplified in certain embodiments disclosed herein.

5           The term "specifically binds", "selectively binds" or "binding specificity" refers to the ability of the humanized antibodies or binding compounds of the invention to bind to a target epitope with a greater affinity than that which results when bound to a non-target epitope. In certain embodiments, specific binding refers to binding to a target with an affinity that is at least 10, 50, 100, 250, 500, or 1000 times greater than the affinity for a non-  
10 target epitope.

As used herein, by "combination therapy" is meant that a first agent is administered in conjunction with another agent. "In combination with" or "In conjunction with" refers to administration of one treatment modality in addition to another treatment modality. As such, "in combination with" refers to administration of one treatment modality  
15 before, during, or after delivery of the other treatment modality to the individual. Such combinations are considered to be part of a single treatment regimen or regime.

"Humoral immunity" or "humoral immune response" both refer to B-cell mediated immunity and are mediated by highly specific antibodies, produced and secreted by B-lymphocytes (B-cells).

20           "Prevention" refers to the use of a pharmaceutical compositions for the vaccination against a disorder.

"Adjuvant" refers to a substance that is capable of potentiating the immunogenicity of an antigen. Adjuvants can be one substance or a mixture of substances and function by acting directly on the immune system or by providing a slow release of an  
25 antigen. Examples of adjuvants are aluminium salts, polyanions, bacterial glycopeptides and slow release agents as Freund's incomplete.

"Delivery vehicle" refers to a composition that helps to target the antigen to specific cells and to facilitate the effective recognition of an antigen by the immune system. The best-known delivery vehicles are liposomes, virosomes, microparticles including  
30 microspheres and nanospheres, polymeres, bacterial ghosts, bacterial polysaccharides, attenuated bacteria, virus like particles, attenuated viruses and ISCOMS.

"Incorporated into" or "encapsulated in" refers to an antigenic peptide that is within a delivery vehicle, such as microparticles, bacterial ghosts, attenuated bacteria, virus like particles, attenuated viruses, ISCOMs, liposomes and preferably virosomes.

As used herein, the terms “peptide,” “polypeptide,” and “protein” are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that may comprise a protein or peptide’s sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. “Polypeptides” include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. The polypeptides include natural peptides, recombinant peptides, synthetic peptides, or a combination thereof.

A “fusion protein” as used herein refers to a protein wherein the protein comprises two or more proteins linked together by peptide bonds or other chemical bonds. The proteins can be linked together directly by a peptide or other chemical bond, or with one or more amino acids between the two or more proteins, referred to herein as a spacer.

In the context of the present invention, the following abbreviations for the commonly occurring nucleic acid bases are used. “A” refers to adenosine, “C” refers to cytosine, “G” refers to guanosine, “T” refers to thymidine, and “U” refers to uridine.

The term “RNA” as used herein is defined as ribonucleic acid.

“Transform”, “transforming”, and “transformation” is used herein to refer to a process of introducing an isolated nucleic acid into the interior of an organism.

The term “treatment” as used within the context of the present invention is meant to include therapeutic treatment as well as prophylactic, or suppressive measures for the disease or disorder. As used herein, the term “treatment” and associated terms such as “treat” and “treating” means the reduction of the progression, severity and/or duration of a disease condition or at least one symptom thereof. The term “treatment” therefore refers to any regimen that can benefit a subject. The treatment may be in respect of an existing condition or may be prophylactic (preventative treatment). Treatment may include curative, alleviative or prophylactic effects. References herein to “therapeutic” and “prophylactic” treatments are to be considered in their broadest context. The term “therapeutic” does not necessarily imply that a subject is treated until total recovery. Similarly, “prophylactic” does not necessarily mean that the subject will not eventually contract a disease condition. Thus,

for example, the term treatment includes the administration of an agent prior to or following the onset of a disease or disorder thereby preventing or removing all signs of the disease or disorder. As another example, administration of the agent after clinical manifestation of the disease to combat the symptoms of the disease comprises “treatment” of the disease.

5           The term “equivalent,” when used in reference to nucleotide sequences, is understood to refer to nucleotide sequences encoding functionally equivalent polypeptides. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions- or deletions, such as allelic variants; and will, therefore, include sequences that differ from the nucleotide sequence of the nucleic acids described herein due  
10 to the degeneracy of the genetic code.

          The term “isolated” as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs or RNAs, respectively that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material,  
15 or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an “isolated nucleic acid” is meant to include nucleic acid fragments, which are not naturally occurring as fragments and would not be found in the natural state. The term “isolated” is also used herein to refer to polypeptides, which are isolated from other cellular proteins and is meant to encompass both  
20 purified and recombinant polypeptides. An “isolated cell” or “isolated population of cells” is a cell or population of cells that is not present in its natural environment.

          A “mutation” as used therein is a change in a DNA sequence resulting in an alteration from its natural state. The mutation can comprise a deletion and/or insertion and/or duplication and/or substitution of at least one desoxyribonucleic acid base such as a purine  
25 (adenine and/or thymine) and/or a pyrimidine (guanine and/or cytosine). Mutations may or may not produce discernible changes in the observable characteristics (phenotype) of an organism.

          As used herein, the term “nucleic acid” refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term  
30 should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

As used herein, "operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in trans or at a distance to control the gene of interest. Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. There are numerous expression control sequences, including promoters which are native, constitutive, inducible and/or tissue-specific, are known in the art that may be used in the compositions of the invention. "Operably linked" should be construed to include RNA expression and control sequences in addition to DNA expression and control sequences.

The term "promoter" as used herein is defined as a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a polynucleotide sequence.

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence, which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements, which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell under most or all physiological conditions of the cell.

An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only when an inducer which corresponds to the promoter is present in the cell.

As used herein, the term "pharmaceutical composition" refers to a mixture of at least one compound useful within the invention with other chemical components, such as carriers, stabilizers, diluents, adjuvants, dispersing agents, suspending agents, thickening agents, and/or excipients. The pharmaceutical composition facilitates administration of the compound to an organism. Multiple techniques of administering a compound exist in the art

including, but not limited to: intravenous, oral, aerosol, parenteral, ophthalmic, pulmonary and topical administration.

The language “pharmaceutically acceptable carrier” includes a pharmaceutically acceptable salt, pharmaceutically acceptable material, composition or carrier, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material, involved in carrying or transporting a compound(s) of the present invention within or to the subject such that it may perform its intended function. Typically, such compounds are carried or transported from one organ, or portion of the body, to another organ, or portion of the body. Each salt or carrier must be “acceptable” in the sense of being compatible with the other ingredients of the formulation, and not injurious to the subject. Some examples of materials that may serve as pharmaceutically acceptable carriers include: sugars, such as lactose, glucose and sucrose; starches, such as corn starch and potato starch; cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt; gelatin; talc; excipients, such as cocoa butter and suppository waxes; oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol; polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; esters, such as ethyl oleate and ethyl laurate; agar; buffering agents, such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline; Ringer’s solution; ethyl alcohol; phosphate buffer solutions; diluent; granulating agent; lubricant; binder; disintegrating agent; wetting agent; emulsifier; coloring agent; release agent; coating agent; sweetening agent; flavoring agent; perfuming agent; preservative; antioxidant; plasticizer; gelling agent; thickener; hardener; setting agent; suspending agent; surfactant; humectant; carrier; stabilizer; and other non-toxic compatible substances employed in pharmaceutical formulations, or any combination thereof. As used herein, “pharmaceutically acceptable carrier” also includes any and all coatings, antibacterial and antifungal agents, and absorption delaying agents, and the like that are compatible with the activity of the compound, and are physiologically acceptable to the subject.

Supplementary active compounds may also be incorporated into the compositions.

As used herein, the term “effective amount” or “therapeutically effective amount” means the amount of the virus like particle generated from vector of the invention which is required to prevent the particular disease condition, or which reduces the severity of and/or ameliorates the disease condition or at least one symptom thereof or condition associated therewith.

A “subject” or “patient,” as used therein, may be a human or non-human mammal. Non-human mammals include, for example, livestock and pets, such as ovine, bovine, porcine, canine, feline and murine mammals. Preferably, the subject is human.

“Titers” are numerical measures of the concentration of a virus or viral vector compared to a reference sample, where the concentration is determined either by the activity of the virus, or by measuring the number of viruses in a unit volume of buffer. The titer of viral stocks are determined, e.g., by measuring the infectivity of a solution or solutions (typically serial dilutions) of the viruses, e.g., on HeLa cells using the soft agar method (see, Graham & Van Der eb (1973) Virology 52:456-467) or by monitoring resistance conferred to cells, e.g., G418 resistance encoded by the virus or vector, or by quantitating the viruses by UV spectrophotometry (see, Chardonnet & Dales (1970) Virology 40:462-477).

A “vector” is a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. In the present disclosure, the term “vector” includes an autonomously replicating virus.

Ranges: throughout this disclosure, various aspects of the invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. This applies regardless of the breadth of the range.

### Description

The invention provides chimpanzee-derived adenoviral vectors useful in vaccine development and gene therapy. These vectors comprise a deletion of the viral early genomic region E1, and a selective deletion of some of the nine open reading frames (ORFs) of the viral early genomic region E3 while retaining others. The disclosed vectors are



particularly useful for vaccine development and therapy. Adenoviral vectors comprising such deletions are disclosed in U.S. Application No. 14/190,787.

The present invention comprises the novel improvement over U.S. Application No. 14/190,787 wherein the adenoviral vector encodes nucleic acid encoding a heterologous protein encoding HIV envelope protein gp140, wherein when the vector is introduced into a cell, the cell stably expresses gp140 protein, for over 12 serial passages of the vector within cells.

The present invention comprises the novel improvement over U.S. Application No. 14/190,787 wherein the adenoviral vector encodes nucleic acid encoding a heterologous protein encoding HIV envelope protein gp160, wherein when the vector is introduced into a cell, the cell stably expresses gp160 protein, for over many serial passages of the vector within cells.

The present invention also comprises the novel improvement over U.S. Application No. 14/190,787 wherein the adenoviral vector encodes nucleic acid encoding a heterologous protein encoding HIV Gag, wherein when the vector is introduced into a cell, the cell stably expresses gag protein, for over many serial passages of the vector within cells.

In one aspect, the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag. In another aspect, the heterologous protein is all or an antigenic portion of the HIV gp140, gp160 or HIV Gag proteins.

In one embodiment, the HIV serotype is HIV-1.

In some embodiments, the chimpanzee-derived adenovirus vector comprises a nucleic acid sequence comprising a constitutive promoter.

In some embodiments, the chimpanzee-derived adenovirus vector of this invention comprises a nucleic acid sequence consists of SEQ ID NOs: 1- 4.

In other embodiments, the present invention relates to a protein expression system comprising a chimpanzee-derived adenovirus vector comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-4. In yet other embodiments, the protein expression system of this invention comprises a chimpanzee-derived adenovirus vector, wherein the vector comprises a nucleic acid sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-8.

In one embodiment, the invention provides a method of generating effector and memory T cell immune responses to a heterologous protein in a mammal. The method comprises first administering to the mammal the chimpanzee-derived adenovirus vector of this invention in an amount effective to elicit an immune response in the mammal; and

second, administering a second effective amount of the chimpanzee-derived adenovirus vector at a subsequent time period, wherein T memory cells directed against the heterologous protein are reactivated in the mammal.

In one embodiment, the invention provides a method of generating an adaptive  
5 B cell immune response to a heterologous protein in a mammal. The method comprises first administering to the mammal the chimpanzee-derived adenovirus vector of this invention in an amount effective to elicit an immune response in the mammal; and second, administering a second effective amount of the chimpanzee-derived adenovirus vector at a subsequent time period, wherein B memory cells directed against the heterologous protein are reactivated in  
10 the mammal.

In some aspects of the invention, the chimpanzee-derived adenovirus vector administered herein to a mammal, in a first and second step, comprises the same or a different: HIV heterologous protein selected from the group consisting of gp140, gp160 and Gag encoded by an adenovirus serotype selected from the group consisting of AdC6 and  
15 AdC7.

Vaccine compositions comprising adenovirus particles made using the adenovirus vectors disclosed herein can be used to induce immunity in a mammal against one or more encoded heterologous proteins or antigenic portions thereof. Immunity can be induced using the disclosed vaccine compositions or dosage units. Immune responses can be  
20 assessed using suitable methods known in the art, as disclosed, for example, in WO2012/02483.

In certain embodiments, the mammal is a human.

#### Heterologous Gene Expression

In one aspect, although the cytomegalovirus immediate early promoter is  
25 exemplified herein as the promoter driving expression of the HIV protein, the invention should not be construed to be limited to this promoter sequence. Promoter sequences that are useful in the invention include any promoter that induces high levels of gene expression. Such promoters may include, but are not limited to those disclosed elsewhere herein.

In one embodiment, a suitable promoter is the immediate early  
30 cytomegalovirus (CMV) promoter sequence. This promoter sequence is a strong constitutive promoter sequence capable of driving high levels of expression of any polynucleotide sequence operatively linked thereto. Another example of a suitable promoter is Elongation Growth Factor -1 $\alpha$  (EF-1 $\alpha$ ). However, other constitutive promoter sequences may also be used, including, but not limited to the simian virus 40 (SV40) early promoter, mouse

mammary tumor virus (MMTV), human immunodeficiency virus (HIV) long terminal repeat (LTR) promoter, MoMuLV promoter, an avian leukemia virus promoter, an Epstein-Barr virus immediate early promoter, a Rous sarcoma virus promoter, as well as human gene promoters such as, but not limited to, the actin promoter, the myosin promoter, the

5 hemoglobin promoter, and the creatine kinase promoter. Further, the invention should not be limited to the use of constitutive promoters. Inducible promoters are also contemplated as part of the invention. The use of an inducible promoter provides a molecular switch capable of turning on expression of the polynucleotide sequence, which it is operatively linked when such expression is desired, or turning off the expression when expression is not desired.

10 Examples of inducible promoters include, but are not limited to a metallothioneine promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter.

In some embodiments, the invention further includes the use of a tissue-specific promoter that drives expression of a given heterologous gene in one or more specific types of cells (e.g., myoglobin promoter, muscle creatine kinase promoter, desmin promoter, 15 mammalian troponin 1 promoter, and skeletal alpha-action promoter). Furthermore, any artificial synthetic promoters known in the art can be used in this invention as these promoters can provide optimal efficiency and stability for the heterologous gene.

Additionally, enhancer sequences regulate expression of the gene contained within a vector. Typically, enhancers are bound with protein factors to enhance the transcription of a gene.

20 Enhancers may be located upstream or downstream of the gene it regulates. Enhancers may also be tissue-specific to enhance transcription in a specific cell or tissue type.

In order to assess the expression of the heterologous gene of interest, the expression vector to be introduced into a cell can also contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of expressing cells from the 25 population of cells sought to be infected through the hybrid-virus vectors. In other aspects, the selectable marker may be carried on a separate piece of DNA and used in a co-infection/transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to enable expression in the host cells. Useful selectable markers include, for example, antibiotic-resistance genes, such as the neomycin resistant gene and the like.

30 Reporter genes are used for identifying potentially infected cells and for evaluating the functionality of regulatory sequences. In general, a reporter gene is a gene that is not present in or expressed by the recipient organism or tissue and that encodes a polypeptide whose expression is manifested by some easily detectable property, e.g.,

enzymatic activity. Suitable reporter genes may include genes encoding luciferase, beta-galactosidase, chloramphenicol acetyl transferase, secreted alkaline phosphatase, or the green fluorescent protein gene (e.g., Ui-Tei et al., 2000 FEBS Letters 479: 79-82).

It will be apparent to one skilled in the art that the invention is not limited to the nature of the heterologous gene that is expressed by the adenovirus vector of the invention. Any suitable heterologous gene can be used where expression of the gene provides a benefit to the mammal. For example, the heterologous gene may be a viral protein whose expression in a mammal confers immunity to infection by the virus.

Similarly, the heterologous gene may be a bacterial antigen, a parasitic antigen, a fungal antigen, a cancer antigen, an antigen involved in a deleterious autoimmune reaction, or any other protein where an immune response directed thereto provides benefit.

## 5 Heterologous proteins

In the present invention, the adenovirus vector of the invention may encode any heterologous protein useful in the invention, and may encode more than one heterologous protein inserted in tandem in the virus vector of the invention. Typically, the heterologous protein is a peptide fragment, polypeptide, protein or fusion protein. Optionally, the  
10 heterologous protein is suitable such that a cell-mediated immune response is induced against it in a mammal following administration of the vector to the mammal.

In one embodiment, the heterologous protein is derived from an HIV protein. In another embodiment, the heterologous protein is derived from HIV envelope glycoprotein. Non-limiting examples of HIV envelope glycoprotein are gp120, gp41, gp160 and gp140. In  
15 yet another embodiment, the heterologous protein is derived from HIV Gag protein.

In some embodiments, the heterologous protein may be derived from a toxic protein such as, but not limited to, the rabies virus glycoprotein.

In some embodiments, the heterologous protein may be derived from a cancer. In such embodiments, heterologous protein is, or is a fragment of, a tumor specific antigen. In  
20 certain embodiments the cancer may be derived from the group including Acute and Chronic Myelogenous Leukemia (AML, CML), Follicular Non-Hodgkins lymphoma, malignant melanoma, Hairy Cell leukaemia, multiple myeloma, carcinoid tumors with carcinoid syndrome and liver and lymph node metastases, AIDS related Kaposi's sarcoma, renal cell carcinoma, adenocarcinoma of the large bowel, squamous cell carcinoma of the head and  
25 neck. The cancer may also be derived from organs and solid tissues, e.g., colon cancer, lung cancer, breast cancer, stomach cancer, prostate cancer, and endometrial cancer. When such

heterologous proteins are used in the compositions and methods of the present invention, the resulting immune response generated may combat cancers and thus the vectors and viruses produced by these vectors are designed to be oncolytic.

5 In other embodiments, the heterologous protein may be associated with the pathology of an autoimmune disease. Organs and tissues commonly affected by autoimmune disorders include, but are not limited to, blood vessels, connective tissues, endocrine glands such as the thyroid or pancreas, joints, muscles, red blood cells and skin. Examples of autoimmune (or autoimmune-related) disorders for which such heterologous proteins may be useful include, but are not limited to, Addison's disease, Celiac disease, Dermatomyositis, 10 Graves' disease, Hashimoto's thyroiditis, Multiple sclerosis, Myasthenia gravis, Pernicious anemia, Reactive arthritis, Rheumatoid arthritis, Sjogren syndrome, Systemic lupus erythematosus and Type I diabetes.

#### Methods of the Invention

The vectors of the invention are useful in a variety of applications useful for immunizing a mammal against disease, and/or treating, preventing or diminishing risk of disease in a mammal.

The invention therefore includes a method of immunizing a mammal against a heterologous protein. The method comprises administering to the mammal a composition comprising a composition comprising a chimpanzee-derived adenovirus (Ad) vector comprising a DNA sequence comprising a deletion in E1, a deletion of E3 ORF3, ORF4, ORF5, ORF6, and ORF7 and a promoter sequence linked to a sequence encoding a heterologous protein, wherein expression of the heterologous protein induces an immune response in the mammal. In one embodiment the chimpanzee-derived Ad vector is AdC6. In another embodiment the chimpanzee-derived Ad vector is AdC7.

The invention further includes a method of treating a mammal in need thereof where the method administering a therapeutically effective amount of a composition encoded by a chimpanzee-derived adenovirus vector comprising a DNA sequence consisting of SEQ ID NOs: 1-4, wherein expression of the heterogeneous gene provides benefit to the mammal. In one aspect, the invention includes a method of generating effector and memory T cell immune responses to a heterologous protein in a mammal. In another aspect, the invention includes a method of generating an adaptive B cell immune response to a heterologous protein in a mammal.

Additionally included in the invention is a method of diminishing the risk that a mammal will develop a disease. The method comprises administering to the mammal a composition comprising a composition comprising a chimpanzee-derived adenovirus vector comprising a DNA sequence comprising a deletion in E1, a deletion of E3 ORF3, ORF4, ORF5, ORF6, and ORF7 and a promoter sequence linked to a sequence encoding a heterologous protein. Expression of the heterogeneous gene (e.g. HIV gp140, gp160 or Gag protein) induces an immune response to the heterologous protein encoded thereby in the mammal, thereby diminishing the risk that the mammal will develop a disease (e.g. HIV-1) associated with the heterologous protein.

#### Adenovirus vector production

Methods of making the adenovirus vector of the invention are described in detail in the Experimental Examples Section herein and in U.S. Application No. 14/190,787 incorporated herein by reference. In general, production, purification and quality control procedures for Adenovirus vectors are well established in the art. Once a vector backbone is created, molecular cloning can be used to create an adenoviral plasmid comprising a coding sequence for an antigenic heterologous protein. The plasmid can be transfected into packaging cells that provide E1 of a suitable adenovirus serotype in trans. Packaging cells are well known in the art, and cells lines such as HEK293 or PERC6 can be used for this purpose. Viral particles are then harvested once plaques become visible. Fresh cells can then be infected to ensure continued replication of the adenovirus. Quality can be assessed using Southern blotting or other methods, such as restriction enzyme mapping, sequencing, and PCR, to confirm the presence of the transgene and the lack of gene rearrangements or undesired deletions.

Vaccine compositions comprising adenovirus particles made using the adenovirus vectors disclosed herein can be used to induce immunity against the encoded antigenic protein. Vaccines can be formulated using standard techniques and can comprise, in addition to a replication-incompetent adenovirus vector encoding a desired protein, a pharmaceutically acceptable vehicle, such as phosphate-buffered saline (PBS) or other buffers, as well as other components such as antibacterial and antifungal agents, isotonic and absorption delaying agents, adjuvants, and the like. In some embodiments vaccine compositions are administered in combination with one or more other vaccines. Dosage units of vaccine compositions can be provided. Such dosage units typically comprise  $10^8$  to  $10^{11}$  adenoviral particles (e.g.,  $10^8$ ,  $5 \times 10^8$ ,  $10^9$ ,  $5 \times 10^9$ ,  $10^{10}$ ,  $5 \times 10^{10}$ ,  $10^{11}$ ). In some

embodiments, the dosage of  $5 \times 10^{10}$  virus particles is of choice. Particularly, this dosage ( $5 \times 10^{10}$ ) suits best humans in clinical trials.

#### Pharmaceutical Compositions and Formulations.

The vector of the invention may be formulated as a pharmaceutical composition.

5           Such a pharmaceutical composition may be in a form suitable for administration to a subject (i.e. mammal), or the pharmaceutical composition may further comprise one or more pharmaceutically acceptable carriers, one or more additional ingredients, or some combination of these. The various components of the pharmaceutical composition may be present in the form of a physiologically acceptable salt, such as in  
10 combination with a physiologically acceptable cation or anion, as is well known in the art.

In one embodiment, the pharmaceutical compositions useful for practicing the method of the invention may be administered to deliver a dose of between  $10^6$  and  $10^{12}$  PFU.

In one embodiment, the pharmaceutical compositions useful for practicing the method of the invention may comprise an adjuvant. Non-limiting examples of suitable are  
15 Freund's complete adjuvant, Freund's incomplete adjuvant, Quil A, Detox, ISCOMs or squalene.

Pharmaceutical compositions that are useful in the methods of the invention may be suitably developed for inhalation, oral, rectal, vaginal, parenteral, topical, transdermal, pulmonary, intranasal, buccal, ophthalmic, intrathecal, intravenous or another  
20 route of administration. Other contemplated formulations include projected nanoparticles, liposomal preparations, resealed erythrocytes containing the active ingredient, and immunologically-based formulations. The route(s) of administration is readily apparent to the skilled artisan and depends upon any number of factors including the type and severity of the disease being treated, the type and age of the veterinary or human patient being treated,  
25 and the like.

Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions suitable for ethical administration to humans, it is understood by the skilled artisan that such compositions are generally suitable for administration to animals of all sorts. Modification of pharmaceutical compositions  
30 suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and perform such modification with merely ordinary, if any,

experimentation. Subjects to which administration of the pharmaceutical compositions of the invention is contemplated include, but are not limited to, humans and other primates, mammals including commercially relevant mammals such as cattle, pigs, horses, sheep, cats, and dogs.

5                   The composition of the invention may comprise a preservative from about 0.005% to 2.0% by total weight of the composition. The preservative is used to prevent spoilage in the case of exposure to contaminants in the environment.

#### Administration/Dosing

10                   The regimen of administration may affect what constitutes an effective amount. For example, the adenovirus vector of the invention may be administered to the subject (i.e. mammal) in a single dose, in several divided dosages, as well as staggered dosages may be administered daily or sequentially, or the dose may be continuously infused, or may be a bolus injection. Further, the dosages may be proportionally increased or  
15                   decreased as indicated by the exigencies of the therapeutic or prophylactic situation.

Administration of the compositions of the present invention to a subject, preferably a mammal, more preferably a human, may be carried out using known procedures, at dosages and for periods of time effective to treat the disease in the subject. An effective amount of the composition necessary to achieve the intended result will vary and will depend  
20                   on factors such as the disease to be treated or prevented, the age, sex, weight, condition, general health and prior medical history of the subject being treated, and like factors well-known in the medical arts. In particular embodiments, it is especially advantageous to formulate the composition in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary  
25                   dosages for the subjects to be treated; each unit containing a predetermined quantity of therapeutic compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical vehicle. The dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the composition and the heterologous protein to be expressed, and the particular therapeutic effect to be achieved.

#### Routes of Administration

30                   One skilled in the art will recognize that although more than one route can be used for administration, a particular route can provide a more immediate and more effective reaction than another route. Routes of administration of any of the compositions\ of the



invention include inhalation, oral, nasal, rectal, parenteral, sublingual, transdermal, transmucosal (e.g., sublingual, lingual, (trans)buccal, (trans)urethral, vaginal (e.g., trans- and perivaginally), (intra)nasal, and (trans)rectal), intravesical, intrapulmonary, intraduodenal, intragastrical, intrathecal, subcutaneous, intramuscular, intradermal, intra-arterial, intravenous, intrabronchial, inhalation, and topical administration.

### Kits

In some embodiments a kit is provided for treating, preventing, or ameliorating an a given disease, disorder or condition, or a symptom thereof, as described herein wherein the kit comprises: a) a compound or compositions as described herein; and optionally b) an additional agent or therapy as described herein. The kit can further include instructions or a label for using the kit to treat, prevent, or ameliorate the disease, disorder or condition. In yet other embodiments, the invention extends to kits assays for a given disease, disorder or condition, or a symptom thereof, as described herein. Such kits may, for example, contain the reagents from PCR or other nucleic acid hybridization technology (microarrays) or reagents for immunologically based detection techniques (e.g., ELISpot, ELISA).

## EXAMPLES

The invention is now described with reference to the following Examples.

These Examples are provided for the purpose of illustration only and the invention should in no way be construed as being limited to these Examples, but rather should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

The results of the experiments are now described in the following examples.

### **Example 1: Advantage of using recombinant AdC6 and AdC7 Vaccines**

E1-deleted Ad vectors of human and simian serotypes have been tested extensively in the clinic. They are well tolerated at immunogenic doses. They induce very

potent cellular responses and are also able to elicit potent and sustained humoral responses to a wide variety of transgene inserts as has been established in animals. Neutralizing antibodies commonly found to human serotypes of Ad vectors can impair immune responses to the transgene product. In the present invention, the combined sequential usage of two serologically distinct AdC vectors (e.g. AdC6 and AdC7) in a heterologous prime-boost regimen (see Example 6) is of particular interest. The rationale is that such a regimen outperforms homologous prime-boost regimens where neutralizing antibodies to the prime vaccine carrier impair immune responses to the boost. This problem is avoided if two serologically distinct AdC vectors are combined in a prime-boost regimen. In some embodiments, the prime-boost with the two serologically distinct AdC vectors is also followed by additional boosts with a protein vaccine.

### **Example 2: Goals and Objectives**

The safety of the AdC6-HIVgp140 and AdC7-HIVgp140 vectors are assessed herein for the first time in humans. The present invention relates to a method of developing a vaccine regimen in which AdC vectors expressing the viral envelope (Env) are combined with other vaccine components. HIV-1 infection is best prevented by vaccines that induce both antibodies that block infection either by neutralization or by preventing passage of the virus through the mucosa. CD8<sup>+</sup> T cells rapidly eliminate cells infected with virus that escaped the antibody barrier. The Env protein, including but not limited to gp140 and gp160, is the primary target of virion binding or neutralizing antibodies while the group-specific antigen (Gag) is a prime target for CD8<sup>+</sup> T cells.

### **Example 3: Preclinical Immunogenicity/Efficacy Studies in mice**

Studies in mice and nonhuman primates were performed herein to evaluate the immunogenicity of study candidates AdC6 and AdC7 vectors. Studies in mice in which animals were primed with an AdC7 vector expressing Env and then boosted with either Env protein constructs or Virus-Like Particles (VLPs) containing Env Clade C were also conducted.

In one of the present study conducted in outbred ICR mice, pre-immunization sera were collected to determine background antibody titers. Animals were then divided into 6 groups of 5 mice each. Groups 1 and 2 were primed 3 times in monthly intervals

intramuscularly (i.m.) with 10 µg of gp145 protein of CO6980v0c22 (gp145<sub>CO6980</sub>) in alum; four weeks later Group 1 was boosted i.m. with 10<sup>10</sup> vp of an AdC7 vector expressing gp140 of Du172, a clade C virus, and Group 2 was boosted with the same vector at 10<sup>9</sup> vp. For Groups 3 and 4 the order was reversed; mice were primed with the AdC7-gp140<sub>Du172</sub> vectors at the two different doses (10<sup>10</sup> vp and 10<sup>9</sup> vp) respectively, and then boosted 8 weeks later 3 times in monthly intervals with gp145<sub>CO6980</sub> in alum. Group 5 was primed with 10<sup>10</sup> vp of an AdC7-gp140<sub>Du172</sub> and were boosted 2 months later with AdC6 expressing Du422, another clade C virus. Group 6 received the same regimen but vectors were used at a reduced dose of 10<sup>9</sup> vp. Pre-immunization sera and sera collected at 2 - 6 weeks after the last dose (Groups 1 and 2: 6 weeks; Groups 3 and 4: 2 weeks; Groups 5 and 6: 4 weeks) were tested for neutralizing antibodies to pseudoviruses (PV) based on two tier 1 clade C viruses (MW065, GS015), one clade C tier 2 virus (TZBD), one clade A/E tier 1 virus (TH023) as well as to MuLV PVs; the latter to assess non-specific neutralization. Sera from one mouse in Groups 1, 2, 4 and 6 each had neutralizing antibodies at baseline; they were excluded from the analysis. As shown in Figs. 1A-1D, all of the regimens induced significant titers of neutralizing antibodies to MW965 PV when compared to non-specific neutralization of MuLV PV.

Some mice also developed antibodies that neutralized GS015 and/or TZBD PV; neutralization of the clade C tier 2 PV was not achieved. The regimen in which the Ad vector was used for priming achieved higher seroconversion rates compared to regimens in which mice were primed with gp145 protein. Ad vectors given in a prime-boost regimen without protein also induced neutralizing antibodies with seroconversion rates depending on vector dose. Titers of neutralizing antibodies tested against MW965 PV were variable; several mice had titers above 1:1000. Highest median titers (1:860) were achieved by group 3. To assess induction of binding antibodies, sera collected at baseline and after each immunization were tested by ELISA on a baculovirus-derived Du172 gp140 (clade C Du 422) protein as described by Bauer et al. (Bauer et al., 2005 Sep;43(9):4426-33). Trends were similar to those obtained by neutralization assays (Fig. 2A). A prime-boost regimen with the protein resulted in low antibody responses after AdC vector boost. Prime-boosting with the two serologically distinct AdC vectors resulted in slightly higher responses and there was no difference between the groups receiving either of the two vector doses. Highest titers were achieved by priming with the AdC7-gp140 vector followed by protein boosts. In this regimen increasing the dose of AdC vector augmented antibody responses. Unexpectedly, maximal titers were achieved after a single protein boost. Ad vector prime followed by the

protein boost or a boost with another Ad vector also induced antibodies to the V2 loop especially at the higher vector dose (Fig. 2B). Overall these results showed that a combination of AdC vector priming followed by protein boosts results in solid neutralization of several tier 1 viruses as well as binding antibody responses to HIV-1.

5

#### **Example 4: Preclinical Immunogenicity/Efficacy Studies Testing in Nonhuman Primates**

AdC7, AdC6 as well as AdC68 and AdC1/C5 vectors expressing sequences from HIV-1 or SIV were tested to assess immunogenicity (Tatsis et al., J Immunol. 2009;182:6587-99) or efficacy against SIV<sub>mac</sub> challenges in nonhuman primates, (Cervasi et al., J Virol. 2013 Jun 26; Lasaro et al., Mol Ther. 2011;19:417-26). Vectors were immunogenic even in animals with pre-existing immunity to human serotype adenoviruses. In the most crucial rhesus macaque (RM) efficacy trial, animals were vaccinated with an AdC7/AdC6 prime-boost regimen using vectors expressing Gag mixed with vectors expressing gp160 of SIV<sub>mac239</sub>. Protection from SIV<sub>mac251</sub> acquisition or disease progression was measured.

The materials and methods employed in the experiments in the study disclosed herein are now described.

#### **20 *Material and Methods***

##### ***Vaccine Vectors***

Ad vectors were derived from the chimpanzee serotypes 6 (AdC6) or 7 (AdC7) and human serotypes 5 (AdHu5) and 26 (AdHu26). The E1- and E3-deleted Ad vectors expressed Gag or gp160 of SIV<sub>mac239</sub> (AdHu5gag/gp160, AdHu26gag/gp160, AdC6gag/AdC6gp160 and AdC7gag/AdC7gp160) or the glycoprotein of rabies virus (rab.gp). Vectors were generated, rescued and expanded on HEK 293 cells obtained from the American Type Culture Collection; they were purified, titrated and quality controlled (Zhou et al., Nat Protoc. 5,1775-85 (2010)). Expression of Gag or gp160 from recombinant viruses was confirmed by Western blot analyses of lysates of infected cells.

##### **30 *Non-Human Primates (NHPs)***

Two to three year-old, healthy and SIV-uninfected Indian origin *Macaca mulatta* were purchased and housed at Bioqual, Inc. (Rockville, MD). Animals were typed for Mamu-A\*01, A\*02, A\*08, A\*11, B\*01, B\*03, B\*04, B\*08 and B\*17 alleles (UW AIDS

Vaccine Research Lab, Madison, WI). All procedures involving handling and sacrifice of animals were performed according to approved protocols and upon approval by the relevant Institutional Animal Care and Usage Committees.

#### *Analyses of Ad-Specific Antibodies*

5 All NHPs were screened prior to enrollment for nAbs to AdC6 and AdC7 vectors (Patel *et al.*, Proc Natl Acad Sci U S A 110, 2975-2980 (2013)) and were found to be seronegative. Some animals were tested for binding Abs to the Ad vectors by ELISA (Patel V, *et al.* Proc Natl Acad Sci U S A 110, 2975-2980 (2013)). Titers were calculated by determining the area under the curve (AUC) obtained by adsorbance at different dilutions  
10 after subtraction of pre-bleed results. Negative values were ignored.

#### *Immunization Regimen*

Thirty-six RMs were enrolled. All animals were injected twice in ~ a monthly interval intra-tracheally with  $1 \times 10^{11}$  vp of an AdHu5rab.gp and AdHu26rab.gp vectors. Animals were bled 2 weeks after the last immunization to determine nAb titers to the AdHu  
15 viruses. Animals were then distributed according to genotypes and nAbs to the AdHu viruses into 3 groups of 12 animals each. Twelve animals were primed intramuscularly with  $5 \times 10^{10}$  vp of AdC7gag mixed with  $5 \times 10^{10}$  vp of AdC7gp160; they were boosted 6 months later with the same dose of AdC7 vectors expressing the same insert. Another 12 animals were primed with AdHu26 vectors and boosted 6 months later with AdHu5 vectors  
20 expressing the same inserts and used at the same doses. The remaining 12 animals were not immunized.

#### *Viral Challenge*

Six months after the boost, experimental and control RMs were challenged rectally 10 times in weekly intervals with 1 infectious dose of SIV<sub>mac251</sub> (most kindly  
25 provided by Nancy Miller, DAIDS, Bethesda, MD).

#### *Plasma Viral Load*

Plasma SIV viral load was determined by quantitative real-time RT-PCR as previously described (Lewis *et al.*, Retrovirology 7, 21 (2010)). Peak viral loads reflect the  
30 highest viral load obtained within an animal. Set-point viral loads reflect viral loads over time by calculating AUC with a Y = 40 as baseline.

#### *Virus Integration*

Genomic DNA was extracted from  $10^6$  peripheral blood mononuclear cells (PBMCs) using DNeasy Blood and Tissue Kit (Qiagen). Ten nanograms of DNA were

amplified by PCR using a mix of forward primers for simian and human Alu sequences, and reverse primers for SIVgag. The following primers were used for the first PCR: simian Alu, 5'-TTCGCGGTGGCTCACGCCTG-3' (SEQ ID NO: 17) ; human Alu, 5'-

TAGTCGGGAGGCTGAGGCAGGAGAA-3' (SEQ ID NO: 18); SIVgagR1, 5'-

5 TCTCTTCTGCGTGAATGCACC-3' (SEQ ID NO: 19); SIVgagR2, 5'-

AAGGCTTTTAAATTTTCTGAGCCTG-3' (SEQ ID NO: 20). The PCR conditions were as

follow: 94°C for 1 min, 20 cycles of 94°C for 30 s, 57°C for 30 s, and 72°C for 30 s, with final elongation at 72°C for 1min. GapDH was used as a sample normalizer in the same

conditions, with primer sequences 5'-TGCCACCCAGAAGACTGTGG-3' (SEQ ID NO: 21)

10 and 5'-ACCAGGAAATGAGCTTGACAAAG-3' (SEQ ID NO: 22). Two microliters of the

amplicon were digested with 10 units of RecJf for 30 minutes at 37°C, followed by enzyme inactivation at 65°C for 20 minutes. The digestion product was used as template for a nested

real-time PCR (50°C for 20s, 95°C for 10 min, and 35 cycles of 95°C for 15 s and 60°C for 1 min). The real-time PCR was performed utilizing the previously described mix of reverse

15 SIVgag primers, and a forward primer specific for the LTR region of SIV: 5'-

AGGAAGAGGCCTCCGGTTG-3' (SEQ ID NO: 23). All real-time PCR samples were

quantified by normalization in comparison to GAPDH sequences using the forward and

reverse primers, respectively: 5'-TCCGGGAAACTGTGGCGTG-3' (SEQ ID NO: 24); 5'-

TCCCGTTTCAGCTCAGGGATG-3' (SEQ ID NO: 25).

## 20 *CD8<sup>+</sup> Cell Depletion*

RM's were injected with antibody depleting anti-CD8alpha (cM-T807R1, NIH Reagent Source, NIH) first subcutaneously at 10mg/kg, then intravenously at 5mg/kg on days 0, 3, 7 and 10.

## *ELISA for Env-specific Abs*

25 Sera of individual RM's were tested for gp160-specific antibodies by an ELISA on plates coated with a baculovirus-derived gp160 protein (Lewis *et al.*, Retrovirology 7, 21 (2010)).

Antibodies to the V2 loop were measured by a peptide ELISA. Briefly, 10mM of V2 peptide was used to coat wells of Nunc 96-well plates (Thermo Fisher Scientific, Rochester, NY) by incubating 50 µl of the peptide dilution at 85 nmol/l in 0.02 mol/l NaCl at 4 °C overnight.

30 Plates were blocked for 2 hours at room temperature with PBS containing 3% bovine serum albumin. After washing, they were incubated for 1 hour with serial dilutions of sera in PBS + 3% bovine serum albumin followed by incubation with 1:30,00 dilution of alkaline

phosphatase- conjugated goat anti-mouse IgG (Sigma) for 1 hour at room temperature. After being washed, plates were incubated for 20 minutes with substrate and then read in an

automated ELISA reader at 405 nm. Titers were calculated by determining the AUC obtained by adsorbance at different dilutions after subtraction of pre-bleed results. Negative values were ignored.

#### *Isolation and Preservation of Lymphocytes*

- 5 PBMCs were isolated (Tatsis *et al.*, J Immunol. 182, 6587–6599 (2009)) and tested immediately after isolation or frozen in 90% FBS and 10% dimethyl sulfoxide (Sigma, St. Louis, MO) at -80°C until testing.

#### *Synthetic Peptides*

- 10 Peptide pools of 15-mers (overlapping by 11 amino acids) spanning the SIV<sub>mac239</sub> Gag and Env proteins were reconstituted in DMSO and pools were prepared from individual peptide stocks obtained from the National Institutes of Health AIDS Research and Reference Reagent Program.

#### *Intracellular Cytokine Staining (ICS)*

- 15 The function of SIV-specific CD8<sup>+</sup> T cells was assessed by ICS after stimulation with SIV Gag or Env peptide pools. All peptides were used at a final concentration of 2 µg of each peptide per ml. When used, frozen cells were thawed and immediately washed with RPMI media, resuspended with RPMI media, rested overnight and then stimulated for 6 hrs with Brefeldin A and Monensin along with CD107a FITC (H4A3). First, cells were stained with anti-CCR7-PE-Cy7 (clone 3D12) at 37°C. Cells were stained  
20 with Aqua-fluorescent reactive dye, anti-CD14-QDot 655 (clone TuK4), anti-CD20-QDot 655 (clone 3G8), anti-CD8-QDot 705 (clone 3B5)(Invitrogen, Carlsbad, CA), anti-CD4-APC-Cy7 (clone OKT4) (Biolegend), anti-CD95-PE-Cy5 (clone DX2), and anti-CD28-Texas Red (clone CD28.2, Beckman Coulter, Fullerton, CA) for 30 min at RT. After fixation and permeabilization with Cytofix/Cytoperm (BD Biosciences, San Jose, CA) for 20 min at RT,  
25 cells were stained with anti-IFN-γ-APC (clone B27), anti-IL-2-PE (clone MQ1-17H12), anti-TNF-α-Alexa 700 (clone MAb11, R&D System) and anti-CD3-Pacific Blue (clone SP34-2) for 1 hr at room temperature. Cells were washed once, fixed with 1% PFA, and then analyzed by FACS using LSRII (BD Biosciences, San Jose, CA) and DiVa software. Flow cytometric acquisition and analysis of samples was performed on at least 400,000 events. Post-  
30 acquisition analyses were performed with FlowJo (TreeStar, Ashland, OR). Data shown on graphs represent values of Gag or Env peptide-stimulated wells from which background values were subtracted. Polyfunctionality graphs were generated using SPICE v5.1 software (NIH, Bethesda MD). Single color controls used CompBeads. Anti-Mouse Igk (BD

Biosciences, San Jose, CA) were used for compensation. Unless otherwise noted, antibodies were purchased from BD (BD Biosciences, San Jose, CA).

### *Statistical Analysis*

Differences in SIV acquisition and decline of viral loads were determined by Mantel-Cox test. Normality of data was determined by D'Agostino & Pearson omnibus normality test. Data that failed the normality test were analyzed by non-parametric tests, such as Wilcoxon-Mann-Whitney test for two groups comparison or Kruskal-Wallis test with Dunn correction for multiple comparisons. In detail, differences in viral loads and set point viral loads were determined by Kruskal-Wallis test with Dunn correction. Differences in integration and the relationship of integration with various other parameters were tested by 2-way Anova or multiple t-tests both with Holm-Sidak correction. Differences in Ab titers and T cell responses between the groups at various time points were determined by Wilcoxon-Mann-Whitney test. Differences in T cell functions between before and after challenge were analyzed by SPICE software by Wilcoxon sign rank tests. Correlations were determined using Spearman correlation with Bonferroni correction of p-values. For correlations adjusted p-values are shown within the text, figures show unadjusted p – values. Analyses were conducted using GraphPad Prism 6, SAS 9.2, and SPICE v5.1.

The results of the experiments are now described in the following examples.

### **SIV acquisition, viral loads, and levels of SIV integration in the different vaccine groups.**

Protection from SIV<sub>mac251</sub> acquisition or virus replication was tested in Rhesus Macaques (RMs) immunized with Ad vectors expressing Gag and gp160 of SIV<sub>mac239</sub>. First to more closely mimic the immune status of humans, AdHu26 and AdHu5 vectors expressing an irrelevant transgene was intra-tracheally administered to 36 healthy Indian-origin RMs. Although this procedure does not fully recapitulate the repeated infections with different Ad serotypes that humans experience during their lifetime it achieves induction of serotype-specific neutralizing (n)Abs as well as non-neutralizing Abs. Most RMs developed moderate nAb titers to AdHu5 and markedly higher titers to AdHu26 (Fig. 3). Non-neutralizing Ad-specific Abs tested in some animals after AdHu administration cross-reacted with SAd-V24, from hereinafter referred to as AdC7 and SAd-V23, from hereinafter referred to as AdC6 (Fig. 9). Animals were distributed with high or low nAb responses to AdHu5 and AdHu26 equally into three groups of twelve RMs each. Each group had eight Mamu-A\*01<sup>+</sup> RMs and groups 1 and 3 each had one Mamu-B\*17<sup>+</sup> animal (Fig. 3). Animals of group 1 were



vaccinated four weeks after the last AdHu pre-exposure with  $5 \times 10^{10}$  vp of AdC7 expressing Gag (AdC7gag) mixed with  $5 \times 10^{10}$  vp of AdC7 expressing gp160 (AdC7gp160). RMs of group 2 were vaccinated with the same doses of AdHu26 vectors expressing the same inserts. RMs of group 3 were not vaccinated and served as controls. Six months after the first vaccine dose RMs of groups 1 and 2 were boosted with AdC6 and AdHu5 vectors, respectively, expressing the same inserts and used at the same doses as for priming. Starting six months after the boost, RMs were challenged rectally in weekly intervals for up to ten times with a low infectious dose (1 mean tissue infective dose) of SIV<sub>mac251</sub> (kindly provided by N. Miller, NIAID). RMs that developed viral loads above 1,000 RNA copies per ml of plasma received no further challenges.

All of the Mamu-A\*01<sup>-</sup>/B17<sup>-</sup> control RMs became infected within two challenges (Fig. 4A). Virus acquisition was slightly delayed in AdHu-vaccinated RMs, which on average became infected by the fourth challenge; this level of protection was not statistically significant when compared to control animals. In contrast, the AdC-vaccinated Mamu-A\*01<sup>-</sup>/B17<sup>-</sup> RMs showed significant protection against SIV<sub>mac251</sub> acquisition when compared to control animals ( $p = 0.0295$  by Mantel-Cox test). Measurement of virus replication also showed significantly lower set-point viral loads (adjusted [adj.]  $p = 0.0209$  by Kruskal-Wallis test with Dunn correction) and peak viral loads (adj.  $p = 0.0209$ ) in Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> RMs of the AdC but not the AdHu vaccine group as compared to controls (Fig. 4B). Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> as compared to MamuA\*01<sup>-</sup>/B17<sup>-</sup> control RMs showed insignificant ( $p = 0.086$ ) increases in resistance to infection with median SIV acquisition after four challenges. On average, AdC-and AdHu-vaccinated Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> animals became infected after the third or fifth challenges respectively, which was not significantly different from acquisition rates of control RMs. Both Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> vaccine groups developed lower peak viral loads (AdC:  $p = 0.0053$ , AdHu:  $p = 0.0007$ ) and set-point viral loads (AdC: adj  $p = 0.0019$ , AdHu: adj  $p = 0.0003$ ) compared to controls. Interestingly all RMs with break-through infections in either of the two vaccine groups regardless of their Mamu genotype controlled viral loads to levels below 1000 copies per ml within a few weeks after the initial SIV acquisition and by 18 weeks after the first challenge all but 2 of the vaccinated RMs (one in each vaccine group) had viral loads below the level of detection. Six of the 12 control animals also showed loss of detectable viral loads although, unlike in the vaccine groups, this was only seen in unvaccinated RMs with controller genotypes. Differences in decline of viral loads were significant comparing controls to AdC ( $p = 0.0277$ ) or AdHu ( $p = 0.0213$ ) vaccinated RMs. Pre-existing nAb titers to AdHu5 or AdHu26 did not

affect peak viral loads, set-point viral loads, number of challenges until infection or time until viral control in either vaccine group.

Relative amounts of integrated SIV were tested at two and twelve weeks after infection in a subset of RMs ( $n = 7$  [AdC],  $= 11$  [AdHu],  $= 4$  [Co]) (Fig. 4C). The one tested animal that did not show detectable viral load at any time after the ten challenges was found to be negative for integrated SIV genome. Detectable levels of integrated SIV genome were found by two weeks after infection in isolated  $CD4^+$  of all RMs with at least one time-point of detectable viremia, with a tendency to increase when tested again at 12 weeks after infection. This increase reached significance for the AdHu group ( $p = 0.015$ ). Of note, at week 12 after infection the relative amounts of integrated SIV in  $CD4^+$  T cells were significantly lower in AdC-vaccinated than in control RMs ( $p = 0.016$ ). In the AdHu group of SIV-infected RMs, the animals that maintained relatively stable levels of integrated SIV (i.e., change below 10 fold) became infected at a later time point as compared to those that showed pronounced increases ( $>100$  fold) during this period ( $p = 0.03$ ). Levels of virus integration or their changes over time were not affected by peak viral loads, time to control, Mamu genotype, pre-existing antibody titers to the AdHu vectors or antibody titers to Env.

#### **Antibody responses upon vaccination and challenge**

To identify correlates of immunological protection conferred by the used vaccine vectors, vaccine-induced SIV-specific immune responses were retrospectively assessed before and after challenges. In all of the vaccinated RMs Env-specific Ab responses were low after priming, increased after the boost and then contracted by the time of challenges (Figs. 5A-5B). After challenges, vaccinated RMs that did not develop detectable viral loads failed to show increases in Env-specific Ab titers, suggesting true sterilizing immunity. All other vaccinated RMs showed pronounced increases in Ab titers after challenges (Figs. 5A-5B). In the Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> groups, AdHu-vaccinated RMs developed significantly higher titers of SIV Env-specific Abs compared to AdC-vaccinated animals ( $p = 0.0003$  by Mann-Whitney) following infection. This most likely reflects the fact that AdC-vaccinated animals of this subcohort failed to acquire the virus or very rapidly controlled viral loads and thereby lacked sufficiently high levels of antigen to optimally increase Env-specific Ab titers. For the same reason Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> AdC-vaccinated RMs developed higher Ab titers compared to Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> RMs ( $p = 0.0006$ ) after challenges. In AdC- but not AdHu-vaccinated RMs (analyzing all animals together regardless of the Mamu genotype), Ab titers after the boost directly correlated with numbers of challenges required to achieve infection ( $r = 0.807$ , adj.  $p = 0.0278$  by Spearman correlation,

Figs. 6A-6B). In the AdHu5 group, correlations were only seen for Ab titers after challenges and set-point viral loads ( $r = 0.720$ , adj.  $p = 0.0425$ ) and peak viral loads ( $r = 0.708$ , adj.  $p = 0.0494$ , Figs. 10A-10D). Control RMs developed robust Ab titers after challenges (Fig. 7C), which were higher than in vaccinated animals with breakthrough infections (AdC: adj.  $p = 0.003$ , AdHu: adj.  $p = 0.0068$ ). Pre-existing Ab titers to either AdHu5 or AdHu26 had no significant effect on Ab responses in the two vaccine groups. Finally binding Abs directed against the V1/V2 loop, which have been linked to protection in humans and RMs (Zolla-Pazner *et al.*, PLoS One. 8, e53629 (2013); Barouch *et al.*, Nature. 482, 89-93 (2012)), were not detected until after challenges. There were no associations between antibody titers at any of the tested time points and levels of SIV integration.

### T cell responses upon vaccination and challenge

Total T cell responses to Gag were measured by intracellular cytokine staining and multicolor flow cytometry in AdC- and AdHu-vaccinated (Figs. 7A-7L) and control RMs (Fig. 11) as the fraction of  $CD4^+$  or  $CD8^+$  T cells showing at least one functional responses (i.e., production of  $IFN\gamma$ , IL-2, or TNF, or surface expression of the degranulation marker CD107). Both vaccine regimens induced total Gag-specific T cells responses of comparable magnitude. The only significant difference in T cell responses between animals with or without controller genotypes was seen in the AdC group (Fig. 7A), where the better protected Mamu-A\*01/B\*17 RMs had significantly higher total Gag-specific  $CD8^+$  cell responses ( $p = 0.042$  by Wilcoxon-Mann-Whitney test) at the time of first challenge. In the AdC but not the AdHu vaccine group Gag-specific effector memory ( $CD8_{EM}$ ) (Figs. 12A-12F) and central memory ( $CD8_{CM}$ ) (Figs. 12B-12E)  $CD8^+$  T cell responses at 4 weeks after the boost correlated with peak viral loads ( $CD8_{CM}$ :  $r = 0.729$ , adj.  $p = 0.036$ ,  $CD8_{EM}$ :  $r = 0.746$ , adj.  $p = 0.0359$ );  $CD8_{EM}$  responses measured shortly after the boost also correlated with set-point viral loads ( $r = 0.725$ , adj.  $p = 0.0392$ ) (Figs. 12C-12E). In the AdHu vaccine group correlations for  $CD8^+$  T cells were only seen in Mamu-A\*01/B\*17 RMs; frequencies of total Gag-specific  $CD8^+$  and  $CD8_{EM}$  cells at the day of challenges showed inverse correlations with time to viral controls (for both  $r = -0.9487$ , adj.  $p < 0.0001$ ). In the same group unlike in AdC-vaccinated RMs total Gag-specific  $CD4^+$  T cells (Fig. 13A and Fig. 13C) and  $CD4_{EM}$  cells (Fig. 13B and Fig. 13D) after challenges inversely correlated with peak viral loads (total  $CD4$   $r = -0.845$ , adj.  $p = 0.011$ ,  $CD8_{EM}$ :  $r = -0.82$ , adj.  $p = 0.0064$ ). In the AdHu5 group RMs with lower levels of SIV integration by 2 weeks after infection ( $<50,000$ ) had higher frequencies of Gag-specific  $CD8_{EM}$  T cells responses before challenge than those with higher levels of integration ( $p = 0.016$ ), while in the same group animals with

low levels of integrated virus by week twelve after infection ( $<10^6$ ) had higher frequencies of Gag-specific CD8<sub>CM</sub> ( $p = 0.003$ ) and CD8<sub>EM</sub> T cells ( $p = 0.037$ ) before challenge (Fig. 14). Env-specific T cell responses, including those of subsets were low and comparable between the vaccine groups and between Mamu-A\*01<sup>+</sup>/B17<sup>+</sup> and Mamu-A\*01<sup>-</sup>/B17<sup>-</sup> RMs (Figs. 15A-15L).

Gag-specific CD8<sup>+</sup> T cells were also specifically analyzed for each individual function, i.e., production of IL-2, IFN- $\gamma$ , TNF- $\alpha$  and degranulation of CD107 in response to SIV-Gag peptides. Functionality of virus-specific CD8<sup>+</sup> T cells between the vaccine groups and within the vaccine groups between Mamu-A\*01<sup>+</sup>/B17<sup>+</sup> and Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> RMs were largely comparable at the different time points tested (Fig. 16). After priming, CD8<sup>+</sup> T cell responses were dominated by cells producing IL-2, and after. The boost responses became more polyfunctional with this trend becoming even more pronounced after challenges. Differences between the two vaccine groups were seen shortly before challenges when animals of the AdHu vaccine groups had higher frequencies of CD8<sup>+</sup> T cells that exhibited all 4 functions ( $p = 0.016$  by Wilcoxon Rank test) or produced TNF- $\alpha$  only ( $p = 0.026$ ). After priming CD4<sup>+</sup> T cell responses of AdC- and AdHu-vaccinated RMs were dominated by cells producing IL-2 only (Fig. 17). After the boost, responses again became more polyfunctional and IFN- $\gamma$  only producing CD4<sup>+</sup> T cells became dominant in the AdHu group. Differences between AdC-vaccinated animals with or without controller genotypes were seen just prior to the first challenge when Mamu-A\*01<sup>-</sup>/B17<sup>-</sup> RMs had higher frequencies of Gag-specific CD4<sup>+</sup> T cells positive for IL-2, CD107a and TNF- $\alpha$  ( $p = 0.021$ ), IL-2 and TNF- $\alpha$  ( $p = 0.021$ ) or TNF- $\alpha$  only ( $p = 0.021$ ). Responses of AdHu-vaccinated animals were not significantly affected by controller genotypes. Pre-existing nAbs to AdHu5 vectors did not affect the magnitude or functions of Gag-specific CD8<sup>+</sup> or CD4<sup>+</sup> T cell responses in either vaccine group. An analysis of Gag-specific T cell subsets just prior to challenges revealed in general comparable functions between the vaccine groups or between Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> and Mamu-A\*01<sup>+</sup>/B\*17<sup>+</sup> RMs in either vaccine group (Fig. 18). Differences were seen mainly for CD4<sub>CM</sub> of AdC-vaccinated RMs; those that were Mamu-A\*01<sup>-</sup>/B\*17<sup>-</sup> showed higher frequencies of cells positive for IL-2, CD107a, and TNF- $\alpha$  ( $p = 0.013$ ), IL-2 and TNF- $\alpha$  ( $p = 0.013$ ), IFN- $\gamma$  and TNF- $\alpha$  ( $p = 0.013$ ), and TNF- $\alpha$  only ( $p = 0.013$ ).

#### **Functional *in vivo* assessment of CD8<sup>+</sup> T cell responses through CD8<sup>+</sup> lymphocyte depletion.**

The antiviral role of CD8<sup>+</sup> T cells in the context of SIV infection of RMs has been directly demonstrated in many studies that used *in vivo* depletion of these cells with

CD8 directed antibodies as pioneered in the publication by Schmitz *et al.*, 1999 (Schmitz *et al.*, Science 283, 857-60 (1999)). In the current invention, the role of CD8<sup>+</sup> T cells in protecting from SIV disease progression was directly assessed by performing CD8<sup>+</sup> lymphocyte depletion in five AdC- and four AdHu-vaccinated RMs at 28 weeks after completion of challenges. All animals, except one RM of the AdHu vaccine group, which had remained virus-free after 10 challenges, developed detectable viral loads following CD8<sup>+</sup> cell depletion (Fig. 8), thus confirming that control of virus replication was mediated by CD8<sup>+</sup> lymphocytes. Once the depleting treatment was stopped and the observed number of CD8<sup>+</sup> lymphocytes returned to the baseline (pre-depletion levels) viral loads rapidly declined in all but one of the AdC-vaccinated RMs. This animal, which did not develop viral loads above 1,000 RNA copies/ml until five weeks after the tenth challenge but was viremic at the time of CD8<sup>+</sup> cell depletion, did not show major increases in viral loads after CD8 depletion, perhaps suggesting CD8<sup>+</sup> T cells had become unable to control SIV replication as a result of the presence and outgrowth of escape mutants.

Overall, testing in mice and nonhuman primates showed that a prime-boost regimen using two serologically distinct AdC vectors markedly increases T and B cell responses to the transgene product (McCoy *et al.*, J Virol. 2007;81:6594-604; Santra *et al.*, Vaccine. 2009;27:5837-45; Tatsis *et al.*, Virology. 2007;367:156-67; Zhou *et al.*, Mol Ther. 2010;18:2182-9; Tatsis *et al.*, J Immunol. 2009;182:6587-99; Lasaro *et al.*, Mol Ther. 2011;19:417-26).

## Example 5: Other Studies

### Mice Studies

No side effects were noted in mice at intramuscular doses as high as  $5 \times 10^{11}$  vp using AdC6 and AdC7 vectors with a variety of different inserts including HIV-1 gag. The highest vaccine dose tested in nonhuman primates (NHPs) for AdC6 and AdC7 vectors expressing a truncated version of HIV-1 gag or the rabies virus glycoprotein was  $10^{12}$  vps. These animals also showed no overt symptoms after immunization in an experiment in which animals were primed with AdC7 vectors, boosted 8 months later with AdC6 vectors and then 4 months after that with AdHu5 vectors to assess immune responses.

## Nonhuman Primate Studies

To assess vector immunogenicity and efficacy a number of nonhuman primate studies were conducted with AdC6 and AdC7 expressing a variety of inserts including, but not limited to, SIVgag, SIVenv, HIV-1env and the rabies virus glycoprotein. Although the primary endpoint of these studies was not to assess vector toxicity, all immunized animals were routinely checked for their health status. Nonhuman primate studies were conducted at three facilities (i.e. at the University of Pennsylvania, at BIOQUAL Inc. (Rockville, Maryland), and at the Yerkes National Primate Research Center (Atlanta, Georgia)). NHP samples (i.e., blood and sera) were screened for Complete Blood Count with differential/absolute numbers (white blood cell counts, red blood cell counts, hemoglobin, hematocrit, mean corpuscular volume, mean corpuscular hemoglobin concentration, polymorphonuclear leukocytes, metamyelocytes, lymphocytes, monocytes, eosinophils, basophiles, and platelets) and blood chemistries (calcium, phosphorus, chloride, lactate dehydrogenase, aspartate aminotransferase, total bilirubin, gamma-glutamyl transferase, alanine aminotransferase, alkaline phosphatase, total protein, total globulin, albumin, blood urea nitrogen, creatinin, glucose, creatine kinase, and aldolase). The NHP samples did not show any abnormalities except for some small increases in liver enzymes that were sometimes observed and thought to be a reflection of anesthesia-related stress.

## Example 6: Ongoing Studies

In one embodiment, the AdC6-HIVgp140 and AdC7-HIVgp140 vectors of this invention are combined with additional vaccines to enhance and broaden HIV-1-specific T and B cell responses.

### Addition of an AdC6-HIVgp140 vector boost:

To optimize B cell responses AdC7-HIVgp140 primed individuals are boosted 6 or more months later with AdC6-HIVgp140 used at the same dose as the priming vector.

### Addition of a Protein Boost:

As an alternative or in addition, subjects from the Phase 1 study receive a protein boost 12 or more months after vaccination with a single AdC Env vector vaccine or 12 or more months after the AdC6-HIVgp140 boost of AdC7-HIVgp140 primed individuals as described above herein. A potential protein vaccine candidate is a gp145 protein derived from an early clade C isolate from Tanzania produced in CHO cells that is under development by the National Institute of Allergy and Infectious Diseases (NIAID).

**AdC6-HIVgag and AdC7-HIVgag:**

In some aspects of this invention, the inclusion of AdC vectors expressing additional HIV antigens broaden and enhance T cell responses. AdC vectors that express gag of a clade B HIV-1 strain (AdC6-HIVgag and AdC7-HIVgag) were developed. Following the completion of the initial Phase 1 trial, additional studies with the AdC6 and AdC7 vectors containing the gag insert are pursued and followed by a study in which subjects receive all four AdC vectors.

**Example 7: Vaccines design, construction and characterization : AdC6 and AdC7****Vectors**

The vaccines of the present invention were based on recombinant viruses derived from clones of two chimpanzee adenoviruses, AdC6 and AdC7 also referred to as SAdV-23 and SAdV-24. The parent viruses were obtained from ATCC (AdC6 – ATCC-VR-592, AdC7 – ATCC-VR-593). The Ad genome contains five segments that encode early gene products, i.e., E1-E5, and five segments that encode five late gene products, i.e., L1-L5. The E1, E2 and E4 gene products regulate the transcription and translation of the later genes and are necessary for viral replication. The E3 gene products subvert immune responses by altering antigen presentation and cytokine and apoptosis pathways but are unnecessary for viral replication. Deletion of the E3 in addition to the E1 domain increases the permitted size of the inserted expression cassette to ~7.5 kilobases (Kb).

To generate the E1-deleted AdC6 molecular clone, the 5' right inverted terminal repeat (ITR) was amplified by Polymerase Chain Reaction (PCR) and cloned into the pNEB193 vector. Using restriction enzyme sites that are unique in assembly but not necessarily unique to the full AdC6 genome, the right half of the AdC6 genome was then cloned piecemeal into the pNEB193 vector. The left ITR was amplified by PCR and cloned into a different pNEB193 vector. Using the same strategy as above, the remainder of the left fragment of the AdC6 genome was assembled into the pNEB193 vector. Approximately 2.6 Kb of the E1 region between *Sna*BI and *Nde*I sites were omitted and replaced with a linker that contains the rare enzyme sites of I-*Ceu*I and PI-*Sce*I. These steps remove the entire E1a and E1b 19-kDa homolog-coding regions and 74% of the E1b 55-kDa homolog-coding region. Finally, using two suitable enzymes, the E1-deleted left fragment of AdC6 was released from the pNEB193 vector and inserted into the vector containing the right fragment of the genome, effectively generating the E1-deleted infectious molecular clone of AdC6.

To delete the E3 domain, a fragment was cut from the E1-deleted AdC6 molecular clone by digestion with SbfI. The ends of this SbfI fragment were joined by ligation and the ~4 Kb E3 region was removed from this SbfI fragment using suitable restriction enzymes, i.e., Eco47III and SmaI. The resulting E3-deleted SbfI fragment was then swapped into the E1-deleted molecular clone to replace the original SbfI fragment and generate an E1/E3-deleted AdC6 molecular clone. For AdC6-HIVgp140 viral molecular clone, which also contains a partial E3 deletion, ORF3, ORF4, ORF5, ORF6 and ORF7 of E3 were removed using similar strategy as described.

To create an E1- and E3-deleted viral molecular clone of AdC7, a similar cloning strategy was adopted. The E1-deleted AdC7 clone was generated first in the pBR322 plasmid to harbor most of AdC7 genome and both ITRs, except the E1 region. Approximately 2.6 Kb between the sites of SnaBI and NdeI were deleted to remove E1 (nucleotide number 455 to 3028). Two sites for endonucleases I-CeuI and PI-SceI were incorporated within the deleted E1 domain to facilitate insertion of the transgene cassette. In the partially E3-deleted viral molecular clone a fragment from nucleotide number 27775 to 31298 was excised removing ORF3, ORF4, ORF5, ORF6 and ORF7 of E3.

Table 1 below illustrates the nucleotide number of the deleted portion of E1 and E3 domain (based on Genbank Accession numbers AY530877 and AY530878 that are sequences for wildtype AdC6 and AdC7 respectively) in the recombinant AdC vector described in this invention.

Table 1. Nucleotide Numbers of the Deleted Portion of E1 and E3 Domain in the rAdC Vectors

| Vector Name   | Nucleotide Number of E1 Deleted Region* | Nucleotide Number of E3 Deleted Region* |
|---------------|-----------------------------------------|-----------------------------------------|
| AdC6-HIVgp140 | 455 – 3022 bp                           | 27835 – 31052 bp                        |
| AdC7-HIVgp140 | 455 – 3028 bp                           | 27775 – 31298 bp                        |

\* Nucleotide numbers are based on Genbank accession numbers that are AY530877 for AdC6 (wildtype) and AY530878 for AdC7 (wildtype) type

#### **Example 8: Vaccines design, construction and characterization : recombinant AdC6 and AdC7 vectors**



Maps of AdC6 and AdC7 vectors expressing Env are shown in Figs. 19A-19B. Maps of pShuttle plasmids containing gp140 (DU172 and DU422) are shown in Fig. 19C. During the manufacturing process, restriction mapping analysis or a PCR-based identification assay is performed on Master Viral Bank and Vaccine Bulk Substance to assess the integrity of the viral genome.

The nucleotide and amino acid sequences of the AdC vectors of the present invention (AdC6 and AdC7) expressing gp140, Gag or gp160 are provided herein Figs. 20-27 (SEQ ID NOs: 1-16).

## **Example 9: Manufacturing Process**

### **Master Viral Bank (MVB)**

The plasmids containing the sequence of the AdC vector with the HIV gene inserts were linearized by restriction enzyme digestion and then transfected into SAFC Pharma's AC-2 cell line that is a HEK-293 based cell line (SAFC<sup>®</sup> Pharma, MilliporeSigma - Carlsbad, California). After the transfections, recombinant viral clones were selected by three rounds of plaque purification. Six to twelve clones from each transfection were produced and an aliquoted. Six clones from each transfection with the highest infectious titers were amplified and tested for production yield (in virus particle and infectious particle), immunogenicity in mice, and genetic integrity (by restriction mapping analysis). Following a selection of one final clone for each construct, each final vector clone was expanded to generate a primary seed stock that was tested (for bioburden, endotoxin, mycoplasma and infectious titer) prior to use in subsequent processes. The primary viral seed stocks were characterized for production parameters (multiplicity of infection and time to harvest) for use in later development and production activities.

The primary viral seed stocks were used to manufacture Master Viral Banks (MVBs) with AC-2 Working Cell Bank under cGMP conditions (SAFC<sup>®</sup> Pharma). AC-2 cells were grown in adherent form in conditioned medium supplied with fetal bovine serum (purchased from Cell Genesys Inc. for AdC-HIVgp140 vectors) prior to adaptation to suspension in serum-free medium. The MVBs were produced in suspension (without fetal bovine serum) in five liter WAVE<sup>™</sup> scale. Cells were harvested, lysed by freeze thawing, and then clarified by low speed centrifugation followed by filtration. The cleared supernatants from cell lysates were filled into approximately two hundred cryovials for each MVB.

Tests performed on each MVB samples and release specifications are listed in Table 2. In some embodiments, the clinical vaccine products release and stability specification of vp to IU ratio to be used is 600 : 1.

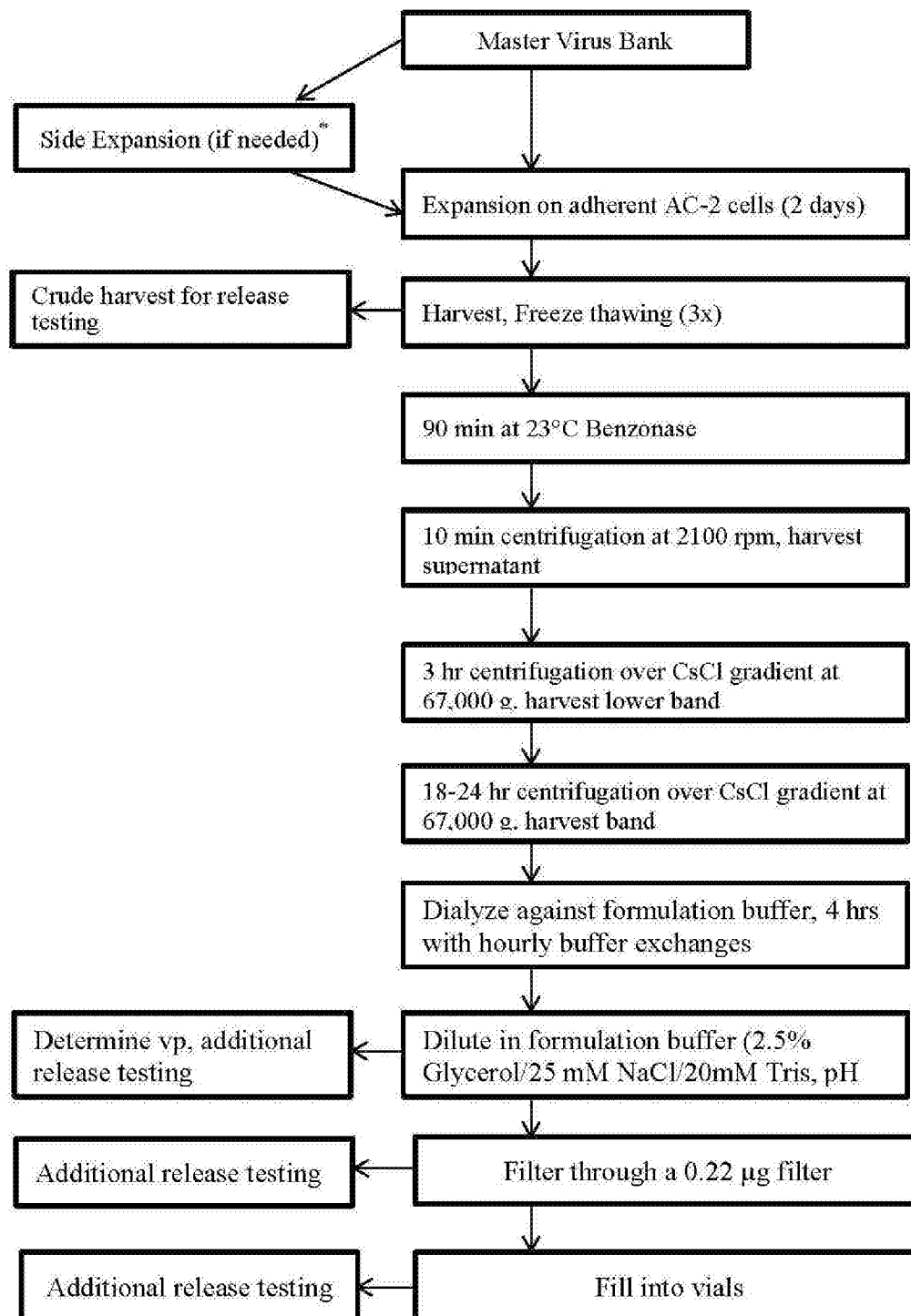
Table 2. Release Tests and Specifications for AdC Recombinant vector MVBs

| Test                                                                                                                                         | Method                                                                        | Release Specification       | AdC6-gp140 | AdC7-gp140 |
|----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|-----------------------------|------------|------------|
| Sterility                                                                                                                                    | Immersion (Direct inoculation) (USP/21 CFR 610.12)                            | No bacteria or fungus found | Pass       | Pass       |
| Sterility Method Suitability                                                                                                                 | Immersion (Direct inoculation) (EP/USP)                                       | No interference             | Pass       | Pass       |
| Mycoplasma                                                                                                                                   | Indirect method and direct cultivation (Points To Consider)                   | Negative                    | Pass       | Pass       |
| Endotoxin                                                                                                                                    | Kinetic chromogenic Limulus Amebocyte Lysate assay                            | < 10 EU/mL                  | Pass       | Pass       |
| In Vitro assay for adventitious viral contaminants                                                                                           | Inoculation of 3 cell lines with hemadsorption and hemagglutination endpoints | Negative                    |            | Pass       |
| In Vivo assay for adventitious viral contaminants                                                                                            | Inoculation of embryonated hen eggs, adult and newborn mice                   | Negative                    |            | Pass       |
| Detection of Porcine Circovirus DNA                                                                                                          | Polymerase chain reaction (PCR)                                               | Negative                    |            | Pass       |
| Detection of Adventitious bovine viruses                                                                                                     | Cultivation on detector cell lines and fluorescent antibody staining (9 CFR)  | Negative                    |            | Pass       |
| Detection of Adventitious porcine viruses                                                                                                    | Cultivation on detector cell lines and fluorescent antibody staining (9 CFR)  | Negative                    |            | Pass       |
| Quantitative PCR (qPCR) assay for potency determination                                                                                      | qPCR assay of hexon from cells infected with serial dilutions of AdC vector   | Vp to IU ratio = 600 : 1    |            |            |
| Detection of 14 viruses (SV-40, HIV-1, HIV-2, HTLV-I, HTLV-II, hepatitis A virus, CMV, EBV, parvovirus B-19, human herpes viruses-6, -7, -8) | Real Time PCR (Human Panel I)                                                 | Negative                    |            | Pass       |
| Quantification of Reverse Transcriptase Activity                                                                                             | QFPERT                                                                        | Negative                    |            | Pass       |
| Detection of adeno-associated virus                                                                                                          | Real-time PcR                                                                 | Negative                    |            | Pass       |

MVBs for both recombinant vectors have been completed and are stored at  $\leq$

5 -65°C at SAFC Pharma under cGMP conditions.

## Manufacturing Flow Chart



\* In the event the MVB is not large enough to provide sufficient material at the stipulated dose level required for preclinical and clinical studies, the virus from the MVB will undergo one round of further expansion and virus from this expansion is used for GMP production.

The above manufacturing flow chart depicts the production process for the AdC6 and AdC7 vaccines. Release testing of the AdC6-HIVgp140 and AdC7-HIVgp140 were finalized.

### **Vaccine Drug Substance**

5                    Production of the Current Good Manufacturing Practice (cGMP) drug substance AdC vector lots are in process, thus far the bulk lot for AdC7-HIV-gp140 has been produced and conditions for AdC6-HIVgp140 production have been established. Several process development (PD) runs were performed for the two gp140-expressing vector constructs utilizing the vector MVBs and AC-2 Working Cell Bank. The PD runs showed  
10                    that viral yields were higher when virus was grown on adherent rather than suspension cells. For this reasons AC-2 cells were grown in adherent form in medium supplied with 10% fetal bovine serum, gamma-irradiated and grown in CellSTACK<sup>®</sup> Cell Culture Chambers (8 for AdC7 and 40 for AdC6). Cells were plated for 3 days and then infected with 0.08 moi of virus per 90% of the cell monolayer shows cytopathic effects (CPEs). Cells were lysed by 3  
15                    rounds of freeze thawing. The lysate were treated for 90 min at 23°C with Benzonase to remove cellular DNA. Debris were then removed by a 10 min low speed (2100 rpm) centrifugation at room temperature. Supernatant is centrifuged at 67,000 g for 3 hrs at 4°C over a CsCl<sub>2</sub> gradient. The viral band were harvested and centrifuged over a CsCl<sub>2</sub> gradient at 67,000 g at 4°C for 18-24 hrs. The band is harvested and dialyzed against formulation  
20                    buffer for a total of 4 hours with hourly buffer exchanges. An aliquot of the dialyzed material is used to determine (vp) content. The material is diluted to 10<sup>12</sup> vp per ml in formulation buffer (2.5% Glycerol / 25 mM NaCl / 20 mM TRIS, pH 8.0) and then filtered through a 0.22 µm filter. The vaccine bulk filled lot were stored at ≤ -65°C under cGMP conditions. Samples from each bulk lot is tested for release and the release specifications and results are listed  
25                    below in Tables 3 and 4.

Table 3. Release Tests and Specifications for Bulk Harvest Lots

| Test                                                                                                                                | Method                                                                                                 | Release Specification    | AdC6-gp140 | AdC7-gp140 |
|-------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|--------------------------|------------|------------|
| Mycoplasma                                                                                                                          | Direct cultivation by PTC/EP/USP                                                                       | Negative                 |            | Pass       |
| Mycoplasmastasis                                                                                                                    | Indirect method by PTC/EP/USP (Points To Consider)                                                     | Negative                 |            | Pass       |
| In Vitro assay for adventitious viral contaminants                                                                                  | Inoculation of 3 cell lines with hemadsorption and hemagglutination endpoints                          | Negative                 |            | Pass       |
| In Vivo assay for adventitious viral contaminants                                                                                   | Inoculation of embryonated hen eggs, adult and newborn mice                                            | Negative                 |            | Pass       |
| Detection of Porcine Circovirus DNA                                                                                                 | Polymerase chain reaction                                                                              | Negative                 |            | Pass       |
| Detection of Adventitious bovine viruses                                                                                            | Cultivation on detector cell lines and fluorescent antibody staining (9 CFR)                           | Negative                 |            | Pass       |
| Detection of Adventitious porcine viruses                                                                                           | Cultivation on detector cell lines and fluorescent antibody staining (9 CFR)                           | Negative                 |            | Pass       |
| Detection of 15 human viruses (SV-40, HIV-1, HIV-2, HTLV I, HTLV II, HAV, HBV, HCV, CMV, EBV, Parvovirus B-19, HHV-6, HHV-7, HHV-8) | Real-time polymerase chain reaction                                                                    | Negative                 |            |            |
| Quantification of reverse transcriptase activity                                                                                    | Ultracentrifugation and quantitative fluorescent product enhanced reverse transcriptase assay (QFPERT) | Negative                 |            | Pass       |
| Quantitative PCR (qPCR) assay for potency determination                                                                             | qPCR assay of hexon from cells infected with serial dilutions of AdC vector                            | Vp to IU ratio = 600 : 1 |            |            |
| Detection of residual host cell DNA                                                                                                 | Polymerase chain reaction assay                                                                        | ≤ 10 ng/dose             |            |            |
| Detection of AAV                                                                                                                    | qPCR                                                                                                   | < 0.2 ng/mL              |            | Pass       |

Table 4. Release Tests and Specifications for Drug Substance Bulk Lots

| Test                                                    | Method                                                                      | Release Specification         | AdC6-gp140 | AdC7-gp140 |
|---------------------------------------------------------|-----------------------------------------------------------------------------|-------------------------------|------------|------------|
| Bioburden                                               | Microbial enumeration test (USP/61)                                         | Negative                      |            | Pass       |
| Determination of virus concentration                    | UV spectrophotometry UV/OD                                                  | Report results                |            | Pass       |
| Endotoxin                                               | Kinetic chromogenic Limulus Amebocyte Lysate assay                          | < 10 EU/mL                    |            | Pass       |
| Detection of residual benzonase                         | Enzyme immunoassay                                                          | < 0.2 ng/mL                   |            | Pass       |
| Detection of Human DNA                                  | qPCR                                                                        | Negative                      |            | Pass       |
| Detection of replication competent adenovirus (RCA)     | Using A549 detector cells                                                   | < 1 RCA/3x10 <sup>10</sup> vp |            |            |
| Quantitative PCR (qPCR) assay for potency determination | qPCR assay of hexon from cells infected with serial dilutions of AdC vector | Vp to IU ratio = 600 : 1      |            |            |
| Viral safety assay                                      | In vivo toxicity in mice and rabbits                                        | Report results                |            |            |

### Vaccine Fill and Finish

Bulk vaccine is diluted in 2.5% Glycerol, 25 mM Sodium chloride, 20 mM Tris pH 8.0 formulation buffer for filling. To fill and finish the final clinical recombinant

- 5 AdC vector vaccines one product fill per vector are performed under cGMP conditions. Following the completion of the product fill at ~ 1 ml for a dose of 5 x 10<sup>10</sup> vp per ml, a review of the lot file and receipt of satisfactory test results for sterility, endotoxin and mycoplasma, a Certificate of Compliance is issued. Moreover, a Certificate of Analysis is issued by the Quality Assurance (SRI International, Menlo Park, California) after obtaining
- 10 all satisfactory release testing results and reviewing the related production batch records. The final release testing for the recombinant AdC vector vaccines filled product is presented in Table 5. The product is stored frozen at ≤ -65°C.

Table 5. Final Release Tests and Specifications for Recombinant AdC Vector Vaccines

| Test                                                    | Method                                                                      | Release Specification        |
|---------------------------------------------------------|-----------------------------------------------------------------------------|------------------------------|
| Appearance                                              | Visual                                                                      | Clear to slightly cloudy     |
| Sterility                                               | Immersion (Direct inoculation)<br>(USP/21 CFR 610.12)                       | No bacteria or fungus found. |
| Endotoxin                                               | Kinetic chromogenic Limulus<br>Amebocyte Lysate assay                       | < 10 EU/mL                   |
| Determination of virus concentration                    | UV spectrophotometry                                                        | Report results               |
| Quantitative PCR (qPCR) assay for potency determination | qPCR assay of hexon from cells infected with serial dilutions of AdC vector | Vp to IU ratio = 600 : 1     |
| Sequencing of viral DNA                                 | Massively Parallel Sequencing                                               | Report results               |
| General safety                                          | 21 CFR 610.11                                                               | No sign of toxicity          |

### Stability

- 5 Stability of filled drug product is tested over time. Vialled vector vaccine (stored at <-65°C) and is tested the first year in 3 monthly intervals for potency and appearance. The second year the vialled vaccine is tested every 6 months and thereafter annually.

### Example 10: preclinical studies

#### 10 Immunogenicity

During selection of the two adenovirus vectors, AdC6 and AdC7, immunogenicity evaluations were conducted in mice and nonhuman primates as described in the Example 8 above.

#### Non-clinical Safety and Biodistribution Studies

- 15 Preclinical safety and biodistribution studies are conducted in accordance with the U.S. FDA "Good Laboratory Practice for Nonclinical Laboratory Studies," as described in 21 CFR Part 58.

1. GLP single dose safety toxicology studies that include Day 4 and Day 29 biodistribution analysis in rabbits with AdC6-HIVgp140 and AdC7-HIVgp140



2. GLP single dose 12 week biodistribution study in rabbits for AdC6-HIVgp140 and AdC7-HIVgp140
3. Prime-boost study in rabbits consisting of AdC7-HIVgp140 prime followed by a AdC6-HIVgp140 boost 29 days later.

Information from these studies is used to define a no-observed-adverse-effect-level (NOAEL) and to identify potential target organs of toxicity. In each of these preclinical studies, New Zealand white rabbits receive a single dose of vector that is higher than the highest dose planned for use in humans.

### Single Vector Dose Ranging Safety Studies with Early Time Point Biodistribution

#### Analysis

The study design for the single-dose definitive safety studies is presented in Table 6. In these studies, New Zealand white rabbits is administered vaccine or control article via intramuscular (i.m.) immunization on Day 1. The study design includes a vehicle control (Group 1) and two vaccine-treatment groups ( $1 \times 10^{10}$  vp Group 2 and  $1 \times 10^{11}$  vp Group 3) with 10 male and 10 female rabbits per dose group. Half of the rabbits per group (n=5/sex) are sacrificed on Day 4 which is 4 days after immunization. The other 5 rabbits per sex per group are sacrificed on Day 29 which is 4 weeks after immunization in order to study the reversibility of toxicity or delayed toxicity of the single immunization.

Table 6. Design of Safety Study for AdC6-HIVgp140 or AdC7-HIVgp140

| Group <sup>A</sup> | Dose Route | Vaccine Dose Level (vp) | Number of Animals       |                             |
|--------------------|------------|-------------------------|-------------------------|-----------------------------|
|                    |            |                         | Main Group <sup>B</sup> | Recovery Group <sup>C</sup> |
| 1                  | i.m.       | Vehicle control         | 5M + 5F                 | 5M + 5F                     |
| 2                  | i.m.       | $1 \times 10^{10}$      | 5M + 5F                 | 5M + 5F                     |
| 3                  | i.m.       | $1 \times 10^{11}$      | 5M + 5F                 | 5M + 5F                     |

<sup>A</sup> Ten per sex per group are immunized once with the vaccine or vehicle.

<sup>B</sup> Main Group, five animals/sex/group are sacrificed 4 days after immunization.

<sup>C</sup> Recovery Group, five animals/sex/group are sacrificed 4 weeks after immunization.

#### The Vaccine Safety Studies include the parameters listed below herein:

- Mortality: at least once daily.
- Clinical Observation: pre dose, 2-4 hr post-dose, once daily for 5 days post-dose, otherwise once weekly, and at necropsy.
- Body Weight: Pre-study, weekly thereafter, and at sacrifice.

- Body Temperature: pre-dose, 3, 24, and 48 hr post-dose or until the rabbit's temperature returns to normal.
- Food Consumption: daily for the 3 days post-dose and otherwise once weekly (quantitatively measured over a 24 hr period).
- 5     • Local Reactogenicity: Local irritation at the injection sites is evaluated by a modified Draize scoring method at pre-dose, 2-4, 24, 48, and 72 hr after each injection. Any animals with irritation at the last time point, are evaluated once daily until irritation resolves..
- Ophthalmology: Pre-Study and post-dose within 1 week prior to scheduled sacrifice.
- 10    • Clinical Pathology: hematology, serum chemistry, and coagulation are pretested, 1 day after immunization (5/sex/group), and at the recovery necropsy.
- Urinalysis: at necropsy
- Antibody Response: Serum samples are collected pretest and at sacrifice and archived for possible antibody analysis (e.g. anti-HIV antibodies, neutralizing antibodies).
- 15    • Necropsy and Organ Weight: All animals at main and recovery sacrifice.
- Histopathology: All tissues in the control and high dose groups at the main study sacrifice. Any target organs is examined in the other dose groups and from the recovery group animals. All gross lesions are examined.
- Biodistribution: All high dose Group 3 rabbits (5/sex/time point) and 3
- 20    rabbits/sex/time point from vehicle control Group 1 are analyzed for biodistribution of the vector at sacrifice (Days 4 and 29).

The final report includes a discussion correlating clinical signs, body weight changes, clinical pathology, hematopoietic and immune function changes, histopathology, and when applicable, biodistribution. Statistical evaluation of body weight, food

25    consumption, body temperature, clinical pathology parameters, and organ weights are conducted. The no observed adverse effect level (NOAEL) and maximum tolerated dose (MTD), is also determined.

### **Clinical Pathology**

Clinical pathology determinations (hematology and clinical chemistry panel)

30    is conducted on blood samples collected at selected time-points from the ear vein without anesthesia. Hematology samples are collected using EDTA as the anticoagulant. Smears for reticulocytes and differentials are prepared within one hour of sample collection (including MeOH fixation but excluding staining and reading). Blood for coagulation tests is collected

using sodium citrate as the anticoagulant and the plasma frozen until analyzed. Clinical chemistry and antibody response samples are collected without the use of an anticoagulant, centrifuged, and the serum stored frozen until analysis.

Hematology evaluations include standard erythrocyte and leukocyte parameters: red and white blood cell (RBC and WBC) counts, hemoglobin, hematocrit, mean corpuscular volume, mean corpuscular hemoglobin and hemoglobin concentration, platelet count, mean platelet volume, reticulocyte count, and differential leukocyte count.

Clinical chemistry evaluations include a standard panel: alanine aminotransferase, aspartate aminotransferase, alkaline phosphatase, albumin, albumin/globulin ratio, blood urea nitrogen, bilirubin, calcium, chloride, cholesterol, creatinine, creatine kinase, globulin, glucose, phosphorus, potassium, total protein, sodium, and triglycerides.

Coagulation parameters include prothrombin time, activated partial thromboplastin time, and fibrinogen.

### **Necropsy/Histopathology**

At sacrifice, terminal body weights and *ante mortem* observations are recorded for each animal and commented on at necropsy. All protocol-specified tissues and the identification mark from each animal are saved in cold, buffered neutral 10% formalin at necropsy. Any gross findings noted at the time of necropsy is recorded and then confirmed in the subsequent microscopic evaluation. Animals in moribund condition are euthanized and receive a full necropsy as for scheduled necropsies. The recommended list of tissues to be retained for conduct of a general and comprehensive evaluation of potential target organs has been standardized. The list of tissues routinely evaluated microscopically is:

Adrenal glands (pair), Aorta, Bone marrow (histology, sternum), Bone marrow (cytology, sternum), Bone (femur with joint surface), Brain (fore-, mid-, and hindbrain), Cecum, Cervix, Colon, Duodenum, Epididymes, Esophagus, Eyes (with optic nerve), Gall bladder, Gross lesions (including tissue masses and abnormal regional lymph nodes), Heart, Identification (tattoo, collected not analyzed), Injection site(s), Ileum, Jejunum, Kidneys, Liver, Lungs with bronchi, Lymph nodes (mandibular, and mesenteric and inguinal or iliac depending on dose site), Mammary gland (from both sexes; to include nipple and surrounding tissue), Ovaries, Pancreas, Pituitary gland, Prostate, Rectum, Salivary gland, Seminal vesicle, Sciatic nerve, Skeletal muscle, Skin (included with mammary gland), Spinal cord (thoracic only), Spleen, Stomach, Testes, Thymus, Thyroid and parathyroid, Trachea, Uterus, Urinary bladder, and Vagina.

### **Toxicologic Evaluations**

Effects on the parameters evaluated in each study, e.g., microscopic lesions, are categorized as vaccine-related or non-vaccine-related, with further clarification, when possible, on whether a vaccine-related lesion is primary or secondary. The evaluation of anatomic pathology results consider and, where possible, integrate related clinical and clinical pathology data.

### **Biodistribution**

Biodistribution analysis is conducted on DNA extracted from the tissues by a quantitative PCR (Q-PCR) assay (with sensitivity of at least 50 copies/ $\mu$ g of genomic DNA) using primers corresponding to the vector insert. Because each of the vaccines is manufactured from different adenovirus serotypes, the biodistribution of each vaccine is assessed. Replicate wells spiked with plasmid encoding the insert are used to monitor PCR inhibition.

The following tissues are collected from each animal at necropsy and analyzed from each of the animals sacrificed 4 days post-dose: blood, bone marrow, brain, heart, lungs, liver, injection site muscle, kidneys, testes/ovaries, draining lymph nodes, and spleens. If vector sequence is detected 4 days post-dose, that tissue is analyzed from later time points. Expression of the transgene is also be tested using quantitative Reverse Transcription (RT)-PCR on RNA isolated from positive tissues. The results of these studies show the distribution of the vector in different tissues as a function of time post-injection.

### **12 Week Biodistribution Study**

The study design for the 12 week biodistribution study of both vaccines tested singly is presented in Table 7. In this study, animals receive a single dose of vehicle or vaccine at  $1 \times 10^{11}$  vp on Day 1 by i.m. injection and are sacrificed 12 weeks later. The tissue list for the 12 week study depends on the results of the prior studies; tissues with detectable vector at 4 weeks post-dose are analyzed for the presence of vector at 12 weeks post-dose. The biodistribution parameters (e.g., methods and endpoints) discussed above is be applied herein. This study includes weekly body weights and clinical observations to monitor the general health of the animals.

Table 7. Design of 12 Week Biodistribution Study for AdC6-HIVgp140 and AdC7-HIVgp140

| Group | Dose Route | Vaccine         | Dose Level (vp)       | Number of Animals Sacrificed at 12 wk |
|-------|------------|-----------------|-----------------------|---------------------------------------|
| 1     | i.m.       | Vehicle control | 0                     | 3M + 3F                               |
| 2     | i.m.       | AdC6-HIVgp140   | $1 \times 10^{11}$ vp | 5M + 5F                               |
| 3     | i.m.       | AdC7-HIVgp140   | $1 \times 10^{11}$ vp | 5M + 5F                               |

## 5 Prime-Boost Safety Study

The study design for the prime-boost safety study is presented in Table 8. New Zealand white rabbits (5 animals/sex/group) are administered by i.m. injection vehicle control or the highest vaccine dose determined to have an acceptable safety profile in the previous single vector safety studies. A single administration of AdC7-HIVgp140 is used as the prime injection on Day 1. A single administration of AdC6-HIVgp140 is used as the boost and occur 4 weeks after the prime. The study is divided into a main and recovery study phase. Animals in the main group are sacrificed on Day 33 which is 4 days after the boost immunization. The recovery group animals are sacrificed on Day 57 which is 4 weeks after the boost immunization. All of the safety study parameters described for the single dose study (as listed above herein) are included in this study with the exception of the biodistribution analysis.

Table 8. Design of Safety Study for Prime-Boost Regimen

| Group <sup>A</sup> | Dose Route | Vaccine Dose (Prime-Boost) | Prime (Day 1)   | Boost (Day 29)  | Number of Animals       |                             |
|--------------------|------------|----------------------------|-----------------|-----------------|-------------------------|-----------------------------|
|                    |            |                            |                 |                 | Main Group <sup>B</sup> | Recovery Group <sup>C</sup> |
| 1                  | i.m.       | 0                          | Vehicle Control | Vehicle Control | 5M + 5F                 | 5M + 5F                     |
| 2                  | i.m.       | $1 \times 10^{11}$ vp      | AdC7-HIV gp140  | AdC6-HIVgp140   | 5M + 5F                 | 5M + 5F                     |

<sup>A</sup> Ten rabbits per sex per group are immunized once with the vaccine prime or vehicle on Day 1 and once with the vaccine boost or vehicle on Day 29.

<sup>B</sup> Main Group, five animals/sex/group are sacrificed on Day 33, 4 days after the boost immunization.

<sup>C</sup> Recovery Group, five animals/sex/group are sacrificed on Day 57, 4 weeks after the boost immunization.

## 25 Example 11: Objectives and Endpoints

*Primary objective*

- To evaluate the safety and tolerability of AdC6HIVgp140 and AdC7HIVgp140 at doses from  $1 \times 10^9$  vp to  $5 \times 10^{10}$  vp in HIV-1 uninfected adults

*Primary endpoints*

- Frequency and severity of local reactogenicity signs and symptoms
- 5 - Frequency and severity of systemic reactogenicity signs and symptoms
- Frequency of AEs categorized by MedDRA body system, MedDRA preferred term, severity and assessed relationship to study products. Detailed description of all AEs meeting DAIDS criteria for expedited reporting.

*Secondary objective*

- 10 - To gain preliminary data on the immunogenicity of AdC6HIVgp140 and AdC7HIVgp140 in HIV-1 uninfected adults

*Secondary endpoints*

- HIV-specific CD4<sup>+</sup> and CD8<sup>+</sup> T-cell response rates
- Magnitude of HIV-specific CD4<sup>+</sup> and CD8<sup>+</sup> T-cell responses
- 15 - Frequency, magnitude and breadth of HIV-specific binding antibody responses as assessed by multiplex assay
- Neutralizing antibody frequency, magnitude and breadth against tier 1 and, if applicable, tier 2 HIV-1 isolates as assessed by area under the magnitude-breadth curves

20

The disclosures of each and every patent, patent application, and publication cited herein are hereby incorporated herein by reference in their entirety.

While this invention has been disclosed with reference to specific embodiments, it is apparent that other embodiments and variations of this invention may be devised by others skilled in the art without departing from the true spirit and scope of the invention. The appended claims are intended to be construed to include all such embodiments and equivalent variations.

25

## CLAIMS

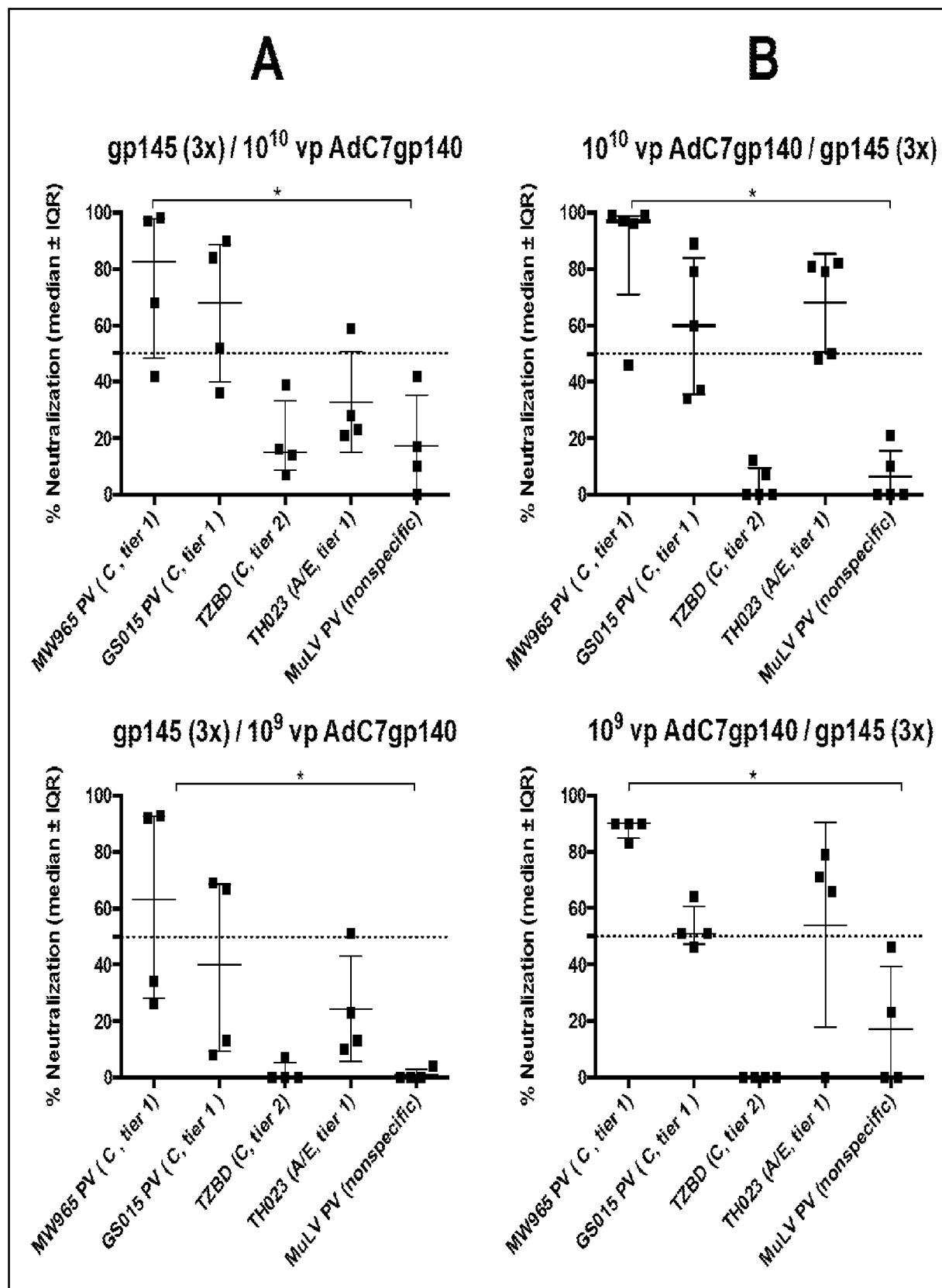
What is claimed:

1. A method of generating a effector and memory T cell immune response to a heterologous protein in a mammal, the method comprising the steps of: (a) administering a composition comprising a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, comprising an early gene E3 wherein the ORF3, ORF4, ORF5, ORF6 and ORF7 are deleted, wherein the early gene E1 is deleted, and wherein the nucleic acid sequence further comprises a promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag to a mammal in an amount effective to elicit an immune response in the mammal; (b) administering a second effective amount of the composition at a second, subsequent time period, wherein the composition administered in (a) and the composition administered in (b) have a different serotype selected from the group consisting of AdC6 and AdC7, and wherein T memory cells directed against the heterologous protein are reactivated in the mammal.
2. The method of claim 1, wherein the composition administered first in (a) and second in (b) comprises a same or a different HIV heterologous protein selected from the group consisting of gp140, gp160 and Gag.
3. A method of generating an adaptive B cell immune response to a heterologous protein in a mammal, the method comprising the steps of: (a) administering a composition comprising a nucleic acid sequence of a chimpanzee-derived adenovirus vector of serotype AdC6 or AdC7, comprising an early gene E3 wherein the ORF3, ORF4, ORF5, ORF6, and ORF7 are deleted, wherein the early gene E1 is deleted, and wherein the nucleic acid sequence further comprises a promoter sequence linked to a sequence encoding a heterologous protein, wherein the heterologous protein is at least one HIV protein selected from the group consisting of gp140, gp160 and Gag to a mammal in an amount effective to elicit an immune response in the mammal; (b) administering a second effective amount of the composition at a second, subsequent time period, wherein the composition administered in (a) and the composition

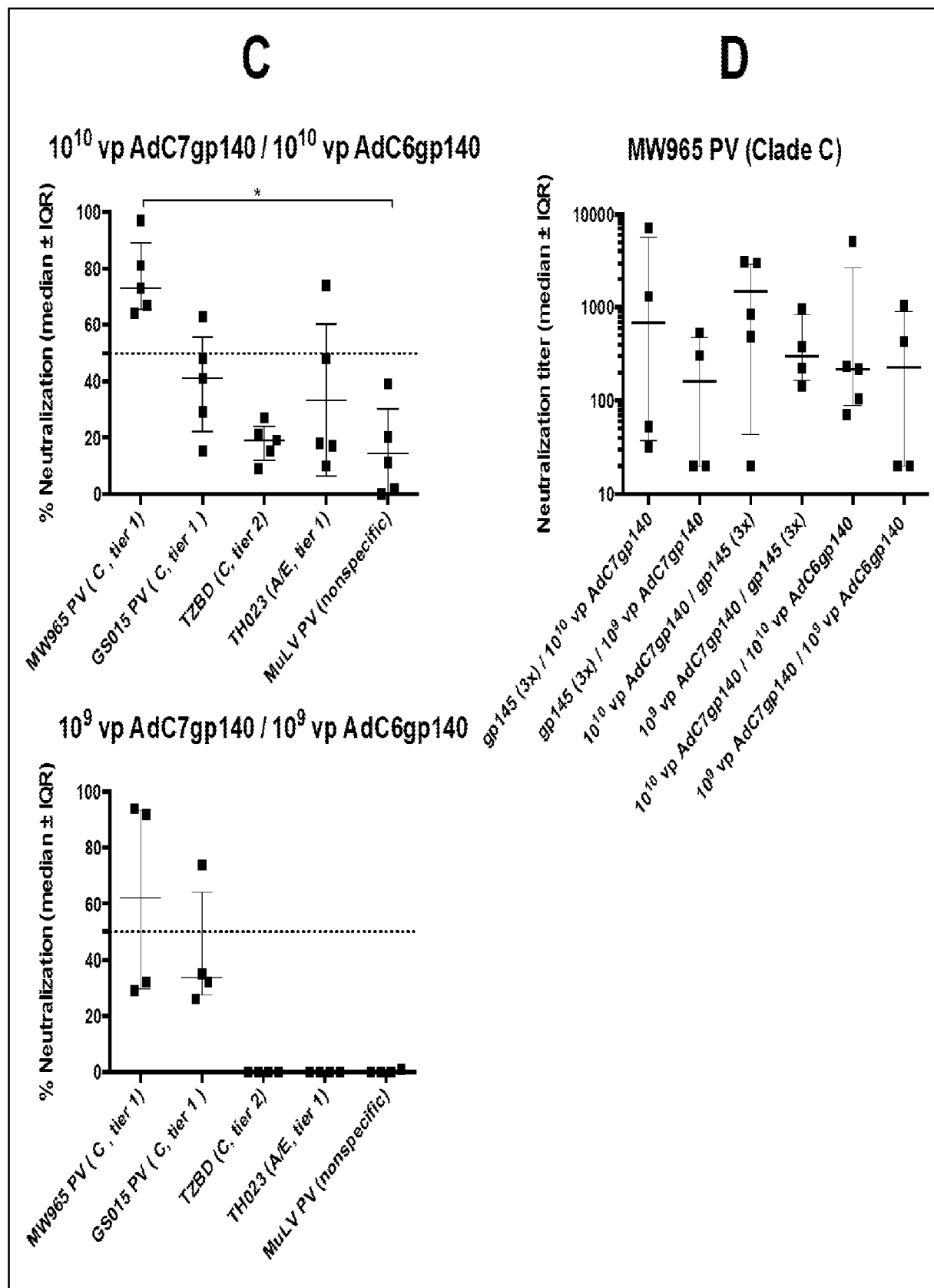
administered in (b) have a different serotype selected from the group consisting of AdC6 and AdC7, and wherein B memory cells directed against the heterologous protein are reactivated in the mammal.

4. The method of claim 1 or claim 3, wherein the mammal is a human.
5. The method of any one of claims 1-4, wherein the promoter is
  - (i) a constitutive promoter; or
  - (ii) a cytomegalovirus immediate early promoter (CMV).
6. The method of any one of claims 1-5, wherein the nucleic acid sequence is selected from the group consisting of SEQ ID Nos: 1-8.





Figs. 1A-1B



Figs. 1C-1D

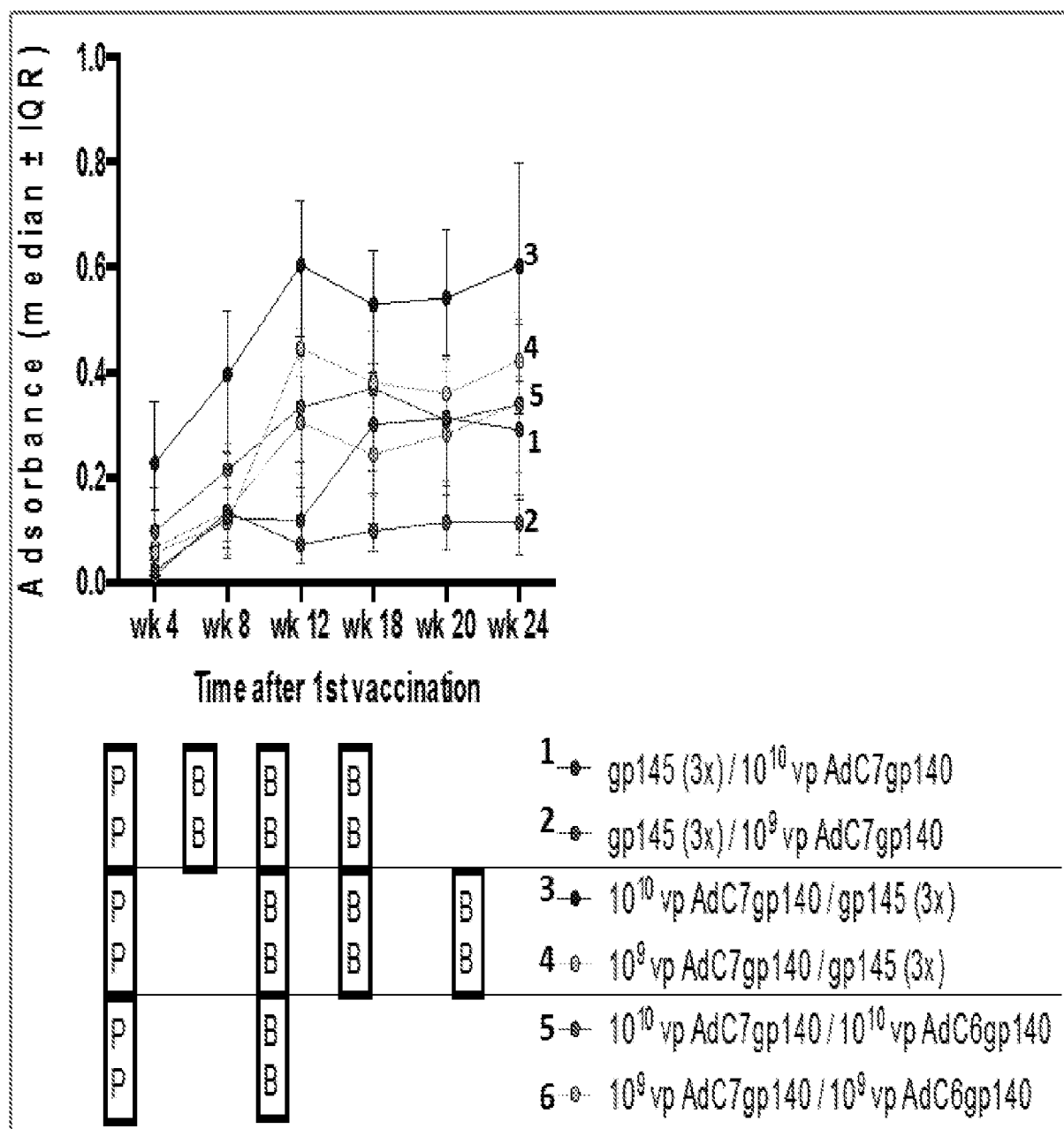


Fig. 2A

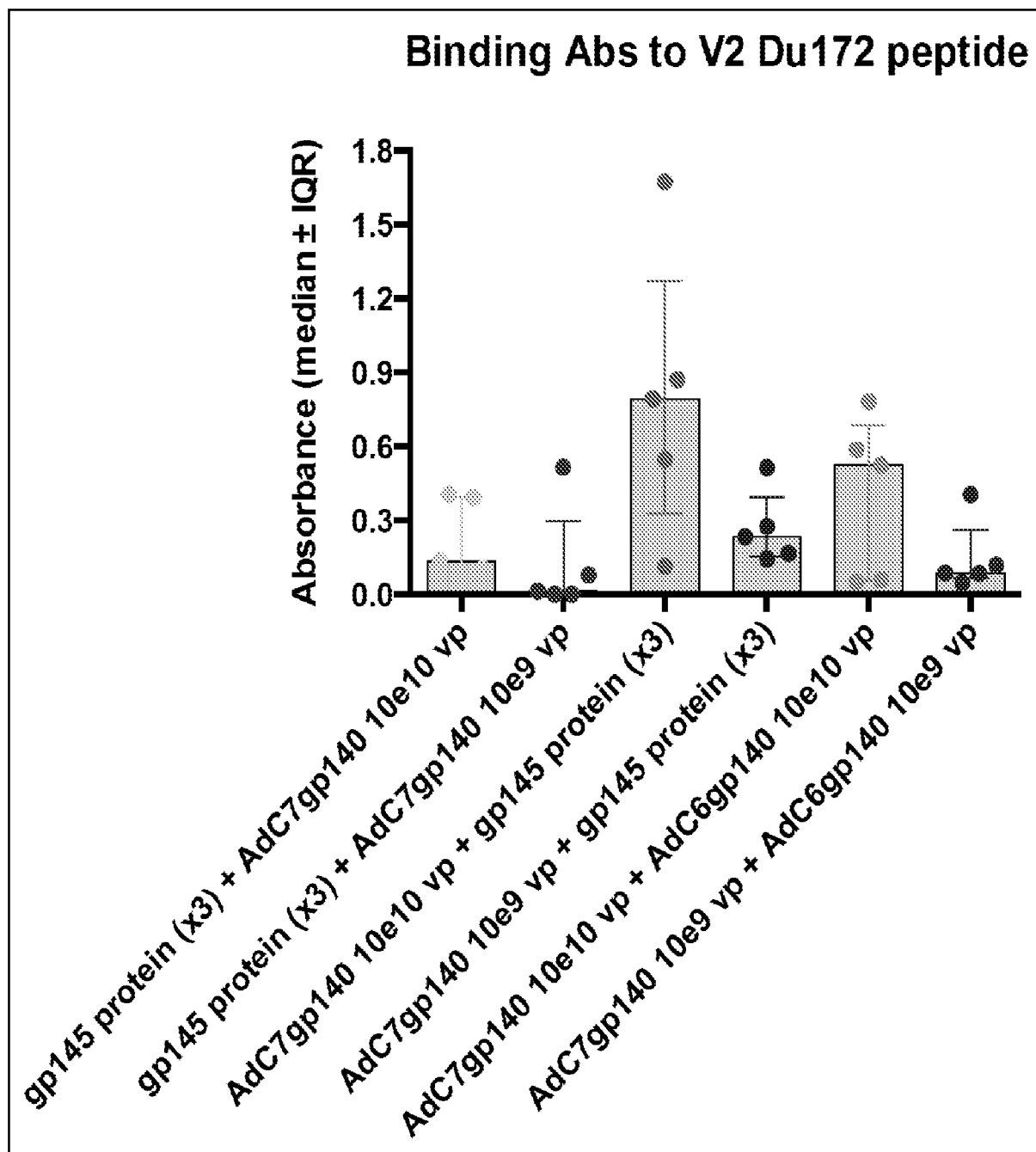


Fig. 2B

| Group/<br>Vaccine             | NHP ID | Genotype | Gender | AdHu5 Titer | AdHu26 Titer |
|-------------------------------|--------|----------|--------|-------------|--------------|
| <b>1</b><br><b>AdC7/C6</b>    | 4825   | -*       | M      | 20          | 640          |
|                               | 4826   | -        | M      | 20          | 640          |
|                               | 4889   | -        | M      | 0           | >1280        |
|                               | 4372   | A01, A02 | F      | 20          | 1280         |
|                               | 4395   | A01, A02 | M      | 0           | 320          |
|                               | 4400   | A01      | M      | 160         | 640          |
|                               | 4552   | A01      | M      | 20          | 160          |
|                               | 4553   | A01      | M      | 40          | >1280        |
|                               | 4770   | A01      | M      | 40          | 10           |
|                               | 4773   | A01      | M      | 80          | 40           |
|                               | 4774   | A01      | M      | 160         | 20           |
|                               | 4894   | A02, B17 | M      | 0           | 160          |
| <b>2</b><br><b>AdHu26/Hu5</b> | 4389   | A02      | F      | 0           | 160          |
|                               | 4892   | A02      | M      | 0           | 1280         |
|                               | 4893   | B01      | M      | 20          | 80           |
|                               | 4916   | -        | M      | 40          | >1280        |
|                               | 4381   | A01, A02 | M      | 40          | 1280         |
|                               | 4394   | A01      | M      | 20          | 1280         |
|                               | 4547   | A01      | M      | 160         | 1280         |
|                               | 4776   | A01      | F      | 40          | 20           |
|                               | 4777   | A01      | M      | 160         | 40           |
|                               | 4778   | A01      | M      | 80          | 80           |
|                               | 4779   | A01      | M      | 20          | 640          |
|                               | 4781   | A01      | M      | 10          | 320          |
| <b>3</b><br><b>None</b>       | 4824   | -        | M      | 0           | 160          |
|                               | 4886   | -        | M      | 0           | 0            |
|                               | 4891   | -        | M      | 0           | 20           |
|                               | 4365   | A01      | F      | 10          | 1280         |
|                               | 4398   | A01, B01 | F      | 10          | 0            |
|                               | 4546   | A01      | M      | 80          | 640          |
|                               | 4769   | A01      | M      | 80          | 20           |
|                               | 4771   | A01      | M      | 40          | 1280         |
|                               | 4772   | A01      | F      | 160         | 80           |
|                               | 4775   | A01      | M      | 640         | 40           |
|                               | 4780   | A01      | M      | 20          | 160          |
|                               | 4392   | A02, B17 | F      | 40          | 0            |

\* animals were not positive for A01, A02, B01 or B17

Fig. 3

## Serum Virus titers

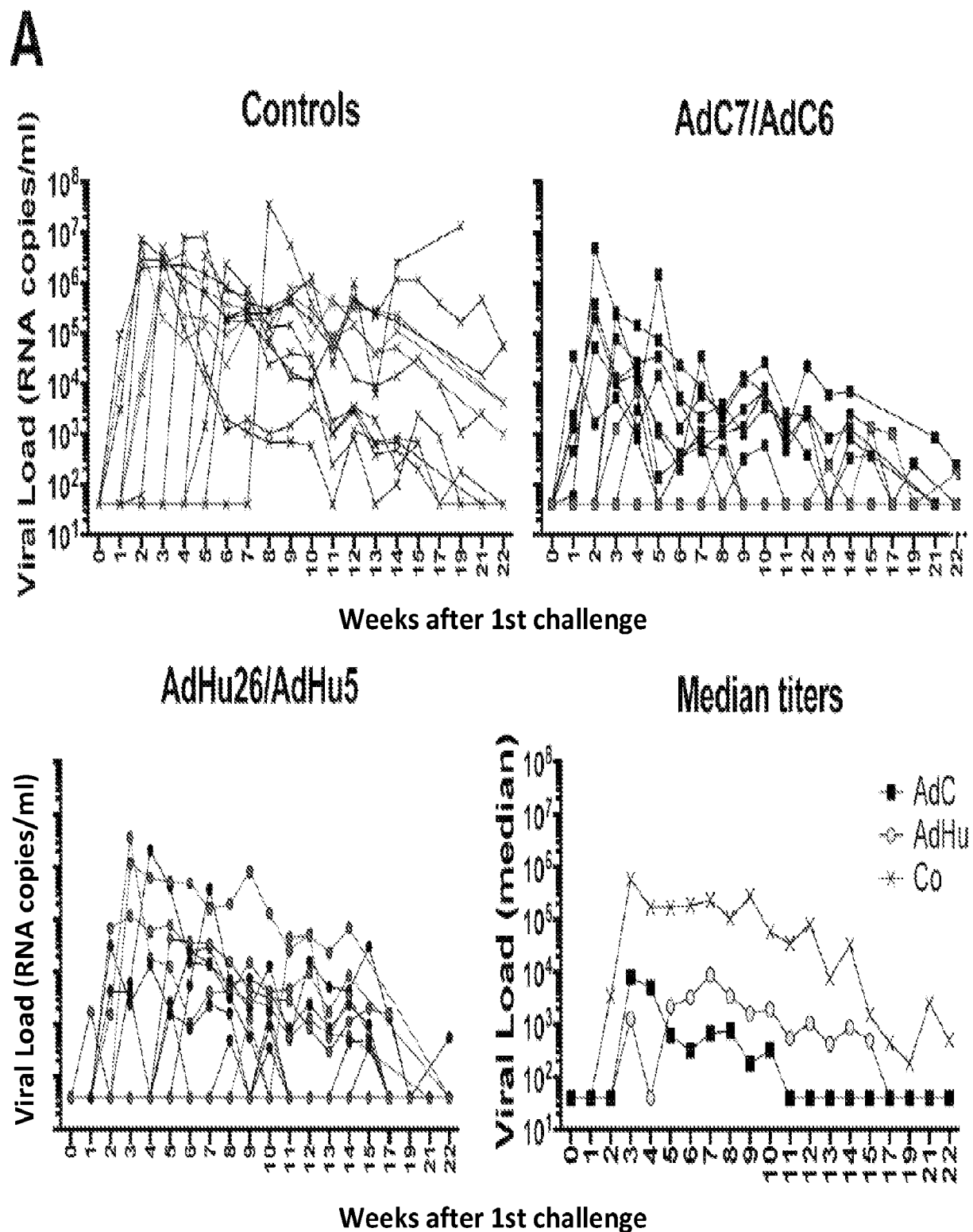
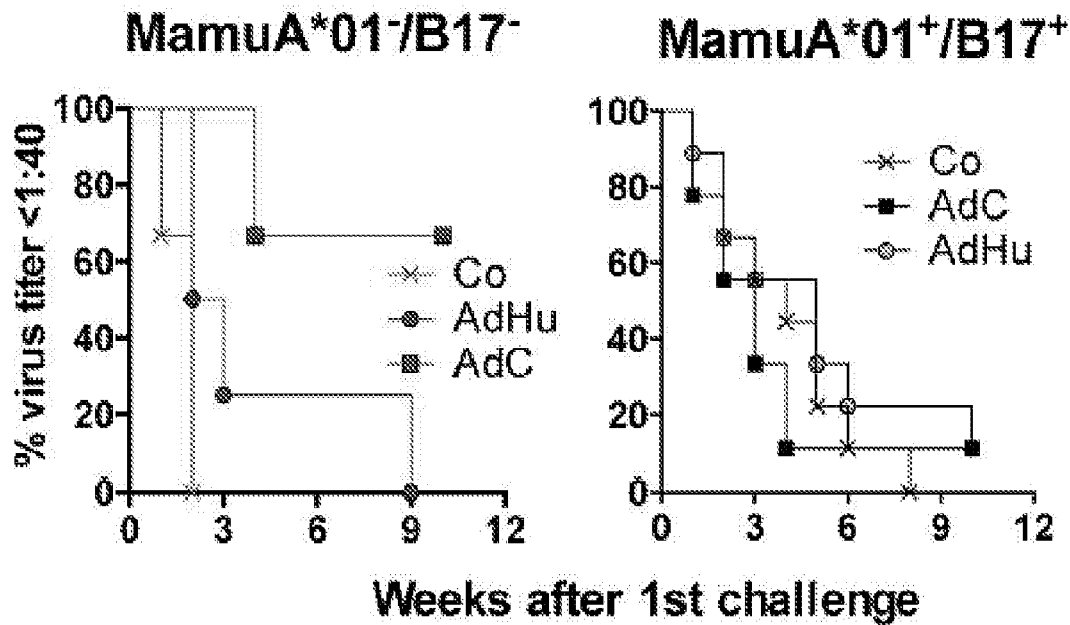
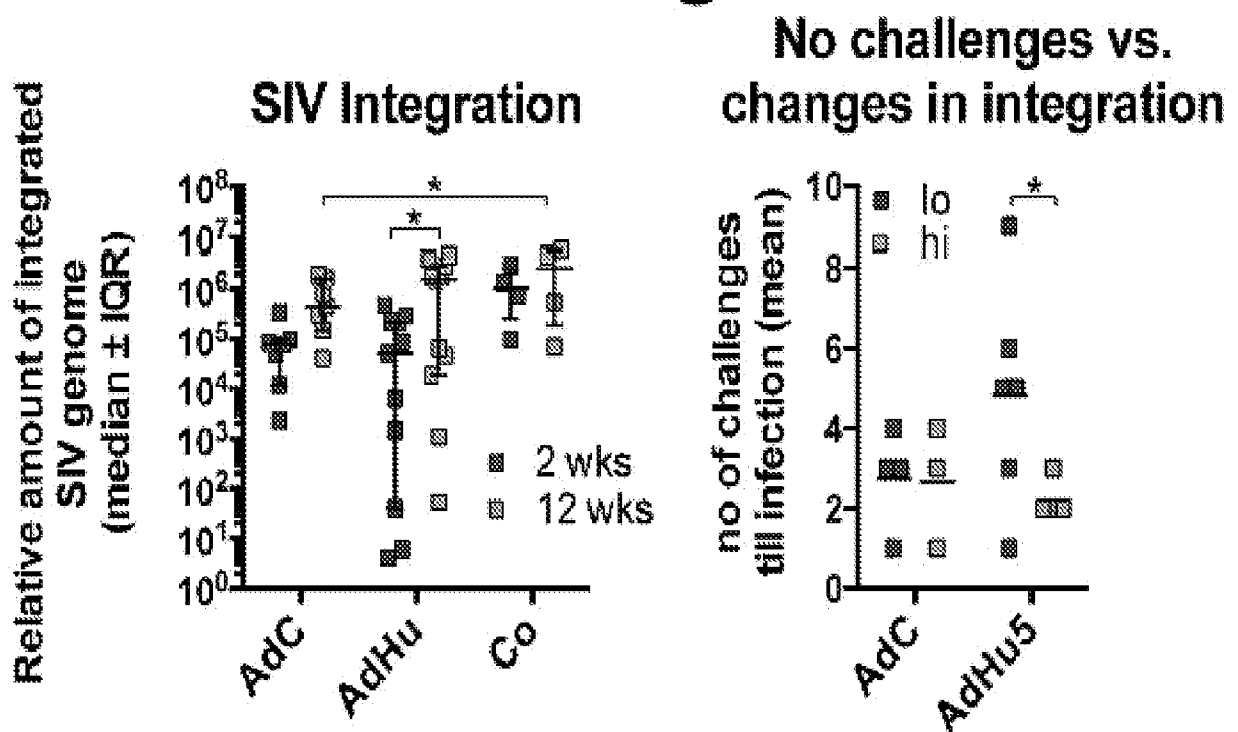


Fig. 4A

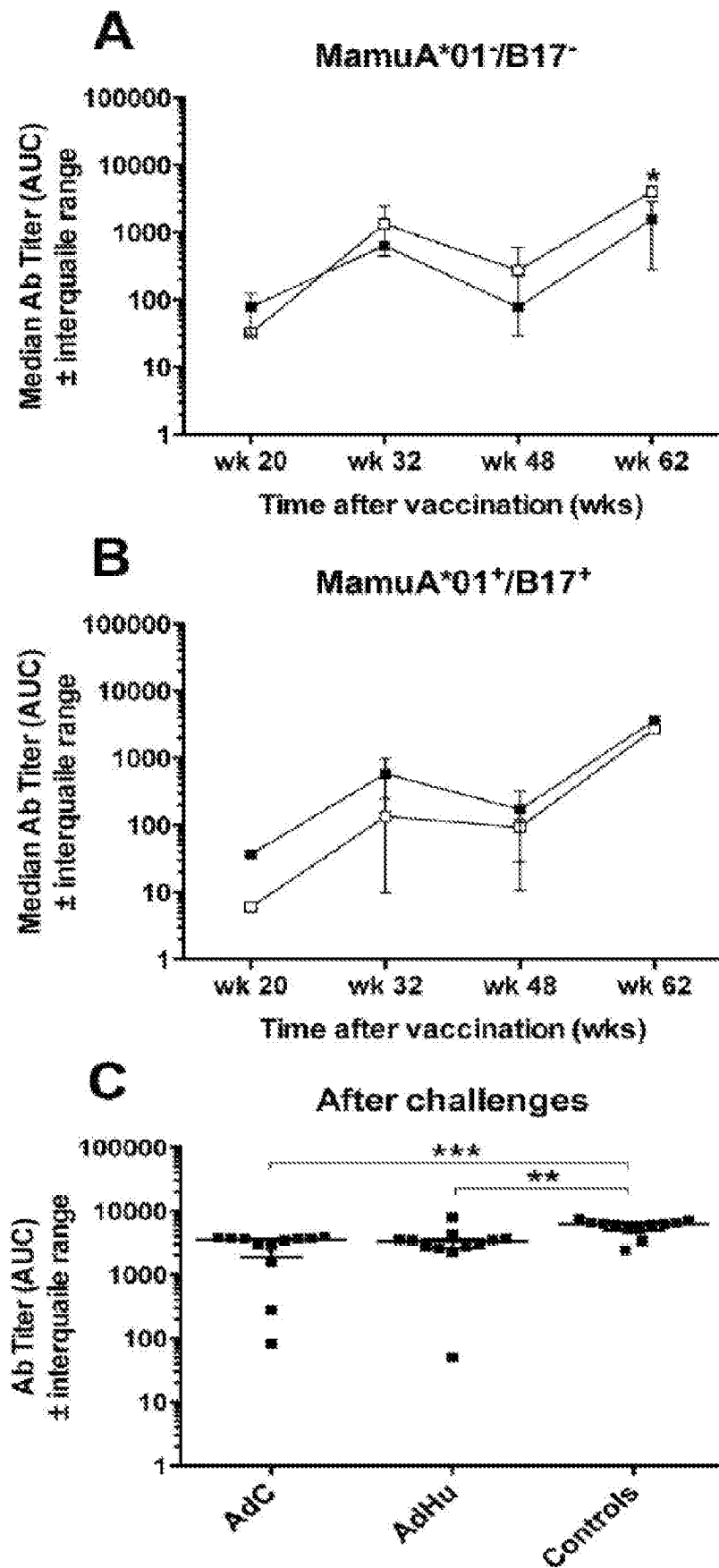
## B Control of serum virus titers



## C Virus integration

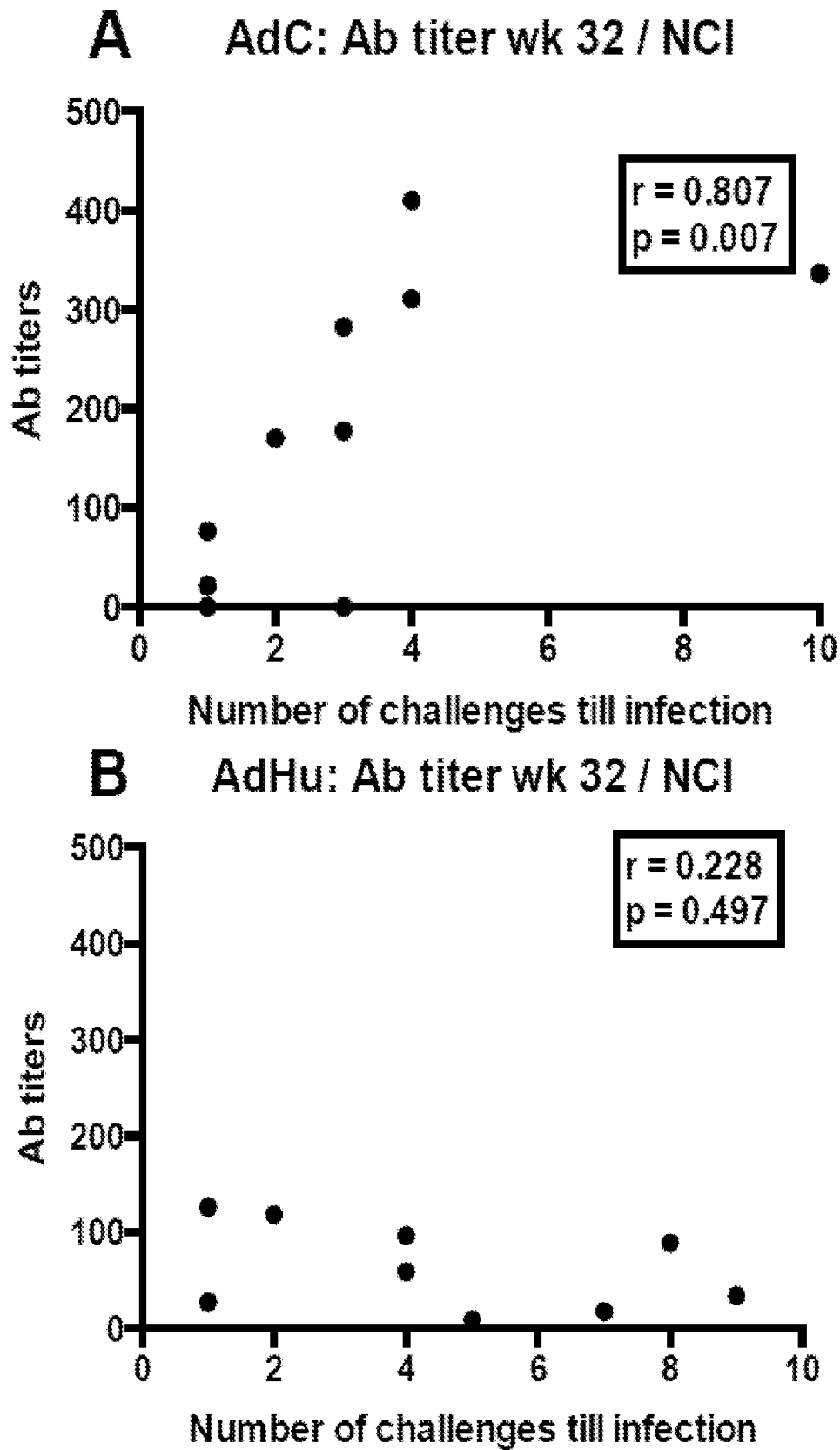


Figs. 4B-4C

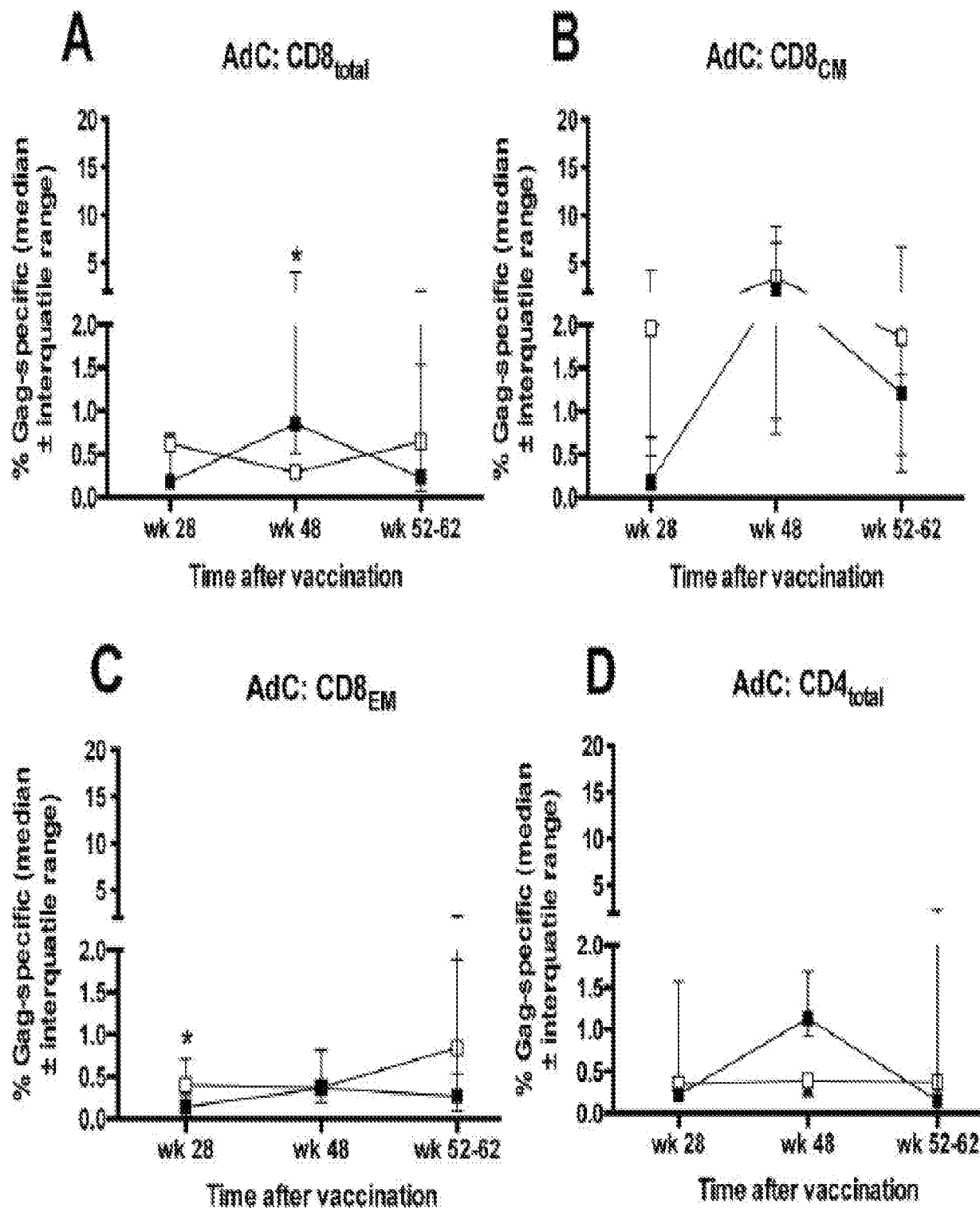


Figs. 5A-5C.

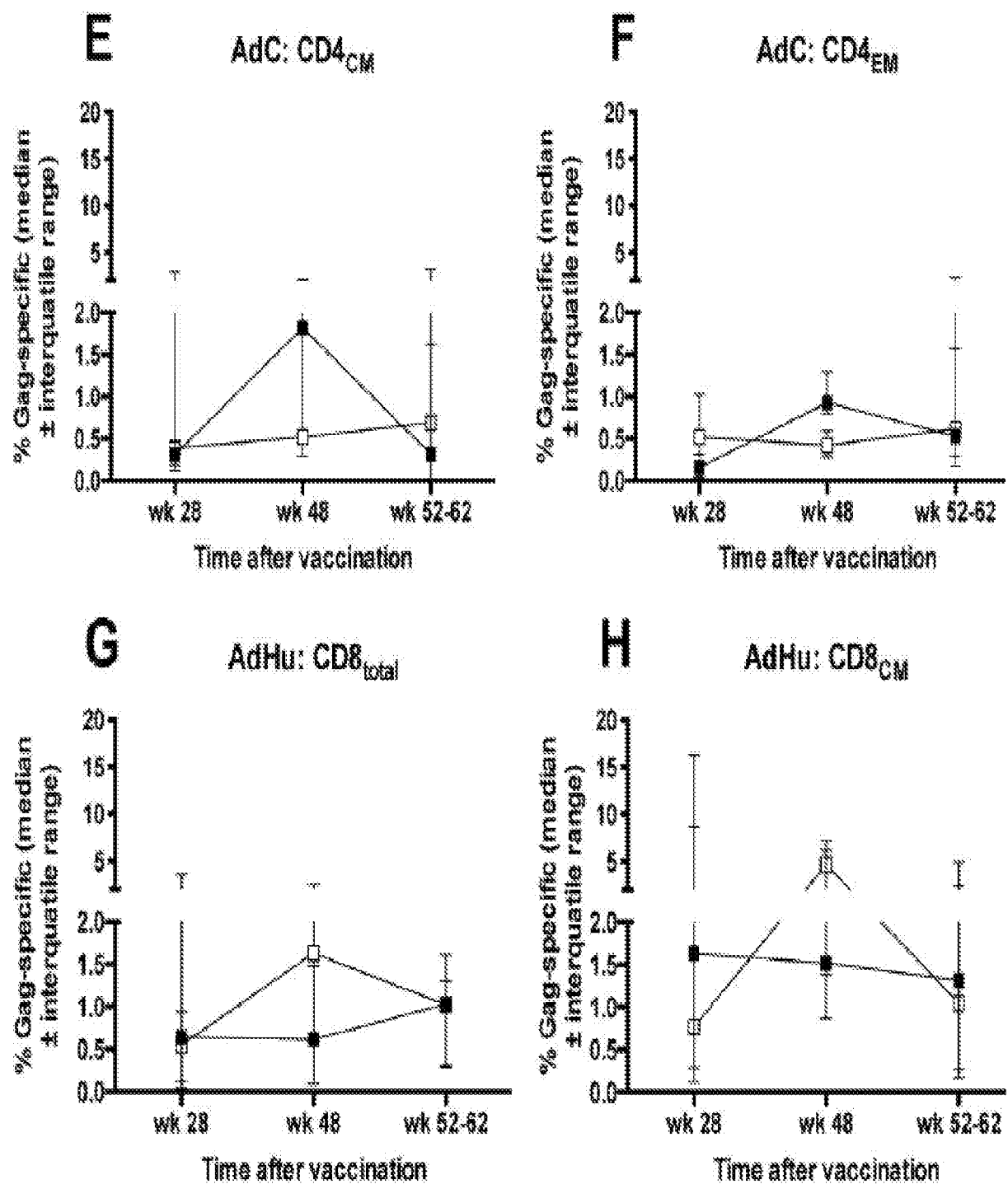




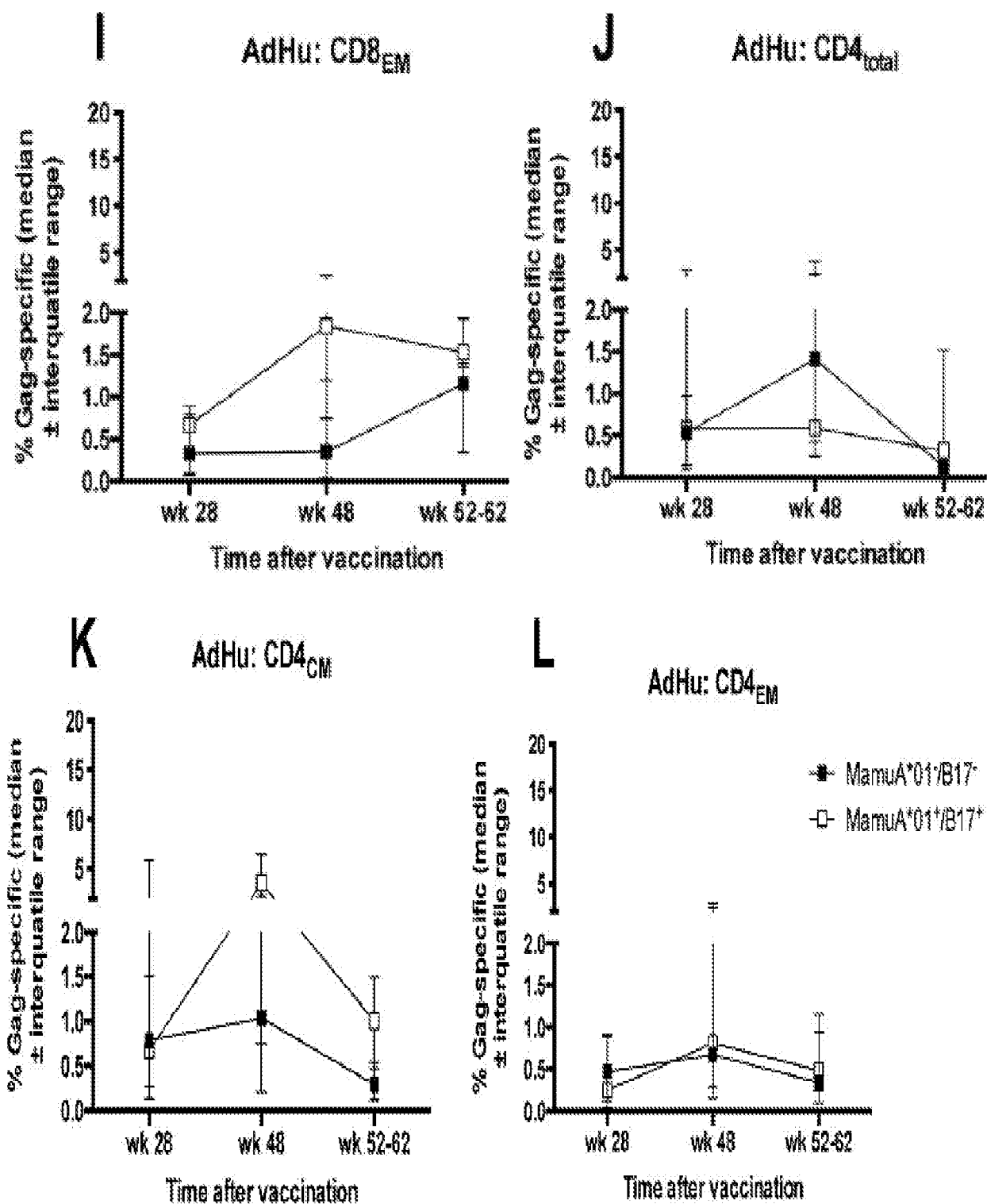
Figs. 6A-6B



Figs. 7A-7D



Figs. 7E-7H



Figs. 7I-7L

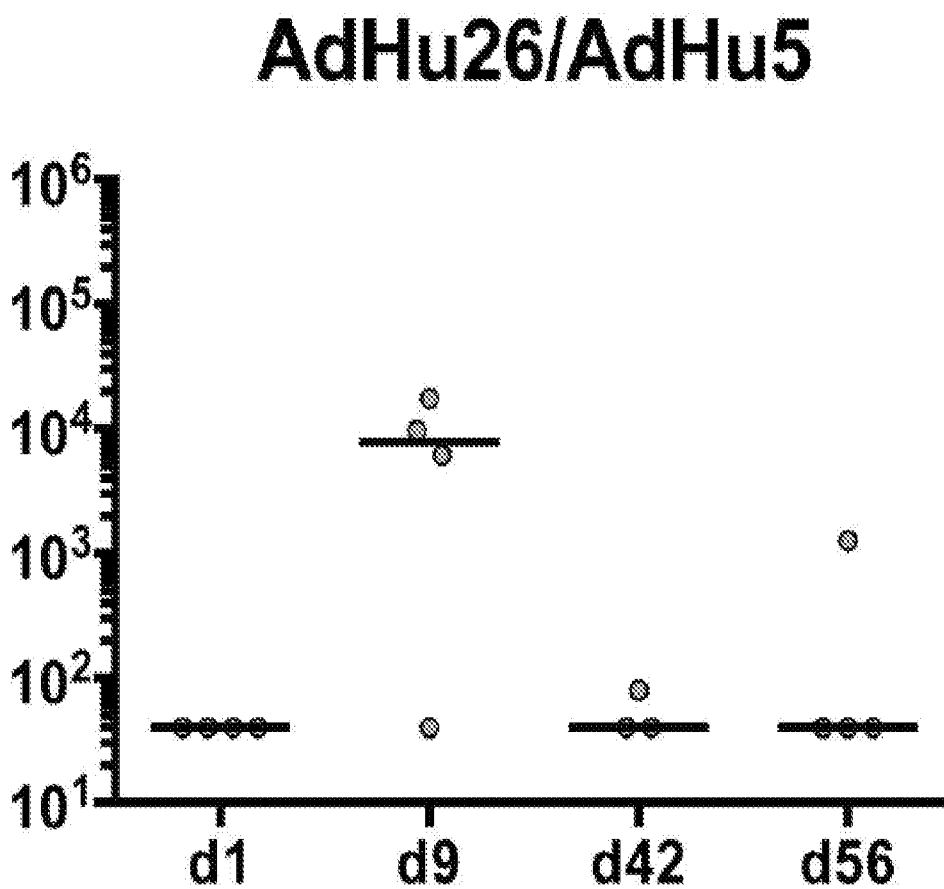
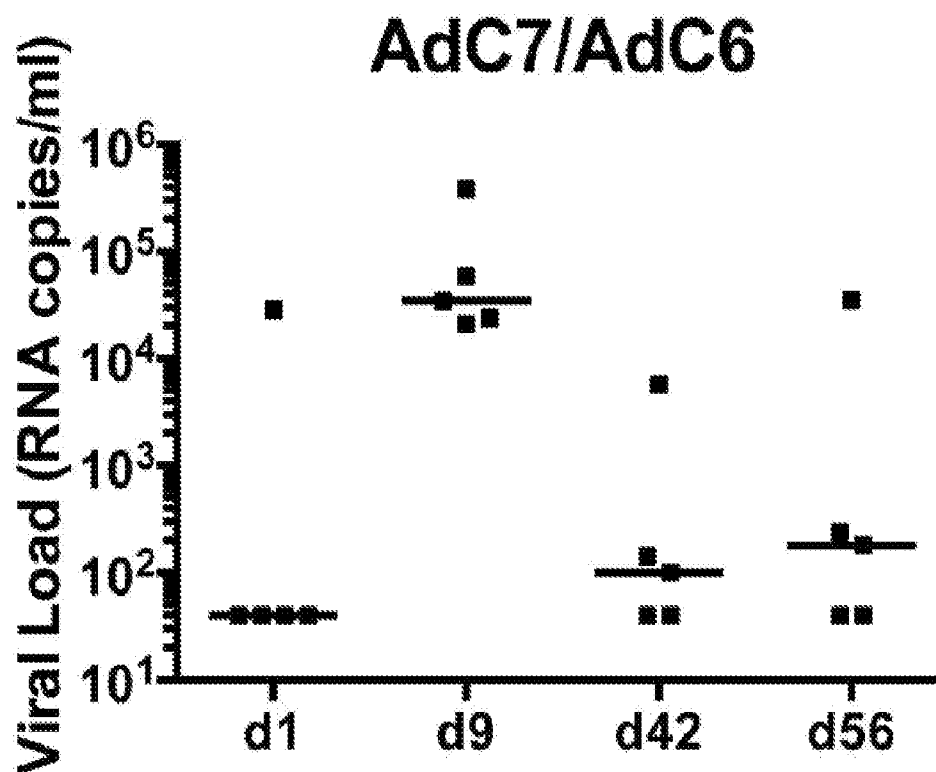


Fig. 8

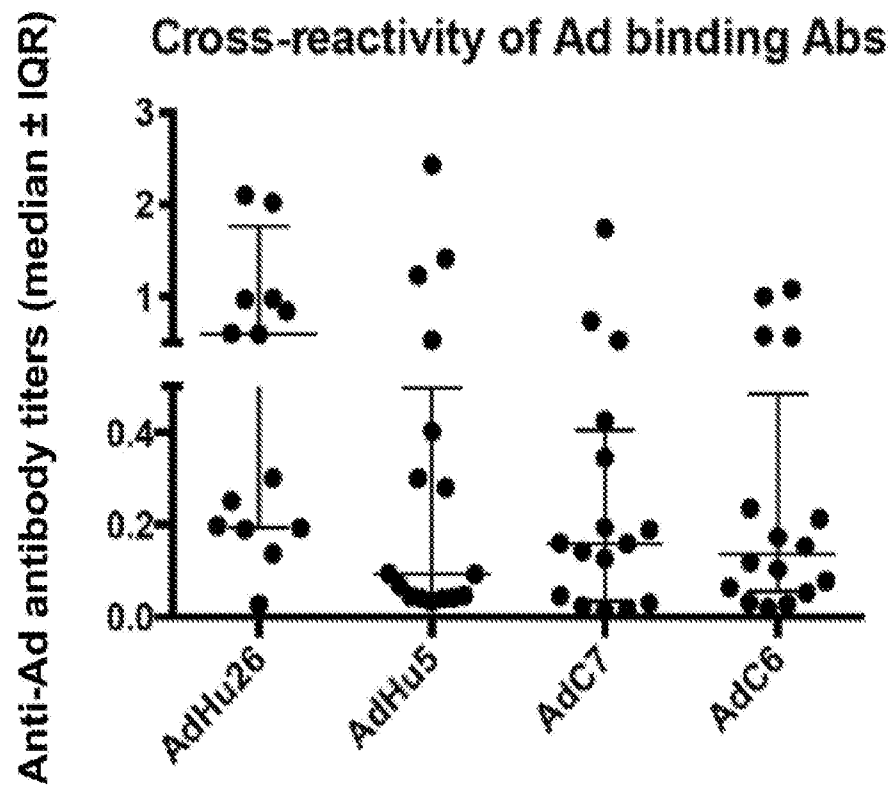
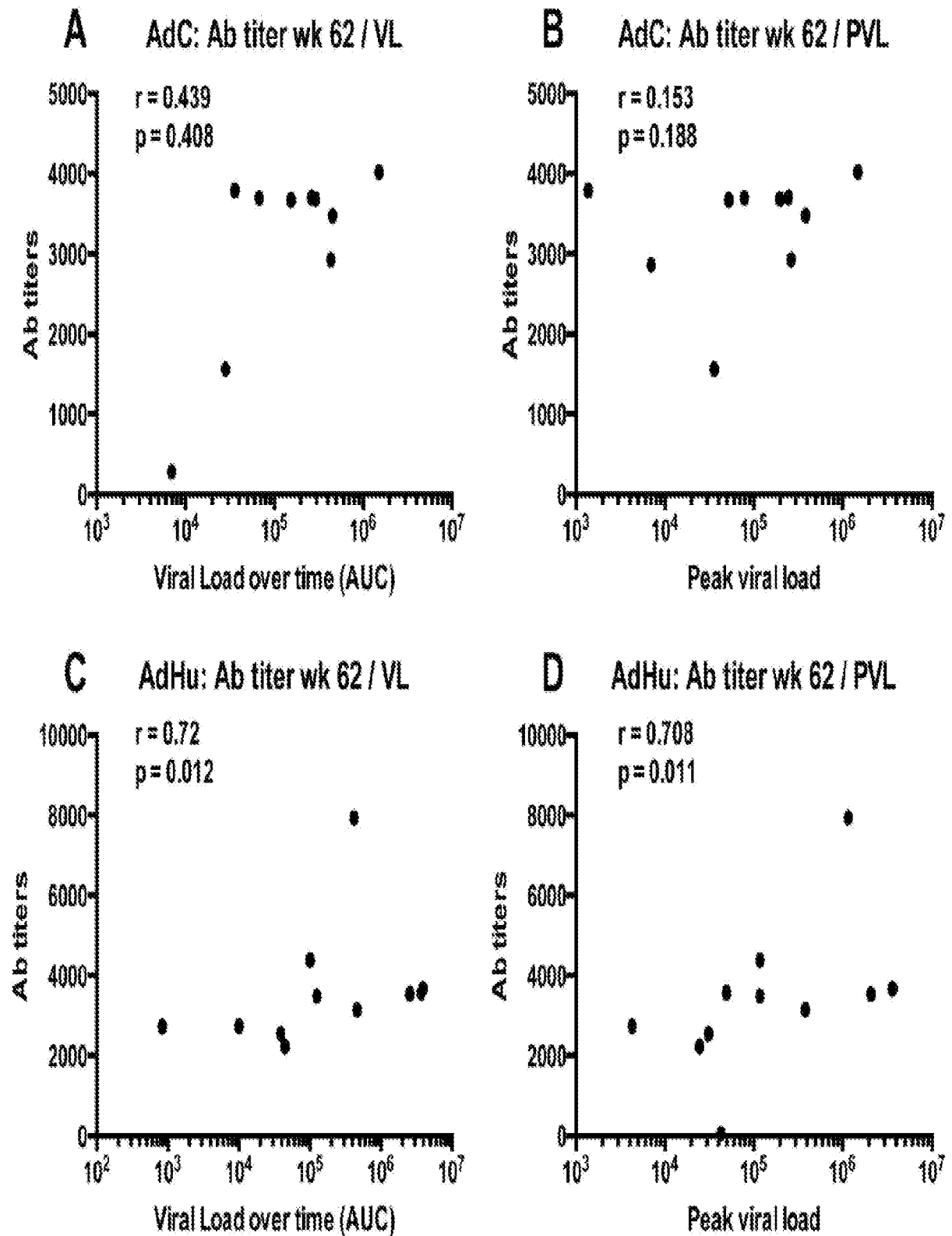


Fig. 9



Figs. 10A-10D

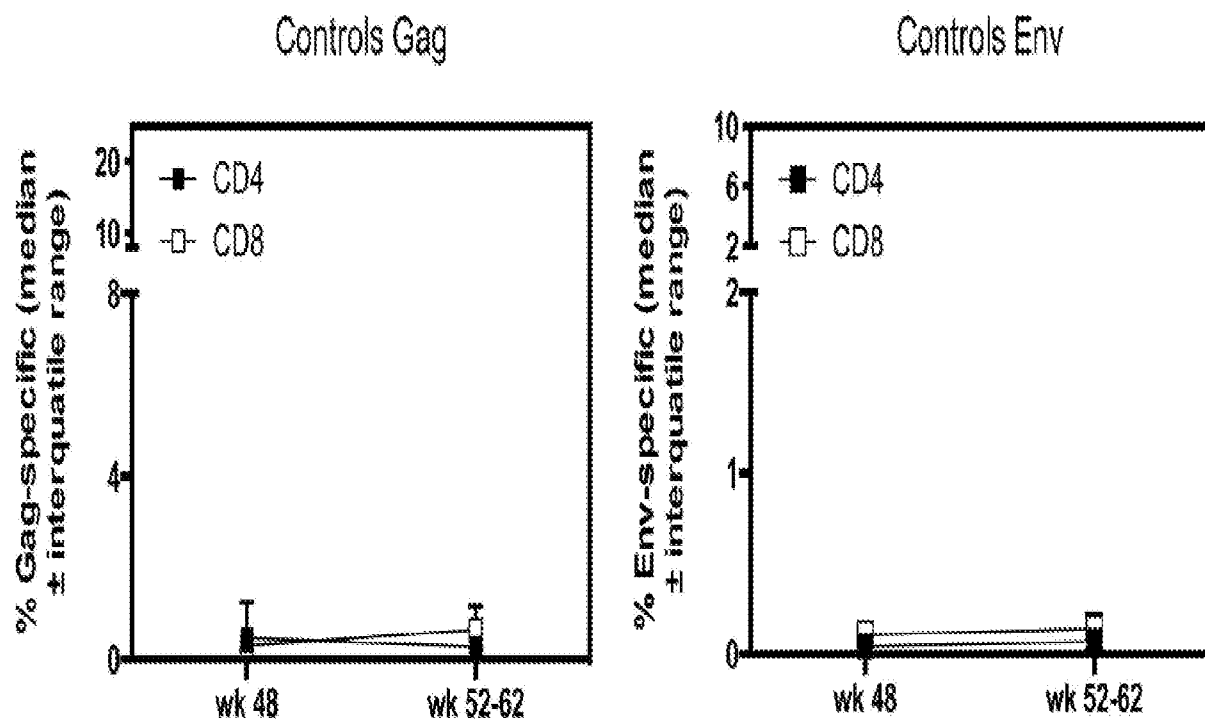
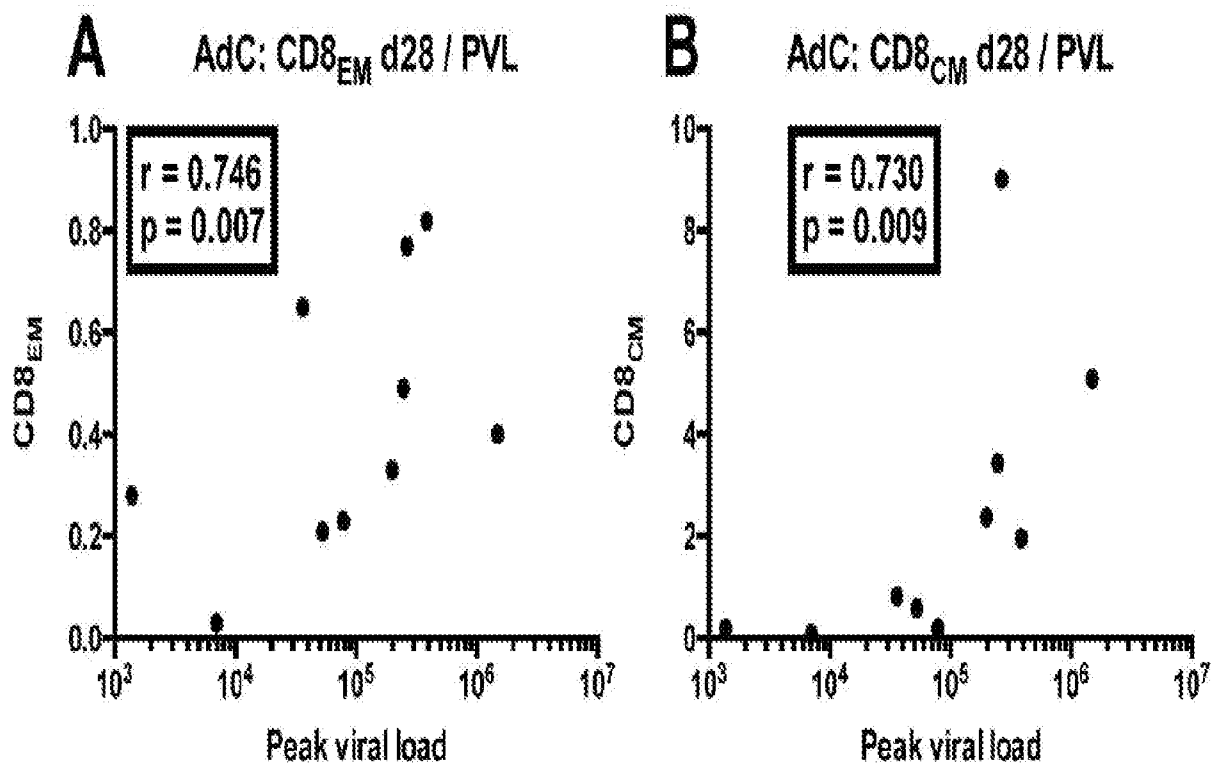
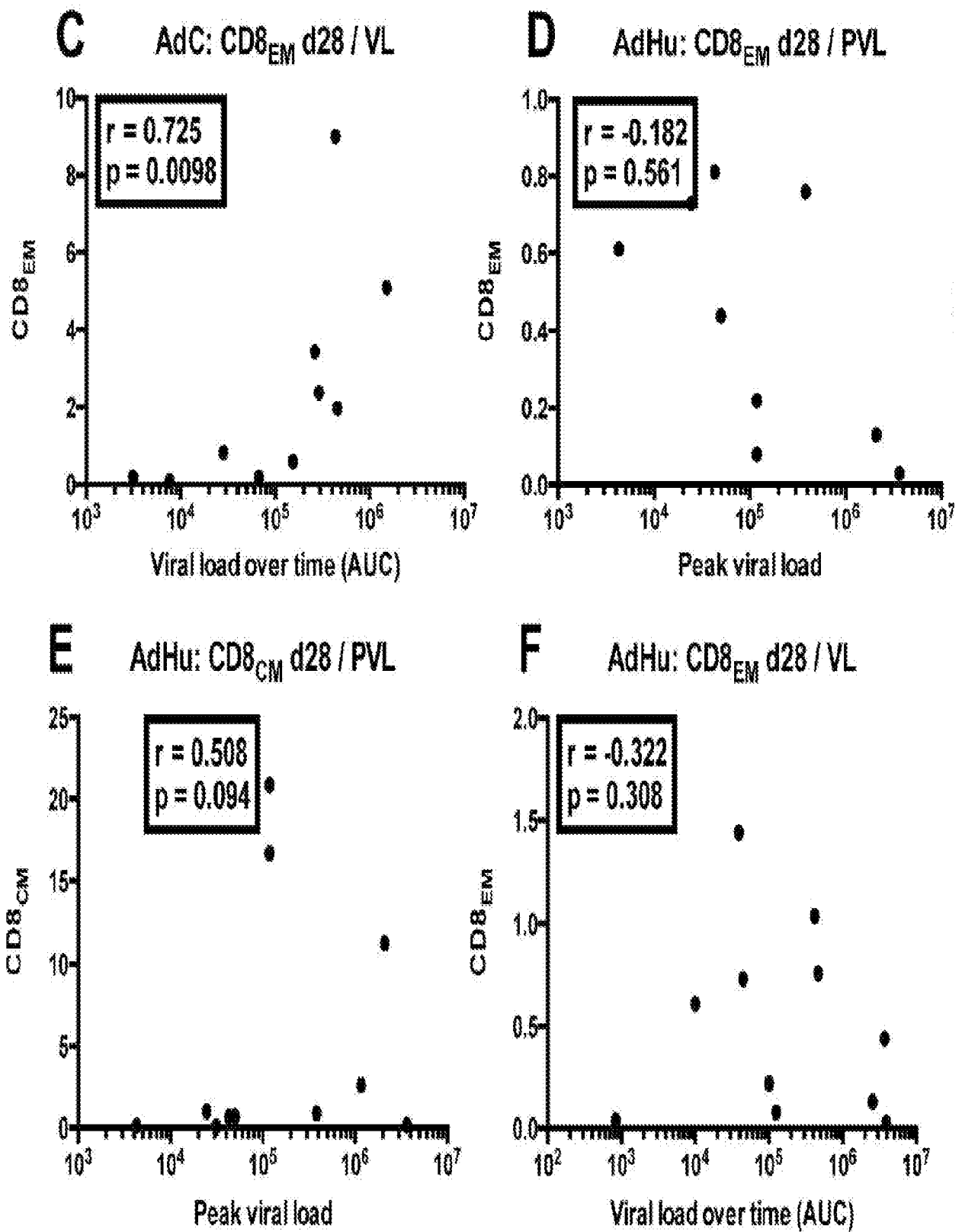


Fig. 11

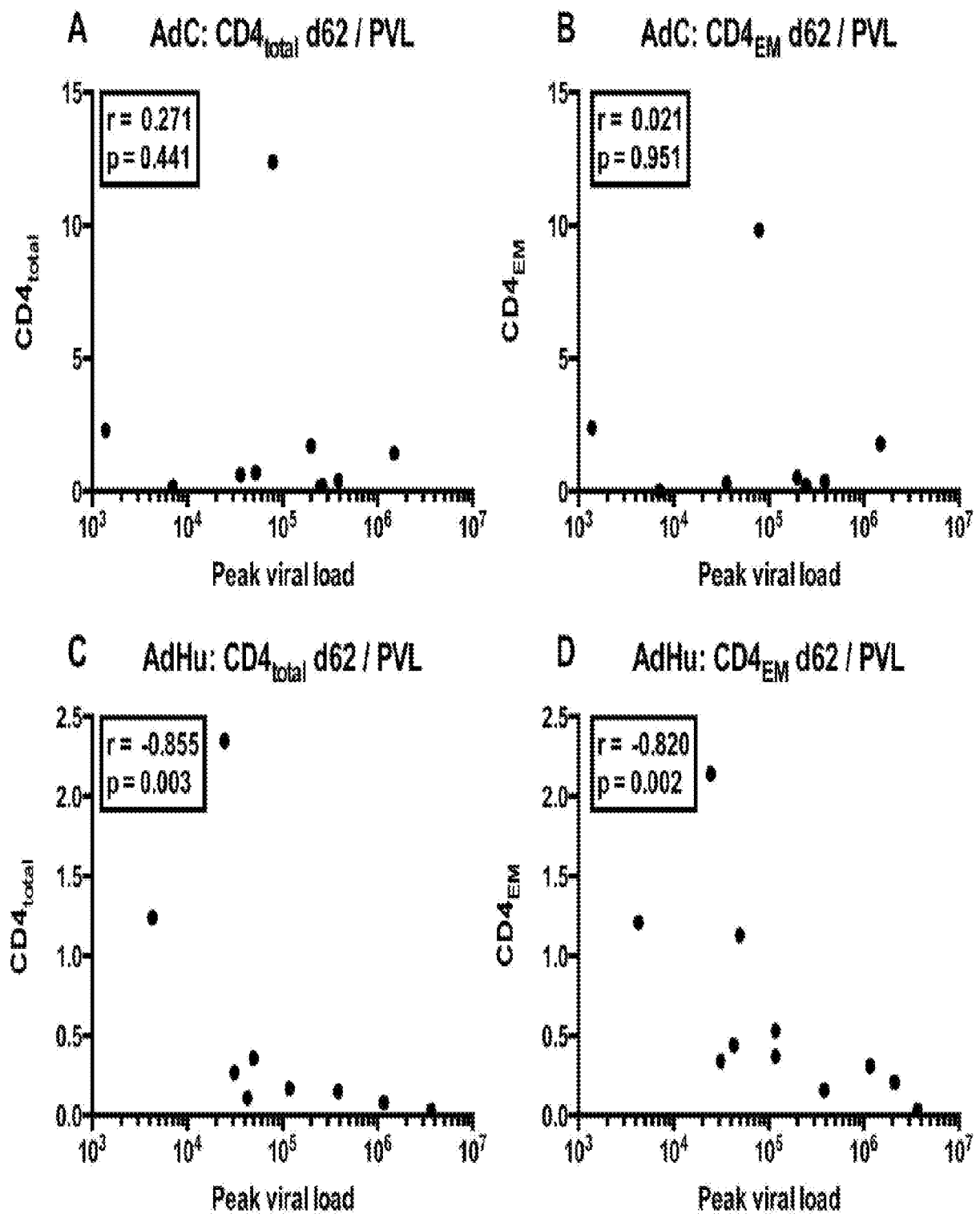


Figs. 12A-12B





Figs. 12C-12F



Figs. 13A-13D

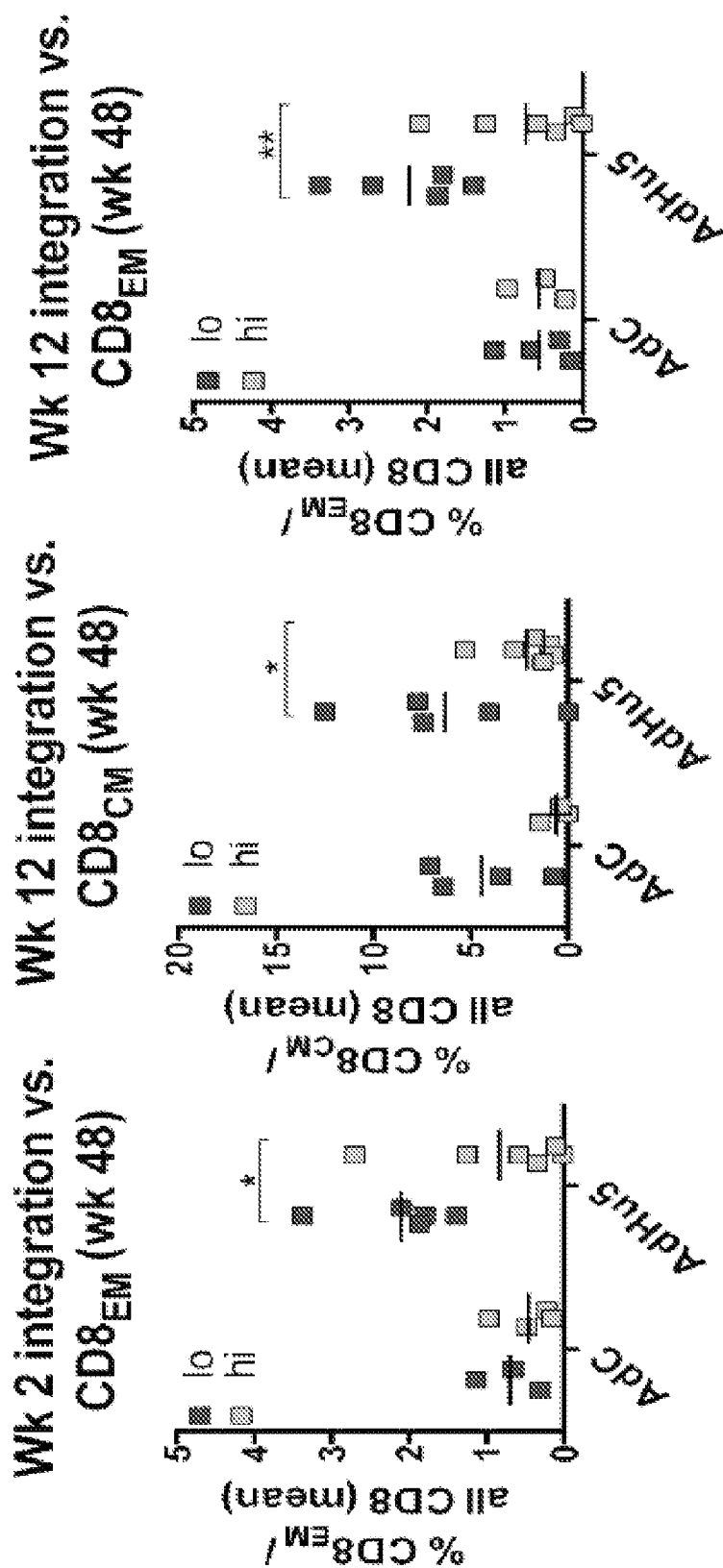
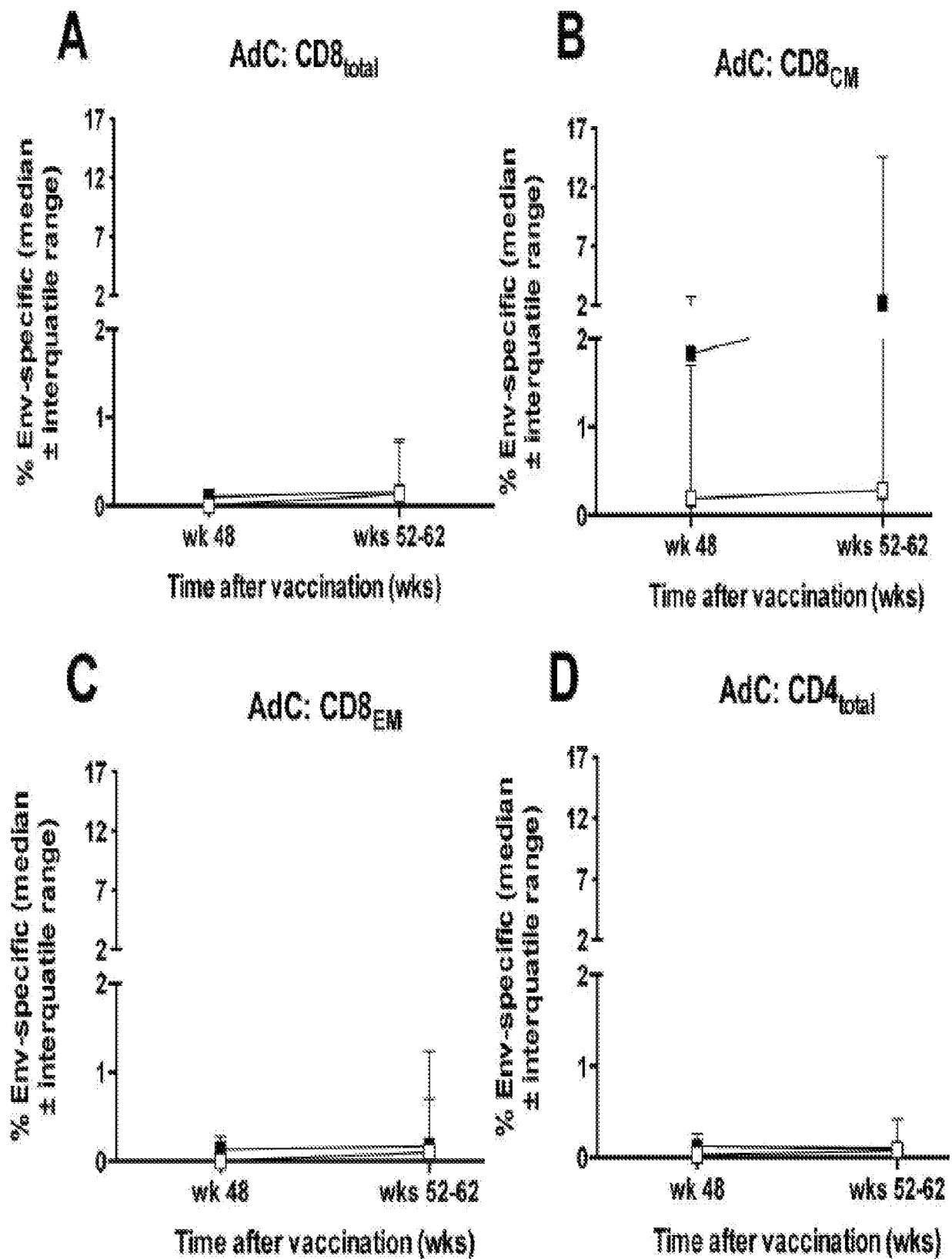
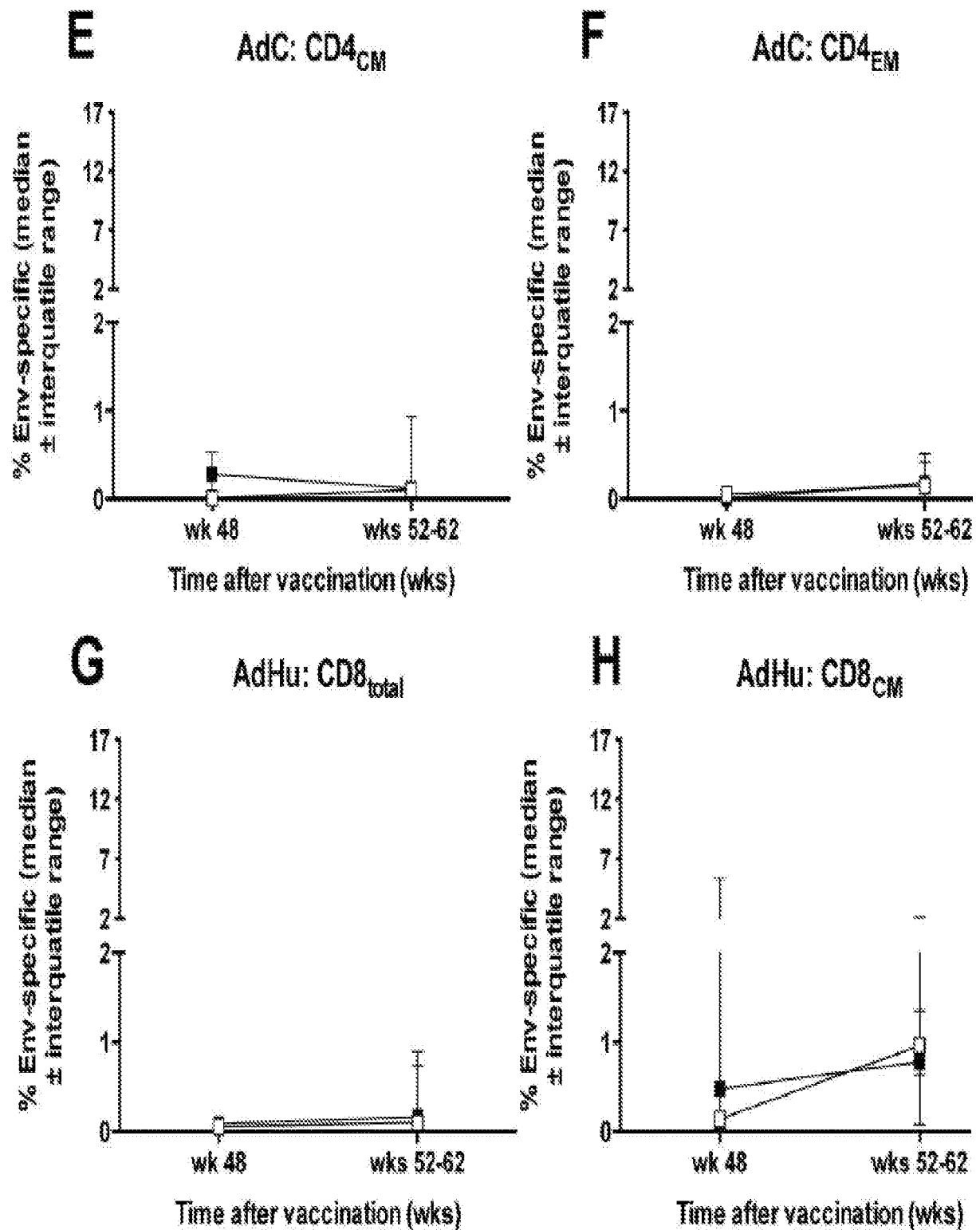


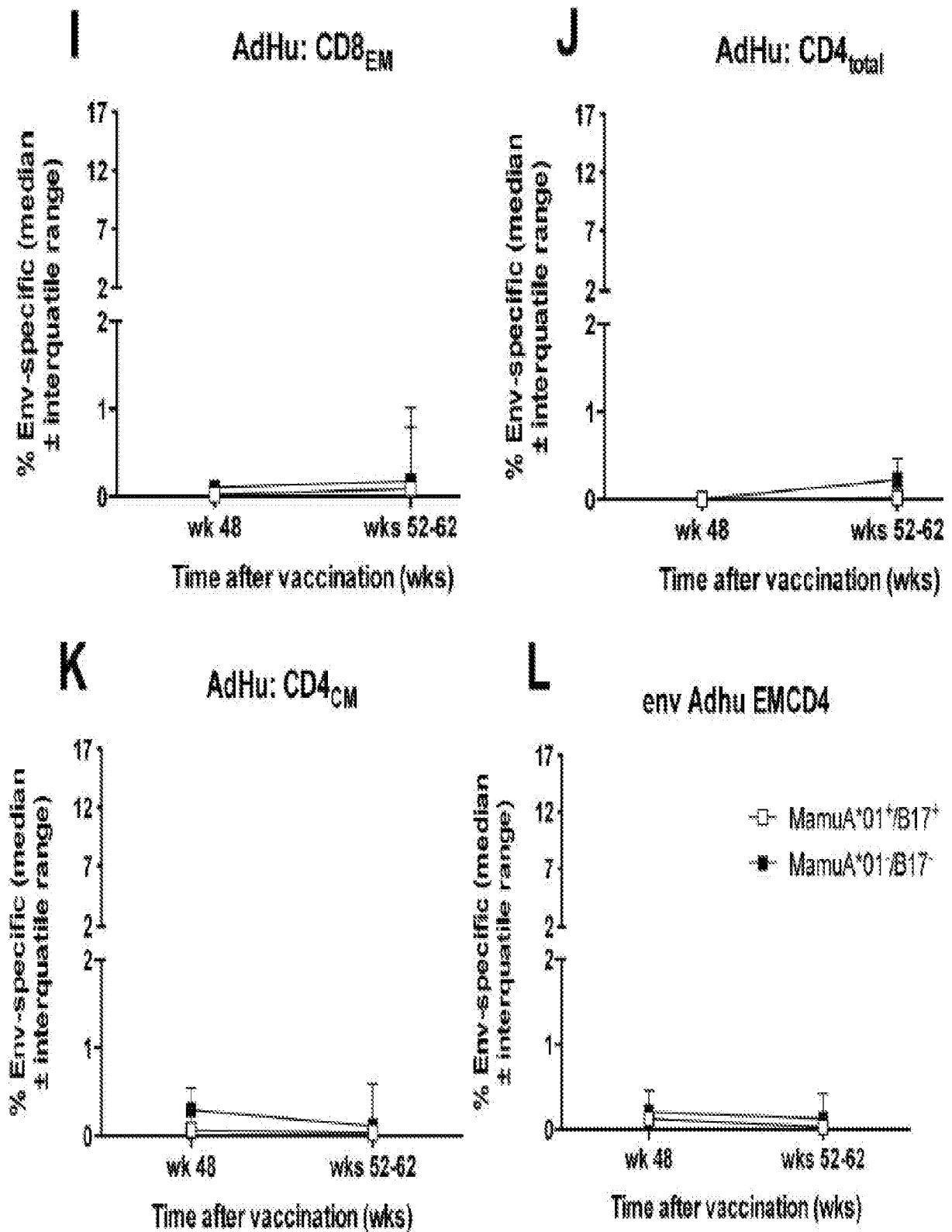
Fig. 14



Figs. 15A-15D



Figs. 15E-15H



Figs. 15I-15L

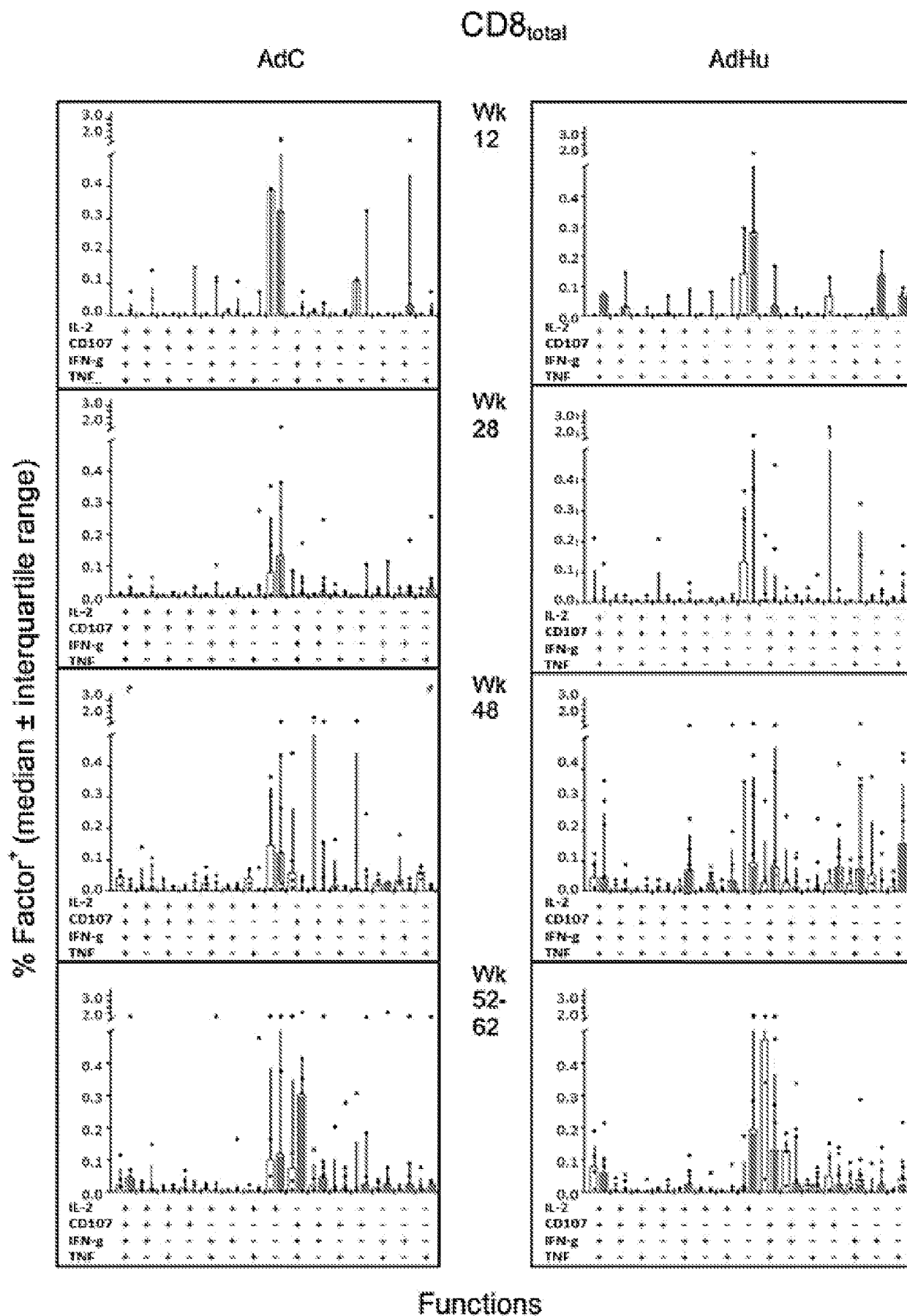


Fig. 16

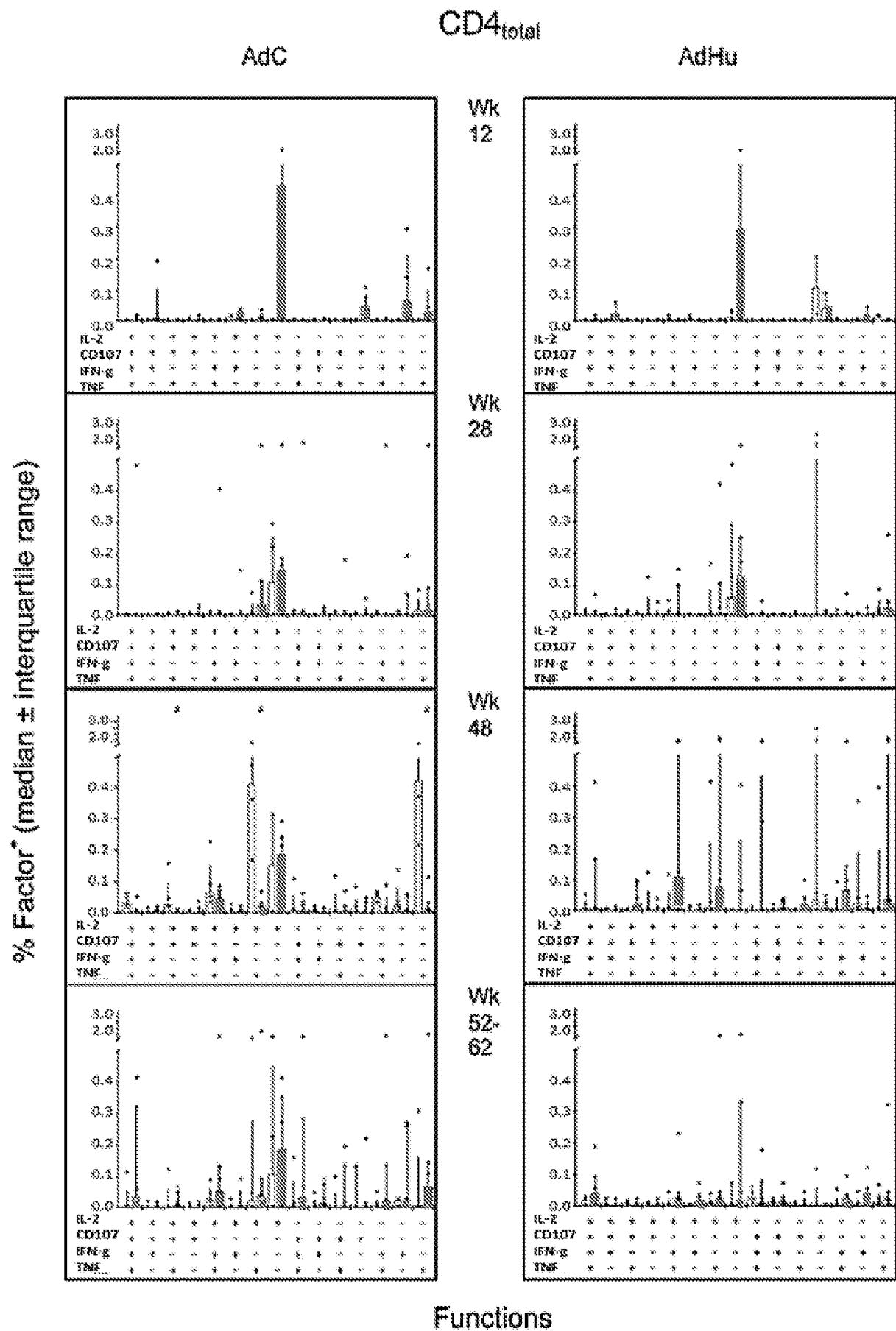


Fig. 17



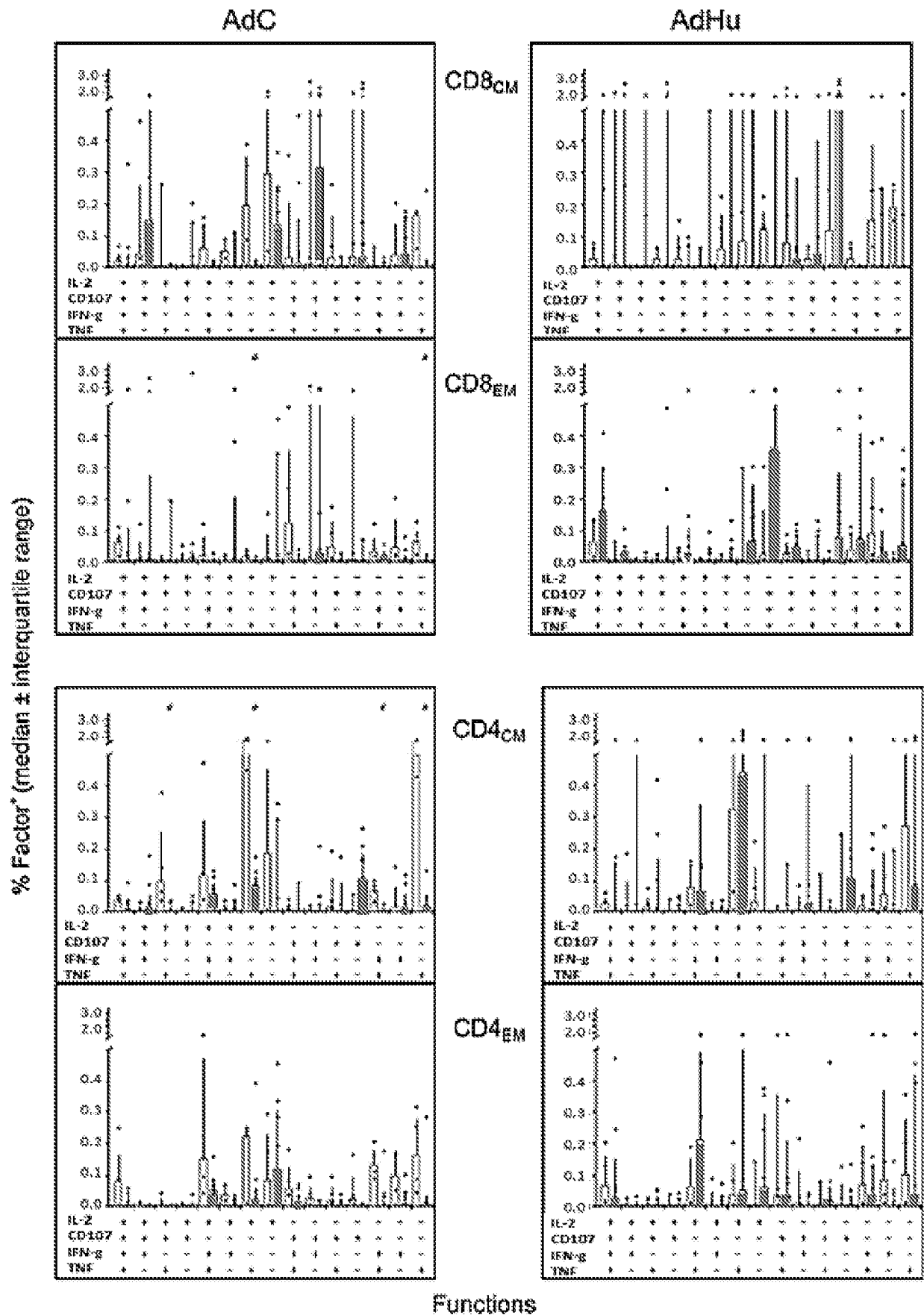


**Fig. 18**

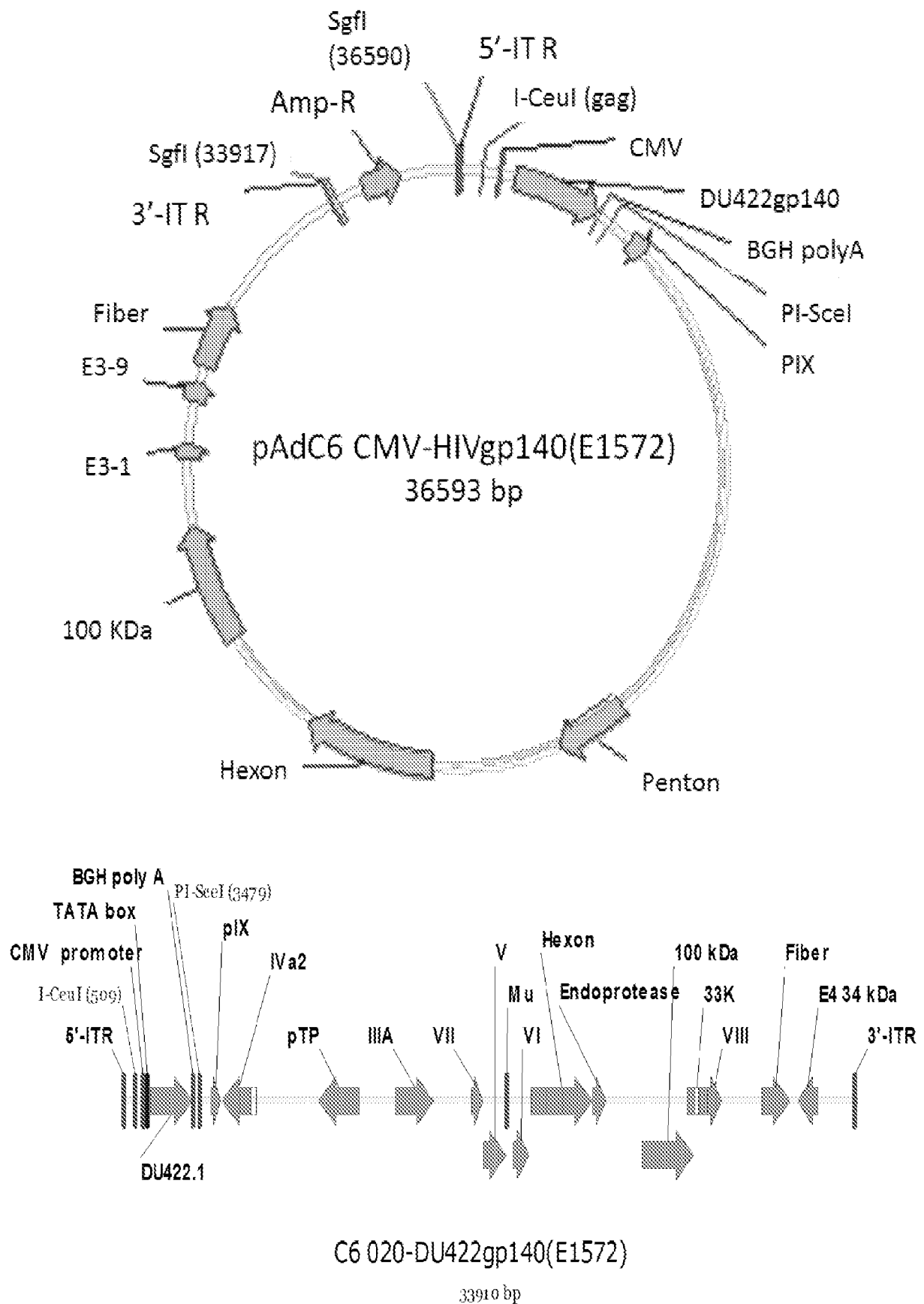


Fig. 19A

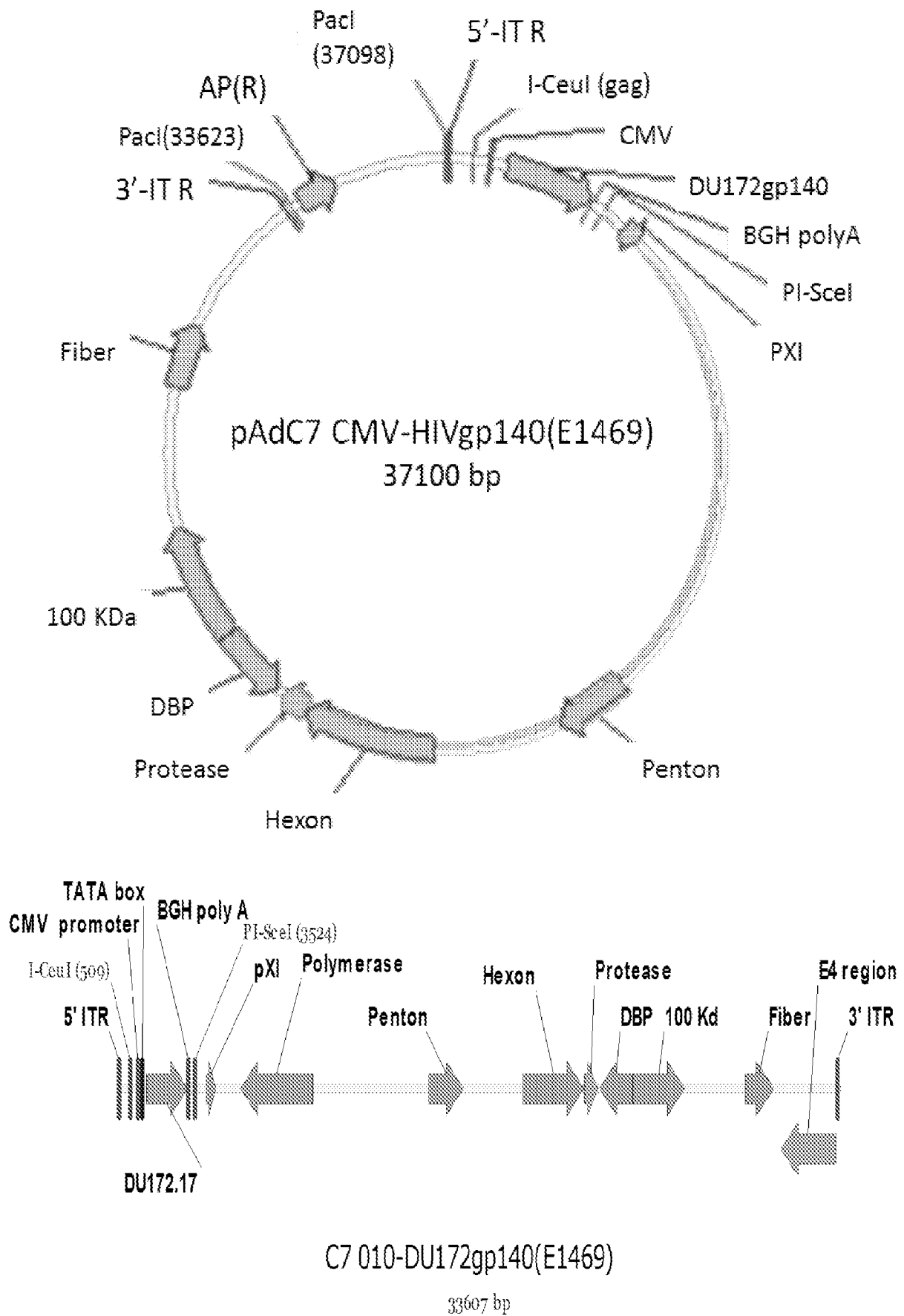


Fig. 19B

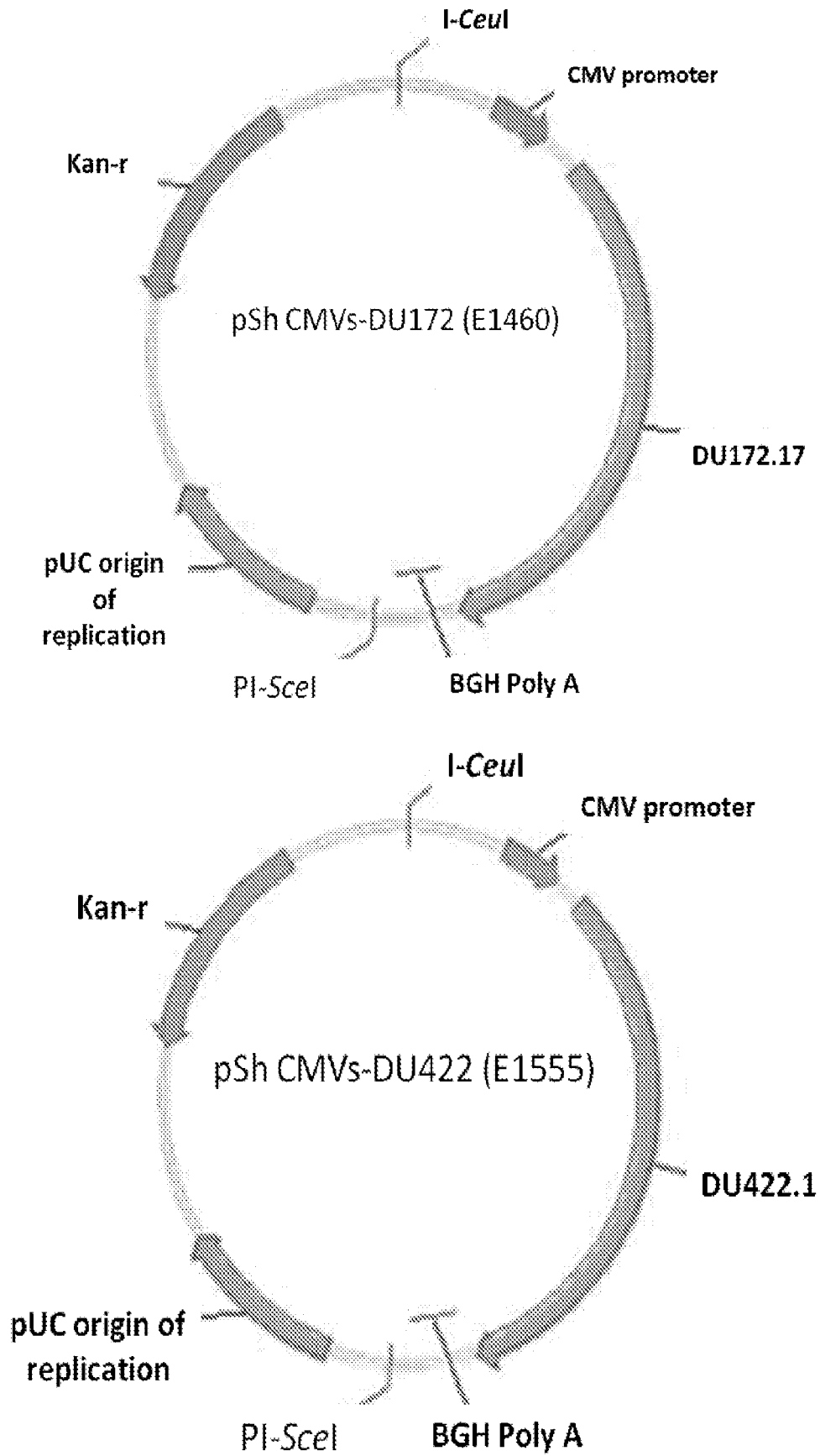


Fig. 19C

Fig. 20A

**AdC6 020-HIVgp140(E1572) Nucleic Acids - SEQ ID NO: 1**

CATCATCAATAATATACCTCAAACCTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCTGCGGGAGCGGCGACCGTTAGGGGCGGGGCGGGTGACGTTTTGATGACGTGGCTATGAGGCGGAGCCGGTTTGCAAG  
TTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTCCCGCGCTCTCTGACAGGAAATG  
AGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGGAAAACCTGAATGAGGAAGTGAAAATCTGAGTAATTTTC  
GCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTTC  
ACCTAAATTTCCGCGTACGGTGTCAAAGTCCGGTGTTTTACGTACGATATCATTTCCCGAAAAGTGCCACCTGACCGTAACTAT  
AACGGTCCTAAGGTAGCGAAAAGCTCAGATCTCCGATCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT  
AAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCT  
TGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGA  
CATTGATTATTGACTAGTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTAC  
ATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACA  
TCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCAAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTGGCACC  
AAAATCAACGGGACTTTCAAATGTCTGAACAACCTCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGT  
CTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAACGC  
AGTCAGTGCTTCTGACACAACAGTCTGAACCTTAAGGCTAGAGTTCGACGCCACCATGCGCGTGCGCGGCATCCCCGCAACT  
GGCCCCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATGATCATCATCTGCCGCGTGGTGGGCAACCTGGACCTGTGGGT  
GACCGTGTAACGCGGTGCCCGTGTGGAAGGAGGCCAAGACCACCCTGTTCTGCGCCTCCGACGCCAAGGCCTACGACAAG  
GAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCAAGGAGATCGTGCTGGAGAACGTGACCG  
AGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACGAGGACATCATCTCCCTGTGGGACCACTCCCTGAAGCC  
CTGCGTGAAAGTGACCCCCCTGTGCGTGACCCCTGAAGTGAAGAAGTGAACATCTCCGCCAACGCCAACGCCACCGCCACCC  
TGAACCTCTCATGAACGGCGAGATCAAGAACTGCTCCTTCAACACCACCCAGAGCTGCGCGACAAGAAGCAGAAGGTGTAC  
GCCCTGTTCTACAAGCCCCGACGTGGTGCCCTGAACGGCGGCGAGCACAACGAGACCGGCGAGTACATCCTGATCAACTGCA  
ACTCCTCCACCATCACCCAGGCTGCCCAAGGTGTCCTTCGACCCCATCCCCATCCACTACTGCGCCCCCGCGGCTACGCCAT  
CCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGCCCTGCAACAACGTGTCCACCGTGCACTGCACCCACGGCATCAAGC  
CCGTGGTGTCCACCCAGCTGCTGCTGAACGGCTCCTGGCCGAGGAGGAGATCATCTGCGCTCCGAGAACCTGACCAACAAC  
ATCAAGACCATCATCTGTCACCTGAACAAGTCCGTGGAGATCAAGTGCACCCGCCCAACAACAACACCCGCAAGTCCGTGCG  
CATCGGCCCGGCCAGACCTTCTACGCCACCGGCGAGATCATCGCGACATCCGCGAGGGCCACTGCAACATCTCCCGCGAGA  
CCTGGAACCTCACCCCTGATCCAGGTGAAGGAGAAGCTGCGCGAGCACTACAACAAGACCATCAAGTTCGAGCCCTCCTCCGGC  
GGCGACCTGGAGGTGACCACCACTCCTTCAACTGCCGCGGCGAGTTCTTCTACTGCGACACCACCAAGCTGTTCAACGAGAC  
CAAGCTGTTCAACGAGTCCGAGTACGTGGACAACAAGACCATCATCCTGCCCTGCCGATCAAGCAGATCATCAACATGTGGC  
AGGAGGTGGGCCGCGCCATGTACGCCCCCCCCATCGAGGGCAACATCACTGCAAGTCCAACATCACCGGCCTGCTGCTGACC  
TGGGACGGCGGCGAGAACTCACCGAGGGCGTGTTCGCCCCGGCGGCGGCAACATGAAGGACAACCTGGCGCTCCGAGCTG  
TACAAGTACAAGGTGGTGGAGATCAAGCCCCGCGGTGGCCCCACCAAGTCCAAGCTGACCGTGACGGCCCGCCAGCTGC  
TGTCGGGCATCTGTCAGCAGCAGTCCAACCTGCTGCGCGCATCGAGGCCAGCAGACCTGCTGCAGCTGACCGTGTGGGG  
CATCAAGCAGCTGCAGACCCGCGTGTGGCCATCGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCCTGTGGGGCTGCTCC  
GGCAAGCTGATCTGCGCCACCGCCGTGCCCTGGAACCTCCTCTGGTCCAACAAGTCCCTGGGCGACATCTGGGACAACATGAC  
CTGGATGCAGTGGGACCGCGAGATCTCCAATACACCAACACCATCTTCCGCTGCTGGAGGACTCCAGAACCAAGCAGGAGA  
AGAACGAGAAGGACCTGCTGGCCCTGGACTCCTGGAAGAACCTGTGGAACCTGGTTCGACATCAACCACTGGCTGTGGTAAGG  
TACCTCTAGAGTCGACCCGGGCGGCCAAACCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTGCCCC  
TCCCCGTCCTTCTTGACCCTGGAAGGTGCCACTCCACTGTCTTTCTAATAAAATGAGGAAATTCATCGCATTTGTCTGA  
GTAGGTGTCAATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCT  
GGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCAGATCTGCAGATCTGAATTCATCTATGTGCGGTGCGG  
AGAAAGAGGTAATGAAATGGCATTATGGGTATTATGGGTCTGCATTAATGAATCGGTCAGATATCGACATATGCTGGCCACCG  
TGCATGTGGCCTCGACCCCCGCAAGACATGGCCCGAGTTCGAGCACAACGTCATGACCCGCTGCAATGTGCACCTGGGCTCC  
CGCCGAGGCATGTTTCATGCCCTACCAAGTGAACATGCAATTTGTGAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAG  
CCTGACGGGGGTGTTTGACATGAATGTGGAGCTGTGGAAAATCTGAGATATGATGAATCCAAGACAGGTGCCGGGCCTGC  
GAATGCGGAGGCAAGCAGCCAGGCTTCAGCCCGTGTGTGTGGAGGTGACGGAGGACCTGCGACCCGATCATTTGGTGTGT  
CCTGCAACGGGACGGAGTTCGGCTCCAGCGGGGAAGAATCTGACTAGAGTGAGTAGTGTGTTGGGGCTGGGTGTGAGCCTGC

Fig. 20B

ATGAGGGGCAGAATGACTAAAATCTGTGGTTTTCTGTGTGTTGCAGCAGCATGAGCGGAAGCGCCTCCTTTGAGGGAGGGGT  
ATTCAGCCCTTATCTGACGGGGCGTCTCCCTCCTGGGCGGGAGTGCCTCAGAATGTGATGGGATCCACGGTGGACGGCCGG  
CCCGTGACGCCCGGAACCTCTCAACCCTGACCTACGCGACCCTGAGCTCCTCGTCCGTGGACGCAGCTGCCGCCGAGCTGCT  
GCTTCCGCCGCCAGCGCCGTGCGCGGAATGGCCCTGGGCGCCGGCTACTACAGCTCTCTGGTGCCAACTCGAGTTCACCAA  
TAATCCCGCCAGCTGAACGAGGAGAAGCTGCTGCTGCTGATGGCCAGCTCGAGGCCCTGACCCAGCGCCTGGGCGAGCTG  
ACCCAGCAGGTGGCTCAGCTGCAGGCGGAGACGCGGGCCGCGGTTGCCACGGTGAAAACCAAATAAAAAATGAATCAATAA  
ATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTTGAATCTTTATTTGATTTTCGCGCGCGGTAGGCCCTGGACCACGG  
TCTCGATCATTGAGCACCCGGTGGATCTTTCCAGGACCCGGTAGAGGTGGGCTTGATGTTGAGGTACATGGGCATGAGCCC  
GTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGTGCTCGGGGATGGTGTGTAATCACCCAGTCATAGCAGGGGCGC  
AGGGCGTGCTGCTGCACGATGCTCTGAGGAGGAGACTGATGGCCACGGGCAGCCCTTGGTGTAGGTGTTGACGAACCTGT  
TGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGATGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTCCCGCCAGATC  
CCGCCGGGGTTTCATGTTGTGACGAGACCACAGCACGGTGTATCCGGTGCACCTGGGGAATTTGTCATGCAACTTGGAAAGG  
AAGGCGTGAAAGAATTTGGAGACGCCCTTGTGACCGCCAGGTTTTTCATGCACTCATCCATGATGATGGCGATGGGCCGTG  
GGCGGGCGCCTGGGCAAAGACGTTTCGGGGGTGCGACACATCGTAGTTGTGGTCCTGGGTGAGCTCGTCATAGGCCATTTTA  
ATGAATTTGGGGCGGAGGGTGGCGACTGGGGACGAAGGTGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGC  
ATCTCCAGGCCTTGAGCTCGGAGGGGGGATCATGTCCACCTGCGGGGCGATGAAAAAACGGTTTCGGGGCGGGGGAG  
ATGAGCTGGGCCGAAAGCAGGTTCCGGAGCAGCTGGGACTTGCCGCAACCGGTGGGGCCGTAGATGACCCCGATGACCGGC  
TGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCTCGCGAGGAGGGGGCCACCTCGTTCATCATCTCGCGCACATGCA  
TGTTCTCGCGCACGAGTTCGCCAGGAGCGCTCGCCCCAGCGAGAGGAGCTTTCAGCGAGGCGAAGTTTTTCAGCGG  
CTTGAGTCCGTGCGCCATGGGCATTTTGAGAGGGTCTGTTGCAAGAGTTCAGACGGTCCAGAGCTCGGTGATGTGCTCTA  
GGGCATCTCGATCCAGCAGACCTCCTCGTTTCGCGGGTGGGGCGACTGCGGGAGTAGGGCACCGATGGGCGTCCAGC  
GAGGCCAGGGTCCGGTCTTCCAGGGCCGAGGGTCCGCGTCAGCGTGGTCTCCGTACGGTGAAAGGGTGCGCGCCGGG  
TGGGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCGGCTGGTTCGAGAACCGTCCCGGTGCGCGCCCTGCGCGTGGCCAGGT  
AGCAATTGAGCATGAGTTCGTAGTTGAGCGCTCGGCCGCGTGGCCCTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGCAG  
ACGGGACAGAGGAGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGACTCGGGGGCGTAGGGCTCCGCGCCGC  
AGCTGGCGCAGACGGTCTCGCACTCCAGAGCCAGGTGAGGTGCGGGCGGTTGGGGTCAAAAACGAGGTTTCTCCGTGCTT  
TTTGATGCGTTTCTTACCTCTGCTCCATGAGCTCGTGCCCCGTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGA  
CTTTATGGGCGGTCTCGAGCGGGGTGCCGCGTCTCGTCTAGAGGAACCCGCCACTCCGAGACGAAGGCCCGGGTC  
CAGGCCAGCACGAAGGAGGCCACGTGGGAGGGGTAGCGGTCTTGTCCACCAGCGGTCCACCTTCTCAGGGTATGCAAG  
CACATGTCCCCCTCGTCCACATCCAGGAAGGTGATTGGCTTGAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGG  
TATAAAGGGGGCGGGCCCTGCTCGTCTCACTGTCTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCC  
CTCTGAAGGCGGGCATGACCTCGGCACTCAGGTTGTGAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTTGGA  
GACGCCTTTCATGAGCCCTCGTCCATTTGGTCAGAAAAGACGATCTTTTGTGTCGAGCTTGGTGCGAAGGAGCCGTAGA  
GGGCGTTGGAGAGCAGCTTGGCGATGGAGCGCATGGTCTGGTCTTTTCTTGTGCGCGCGTCTTGGCGGCGATGTTGAGC  
TGACGTACTCGCGGCCACGCACTTCCATTCCGGGAAGACGGTGGTGAGCTCGTCGGGCACGATTCTGACCCGCCAGCCGC  
GGTTGTGCAGGGTGATGAGGTCCACGCTGGTGGCCACCTCGCCGCGCAGGGGCTCGTTGGTCCAGCAGAGGCGCCGCCCTT  
GCGCGAGCAGAAGGGGGGCGAGCGGTCCAGCATGAGCTCGTGGGGGGGTGCGCTCCACGGTGAAGATGCCGGGCAGGA  
GCTCGGGGTGCAAGTAGCTGATGCAGGTGCCAGATTGTCCAGCGCCGCTTGCCAGTCGCGCACGGCCAGCGCGCGCTCGTA  
GGGGCTGAGGGGCGTGCCCCAGGGCATGGGTGCGTGAGCGCGGAGGCGTACATGCCGAGATGTCGTAGACGTAGAGGG  
GCTCTCGAGGACCCGATGTAGGTGGGTAGCAGCGCCCCCGCGGATGCTGGCGCGCACGTAGTCGTACAGCTCGTGCGA  
GGGCGGAGGAGCCCGTGCCGAGGTTGGAGCGTTGCGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGA  
GTTGGAGGAGATGGTGGGCTTTGGAAGATGTTGAAGTGGGCGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTA  
GGAGTCTGCACTTGGCGACGAGCTCGGCGGTGACGAGGACGTCCAGGGCGCAGTAGTCGAGGGTCTCTTGATGATGTC  
ATACTTGAGCTGGCCCTTCTGCTTCCACAGCTCGCGGTTGAGAAGGAACTCTTCGCGTCTTCCAGTACTTTCGAGGGGGAA  
CCCGTCTGATCGGCACGGTAAGAGCCACCATGTAGAACTGTTGACGGCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGA  
GGGCGTAAGCTTGCAGCGCTTGCAGGGAGGTGTGGGTGAGGGCGAAGGTGTGCGCACCATGACCTTGAGGAACTGGT  
GCTTGAAGTCGAGGTCTGCGAGCCGCCCTGCTCCAGAGTTGGAAGTCCGTGCGCTTCTGTAGGCGGGGTAGGCAAAGC  
GAAAGTAACATCGTTGAAGAGGATCTTCCCCGCGCGGGGCATGAAGTTGCGAGTGATGCGGAAAGGTGGGGCACCTCGGC  
CCGTTGTTGATGACCTGGGCGGCGAGGACGATCTCGTCAAGCCGTTGATGTTGTGCCCGACGATGTAGAGTTCACGAATC  
GCGGGCGGCCCTTGACGTGGGGCAGCTTCTGAGCTCGTCTAGGTGAGCTCGGCGGGTCTGCTGAGCCCGTGTGCTCGAG

[illegible]

Fig. 20D

TGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATCGACGGGTTTACAT  
GCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCGCAACGACAGGATGCACCGCGCGGTGAGCGC  
CAGCCGCCGGCGCGAGCTGAGCGACCAGGAGCTGATGCACAGCCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGG  
AGAGTACTTTGACATGGGCGCGGACCTGCGCTGGCAGCCCAGCCGCCGGGCCTTGAAGCTGCCGGCGGTTCCCCCTACGT  
GGAGGAGGTGGACGATGAGGAGGAGGAGGGCGAGTACCTGGAAGACTGATGGCGCGACCGTATTTTGTAGATGCAGCA  
ACAGCCACCGCCGCCGCTCTGATCCCGCATGCGGGCGGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATT  
GGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAATCCCGAAGCCTTTAGACAGCAGCCTCAGGCCAACCGGCTC  
TCGGCCATCCTGGAGGCCGTGGTGCCCTCGCGCTCGAACCCACGCACGAGAAGGTGCTGGCCATCGTGAACCGCGCTGGTGG  
AGAACAAGGCCATCCGCGGTGACGAGGCCGGGCTGGTGTAACGCGCTGCTGGAGCGCGTGCCCCGCTACAACAGACCA  
ACGTGCAGACGAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCGGTGTCGACGCGGAGCGGTTCCACCGCGAGTCGA  
ACCTGGGCTCCATGGTGGCGCTGAACGCCTTCTGAGCACGCAGCCCGCAACGTGCCCCGGGGCCAGGAGGACTACACCAA  
CTTCATCAGCGCGCTGCGGCTGATGGTGGCCGAGGTGCCCCAGAGCGAGGTGTACAGTCGGGGCCGGACTACTTCTTCAG  
ACCACTGCCAGGGCTTGAGACCGTGAACCTGAGCCAGGCTTTCAAGAACTTGCAGGGACTGTGGGGCGTGCAGGCCCGG  
TCGGGGACCGCGCGACGGTGTGAGCCTGCTGACGCCGAACCTCGCGCCTGCTGCTGCTGCTGGTGGCGCCCTTACGGACAG  
CGGCAGCGTGAGCCGCGACTCGTACCTGGGCTACCTGCTTAACCTGTACCGCGAGGCCATCGGACAGGCGCAGCTGGACGAG  
CAGACCTACCAGGAGATACCCACGTGAGCCGCGCGCTGGGCCAGGAGACCCGGGCAACCTGGAGGCCACCCTGAATTC  
TGCTGACCAACCGTGCAGAAAGATCCCGCCCCAGTACGCGCTGAGCACCGAGGAGGAGCGCATCCTGCGCTACGTGCAGCA  
GAGCGTGGGGCTGTTCTGATGCAGGAGGGGGCCACGCCAGCGCGGCGCTCGACATGACCGCGCGCAACATGGAGCCCAG  
CATGTACGCCCGCAACCGCCGTTTCATCAATAAGCTGATGGACTACTTGATCGGGCGGGCCCATGAACCTCGGACTACTTTAC  
CAACGCCATCTTGAACCCGCACTGGCTCCCGCCGCCGGGTTCTACACGGGCGAGTACGACATGCCCGACCCCAACGACGGGT  
TCCTGTGGGACGACGTGGACAGCAGCGTGTCTCGCCGCGTCCAGGAACCAATGCCGTGTGGAAGAAAGAGGGCGGGGACC  
GGCGGCCGTCTCGGCGCTGTCCGGTCGCGCGGGTGTCTGCGCGGGCGGTGCCGAGGCCGCCAGCCCTTCCGAGCCTGCC  
CTTTTCGTGAACAGCGTGCGCAGCAGCGAGCTGGGTGCGCTGACGCGACCGCGCCTGCTGGGCGAGGAGGAGTACCTGAAC  
GACTCCTTGTGAGGCCCCGAGCGCGAGAAGAACTTCCCAATAACGGGATAGAGAGCCTGGTGGACAAGATGAGCCGTGGA  
AGACGTACGCGCACGAGCACAGGGACGAGCCCCGAGCTAGCAGCGCAGGCACCCGTAGACGCCAGCGGCACGACAGGCAGC  
GGGACTGGTGTGGGACGATGAGGATTCCGCCGACGACAGCAGCGTGTGGACTTGGGTGGGAGTGGTGGTAACCCGTTCCG  
CTCACCTGCGCCCCGTATCGGGCGCTGATGTAAGAACTGAAAAAATAAAAGACGGTACTACCAAGGCCATGGCGACCAG  
CGTGCGTTCTTCTCTGTTGTTGTAGTAGTATGATGAGGCGCGTGTACCCGAGGGTCTCTCCTCGTACGAGAGCGTGATG  
CAGCAGGCGGTGGCGGCGCGATGCAGCCCCGCTGGAGGCGCCTTACGTGCCCCGCGGTACCTGGCGCTACGGAGGGG  
CGGAACAGCATTCTTACTCGGAGCTGGCACCTTGTACGATACCACCCGTTGTACCTGGTGGACAACAAGTCGGCAGACAT  
CGCCTCGTGAACCTACCAGAACGACCACAGCAACTTCTGACCACCGTGGTGCAGAACAAACGATTTACCCCCACGGAGGCCA  
GCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCCAGTGAACCAACATCATGCACACCAACATGCCAACGT  
GAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGGGTGTGGTCTCGCGCAAGACCCCCAACGGGGTGGATGATGATTAT  
GATGGTAGTCAGGACGAGCTGACCTACGAGTGGGTGGAGTTTGAGCTGCCGAGGGCAACTTCTCGGTGACCATGACCATCG  
ATCTGATGAACAACGCCATCATCGAACAATACTTGGCGGTGGGGCGGCAGAACGGGGTGTGGAGAGCGACATCGGCGTGA  
AGTTGCACACGCGCAACTTCCGGCTGGGTGGGACCCCGTGACCGAGCTGGTGTGTCGGGGCGGTGTACACCAACGAGGCCCT  
CCACCCCGACATCGTCTGCTGCCCCGCTGCGGCGTGGACTTCACCGAGAGCCGCTCAGCAACCTGCTGGGCATCCGCAAGC  
GGCAGCCCTTCCAGGAGGGCTTCCAGATCCTGTACGAGGACCTGGAGGGGGGCAACATCCCCGCGCTCTTGATGTGCAAGC  
CTACGAGAAAAGCAAGGAGGATAGCACCGCCGCGCGGACCGCAGCCGTGGCCACCGCCTTACCGAGGTGCGGGGCGATAA  
TTTTGCTAGCGCTGCGGCAGCGGCCGAGGCGGTGAAACCGAAAGTAAGATAGTCATCCAGCCGGTGGAGAAGGACAGCAA  
GGACAGGAGCTACAACGTGCTCGCGGACAAGAAAAACACCGCCTACCGCAGCTGGTACCTGGCCTACAACCTACGGCGACCCC  
GAGAAGGGCGTGCGCTCCTGGACGCTGCTACCACTCGGACGTACCTGCGGCGTGGAGCAAGTCTACTGGTCGCTGCCCCG  
ACATGATGCAAGACCCGTCACCTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGCGCGGAGCTCTGCCGTC  
TACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTACCTCGCTCACGCACGTCTTCAACCGC  
TTCCCCGAGAACCAGATCCTCGTCCGCCGCCCGCGCCACCATTACCACCGTCAGTGAACACGTTCTGCTCTCACAGATCAC  
GGGACCCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGCGTGACCGTCACTGACGCCAGACGCCGACCTGCCCTACG  
TCTACAAGGCCCTGGGCGTAGTCGCGCCGCGCGTCTCTCGAGCCGCACCTTCTAAAAATGTCCATTCTCATCTCGCCAGTA  
ATAACACCGGTTGGGGCTGCGCGCGCCAGCAAGATGTACGGAGGCGCTCGCAACGCTCCACGCAACACCCCGTGCAGCT  
GCGCGGGCACTTCCGCGTCCCTGGGGCGCCTCAAGGGCGCGTGCAGCTCGCGCACCAACCGTCGACGACGTGATCGACAG  
GTGGTGGCCGACGCGCGCAACTACACGCCGCCCGCGCGCCGCTCTCCACCGTGGACGCCGTATCGACAGCGTGGTGCCG



Fig. 20E

ACGCGCGCCGGTACGCCCCACCAAGAGCCGGCGGGCGGCATCGCCCGGGCGGACCGGAGCACCCCGCCATGCGCGCGG  
CGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAGACGCGCGGCCTCCGGCAGCA  
GCAGCGCCGGCAGGACCCGAGACGCGCGGCCACGGCGGGCGGGCGGCCATCGCCAGCATGTCCCGCCCGCGCGCGGCA  
ACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCCGTGCGCACCCGCCCCCTCGCACTTGAAGATGCTGACTT  
CGCGATGTTGATGTGTCCAGCGGCGAGGAGGATGTCCAAGCGCAAATAACAAGGAAGAGATGCTCCAGGTATCGCGCCTGA  
GATCTACGGCCCCGCGGCGGCGGTGAAGGAGGAAAGAAAGCCCGCAAACCTGAAGCGGGTCAAAAAGGACAAAAGGAGG  
AGGAAGATGACGGAAGTGTGGAGTTTGTGCGCGAGTTCGCCCCCGGGCGGCGGTGCAAGTGGCGGGGCGGAAAGTGAAAC  
CGGTGCTGCGGCCCGGCACACGGTGGTCTTACGCCCCGGCGAGCGTTCGGGCTCCGCCTCCAAGCGCTCCTACGACGAGGT  
GTACGGGGACGAGGACATCCTCGAGCAGGCGGTGAGCGTCTGGGCGAGTTTGCCTACGGCAAGCGCAGCCGCCCGCGCC  
CTTGAAAGAGGAGGCGGTGTCCATCCCGTGGACACGGCAACCCACGCCGAGCCTGAAGCCGGTGACCCTGCAGCAGGTG  
CTACCGAGCGCGGCGCCGCGCGGGGCTTCAAGCGGAGGGCGGCGAGGATCTGTACCCGACCATGCAGCTGATGGTGCCC  
AAGCGCCAGAAGCTGGAGGACGTGCTGGAGCACATGAAGGTGGACCCGAGGTGCAGCCCGAGGTCAAGGTGCGGCCCATC  
AAGCAGGTGGCCCCGGGCGTGGGCGTGACACCGTGGACATCAAGATCCCCACGGAGCCCATGGAACCGCAGACCGAGCCC  
GTGAAGCCCAGCACACCATGGAGGTGCAGACGGATCCCTGGATGCCAGCACACAGCTTCCACAGCACTCGCCGAAGAC  
GCAAGTACGGCGCGGCCAGCCTGCTGATGCCAACTACGCGCTGCATCCTTCCATCATCCCCACGCCGGGCTACCGCGGCACG  
CGTTCTACCGCGCTACACCAGCAGCCGCCCGCAAGACCACCCCGCGCGTCTGTCGAGCCGCCGCGCAGCAGACCCGC  
GACTTCCGCTTGGTGCGGAGAGTGTATCGCAGCGGGCGCGAGCCTCTGACCTGCCGCGCGCGCTACACCCGAGCATC  
GCCATTTAACTACGCCTCTACTTGCAGATATGGCCCTCATATGCCGCTCCGCGTCCCCATTACGGGTACCGAGGAAGAAA  
GCCGCGCGGTAGAAGGCTGACGGGGAACGGGCTGCGTCGCCATCACACCGCGCGGCGCGCCATCAGCAAGCGGTTGGG  
GGGAGGCTTCTGCCGCGCTGATCCCCATCATCGCCGCGCGATCGGGGCGATCCCCGGCATAGCTTCCGTGGCGGTGCAG  
GCCTCTCAGCGCCACTGAGACACAAAAAGCATGGATTTGTAATAAAAAAAATGGACTGACGCTCCTGGTCTGTGATGT  
GTGTTTTAGATGGAAGACATCAATTTTTCGTCCTGGCACCGCGACACGGCACGCGGCCGTTTATGGGCACCTGGAGCGACA  
TCGGCAACAGCCAACTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGAGCGGGCTTAAGAATTCGGGTCCACGCTCAA  
AACCTATGGCAACAAGGCGTGGAACAGCAGCACAGGGCAGGCGCTGAGGGAAAAGCTGAAAGAACAGAACTTCCAGCAGAA  
GGTGGTTGATGGCCTGGCCTCAGGCATCAACGGGGTGGTTGACCTGGCCAACAGGCGGTGCAGAAACAGATCAACAGCCGC  
CTGGACGCGGTCCCGCCCCGCGGGTCCGTGGAGATGCCCCAGGTGGAGGAGGAGCTGCCTCCCCTGGACAAGCGCGGCGAC  
AAGCGACCGGTCCCGACGCGGAGGAGACGCTGCTGACGCACACGACGAGCGCCCGCTACGAGGAGGCGGTGAAACTG  
GGCCTGCCACACGCGGCCCGTGGCGCCTCTGGCCACCGGAGTGCTGAAACCCAGCAGCAGCCAGCCCGCGACCTGGACT  
TGCTCCGCTCGCCCTCCACAGTGGCTAAGCCCTGCCCGGTGGCCGTGCGTGCAGCGCCCCCGAGGCCGCCCGCAG  
GCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGGGAGTGAGAGTGTGAAGCGCGCGCGTCTATTAAAAAGACAC  
TGTAAGCGCTTAACCTGCTTGTGTGTATGTATGTCCGCCGACCAGAAGGAGGAGTGTGAAGAGGCGCGTCCCGAGTT  
GCAAGATGGCCACCCATCGATGCTGCCCCAGTGGGCGTACATGCACATCGCCGACAGGACGCTTCGGAGTACCTGAGTCC  
GGGTCTGGTGCAGTTCGCCCCGCGCACAGACACCTACTTCAGTCTGGGGAACAAGTTAGGAACCCACGGTGGCGCCACGC  
ACGATGTGACCACCGACCGCAGCCAGCGGTGACGCTGCGCTTCGTGCCCGTGGACCGGAGGACAACACCTACTCGTACAA  
AGTGCGCTACACGTGGCCGTGGGCGACAACCGGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGTGGAC  
CGGGGCCCTAGCTTCAAACTACTCTGGCACCGCTACAACAGCCTAGTCCCAAGGGAGCTCCCAATTCAGCCAGTGGGA  
GCAAGCAAAAACAGGCAATGGGGGAACATGGAACACACACATATGGTGTGGCCCCAATGGGCGGAGAGAATATTACAAA  
AGATGGTCTTCAAATTGGAAGTACGTTACAGCGAATCAGAATAAACCAATTTATGCCGACAAAACATTTCAACAGAACCGC  
AAGTAGGAGAAGAAAATTGGCAAGAACTGAAAACCTTTATGGCGGTAGAGCTCTAAAAAAGACACAAACATGAAACCTTG  
CTATGGCTCCTATGCTAGACCACCAATGAAAAAGGAGGTCAAGCTAACTTAAAGTTGGAGATGATGGAGTTCAAACCAAG  
AATTCGACATAGACCTGGCTTTCTTTGATACTCCCGGTGGCACCGTGAACGGTCAAGACGAGTATAAAGCAGACATTGTCATGT  
ATACCGAAAACACGTATTTGGAACTCCAGACACGCATGTGGTATACAAACCAGGCAAGGATGATGCAAGTTCTGAAATTAAC  
CTGGTTTACGAGTCTATGCCAACAGACCAACTACATTGGGTTCAGGGACAACCTTATCGGTCTTATGTAACACAGCACT  
GGCAATATGGGTGTGCTTGTGCTGAGGCTCCAGCTGAATGCTGTGGTTGATTGCAAGACAGAAAACCGAGCTGTCTTA  
CCAGCTCTTGTGCTTACTTTGGGTGACAGAACCCGGTATTTAGTATGTGGAACAGGCGGTGGACAGTTATGACCCCGATG  
TGCGCATCATGAAAACCATGGTGTGGAGGATGAATTGCCAACTATTGCTTCCCCTTGGACGGCTCTGGCACTAACGCCGCA  
TACCAAGGTGTGAAAGTAAAGATGGTCAAGATGGTGATGTTGAGAGTGAATGGGAAAATGACGATACTGTTGCAGCTCGAA  
ATCAATTATGTAAGGTAAATTTTCGCCATGGAGATTAATCTCCAGGCTAACCTGTGGAGAAGTTTCTCTACTCGAACGTGG  
CCCTGTACCTGCCCCGACTCTACAAGTACAGCCGACCAACGTACGCTGCCGACCAACACCAACACCTACGATTACATGAATG  
GCAGAGTGACACCTCCCTCGTGGTAGACGCTACCTAACATCGGGGCGCGTGGTGTGCGTGGACCCCATGGACAACGTCAAC

Fig. 20F

CCCTTCAACCACCAACGCGGGCCTGCGCTACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAG  
GTGCCCCAAAAGTTTTTCGCCATCAAGAGCCTCTGCTCCTGCCCGGTCTACACCTACGAGTGGAAGTTCGCAAGGACGTC  
AACATGATCCTGCAGAGCTCCCTAGGCAACGACCTGCGCACGGACGGGGCCTCCATCGCCTTACCAGCATCAACCTCTACGC  
CACCTTCTCCCATGGCGCACAAACCCGCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCTTCAACGA  
CTACCTCTCGGCGGCAACATGCTCTACCCCATCCCGGCAACGCCACCAACGTGCCATCTCCATCCCCTCGCGCAACTGGGC  
CGCCTTCCGCGGATGGTCTTACGCGCCTGAAGACCCGCGAGACGCCCTCGCTCGGCTCCGGGTTGACCCCTACTTCTGCTA  
CTCGGGCTCCATCCCCTACCTAGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTC  
AGCTGGCCCCGCAACGACCGCTCCTGACGCCCCACGAGTTCGAAATCAAGCGCACCGTCGACGGAGAGGGATACAACGTGG  
CCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCCACTACAACATCGGCTACCAGGGCTTCTACGTGCC  
GAGGGCTACAAGGACCGCATGTACTCTTCTCCGCAACTTCCAGCCCATGAGCCGCCAGGTCTGGACGAGGTCAACTACAA  
GGACTACCAGGGCGTCACCCTGGCTACCAGCACAACACTCGGGCTTCGTGCGCTACCTCGCGCCACCATGCGCCAGGGCC  
AGCCCTACCCGCCAACTACCCTACCCGCTCATCGCAAGAGCGCGTCGCCAGCGTCACCCAGAAAAAGTTCCTCTGCGACC  
GGGTCTGTGGCGCATCCCCTTCTCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATGCTCTACGCCA  
ACTCCGCCACGCGCTAGACATGAATTTCAAGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTTCAAGTCTTCA  
CGTCGTCCGAGTGACCAAGCCCCACCGCGCGTCATCGAAGCGTCTACCTGCGCACGCCCTTCTCGGCCGCAACGCCACCA  
CCTAAGCCGCTCTTGCTTCTTGAAGATGACGGCGGGTCCGGCGAGCAGGAGCTCAGGGCCATCCTCCGCGACCTGGGCTGC  
GGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCCCTGGATTTCATGGCCCCGACAAGCTGGCTGCGCCATCGTGAACAC  
GGCCGGCCGCGAGACCGGGGCGAGCACTGGCTGGCCTTCGCTGGAACCCGCGCTCCACACATGCTACCTTCTGACCCCT  
TCGGGTTCTCGGACGAGCGCTCAAGCAGATCTACCAGTTCGAGTACGAGGGCTGCTGCGTCGACGCGCTTGGCCACCGA  
GGACCGTGTGTCACCTGAAAAAGTCCACCCAGACCGTGCAGGTCGCGCTCGGCCGCTGCGGGCTTCTGCTGTCATGT  
TCCTGCACGCTTCTGTCAGTGGCCCGACCGCCCATGGACAAGAACCCACCATGAAGTACTGACGGGGGTGCCAACGGC  
ATGCTCCAGTCGCCCCAGGTGGAACCCACCTGCGCCGCAACCAGGAAGCGCTCTACCGCTTCTCAATGCCCACTCCGCTAC  
TTTCGCTCCACCGCGCGCATCGAGAAGGCCACCGCTTCGACCGCATGAATCAAGACATGTAAAAAACCGGTGTGTGTAT  
GTGAATGCTTTATTATAATAAACAGCACATGTTATGCCACCTTCTCTGAGGCTCTGACTTTATTAGAAATCGAAGGGTTCT  
GCCGGTCTCGGCATGGCCCGCGGGCAGGGATACGTTGCGGAAGTGGTACTTGGGCAGCCACTGAACTCGGGGATCAGCAG  
CTTGGGCACGGGAGGTGCGGGAACGAGTCGCTCCACAGCTTGCAGGTGAGTTGAGGGCGCCAGCAGGTGCGGCGCGGA  
GATCTTGAATCGCAGTTGGGACCCGCGTTCGCGCGGAGAGTTGCGGTACACGGGGTTGCAGCACTGGAACACCATCAGG  
GCCGGTGCTTCACGTTGCCAGACCGTCGCGTCGGTGATGCCCTCCAGTCCAGATCCTCGGCGTTGGCCATCCGAAGGG  
GGTCATCTTGCAAGTCTGCGGCCCATGCTGGGCACGACCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATC  
ATCTGGGCTGCTCGGAGCTCATGCCCGGTACATGGCCTTCATGAAAGCTCCAGCTGGCGGAAGGCTGCTGCGCTTGCC  
GCCCTCGGTGAAGAAGACCCGCGAGGACTTGCTAGAGAACTGGTGGTGGCGCAGCCGGCGTCGTGCACGCAGCAGCGCGC  
GTGTTGTTGGCAGCTGCACACGCTGCGCCCCAGCGTTCTGGGTGATCTTGGCCGGTTGGGGTTCTCTTACGCGCGC  
GCTGCCCGTTCTCGCTCGCCACATCCATCTCGATAGTGTGCTCCTTCTGGATCATCACGGTCCCGTGCAGGCACCCGAGCTTGC  
CCTCGGCTTCTGGTGACGCGTGCAGCCACAGCGCGCAGCCGGTGCACTCCAGTTCTTGTGGCGATCTGGGAGTGCGAGTG  
CACGAAGCCCTGCAGGAAGCGGCCATCATCGCGTCAAGGTCTTGTGCTGGTGAAGGTGAGCGGGATGCCGCGGTGCTCC  
TCGTTACATACAGGTGGCAGATGCGGCGGTACACCTCGCCCTGCTCGGCATCAGCTGGAAGGCGGACTTCAGGTGCTCTC  
CACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCCATGCCCTTCTCCAGGCCGAAACGATCGGCAGGCTCAGGGGGTCT  
TCACCGCCATTGTCATCTAGTCGCGCGCCGAGAGTCAAGGGGTGCTTCTCGTCCAGGGTCTCAAACACTCGCTTGGCGTCT  
TCTCGATGATGCGCACGGGGGAAAGCTGAAGCCACGGCCGCGAGCTCCTCCTCGGCTGCTTTCTGCTCCTCGCTGTCTGG  
CTGATGTCTTCAAAGGCACATGCTTGGTCTTGGCGGGTTCTTTTTGGGCGGAGAGGGCGGCGCGATGTGCTGGGAGAGC  
GCGAGTTCTGTTACACGACTATTTCTTCTTGGCCGTGCTCCGAGACCACGCGCGGTAGGCATGCCTTCTTGGGGCA  
GAGGCGGAGGCGACGGGCTCTCGCGTTCCGCGGGCGGCTGGCAGAGCCCTTCCGCGTTCCGGGGTGGCTCCTGGCGGC  
GCTGCTCTGACTGACTTCTCCGCGGCCGCGCATTTGTTCTCTAGGGAGCAACAACAAGCATGGAGACTCAGCCATCGTCG  
CCAACATCGCCATCTGCCCCCGCGCCACCGCCGACGAGAACCAGCAGCAGAATGAAAGCTTAACCGCCCCGCGCCGAGCCC  
CACCTCCGACGCGCGGCCCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGACCTGGGCTACGTGACGCCCCGCGAG  
CACGAGGAGGAGCTGGCAGCGCGCTTTTACGCCCCGAAGAGAACCACCAAGAGCAGCCAGAGCAGGAAGCAGAGAACGA  
GCAGAACCAGGCTGGGCACGAGCATGGCGACTACCTGAGCGGGGAGAGGACGTGCTCATCAAGCATCTGCCCCGCAATG  
CATCATCGTCAAGGACGCGCTGCTCGACCGCGCCGAGGTGCCCTCAGCGTGGCGGAGCTCAGCCGCGCTACGAGCGCAAC  
CTTCTCTCGCGCGCGTGGCCCCAAGCGCCAGCCAAACGGCACCTGTGAGCCCAACCGCGCCTCACTTCTACCCGGTCTTC  
GCGGTGCCCCGAGGCGCTGGCCACCTACCACCTTTTTTCAAGAACCAAGGATCCCCGTCTCTGCGCGCCAACCGCACCCGC

Fig. 20G

GCCGACGCCCTGCTCAACCTGGGCCCCGGCGCCCGCTACCTGATATCACCTCCTTGAAGAGGTTCCCAAGATCTTCGAGGG  
TCTGGGCAGCGACGAGACTCGGGCCGGAACGCTCTGCAAGGAAGCGGAGAGGAGCATGAGCACCACAGCGCCCTGGTGGA  
GTTGGAAGGCGACAACGCGCGCCTGGCGGTCTCAAGCGCACGGTCGAGCTGACCCACTTCGCCTACCCGGCGCTCAACCTGC  
CCCCAAGGTCATGAGCGCGTCATGGACCAGGTGCTCATCAAGCGCGCTCGCCCTCTCGGAGGAGGAGATGCAGGACCC  
CGAGAGTTCGACGAGGGCAAGCCGTGGTCAGCGACGAGCAGCTGGCGCGCTGGCTGGGAGCGAGTAGCACCCCCAGAG  
CCTGGAAGAGCGGGCGCAAGCTCATGATGGCCGTGGTCTGGTGACCGTGGAGCTGGAGTGTCTGCGCCGCTTCTTGCCGAC  
GCGGAGACCCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGGCACGGGTTCTGCGCCAGGCTGCAAGATCTCCA  
ACGTGGAGCTGACCAACCTGGTCTCTACATGGGCATCTGACGAGAACCCTGGGGCAAAACGTGCTGCACACCACCTG  
CGCGGGGAGGCCCCGCGGACTACATCCGCGACTGCGTCTACCTGTACCTTGCCACACCTGGCAGACGGGCATGGGCGTGT  
GGCAGCAGTGCCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCTGCAAGAAGCTCAAGGCCCTGTGGACCGGGTT  
CGACGAGCGTACCACCGCTCGGACCTGGCCGACCTCATCTTCCCGAGCGCTGCGGCTGACGCTGCGCAACGGGTGCCCG  
ACTTTATGAGCCAAAGCATGTTGCAAACTTTGCTCTTTCATCTCGAACGCTCCGGGATCTGCCCGCCACCTGCTCCGCGCT  
GCCCTCGGACTTCGTGCCGCTGACCTTCCGCGAGTGCCCCCGCGCTCTGGAGCCACTGCTACTTGCTGCGCTGGCCAACTA  
CCTGGCCTACCACTCGGACGTGATCGAGGACGTGAGCGGGCAGGGTCTGCTGGAGTGCCACTGCCGCTGCAACCTCTGCACG  
CCGCAACGCTCCCTGGCCTGCAACCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGCCCCGGCGA  
CGGCGAGGGCAAGGGGGGTCTGAACTACCCCGGGGTGTGGACCTCGGCCTACTTGCGCAAGTTCGTGCCGAGGACTAC  
CATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCAGCGGCCAAGGCCGAGCTGTGGCCTGCGTCATCACCCAGGGGGC  
CATCTGGCCCAATTGCAAGCCATCCAGAAATCCGCGCAAGAATTCTGCTGAAAAAGGGCCACGGGTCTACTTGACCCCC  
AGACCGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCGAGGAAGCAGCAAGAAGCTGAAAGTGAGCTGCCGCCG  
CCGGAGGATTTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGGAGGAGGAGATGGAAGACTGGGACAGCACTCAGGCAG  
AGGAGGACAGCCTGCAAGACAGTCTGGAGGAGGAAGACGAGGTGGAGGAGGCAGAGGAAGAAGCAGCCGCCGACAGACC  
GTCGTCTCGGCGGAGAAAGCAAGCAGCACGGATACCATCTCGCTCCGGGTCCGGGTGCGGGCGGCCGGCCACAGTAG  
GTGGGACGAGACCGGGCGCTTCCCGAACCCACCCAGACCGGTAAAGAGGAGCGGCAGGGATACAAGTCTGGCGGGG  
GCACAAAAACGCCATCGTCTCTGCTTGAAGCTGCGGGGGCAACATCTCTTACCCGGCGCTACCTGCTTCCACCGCGG  
GGTGAACCTCCCCGCAACATCTTGCACTACTACCGTCACTCCACAGCCCTACTACTGTTTCCAAGAAGAGGCAGAAACCCA  
GCAGCAGCAGAAAAACAGCGGCAGCAGCAGCTAGAAAATCCACAGCGCGGCAGGTGGACTGAGGATCGCGGCGAACGAG  
CCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTTCCCACCTCTATGCCATCTTCCAGCAGAGTCGGGGGCAGGAGCAGG  
AACTGAAAGTCAAGAACCCTTCTGCGCTCGCTACCCGAGTTGTCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTC  
TCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGTCACTCTTAAAGAGTAGCCCGCGCCCGCCACACACGGAAAAAG  
GCGGGAATTACGTACCACTGCGCCCTTCCCGGACCATCATGAGCAAGAGATTCCACGCTTACATGTGGAGCTACCAG  
CCCCAGATGGGCTGGCCGCGCGCGCCAGGACTACTCCACCCGATGAAGTGGCTCAGTGCCGGGGCCCGCATGATCTC  
ACGGGTGAATGACATCCGCGCCACCGAAACAGATACTCTAGAACAGTCAGCGATCACCGCCACGCCCCGCCATCACCTTA  
ATCCGCGTAATTGGCCCGCGCCCTGGTGTACCAGGAAATCCCCAGCCACGACCGTACTACTTCCGCGAGACGCCAGGCC  
GAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCCGGCGGCGCCGCCCTGTGTGTCACCGCCCCGCTCAGGGTATAAAGCG  
GCTGGTGATCCGAGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAGCTCTTGGTGGTCTGCGACCTGACGGAGTCTTC  
CAACTCGCCGATCGGGGAGATCTTCTTACGCTCTGTCAGGCGTCTGACTTTGGAGAGTTCGTCTCGACGCCCGCTCG  
GGCGGCATCGGCACTCTCAGTTCTGTGGAGGAGTTCACCTCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCGGCCACTAC  
CCGGACGAGTTCATCCGAACCTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAATGTCCATGGTGGCGCAGCTG  
ACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGC  
TGCCCCGAGGAGCACCTCAGGGCCAGCCACGGAGTGCGGATCATCGTGAAGGGGGCTCGACTCCACCTGCTTCGGAT  
CTTCAGCCAGCGACCGATCTGGTCGAGCGCGAACAAGGACAGACCCTTCTACTTTGTACTGCATCTGCAACCACCCCGCCT  
GCATGAAAGTCTTTGTTGTCTGCTGTACTGAGTATAATAAAGCTGAGATCAGCGACTACTCCGACTCGATTGTGGTGTTC  
CTGCTATCAACCGGTCCCTGTTCTTACCGGGAACGAGACCGAGCTCCAGCTCCAGTGAAGCCCCACAAGAAGTACCTCACCT  
GGCTGTTCCAGGGTCCCCGATCGCGTTGTCAACCACTGCGACAACGACGGAGTCTGCTGAGCGGCCCTGCCAACCTTACTT  
TTTCCACCCGAGAAGCAAGCTCCAGCTCTTCAACCTTCTTCCCGGGACCTATCAGTGCGTCTCAGGACCTGCCATCACAC  
CTTCCACCTGATCCGAATACCACAGCGCCGCTCCCCGCTACTAACAACCAAACTACCCACCAACGCCACCGTCGCGACCTTTCC  
TCTGAATCTAATAACCACTACCGGAGGTGGCTTCTGCTGTTAGTGCTCCCCGTCCCGTCGACCCCCGGTCCCCACTCAGTCCCC  
CGAGGAGGTTGCAAAATGCAAAATCCAAGAACCTGGAATTCCTCAAATGCTACCGCAAAAAATCAGACATGCATCCAGCT  
GGATCATGATCATTGGGATCGTGAACATTCTGGCCTGCACCTCATCTCTTTGTGATTACCCCTGCTTTGACTTTGGTTGGAA  
CTCGCCAGAGGCGCTCTATCTCCCGCTGAACCTGACACACCACCACAGCAGCAACCTCAGGCACACGCACTACCAACCACCA

Fig. 20H

GCCTAGGCCACAATACATGCCATATTAGACTATGAGGCCGAGCCACAGCGACCCATGCTCCCCGCTATTAGTTACTTCAATCT  
AACCGGCGGAGATGACTGACCCACTGGCCAATAACAACGTCAACGACCTTCTCCTGGACATGGACGGCGCCTCGGAGCA  
GCGACTCGCCAACTTCGATTCGTGAGCAGCAGGAGAGAGCCGTCAAGGAGCTGCAGGACGGCAGATGCCATCCACCAAGTGC  
AAGAGAGGCATCTTCTGCCTGGTGAACAGGCCAAGATCTCTACGAGGTACCCAGACCGACCATCGCTCTCTACGAGCT  
CCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTGGAGTCAACCCCATCGTCATCACCAGCAGTGGGGGATACCAAGGGGT  
GCATCCACTGCTCCTGCGACTCCCCGACTGCGTCCACACTCTGATCAAGACCTCTGCGGCCTCCGCGACCTCTCCCATGAA  
CTAATCACCCCTTATCCAGTGAAATAAAGATCATATTGATGATGATTTAAATAAAAAAATAATCATTTGATTTGAAATAAAGA  
TACAATCATATTGATGATTTGAGTTTAAACAAAAATAAAGAATCACTTACTTGAAATCTGATACCAGGTCTCTGTCCATGTTTTCT  
GCCAACACCACCTCACTCCCTCTTCCAGCTCTGGTACTGACGGCCCCGGGGCTGCAAACTTCTCCACACGCTGAAGGGG  
ATGTCAAATTCCTCTGTCCCTCAATCTTCATTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGA  
CCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCTTCATCAACCCCCCTTCGTCTCTTCAGATGGATTCGAAGAG  
AAGCCCTGGGGTGTGTCCCTGCGACTGGCTGACCCCGTCAACCAAGAACGGGGAAATCACCTCAAGCTGGGAGAGG  
GGGTGGACCTCGACTCGTGGGAAAACTCATCTCAACACGGCCACCAAGGCCGCCGCCCTCTCAGTATTTCAAACAACACC  
ATTTCCCTTAAACTGCTGCCCTTTCTACAACAACATGGAATTTAAGCCTCAATGTCTCCACACCATTAGCAGTATTTCCAC  
ATTTAACACTTTAGGCATAAGTCTTGAAACGGTCTTACAGACTTCAAATAAGTTGTTGACTGTACAATAACTCATCTCTTACA  
TTCAGCTCAAATAGCATCACAGTAAAAACAGACAAAGGGCTATATTAACCTCCAGTGGAACAGAGGACTTGAGGCTAATAT  
AAGCTAAAAAGAGGACTAGTTTTGACGGTAATGCTATTGCAACATATATTGAAATGGCTTAGACTATGGATCTTATGATAG  
TGATGGAAAAACAGACCGTAATTACCAAAATGGAGCAGGATTAATTTTGATGCTAACAAAGCAATAGCTGTCAAACCTAG  
GCACAGGTTTTAAGTTTTGACTCGCTGGTGCCTTGACAGCTGGAACAAACAGGATGACAAGCTAACACTTTGGACTACCCCT  
GACCCAAGCCCTAATTGTCAATTACTTTAGACAGAGATGCCAAATTTACTCTCTGTCTTACAAAATGCGGTAGTCAAATACTAG  
GCACTGTGGCAGTGGCGGTGTTACTGTAGGATCAGCACTAAATCCAATTAATGACACAGTCAAAAGCGCCATAGTTTTCTTA  
GATTTGATTCGATGGTGTACTCATGTCAAACCTCATCAATGGTAGGTGATTACTGGAATTTAGGGAGGGACAGACCACTCAA  
AGTGTAGCCTATACAAATGCTGTGGGATTCATGCCAAATATAGGTGCATATCCAAAAACCAAAGTAAACACCTAAAAATAG  
CATAGTCAGTCAGGTATATTTAACTGGAGAACTACTATGCCAATGACACTAACCTAATTTCAATGGCACTGATGAAAAAGA  
CACAACCCCAAGTTAGCACCTACTCTATGACTTTTACATGGCAGTGGACTGGAGACTATAAGGACAAAAATATTACCTTTGCTAC  
CAACTCATTTCTTTTTCTACATCGCCAGGAATAATCCCACCCAGCAAGCCAACCCCTTTTCCACACCTTTGTCTATATGGA  
AACTCTGAACAGAAAAATAAGTTCAAGTGTGTTTATGAATCAACAGTTTTACAGGACTCGAGCAGTTATTTTCTCCACCT  
CCCAGGACATGGAATACACCAACCTCTCCCCCGCAGCGCTTGAACTGAACTGCAATGCCATTGGTGTCTTTTGCTCT  
CCACGTTCCACACAGTTTCAGAGCGAGCCAGTCTCGGATCGGTGAGGAGATGAAACCTCCGGGCACTCCCGCATCTGCACC  
TCACAGCTCAACAGCTGAGGATTGCTCTCGGTGGTGGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATC  
ATAGTCCGCGAACGGGATCGGCCGGTGGTGTGCATCAGGCCCGCAGCAGTCTGCTGCCGCCGCCGCTCCGTCAAGCTGCTG  
CTCAGGGGGTTCGGGTCCAGGACTCCCTCAGCATGATGCCACGGCCCTCAGCATCAGTCGTCTGGTGGCGGGCGCAGC  
AGCGCATGCGAATCTCGCTCAGGTCACTGCAGTACGTGCAACACAGGACCACAGGTTGTTCAACAGTCCATAGTTCAACACG  
CTCCAGCCGAACTCATCGCGGAAGGATGTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAAATCAAGTGGCGCTCCCT  
CCAGAAGACGCTGCCATGTACATGATCTCCTGGGCATGTGGCGGTTACCACTCCCGGTACCACATCACCTCTGGTTGAA  
CATGCAAGCCCGGATGATCTCGGGAACCAAGGCCAGCGCCCGCCCGCATGCAAGCAGAAGAGACCCCGATCCCGG  
CAATGACAATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCAGGCATAT  
GCTCATGATCTCTCAGCACTCTCAGTCTCTCGGGGTCAAAACCATATCCAGGGCACGGGGAATCTTGACAGGACAGCGA  
ACCCCGCAGAACAGGGCAATCCTCGACATAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTATCC  
TCCACAGAGAAGCGCGGGTCTCGGTCTCTCAGCGTGGTAAGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGCT  
GATCGTGTCTCGACCGTGTCTGATGCAAGTGTCTTCGGACATTTCTGTAATGCTGTAGCAGAACCTGGTCCGGGCGCTGCA  
CACCGATCGCGGGCGGGTCTCGGCGCTTGGAACGCTCGGTGTTAAAGTTGTAACACAGCCACTCTCTCAGACCGTGCAGCA  
GATCTAGGGCCTCAGGAGTATGAAGATCCCATCATCCTGATAGCTCTGATCACATCGACCACCGTGAATGGGCCAGGCCC  
AGCCAGATGATGCAATTTTGTGGTTTGGTGACGGCGGGGAGGGAAGAACAGGAAGAACCTGATTAATCTTAATCCA  
AACGGTCTCGGAGCACTTCAAATGAAGGTCAAGGATGAGGACCTCGACCTCTCGCCCCGCTGTGTTGGTGAATAACCAAG  
GTCAAAGGTGATACGGTCTCGAGATGTTCCACGGTGGCTTCAGCAAAGCCTCCACGCGCACATCCAGAAACAAGACAATAG  
CGAAAGCGGGAGGGTCTCTAATCTCAACCATCATGTTACACTCTGCACCATCCCCAGATAATTTTCATTTTCCAGCCTTG  
AATGATTGCAACTAGTTCTGAGGTAAATCCAAGCCAGCCATGATAAAAAGCTCGCGCAGAGCACCTCCACCGGCATTCTAA  
GCACACCTCATAATTCCAAGATATTCTGCTCCTGGTTACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGA  
TCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTTTTATATCGTCTCCGAAATTTTAGCCATAGGACCCCCAGGAATAA  
GAGAAGGGCAAGCCACATTACAGATAAACCGAAGTCCCCCAGTGAGCATTGCCAATGTAAGATTGAAATAAGCATGCTG  
GCTAGACCCGGTGATATCTCCAGATAACTGGACAGAAAAATCGGGTAAGCAATTTTAAGAAAAACAACAAAAAGAAATCTT  
CCAGGTGCAGTTTAGGGCTCGGGAACAACGATGGAGTAAGTGCAAGGGTGGTTCAGCATGGTTAGTTAGCTGATCTG  
TAAAAAACAACAAAAATAAACATTAACCATGCTAGCCTGCGGAACAGGTGGTAAATCGTTCTCTCCAGCACCAGCAGGCC  
ACGGGGTCTCCGGCGCGACCTCGTAAAAATGTGCTATGATTGAAAACCATCACAGAGAGACGTTCCGGTGGCCGGCGT  
GAATGATTGAGAAGAAGCATACCCCCGGAACATTGGAGTCCGTGAGTGAAAAAAGCGGCCGAGGAAGCAATGAGGCA  
CTACAACGCTCACTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAAATTTTCAAGTGCCTAAAAATGTAATTA  
CTCCCTCTGCAAGGCAGCGAAGCTCCGATCCCTCAGATACACATACAAAGCCTCAGCGTCCATAGCTTACCAGCGGCA  
GCAGCAGCGGCACACAACAGGCGCAAGAGTCAGAGAAAAGACTGAGCTCTAACCTGTCCGCCCGCTCTCTGCTCAATATATAG  
CCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAGCACAGCCAGAAACC  
GGTGACACACTCAGAAAAATACGCGCACTTCTCAACGGCCAACTGCCGTCAATTTCCGGGTTCACACGCTACGTCATCAAAA  
CACGACTTTCAAATTCGTCGACCGTTAAAAACATCACCGCCCCGCTAACGGTCGCGCTCCCGCAGCCAATCACCTTCT  
CCCTCCCCAAATTCAAACAGCTCATTTGCATATTAACGCGCACCAAAAGTTTGAGGTATATTATTGATGATG

Fig. 20I

**AdC6 020-HIVgp140(E1572) Amino acids – SEQ ID NO: 9****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVICGSGDR\*GRGG\*RFDDVAMRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFL  
GGCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDRLRGGFYRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RKLR  
PDPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMKNLRRVRRFALLRDVRARYTR\*H\*LLTSMPSTPPIDVN  
DGKWPAWHYAQYMTLWDFPTWQYIYVLVIAITMVMRWFQYINGRG\*RFDSRGFPSLHPIDVNGSLFWHQNRDFPKCRNNSA  
PLTQMGGRRVRWEVYISRARLVNRQITRSFIADVYHS\*IANAVSASDTTVSNLRLEFDATMRVRGIPRNWPQWWIWGILGFWMI  
CRVVGNDLWVTVYGVVWKEAKTTLFCASDAKAYDKEVHNWATHACVPTDNPQEIENVTFENFMWKNDMVDQMHE  
DIISLWDQSLKPCVKLTPLCVTLNCKNVNISANANATATLNSSMNGEIKNCSFNTTTEL RDKKQKVYALFYKPDVPLNGGEHNETGE  
YILINCNSSTITQACPKVSFDPPIHYCAPAGYAILKCNKTFNGTGPCNNVSTVQCTHGIKPVVSTQLLNGSLAEEEEIIVRSENLTNNIK  
TIIVHLNKSVEIKTRPNNNTRKSVRIGPGQTFYATGEIIGDIREAHCNISRETWNSTLIQVKEKLREHYNKTIKFEPSSGGDLEVTTHSF  
NCRGEFFYCDTTKLFNETKLFNESEYVDNKTIILPCRIKQIINMWQEVGRAMYAPPIEGNITCKSNITGLLTWDGGENSTEGVFRPG  
GGNMKDNWRSELYKYKVVEIKPLGVAPTSKLTQARQLLSGIVQQSNLLRAIEAQHLLQLTVWGKQLQTRVLAIERYLKQQQL  
LGLWGCSGLKICATAVPWNSSWSNLSLGDWDNMTWMQWDREISNYTNTIFRLLEDSDNQQEKNEKDLLALDSWKNLWNWF  
DITNLW\*GTSRVDPGGQTADQPRCLLVASHLLFAPPPCLP\*PWKVPLPSFPNKMRLHRIV\*VGVLFWGVGWGRTARGRIG  
KTIAGMLGMRWALWLLRRKEPADLQI\*IHLCRVRRKR\*\*NGIMGIMGLH\*\*IGQISTYAGHRACGLAPPQDMARVRAQRHDPLQ  
CAPGLPPRHVHALPVQHAICEGAAGARCHVQSEPDDGV\*HECGAVENSEI\*\*IQDQVPGLRMRRQARQASARVCGGDDGGPATRS  
FGVVLQRDGVRLQRGR\*LE\*VVFAGCEPA\*GAE\*LKSVFVCLQQHERKRL\*GRGIQPLSDGASPLLGCSASECDGIHGGPAR  
AARELFNPDRLDPPELLVRGRSCRRSCFRQRARRNGPGRRLQLSGGQLEFHQ\*SRQPERGEAAAADGPARGPDPAPGRADPAG  
GSAAGGDAGRGCHGENQIKNESINKRRRLILTQSLESLEDFSRVAGPGPPVSIIEHPVDLFQDPVEVGLDVEVHGHEPVPGEVAPL  
QGLVLGDGVVNHPIAGAQGVVLHDVLEEEDGHGQPLGVGVDEPVELGGMHAGGDEMHLGLDLEIGDVPAPQIPGVHVVD  
HQHGVSGALGEFVMQLGREGVKEFGDALVTAQVFHALIHDDGDGPVGGGLGKDVSGVGHIVVVVLGELVIGHFNEFGAEGARLG  
DEGALDPGGVVALADLHPLGLELGGGDHVLRGDEKNGFRGGGDELGRKQVPEQLGLAATGGAVDDPDRLQVVVEGETAAVL  
AEEGGHLVHHLAHMHVLAHEFRQEALAPQREELLQRGEVFQRLESVGHGHFGEGLLQEFQTVPELGDVL\*GISIQQTSSFRGLGRL  
RE\*GTRRWASSEARVRSFQGRVRVSVSVTVKGCAPGWALARVRFRILRLVENRSRSPACASAR\*QLSMSS\*LSASAAWPLARSL  
PLEVCPQTGQRDLRA\*SLGARKTDSGA\*ASAPQLAQTVSHSTSQVRSRGLSKTRFPFCFLMRFLPLVSMSSCPRWVTKRLSVSP\*  
TDFMGRSSSGVPRSS\*RNPAHSETKARVQASTKEATWEG\*RSLSSTSGTSRVCCKHMSPSSTSRKVI GL\*V\*AT\*PGVPAGGV\*KG  
AGPCSSSLSSGSLRSASCWGRYLSKAGMTSALRLSVSRNEEDLITVPLETFMSPSSIWSEKTI FLLSSLVAKEP\*RALESSLAMER  
MVWFFLSARSLAAMLSCYSRATHFHSGKTVSSSGTILTRQPRLCRVMRSTLVATSPRRGSLVQQRPPLEQKGGSGSSMSSSG  
GSASTVKMPGRSSGSK\*LMQVRLSSAACQSRASARS\*GLRGVPQGMGCVSAEAYMPQMS\*T\*RGSSRTPM\*VG\*QRPPRML  
ART\*SYSSCEGARSPVRLERCFSAR\*TIWRKMAWELEEMVGLWKMLKWAWGRPTESLMKWA\*ESCLATSSAVTRTSRAQ\*S  
RVSWMMSYLSWPFCHSSRLRRNSSRSFQYSSRGNPS\*SAR\*EPTM\*NWLTAL\*AQQPFSTGRA\*ACAALRREVWVRKVSRTM  
TLRNWCLKSRSSQPPCSQSWKSVRFL\*AGLGKAKVTSKRLILPARGMKLRVMRKGWGT SARLLMTWAARTISSKPLMLCPTM\*SS  
TNRGRPLTWGSFLSS\*VSSAGSLSPCCSRAQSATWGLALRKEVQRSTARAVCKRSRY\*RNCWPTAIFSGVTQ\*KVRGSPCQRSHLS  
WRARSWASSTSGGSPESFMTSMKGTSCLPKDIQV\*VSTS\*VRKSLSVRGCEPMGKNWISCHQLEEWLLM\*WK\*KCRRRAEHSC  
LCLYKRQCQSRCTGCTCTCTWVPLARNFSGQWSAGGCISCCTTSWPSAWPSSASMVVMLTSPRGRQVQTSARTGRRARTRA  
RRPELSRVLRRCGVRVSGGARLTCSRFSRARGRSRWYLISTAPLVATSTACRVPCPWGATTVPFRFLGAASMSVRSGGEDARRA  
AGAARGPEAGAAGARRRRARAGSGTAPGEDWRERRRDG\*RPGSDASG\*RPDP\*V\*T\*KVRQNRQSRYP\*RRPAAGSLARRPSC  
PGRRSRS\*TARSPPEGLRGRARRWPRGRWRCGP\*AARRRSCRPRRGRCPRLRRGRARA\*PPGRG\*ARRGA\*RRPSRCGAG  
RGS\*AWWRCAR\*RRST\*SSGGAASR\*RRPGLSPVPWPRRSPRS\*KTGSCAPRRSTPPPEDG\*ARRWWRAPRARRPRGAPLPSP  
PLPPPLTSLLLPPQEAVAGEGPCVAGGARADGR\*SARWSPRAGDAWSR\*RRARPRGAAA\*RRRRASPGGRRGGLRWAGRGR\*R  
CILSIDP\*GLRART\*ASRDPRDPKTAERRLRASRSRKVG\*ARFLVLRVFGREAGGCCW\*\*S\*SRRS\*DGGWWRGAPGPWARLAG  
CADGRPCPRRGPDTRWGPCSSPA\*AAPRAPPPRPRGRACA\*ARTRAAAGRAPGRRRRAR\*GWPAGSG\*GWSGSRRSRRSGGRL  
RC\*WCRSSWP\*RTS\*RSRGRVARARGT\*GASRRACRRCSRARRARGTGIRRGSAAGGAAIARWRGRARRARGPRA\*GGGSRRC  
TWTSR\*CCCCRRRAGTRGRGSRCCAAAGSSSWWPRSGP\*GARSRGCSRHTGKNESGQRLDSVAWRLSERVGLRVYPGSNLES  
GWSRS\*RGTGTPVSTQAC\*RNLDQTEAGRFLALVAGHEKLVS AESGRPRWLA AVVWRKNRQGCVA VCPGSSLSARRRPDSAA NV  
GVAAPSFPRPLSQPTSPVTERAPLFFSCVFARCIPIYCGRCAPT LHHNRPYRSSNSRRFCPRPSSSQPLPRPP\*AEPAFSMTWPWKR  
ARGWRGWGRRRRSGTRACR\*KGT LARPTCPSTCSETGAARSPRRCAPASTRGSGCGAAWTESGC\*GTRISRRTS\*RGAPRAR  
TWPRPTWSRRTSRP\*RRRATSKNPSTTTCAR\*SRARR\*PWA\*CTCGTCWRPSCRTPRASR\*RRSCFWWCSTVGTTRRSGRRC\*ISP

Fig. 20J

SPRAAGSWTW\*TFCRASWCRSAGCRCPRSWRPSTSRC\*VWASTTLGRSTRPRTCP\*TRR\*STGFTCA\*P\*KC\*P\*ATIWGCTATT  
 GCTAR\*APAAGAS\*ATRS\*CTACSGP\*PGPGPRGRATLTWARTCAGSPAAGPWKLPAPVPTWRRWTMRRRRRASTWKTGDATVF  
 LLDAATATAAAS\*SRDAGGAAEPAVRH\*LLGRDPGHATHHGADDPQSRL\*TAASGQPALGHPGGRGALALEPHAREGAGHRE  
 RAGGEQGHPR\*RGRAGVQRAAGARGPLQQHQRADDEPGPHGDRRARGGVAARAVPPRVEPLHGGAERLPEHAARQRAPGPG  
 GLHQLHQRAAADGGRGAPERGVVAGALLPDQSPGLADREPEPGFQELAGTVGRAGPGRGPRDGVEPADAELAPAAAAGGAL  
 HGQRQREPLVPGLPA\*PVPRGHRTGARGRADLPGDHPREPRAGPGGPGQPGGHPPELADQPVAEDPAPVRAEHRGGAHPALR  
 AAERGAVPDAGGGHAQRGARHDAQHGAQHVRPQPPVHQ\*ADGLLASGGRHELGLLYQRHLEPALAPAARVLHGRVRHARPQ  
 RRVVPGRRGQQRVLAASRNQCRVEERGRGPAAVLGAVRSRGCCRGARGRQPLPEPALFAEQRAQQRAGSADATAPAGRGV  
 ERLLEARAREELPQ\*RDREPGGQDEPLEDVARAQGRAPS\*QRRHP\*TPAARQAAGTGVGR\*GFRRRQQRVGLGWEWW\*PV  
 RSPAPPYRAPDVRI\*KNRRYSRPPWRPACVLLCCL\*\*YDEARVPGSSSLVRERDAAGGGGGDAAPAGGALRAPVPGAYGGAE  
 QHSLLAGATLVRYHPVPGGQVGRHRLAELPERPQQLPDHRGAEQRFPHGGQHPDHQL\*RALAVGRPAENHHAHQHAQRE  
 RVHVQQVQVQAGDGLAQDPQRGG\*\*L\*W\*SGRADLRVGGV\*AARGQLLDHHRSDQRHHRQLGGGAAERGAGERHRE  
 VRHAQLPAGLGRDRAGDAGRVHQRLPPRHRPAARLRRGLHREPPQQPAGHPQAAALPGGLPDVVRGPGGGQHPRALGCRSL  
 REKQGG\*HRRGDRSRGHRLYRGAGR\*FC\*RCGSGRGG\*NRK\*DSHPAGGEGQQGQELQRRARGQEKHRLPQLVPLQLRRPREG  
 RALLDAHHHLGRHLRRGASLLVAARHDARPHLPHASS\*QLPGGGRRAPARLLQELLQRAGRLAAAARLHLAARLQPLPREPD  
 PRPPARAHYHRQ\*KRSCSHSRDPAQAQYQPGSPARDH\*RQTPHLPLRLQGPRGSRAPLEPHLLKNVHSHLAQ\*\*HRLGPA  
 RAQQDVRRRSPTLHATPRARARALPRSLGRPQGPRALAHRRRRDRPGGGRRALHARRRRLHRRRRHRQRRGRRAPVRPHQ  
 EPAAAHRAPEHPRHARGASLAAQQAAGTQGHAGGGQTRGLRQQQRRQDPQTRGHGGGGGHRQHVPAAARQVVGARR  
 RHRCARARAHPPPSHLKMLTSLRC\*CVPAARRMSKRKYKEEMLQVIAPEIYGPAAAVKEERKPRKLKRVKDKKEEEDDGLVEFVREF  
 APRRRVQWRGRKVKPVLPRGTTVVFTPGERSGSASKRSYDEVYGEDILEQAVRLGEFAYGKRSRPAPLKEEAVSIPLDHGNPTPSL  
 KPVTLLQQLPSAAPRRGFKREGGEDLYPTMQLMVPKRQKLEDVLEHMKVDPEVQPEVKVRPIKQVAPGLGVQTVDIKIPTMET  
 QTEPVKPSTSTMEVQTDPMWPAPASTSTRRRRKYGAASLLMPNYALHPSIIPGYPGRTRFYRGYTSSRRRKTTRRRRRSRRSSTAT  
 SALVRRVYRSGREPLTLPRARYHPSIAI\*LPPPTCRYGPHMPPRPHYGLPRKKAAP\*KADGERAASPSPAAARHQQAVGGRLPAR  
 ADPHHRRGDRGDRHRSFRGGAGLSAPLRHKKAWICNKKKNGTLTLLV\*CVFLDGRHQFFVPGTATRAAVYGHLEHRHQPTERG  
 RLQLEQSLERA\*EFRVHAQNLWQQGVEQQRHAGAEGKAERTELPAGG\*WPGLRHQRG\*PGQPGRAETDQPPGRGPARGV  
 RGDAPGGGGAASPGQARRQATASRRGGDAADAHGRAAPVRGGGETGPAHHAARGASGHRSAETQQQPARDPGLASASPLHSG  
 \*APAAGGRRVARPPPPGELAHESEQHRGSGSAECEAPLLKDTVALNLLVCVYMYVRRPEGGV\*RGASPSCKMATPSMLPQW  
 AYMHIAGQDASEYLSPLVQFARATDTYFSLGNKFRNPTVAPTHDVTDRSQRLLRFPVDREDNTYSYKVRYTLAVGDNRVLDM  
 ASTYFDIRGVLDRGPSFKPSGTAYNSLAPKGPANSSQWEQAKTGNGGTMETHTYGVAPMGGENITDKGLQIGTDVTANQNKPIY  
 ADKTFQPEPQVGEENWQETENFYGGALKKDTNMKPCYGSYARPTNEKGGQAKLVGDDGVPTKEFDIDLAFDTPGGTVNGQD  
 EYKADIVMYTENTYLETPDTHVYKPGKDDASSEINLVQSQMPNRPNYIGFRDNFIGLMYYNSTGNMGMVLGQASQLNAVVDLQD  
 RNTELSYQLLLDSLDRTRYFSMWNQAVDSYDPDVRIENHGVDELPNYCFPLDGSNTAAAYQGVKVKDQDGDVESEWENDD  
 TVAARNQLCKGNIFAMEINLQANLWRSFLYSNVALYLPDSYKYTPTNTVLTPTNTNTYDYMNGRVTTPPSLVDAYLNIGARWSLDPM  
 DNVNPFNHHRNAGLRYSMILLGNGRYVPFHIQVPQKFFAIKSLLLPGSYTYEWNFRKDVNMILQSSLGNDLRTDGASIAFTSINLY  
 ATFFPMAHNTASTLEAMLRNDTNDQSFNDYLSAANMLYPIANATNPISIPSRNWAARFGRWSFTRLKTRETPSLGSGFDYFVYS  
 GSIPLYDGTFFLYNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLVQMLAHYNIGYQGFYVPEGYK  
 DRMYSFERNFQPMRQVVDENVYKDYQAVTLAYQHNSGFGVGLAPTMRQGGQYPANYPYPLIGKSAVASVTQKFLCDRVMW  
 RIPFSSNFMSMGALDGLQNMLYANSAHALDMNFEVDPMDESTLLYVFEVFDVVRVHQPHRGVIEAVYLRTPFSAAGNATT\*AAL  
 ASCKMTAGSGEQELRAILRDLGCGPCFLGTDFDKRPFPMAPHKLACAIVNTAGRETGGEHWLAFAWNPRSHTCYLFDPFGFSDERL  
 KQIQFEYEGLLRRSALATEDRCVTLEKSTQTVQGPRAACGLFCCMFLHAFVHWPDRPMDKNPTMNLTLGVPNGMLQSPQVEP  
 TLRRNQEALYRFLNAHSAYFRSHRARIKATAFDRMNQDM\*KTGVCM\*MLYS\*\*TAHVYATFSEALTFRNRRGSAGSRHGPRAGI  
 RCGTGTWAAT\*TRGSAAWARGGRGTSRSTACA\*VAGRPAGRARRS\*NRWDPRSARESCGTRGCTGTSPGPGASRLPAPSRR\*  
 CPPRPDPRRWPSRRGSSCRSAAPCWARSACGCNRSAGGSASSGPARSSCPGTWPS\*KPPAGGRPAAPCRPR\*RRPRRTC\*RTG  
 WWRSRRRARSSARRCWPAAPRCAPSGSG\*SWPGWGPSARAARSRSRPHPSR\*CAPSGSSRSRAGTAACPRLRCSRAATARSCT  
 PSSCGRSGSASARSPAGSGPSSRSGSCCW\*RSAGCRGAPRSHTGGRCGGTTPPARASAGRRTSGRSPRGTPSAASSLPCSPRPK  
 RSAGSGGSSPLSS\*SPPPSGGRSRPGSQTACRPSR\*CARGES\*SPRPPAPRPAFRPRCPG\*CLAKAHAWSCGVSWAAEAAA  
 MCWESASSRSPRLFLLLGRRPRPRGGRHASSGAEEATGSRGSAGGWQSPFRVRCAPGGAALDFLRGRPLCSPREQQQAWRL  
 SHRRQHRHLPPLPPPTTRTSSRMKA\*PPRRPAPPPTPRPQTCKRWRNPSRLTAT\*RPSTRRSWQRAFPKRTTKSSQSRKQRT  
 SRTLGLTSMATT\*AGQRTCSSIWPAANASSRTRCSTAPRCPSAWRSSAAPTATSSRRACPPSASPTAPVSPTRASTSTRSSRCPRP  
 WPPTTSFRTKGSPSPAAPTAPAPTPCSTWAPAPAYLISPWWKFRPSSRVWAATRLGPRTLCKEAERSMSTTAPWWSWKATTRA

Fig. 20K

WRSSSARSS\*PTSPTRRSTCPPRS\*APSWTRCSSAPRPSRRRCRTPRVRTRASPWSATSSWRAGWERVAPPRAWKSGASS\*WP  
 WSW\*PWSWSVCAASLPTRRPCARSRRCTTSSGTGSCARPARSPTWS\*PTWSPTWASCTRTAWGKCTCTPPCAGRPAATTSATA  
 STCTSATPGRRRAWACGSSAWRSRT\*KSSASSCRRTSRPCGPGSTSVPPPRTWPTSSSPSACG\*RCATGCPTL\*AKACCKTFALSSSN  
 APGSCPPPAPRCPTSCR\*PSASAPRRSGATATCCAWPTTWPTTRT\*SRTSAARVCWSATAAATSARRTAPWPAATPSC\*ARPRSSA  
 PSSCKAPATARARGV\*NSPRGCGPRPTCASSCPRTTIPSRSGSTRTNPSRPRPSCRPPASSPRGPSWPNCCKPSRNPKNFC\*KRATGST  
 WTPRPERSSTPASPRMPRGSSKKLVLPPEDEEDWESSQAEEEEMEDWDSTQAEEDSLQDSLEEEDEVEEAEAAAAARPSSS  
 AEKASSTDISAPGRGRGGRAHSRWDETGFRPNPTTQTGKKERQGYKSWRGHKNVSVCLQACGGNISFTRRYLLFHRGVNFPNRNI  
 LHYRHLHSPYYCFQEEAETQQQKTSGSSS\*KIHSGGRWTEDEGERAGADPGAEEPDLSHPLCHLPAESGAGAGTESQEPFSALA  
 HPQLSVSQERRPTSASHSRGRGSLQQLVLAHS\*RVARARPHTEKGGNYVTTCALRPTIMSKEIPTYMWSYQPMGLAAGAAQD  
 YSTRMNWLSAGPAMISRVNDIRAHNRNILLEQSAITATPRHHLNPRNWPAALVYQEIPOPTTVLLPRDAQAEVQLTNSGVQLAGG  
 AALCRHRPAQGIKRLVIRGRGTQLNDEVVSSSLGLRDPGVFQLAGSGRSSFTPRQAVLTLESSSSQPRSGGIGTLQFVEEFTPSVYFNP  
 FSGSPGHYPDEFIPNFDaisesVDGYD\*MSHGGAADLARLRHLHDHCRFRFCFARDLAEFAYFELPEEHPQGAHVRIIVEGGLDSDL  
 LRIFSQRPIVEREQGQTLTLYCICNHPGLHESLCCLLCTEYNKS\*DQRLRLRLWCSCYQVPVLRHRERDRAPAPV\*APQEVPHLAV  
 PGLPDRRCQPLRQRRSPAERPCCQPYFFHPQKQAPALPTLPPRDLVRLRTLPSHLPPDEYHSAAPRY\*QPNYPPTPPSRPFL\*I\*YHY  
 RRWLLLLVLPRPVDPRSPTQSPEEVRKCKFQEPWFKLCYRQKSDMHPSWIMIIGIVNILACTLISFVIYPCDFGWNSEALYLPPEP  
 DTPPQQQQAHALPPPQPRPQYMPILDYEAEPQRPMLPAISYFNLTGGDD\*PTGQ\*QRQRPSPGHGRPRLGAATRPTSHSSAAGE  
 SRQGAAGRHSHPVQERHLLPGETGQDLLRGHPDRPSLLRAPAAPEVHLPGRSQPHRHHPAVGRYQGVHPLLLRLRPLRPHSD  
 QDPLRPPRPPHELITPLSEIKIILMMI\*IKKIII\*FEIKIQSY\*\*FEFNKNKESLT\*NLIPGLCPCFLPTPPHSLPSSGTAGPGGLQTSSTR  
 \*RGCQIPVPQSSFYLLSDVQKARPGG\*\*LRPRLPLRCRQRTDRALHQPLRLFRWIPREAPGGVVPATG\*PRHHQERGNHPQAGR  
 GGGPRLVGKTHLQHGHHQRRPSQYFKQHHPF\*NCCPFLQQQWNFKPQCLHTISSISHI\*HFRHKSWKRSSDFK\*VVDCTTNSSSYI  
 QLK\*HHSKNRQRAIY\*LQWKQRT\*G\*YKPKKRTSF\*R\*CYCNIYWKWLRLWL\*\*\*WKNKTRNYQNWRIKF\*C\*QSNQCQTRHR  
 FKF\*LRWCLDSWKQTG\*QANTLDYP\*PKP\*LSITFRQRCQIYSLSYKMR\*SNTRHCGSGGCYCRISTKSN\*\*HSQKRHSFP\*I\*FRWC  
 THVKLINGR\*LLEL\*GGTDSKCSLYKCCGIHAKYRCISKNPK\*NT\*K\*HSQSGIFNWRNYYANDTNHNFQWH\*\*KRHNPS\*HLLYD  
 FYMAVDWRL\*GQKYLYCQLILFFLHRPGIIPPSKPTPFPTTFVYMETLKQKNKVQVFY\*INSFTGLEQLFFLHPRTWNTPPSPPAQ  
 \*TSECHW\*WTCFWSPRSTQFQSEPVS DRSRGR\*NPPGTPASAPHSSAEDCPRWWSGSRSLSGRSRRAAVGIIVRERDRPVVSHQAPQ  
 QSLPPPLRQAAAQGVVRVQGLPQHDAHGPQHQS SGAAGAAHANLAQVTAVRATQDHQVQVQSSIVQHAPAETHRGKDATHVA  
 VVPDPQVNQVALPPEDAAHVHDLGHVAVHHLVPVPHHPLVEHAAPDDPAEPQGHQHRPARHAARKRIPAMTMEDPPLVPVDHL  
 GAEQVYVGTAAQAYAHASLQHSQLLGGQNHIPGHGELLQDSEPRRTGQSSHITYIVHGQGIARQHRVILHQRSAGLGLLTAW\*GGR  
 PIRVMAGRG\*SCSRPCHDAVAFGHFRTCCSRTWSGRCTPIAGGGLGAWNARC\*SCKTATLSDRAADLGPQE\*\*RSHHA\*\*L\*SHR  
 PPWNGPGPAR\*CNFVGFR\*RRGREEQEEP\*LTFNPNGLGALQNEGHGDGTSRPRCVGGK\*QPGQR\*YGSRDVPRWLPAPKPPRA  
 HPETRQ\*RKREGSLIPQSCYTPAPSPDNFHFSSLE\*FELVPEVNPSQP\*\*KARAEHPPPAFLSTPS\*FQDILLVHLQQIDKRNKISAA  
 IPELLPQQ\*L\*VLFHIVSEIFSHRTPRNKRASHITDKPKSPVSIACKIEISMLARPGDIFQITGQKIG\*AIFKKINKRKIFQVHV\*GLGN  
 NDGVSARGAFQHG\*LADL\*KNKK\*NIKPC\*PGEQVGKSFSPAPGRPRGLRRDPRKNCRYD\*KPSQRDVPGGRR\*FEKKHTPPEH  
 WSP\*VKKSGRGSNEALQRLSSPAKRCHADEAQNFQVRKKCNYSPPAQAAKLPIPPDTHTKPQRP\*LTERQQQRHTTGARVREKTE  
 L\*PVRPLSAQYIAPDLH\*RGQSLKIPAK\*SHTPSTRPETGDTLRKIRALPQTAKLPSPGSHATSSKHDFQIPSTVKNITRPAPNGRRS  
 RSQSPSSLPKFKQLICILTRTKSLRYIID

Fig. 21A

**AdC6 010-HIVgag (E1026) Nucleic Acids – SEQ ID NO: 2**

CATCATCAATAATATACCTCAAACCTTTTGGTGCGCGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCTGCGGGAGCGGCGACCGTTAGGGGCGGGCGGGTGACGTTTTGATGACGTGGCTATGAGGCGGAGCCGGTTTGCAAG  
TTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTCCCGCGCTCTCTGACAGGAAATG  
AGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAAAACCTGAATGAGGAAGTGAAAATCTGAGTAATTTTC  
GCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTTC  
ACCTAAATTTCCGCGTACGGTGTCAAAGTCCGGTGTTTTTACGTACGATATCATTTCCCGAAAAGTGCCACCTGACCGTAACTAT  
AACGGTCTTAAGGTAGCGAAAGCTCAGATCTCCCGATCCCTATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTT  
AAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCT  
TGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGA  
CATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC  
TTACGGTAAATGGCCCCGCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGC  
CAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGC  
CAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCCGCTGGCATTATGCCCACTACATGACCTTATGGGACTTTCCTA  
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGT  
TTGACTCACGGGGATTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTGGCACCAAAATCAACGGGACTTTCCTAA  
AATGTCGTAACAACTCCGCCCATTTGACGCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTA  
GTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGTGCTTCTGACACAACA  
GTCTCGAACTTAAGCTGCAGAAGTTGGTCGTGAGGCACTGGGCAGGTAAGTATCAAGGTTACAAGACAGGTTTAAGGAGACC  
AATAGAAACTGGGCTTGTGAGACAGAGAAGACTCTTGCGTTTCTGATAGGCACCTATTGGTCTTACTGACATCCACTTTGCCT  
TTCTCTCCACAGGTGTCCACTCCAGTTCAATTACAGCTCTTAAGGCTAGAGTACTTAATACGACTCACTATAGGCTAGCGCCAC  
CATGGGCGCCAGAGCCAGCGTGTGAGCGGGGAGAGCTGGATCGCTGGGAAAAGATTAGACTGAGGCCCGGAGGGAAGA  
AAAAGTACAAGCTGAAACACATCGTGTGGGCCAGCAGGGAGCTGGAGCGCTTCGCCGTGAACCCCGACTGCTGGAGACCTC  
CGAAGGTGTGCGCAGATCTGGGGCAGCTGCAGCCTTCCCTGCAGACAGGCTCCGAGGAGCTGCGGTCTCTGTATAATACA  
GTGGCCCACTGTACTGTGTGCACCAAGCGGATTGAGGTGAAGGATACAAAAGAGGGCCCTGGAGAAGATTGAGGAGGAGCAG  
AACAAGAGCAAGAAGAAAGCCAGCAGGCGCCGCCGACACCGGCAATAGCTCCAGGTGAGCCAGAATATCCAATTGTGC  
AGAATCTGCAGGGCCAGATGGTGCACCAGGCCATTTCCCCACGGACACTGAACGCCTGGGTGAAGGTGGTGGAGGAGAAGG  
CCTTCAGCCCCGAAGTGATCCCTATGTTTTCCGCCCTGTCCGAAGGCGCCACCCCTCAGGACCTGAACACCATGCTGAACACAG  
TGGGGGGACACCAGGCCGCCATGCAGATGCTGAAGGAAACCATCAACGAGGAGGCGCCGAGTGGGATCGGCTGCACCCCG  
TGCACGCCGGGCCAATCGCCCTGGCCAGATGAGGGAGCCCAGAGGCTCTGACATCGCCGGCACCATCTACCTGCAGGA  
ACAGATCGGGTGGATGACCAATAACCCACCAATCCAGTGGGCGAGATCTACAAGAGGTGGATTATTCTGGGACTGAACAAA  
ATTGTGCGCATGTATTTCCCTACATCCATCCTGGACATCAGGCAGGGCCCTAAGGAACCTTTCCGCGACTACGTGGATCGGTTT  
TACAAAACCTGCGCGCCGAGCAGGCCAGCCAGGAAGTGAAGAATTGGATGACAGAGACCCTGCTGGTGCAGAACGCCAATC  
CTGACTGTAAAACCATCCTGAAGGCCCTGGGCCCTGCCGCCACACTGGAGGAAATGATGACCGCTGCCAGGGCGTGGGCGG  
CCCTGGCCACAAAGCCAGGGTGCTGGCCGAGGCCATGTCTCAGGTGACCAACTCTGCCACAATTATGATGCAGCGGGGGAAC  
TTTCGGAACCAGAGGAAGACCGTGAAGTGCTTCAACTGTGGCAAGGAGGGACACATCGCCAAGAATTGCCGCGCCCCACGGA  
AGAAGGGGTGTTGGAAATGCGGGAAGGAGGGCCACCAGATGAAAGACTGCACAGAGCGGCAGGCCAACTTTCTGGGCAAG  
ATTTGGCCAGCCACAAGGGCCGCCCGGAACTTTCTGCAGTCCAGGCCTGAGCCTACCGCCCCCTGAGGAATCCTTCGG  
GTTCCGGCAGGAGACAACACCCCAAGCCAGAAGCAGGAACCCATCGACAAAAGAGCTGTACCCCTGGCCAGCCTGAGATCC  
CTGTTCCGGAATGACCCAGCTCTCAGTGATGATCTAGCGTTTAAACGGGCCCTCTAGAGTCGACCCGGGCGGCCAAACCGCT  
GATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCGTGCCTTCCTTGACCTGGAAGGTGCCAC  
TCCCACTGTCCTTTCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGG  
GCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGG  
AAAGAACCAGCAGATCTGCAGATCTGAATTCATCTATGTGCGGTGCGGAGAAAGAGGTAATGAAATGGTATTATGGGTATTAT  
GGGTCTGCATTAATGAATCGGTGAGATATCGACATATGCTGGCCACCGTGCATGTGGCCTCGCACCCCCGCAAGACATGGCCC  
GAGTTCTGAGCACAACGTCATGACCCGCTGCAATGTGCACCTGGGCTCCCGCCGAGGCATGTTATGCCCTACCACTGCAACAT  
GCAATTTGTGAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGCTG  
TGGAAAATTCTGAGATATGATGAATCCAAGACCAGGTGCCGGCCTGCGAATGCGGAGGCAAGCACGCCAGGCTTCAGCCCG  
TGTGTGTGGAGGTGACGGAGGACCTGCGACCCGATCATTTGGTGTGCTGCTGCAACGGGACGGAGTTCGGCTCCAGCGGGGA



Fig. 21B

AGAATCTGACTAGAGTGAGTAGTGTGGGGCTGGGTGTGAGCCTGCATGAGGGGCAGAATGACTAAAAATCTGTGGTTTTCT  
GTGTGTTGCAGCAGCATGAGCGGAAGCGCCTCTTTGAGGGAGGGGTATTAGCCCTTATCTGACGGGGCGTCTCCCTCCTG  
GGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCCCGTGCAGCCCGCGAACTCTTCAACCTGACCTAC  
GCGACCTGAGCTCCTCGTCCGTGGACGCAGCTGCCGCCGACGTGCTGCTCCGCCGCCAGCGCCGTGCGCGGAATGGCCCT  
GGGCGCCGGCTACTACAGCTCTCTGGTGGCCAACTCGAGTTCACCAATAATCCGCCAGCCTGAACGAGGAGAAGCTGCTGC  
TGCTGATGGCCAGCTCGAGGCCCTGACCCAGCGCCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGCAGGCGGAGACGC  
GGGCGCGGTTGCCACGGTGAAAACCAATAAAAAATGAATCAATAAAATAAACGGAGACGGTTGTTGATTTAACACAGAGT  
CTTGAATCTTTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACGGTCTCGATCATTGAGCACCCGGTGGATCTTTCCAG  
GACCCGGTAGAGGTGGGCTTGATGTTGAGGTACATGGGCATGAGCCGTCGCCGGGGTGGAGGTAGCTCCATTGCAGGGC  
CTCGTGCTCGGGGATGGTGTGTAATCACCCAGTCATAGCAGGGGCGCAGGGCGTGGTGTGCACGATGTCCTTGAGGAGG  
AGACTGATGGCCACGGGCAGCCCTTGGTGTAGGTGTTGACGAACCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATG  
AGATGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTCCCGCCAGATCCCGCCGGGGTTCATGTTGTGCAGGACCACCAG  
CACGGTGTATCCGGTGCACTTGGGGAATTTGTATGCAACTTGGAAGGGAAGGCGTGAAAGAATTTGGAGACGCCCTTGTGA  
CCGCCAGGTTTTCCATGCACTCATCATGATGATGGCGATGGGCCCGTGGGCGGCGGCCTGGGCAAAGACGTTTCGGGGGT  
CGGACACATCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAATGAATTTGGGGCGGAGGGTGCCCGACTGGGG  
GACGAAGGTGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGCATCTCCAGGCCCTGAGCTCGGAGGGGGGGATC  
ATGTCCACCTGCGGGGCGATGAAAAAACGGTTTCGGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAGGTTCCGGAGCAGC  
TGGGACTTGCCGAACCGGTGGGGCCGTAGATGACCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCG  
TCCTCGCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACATGCATGTTCTCGCGCACGAGTTCGCCAGGAGGCGCTC  
GCCCCCAGCGAGAGGAGCTCTGCAGCGAGGCGAAGTTTTTACAGCGCTTGTAGTCCGTGCGCCATGGGCATTTTGAGAGG  
GTCTGTTGCAAGAGTTCAGACGGTCCAGAGCTCGGTGATGTGCTCTAGGGCATCTCGATCCAGCAGACCTCCTCGTTTCGC  
GGGTTGGGGCGACTGCGGAGTAGGGCACAGGCGATGGGCGTCCAGCGAGGCCAGGGTCCGGTCTTCCAGGGCCGCAG  
GGTCCGCGTCAGCGTGGTCTCCGTACCGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGCGAGGGTGCGCTTCAGGCTCATC  
CGGCTGGTCGAGAACCGTCCCGGTGGGCGCCCTGCGCGTCGGCCAGGTAGCAATTGAGCATGAGTTCGTAGTTGAGCGCCT  
CGGCCGCGTGGCCCTTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGCAGACGGGACAGAGGAGGACTTGAGGGCGTAGA  
GCTTGGGGGCGAGGAAGACGGAAGTTCGGGGCGTAGGGCGTCCGCGCCGACGTGGCGCAGACGGTCTCGCACTCCACGAGCC  
AGGTGAGGTGCGGGCGGTTGGGGTCAAAACGAGGTTTCTCCGTGCTTTTGATGCGTTTCTACCTCTGGTCTCCATGAGCT  
CGTGTCGCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACTTATGGGCCGGTCTCGAGCGGGGTGCCGCG  
GTCTCGTCGTAGAGGAACCCCGCCACTCCGAGACGAAGGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGAGGG  
GTAGCGGTGCTGTCCACCAGCGGGTCCACCTTCTCCAGGGTATGCAAGCACATGTCCCCTCGTCCACATCCAGGAAGGTGA  
TTGGCTTGTAAGTGTAGGCCACGTGACCGGGGTCCCGGCCGGGGGGTATAAAAGGGGGCGGGCCCTGCTCGTCTCACT  
GTCTCCGGATCGTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTGAAGGCGGGCATGACCTCGGCACTCAGGT  
TGTCAGTTTCTAGAAACGAGGAGGATTGATATTGACGGTGCCGTTGGAGACGCTTTCATGAGCCCTCGTCCATTTGGTCAG  
AAAAGACGATCTTTTGTGTGCGAGCTTGGTGGCGAAGGAGCCGTAGAGGGCGTTGGAGAGCAGCTTGGCGATGGAGCGCAT  
GGTCTGGTTCTTTCTGTGCGCGCGCTCCTTGGCGGCGATGTTGAGCTGCACGTAAGTTCGCGCGCCACGCACTTCCATTGGG  
GAAGACGGTGGTGAGCTCGTGGGCACGATTCTGACCCGCCAGCCGCGGTTGTGCAGGGTGATGAGGTCCACGCTGGTGGC  
CACCTCGCCGCGCAGGGGCTCGTTGGTCCAGCAGAGGCGCCCGCCCTTGCGCGAGCAGAAGGGGGGCGAGCGGGTCCAGCAT  
GAGCTCGTGGGGGGGTGCGGTCACGGTGAAGATGCCGGGAGGAGCTCGGGGTGAAGTAGCTGATGCAGGTGCCCCA  
GATTGTCCAGCGCCGCTTGCAGTCGCGCACGGCCAGCGCGCTCGTAGGGGCTGAGGGGCGTGCCCCAGGGCATGGGGT  
GCGTGAGCGCGGAGGCGTACATGCCGAGATGTGCTAGACGTAGAGGGGCTCCTCGAGGACGCCGATGTAGGTGGGGTAGC  
AGCGCCCCCGCGGATGTGGCGCGCACGTAGTCGTACAGCTCGTGCGAGGGCGCGAGGAGCCCCGTGCCGAGGTTGGAGC  
GTTGCGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAGTTGGAGGAGATGGTGGGCCTTTGGAAGATGT  
TGAAGTGGGCGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTAGGAGTCTGACGCTTGGCGACGAGCTCGGCGG  
TGACGAGGACGTCCAGGGCGCAGTAGTCGAGGGTCTCTGGATGATGTCATACTGAGCTGGCCCTTCTGCTTCCACAGCTCG  
CGGTTGAGAAGGAAGTCTTCCGCGTCTTCCAGTACTCTTCCAGGGGGAACCCGCTGATCGGCACGGTAAGAGCCCACCAT  
GTAGAAGTGGTTGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCAGGGGAGGGCGTAAGCTTGCAGCGCCTTGCAGGGGAG  
GTGTGGGTGAGGGCGAAGGTGTGCGCACCATGACCTGAGGAACTGGTGTGAGTGAAGTCGAGGTGTCGAGCCGCCCTGCT  
CCCAGAGTTGGAAGTCCGTGCGCTTCTGTAGGCGGGGTAGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTCCCCG  
GCGGGGCATGAAGTTGCGAGTGATGCGGAAAGGCTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGGACGAT  
CTCGTCGAAGCCGTTGATGTTGTGCCGACGATGTAGAGTTCACGAATCGCGGGCGGCCCTTGACGTGGGGCAGCTTCTGA

**Fig. 21C**

[illegible]

Fig. 21C

GGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGCTGAGTCTGGGCAAGTACTACGCTAGGAAGATCTACA  
AGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAG  
CGACGATCTGGGGGTGTACCGCAACGACAGGATGCACCGCGCGGTGAGCGCCAGCCCGCGCGGAGCTGAGCGACCAGGA  
GCTGATGCACAGCCTGCAGCGGGCCCTGACCGGGGCCGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCG  
CTGGCAGCCCAGCCCGCGGGCCTTGGAAGCTGCCGGCGGTTCCCTCTACGTGGAGGAGGTGGACGATGAGGAGGAGGAGG  
GCGAGTACCTGGAAGACTGATGGCGCGACCGTATTTTGTAGATGCAGCAACAGCCACCGCGCGCCTCTGATCCCGCGA  
TGCGGGCGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCT  
GACGACCCGCAATCCCGAAGCCTTTAGACAGCAGCCTCAGGCCAACCGGCTCTCGGCCATCTGGAGGCGGTGGTGCCTCGC  
GCTCGAACCCACGCACGAGAAGGTGCTGGCCATCGTGAACGCGTGGTGAGAAACAAGGCCATCCGCGGTGACGAGGCCG  
GGCTGGTGTAACGCGCTGCTGGAGCGCTGGCCGCTACAACAGCACCAACGTGCAGACGAACCTGGACCGCATGGTGAC  
CGACGTGCGCGAGGCGGTGTCGACGCGGAGCGGTTCCACCGCGAGTGAACCTGGGCTCCATGGTGGCGCTGAACGCCTTC  
CTGAGCACGACGCCCGCAACGTGCCCCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCGCTGCGGCTGATGGTGGCCG  
AGGTGCCCCAGAGCGAGGTGTACAGTCGGGGCCGACTACTTCTCCAGACCAGTCGCCAGGGCTTGACAGCCGTGAACCT  
GAGCCAGGCTTTCAAGAACTTGACGGGACTGTGGGGCGTGACGGCCCCGTGCGGGGACCGCGCGACGGTGTGAGCCTGCT  
GACGCCGAACCTCGCGCTGCTGCTGCTGCTGGTGGCGCCCTTACGACAGCGGCAGCGTGAGCCGCGACTCGTACCTGGGC  
TACCTGCTTAACCTGTACCGCGAGGCCATCGGACAGGCGCACGTGGACGAGCAGACCTACCAGGAGATACCCACGTGAGCC  
GCGCGCTGGGCCAGGAGGACCCGGGCAACCTGGAGGCCACCTGAACTTCTGCTGACCAACCGGTGCGAGAAGATCCCGCC  
CCAGTACGCGCTGAGCACCGAGGAGGAGCGCATCTGCGCTACGTGCAGCAGAGCGTGGGGCTGTTCTGATGCAGGAGGG  
GGCCACGCCAGCGCGGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCCGCAACCGCCCGTTCATCAAT  
AAGCTGATGGACTACTTGATCGGGCGGCCCATGAACTCGGACTACTTTACCAACGCCATCTGAACCCGCACTGGCTCCCG  
CCGCCCCGGTTCTACAGGGCGAGTACGACATGCCGACCCCAACGACGGGTTCTGTGGGACGACGTGGACAGCAGCGTGT  
TCTCGCCGCTCCAGGAACCAATGCCGTGTGGAAGAAAGAGGGCGGGGACCGGGCGGCGTCTCGGGCGTGTCCGGTGC  
CGGGTGTGCGCGGCGGTGCCGAGGCCGCCAGCCCTTCCGAGCCTGCCCTTTCTGCTGAACAGCGTGCGCAGCAGCGA  
GCTGGGTGCGCTGACCGACCGCGCTGCTGGGCGAGGAGGAGTACCTGAACGACTCCTTGTGAGGCCGAGCGCGAGAA  
GAACTTCCCAATAACGGGATAGAGAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTACGCGCAGCAGCAGGGACGA  
GCCCCGAGTAGCAGCGCAGGCACCCGTAGACGCCAGCGGCACGACAGGCAGCGGGGACTGGTGTGGGACGATGAGGATTC  
CGCCGACGACAGCAGCGTGTGGACTTGGGTGGGAGTGGTGGTAACCCGTTGCTCACCTGCGCCCCGTATCGGGCGCCTG  
ATGTAAGAATCTGAAAAATAAAGACGGTACTCACCAAGGCCATGGCGACACGCGTGCCTTCTCTGTTGTTGTAGTAG  
TATGATGAGGCGCGTGTACCCGGAGGGTCTCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGGTGGCGGCGGCGATGCA  
GCCCCGCTGGAGGCGCCTTACGTGCCCCGCGGTACCTGGCGCTACGGAGGGGCGGAACAGCATTGTTACTCGGAGCTG  
GCACCTTGTACGATAACACCGGTTGTACCTGGTGGACAACAAGTCGGCAGACATCGCCTCGCTGAACTACCAGAACGACCA  
CAGCAACTTCTGACCACCGTGGTGCAGAACACGATTTACCCCCAGGAGGCCAGCACCAGACCATCAACTTTGACGAGC  
GCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCAACGTGAACGAGTTCATGTACGCAACAAGTTC  
AAGGCGCGGGTGTGGTCTCGCGCAAGACCCCCAACGGGGTGGATGATGATTATGATGGTAGTCAGGACGAGCTGACCTAC  
GAGTGGGTGGAGTTTGTAGCTGCCCCAGGGCAACTTCTCGGTGACCATGACCATCGATCTGATGAACAACGCCATCATCGACAA  
CTACTTGGCGGTGGGGCGGCAGAACGGGGTGTGGAGAGCGACATCGGCGTGAAGTTCGACACGCGCAACTTCCGGCTGGG  
CTGGGACCCCGTGACCGAGCTGGTGTATGCCGGGCGTGTACCAACGAGGCTTCCACCCGACATCGTCTGCTGCCCGGCT  
GCGGCGTGGACTTCACCGAGAGCCGCTCAGCAACCTGCTGGGCATCCGCAAGCGGCAGCCCTTCCAGGAGGGCTTCCAGAT  
CCTGTACGAGGACCTGGAGGGGGGCAACATCCCCGCGCTCTGGATGTGCAAGCCTACGAGAAAAGCAAGGAGGATAGCAC  
CGCCGCGGCGACCGCAGCCGTGGCCACCGCCTTACCGAGGTGCGGGGCGATAATTTTGCTAGCGCTGCGGCAGCGGCCGAG  
GCGGCTGAAACCGAAAGTAAGATAGTCATCCAGCCGTGGAGAAGGACAGCAAGGACAGGAGCTACAACGTGCTCGCGGAC  
AAGAAAAACACCGCTACCGCAGCTGGTACCTGGCCTACAACTACGGCGACCCCGAGAAGGGCGTGCGCTCTGGACGCTGC  
TACCACCTCGGACGTCACTGCGGCTGGAGCAAGTCTACTGGTGCCTGCCCACATGATGCAAGACCCGGTCACTTCCGC  
TCCACGCGTCAAGTTAGCAACTACCGGTGGTGGGCGCCGAGTCTGCGCGTCTACTCAAGAGCTTCTTCAACGAGCAGGC  
CGTCTACTCGCAGCAGTGCAGCGCTTCACTCGCTCACGCAGTCTTCAACCGCTTCCCCGAGAACCAGATCCTCGTCCGCCC  
GCCCGCGCCACCATACCACCGTCAGTGAACCGTTCCTGCTCTCACAGATCACGGGACCCTGCCGTGCGCAGCAGTATCCG  
GGGAGTCCAGCGCGTGACCGTCACTGACGCCAGACGCCGACCTGCCCTACGCTACAAGGCCCTGGGCGTAGTCGCGCCG  
CGCGTCTCTCGAGCCGACCTTCTAAAAATGTCCATTCTCATCTCGCCAGTAATAACACCGGTTGGGGCTGCGCGCGCCC  
AGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGCAGCGTGCAGGGGCACTTCCGCGCTCCCTGGGGCG  
CCCTCAAGGGCCGCTGCGCTGCGCACCAACCGTCGACGACGTGATCGACAGGTGGTGCCGACGCGCGCAACTACACGCC

Fig. 21D

CGCCGCCGCGCCCGTCTCCACCGTGGACGCCGTATCGACAGCGTGGTGGCCGACGCGCGCCGGTACGCCCGCACCAAGAGC  
CGGCGGCGGCGCATCGCCCGGCGGCACCGGAGCACCCCGCCATGCGCGCGGCGGAGCCTTGCTGCGCAGGGGCCAGGCGC  
ACGGGACGCGAGGGCCATGCTCAGGGCGGCCAGACGCGCGGCCCTCCGGCAGCAGCAGCGCCGGCAGGACCCGACAGCGCG  
GGCCACGGCGGCGGCGGCGGCCATCGCCAGCATGTCCCGCCCGCGGCGCGGCAACGTGTACTGGGTGCGCGACGCCGCCAC  
CGGTGTGCGCGTGCCCGTGCACCCGCCCCCTCGCACTTGAAGATGCTGACTTCGCGATGTTGATGTGTCCAGCGGCGAG  
GAGGATGTCCAAGCGCAAATACAAGGAAGAGATGCTCAGGTATCGCGCCTGAGATCTACGCCCCGCGGCGGCGGTGAA  
GGAGGAAAGAAAGCCCCGAAACTGAAGCGGGTCAAAAAGGACAAAAAGGAGGAGGAAGATGACGGAAGTGGTGGAGTTTG  
TGCGCGAGTTGCCCCCGGCGGCGCGTGCAGTGGCGCGGCGGAAAGTGAACCGGTGCTGCGGCCGGCACCACGGTGG  
TCTTACGCCCGGCGAGCGTTCCGGCTCCGCCTCAAGCGCTCTACGACGAGGTGTACGGGGACGAGGACATCCTCGAGCA  
GGCGGTGAGCGTCTGGGCGAGTTTTCGTACGGCAAGCGCAGCCGCCCGCGCCCTTGAAGAGGAGGCGGTGTCCATCCC  
GCTGGACCACGGCAACCCACGCCGAGCCTGAAGCCGGTGACCCTGCAGCAGGTGCTACCGAGCGCGGCGCGCGCCGGGG  
CTTCAAGCGCGAGGGCGGCGAGGATCTGTACCCGACCATGCAGCTGATGGTGCCCAAGCGCCAGAAAGCTGGAGGACGTGCT  
GGAGCACATGAAGGTGACCCCGAGGTGCAGCCCGAGGTCAAGGTGCGGCCATCAAGCAGGTGGCCCCGGGCTGGGCGT  
GCAGACCGTGGACATCAAGATCCCCACGGAGCCCATGAAACGCAGACCGAGCCCGTGAAGCCAGCACCAGCACCATGGAG  
GTGCAGACGGATCCCTGGATGCCAGCACCAGCTTCCACCAGCACTCGCCGAAGACGCAAGTACGGCGCGGCCAGCCTGTGA  
TGCCCAACTACGCGCTGCATCCTTCATCATCCCCACGCCGGGCTACCGCGGCACGCGCTTCTACCGCGGTACACCAGCAGCC  
GCCGCCGAAGACCACACCCCGCGCCGTCGTGCGAGCCGCCGAGCAGCACCAGCGACTTCGCGCTTGGTGCGGAGAGTGTA  
TCGCAAGCGGCGCGAGCCTCTGACCCTGCCGCGCGCGCTACCACCCGAGCATCGCCATTTAACTACCGCTCTACTTGCA  
ATATGGCCCTCACATGCCGCTCCGCGTCCCATACGGGCTACCGAGGAAGAAAGCCGCGCCGTAGAAGGTGACGGGGAA  
CGGGTGCCTGCGCATCACACCGGCGGCGCGGCCATCAGCAAGCGGTTGGGGGAGGCTTCTGCCGCGCTGATCCCC  
ATCATGCGCGGCGATCGGGGCGATCCCCGGCATAGCTTCCGTGGCGGTGCAGGCCTCTCAGCGCCACTGAGACACAAAA  
AGCATGGATTTGTAATAAAAAAAAAAATGGACTGACGCTCCTGGTCTGTGATGTGTGTTTTAGATGGAAGACATCAATTTT  
CGTCCCTGGCACCGCGACACGGCACGCGGCCGTTTATGGGCACCTGGAGCGACATCGGCAACAGCCAAGTGAACGGGGGCGC  
CTTCAATTGGAGCAGTCTCTGGAGCGGGCTTAAGAATTTCCGGTCCACGCTCAAAACCTATGGCAACAAGGCGTGGAACAGCA  
GCACAGGGCAGGCGCTGAGGAAAAAGCTGAAAGAACAGAACTTCCAGCAGAAGGTGGTTGATGGCCTGGCCTCAGGCATCA  
ACGGGTGGTTGACCTGGCAACACAGGCGGTGCAGAAACAGATCAACAGCCGCTGGACGCGGTCCCGCCCGCGGGGTCCGT  
GGAGATGCCCCAGGTGGAGGAGGAGTGCCTCCCTGGACAAGCGCGGCGACAAGCGACCGCGTCCCGACGCGGAGGAGA  
CGTGCTGACGCACACGGACGAGCCGCCCGTACGAGGAGGCGGTGAAACTGGGCCTGCCACCACGCGGCCCGTGGGCG  
CTCTGGCCACCGGAGTGCTGAAACCCAGCAGCAGCCAGCCCGCGACCTGGACTTGCTCCGCCTCGCCCCCTCCACAGTGGCT  
AAGCCCTGCCGCCGTGGCCGTGCGCTGCGCGCCCCCGAGGCCGCCCGCAGGCGAACTGGCAGAGCACTCTGAACAGCA  
TCGTGGGTCTGGGAGTGCAAGTGTGAAGCGCGCGCGTCTATTAAAAGCACTGTAGCGCTTAACCTGCTGTGTGTGT  
ATATGTATGTCCGCCGACCAGAAGGAGGAGTGTGAAGAGGCGCGTCCCGAGTTGCAAGATGGCCACCCCATCGATGCTGCC  
CCAGTGGGCGTACATGCACATCGCCGGACAGGACGCTTGGAGTACCTGAGTCCGGGTCTGGTGCAGTTCGCCCCGCCACA  
GACACCTACTCAGTCTGGGGAACAAGTTTAGGAACCCACGGTGGCGCCACGCACGATGTGACCACCGACCGCAGCCAGC  
GGCTGACGCTGCGCTTCTGCGCGTGGACCGGAGGACAACACCTACTCGTACAAAGTGCCTACACGCTGGCCGTGGGCGA  
CAACCGCGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGCTGGACCGGGGCCCTAGCTTCAAACCTACTCTG  
GCACCGCCTACAACAGCCTAGCTCCCAAGGGAGCTCCCAATTCAGCCAGTGGGAGCAAGCAAAAACAGGCAATGGGGGAAC  
TATGGAAACACACATATGGTGTGGCCCAATGGGCGGAGAGAATATTACAAAAGATGGTCTTCAAATTGGAAGTACGTTA  
CAGCGAATCAGAATAAACCAATTTATGCCGACAAAACATTTCAACCAGAACCGCAAGTAGGAGAAGAAAATTGGCAAGAAAC  
TGAAAACCTTTATGGCGGTAGAGCTCTAAAAAAGACACAAACATGAAACCTTGCTATGGCTCCTATGCTAGACCCACCAATGA  
AAAAGGAGGTCAAGCTAACTTAAAGTTGGAGATGATGGAGTTCAACCAAGAATTCGACATAGACCTGGCTTTCTTGATA  
CTCCCGGTGGCACCGTGAACGGTCAAGACGAGTATAAAGCAGACATTGTGATGTATACCGAAAACACGTATTTGGAACTCCA  
GACACGCATGTGGTATACAAACCAGGCAAGGATGATGCAAGTTCTGAAATTAACCTGGTTCAGCAGTCTATGCCAACAGACC  
CAACTACATTGGGTTACGGGACAATTTATCGGTCTTATGTACTACAACAGCACTGGCAATATGGGTGTGCTTGCTGGTCAGGC  
CTCCAGCTGAATGCTGTGGTTGATTGCAAGACAGAAACACCGAGCTGTCTACCAGCTTGTCTGACTCTTTGGGTGACAG  
AACCCGGTATTTAGTATGTGGAACAGGCGGTGGACAGTTATGACCCGATGTGCGCATCATCGAAAACCATGGTGTGGAG  
GATGAATTGCCAACTATTGCTTCCCTTGGACGGCTCTGGCACTAACGCCGCATACCAAGGTGTGAAAGTAAAGATGGTCA  
AGATGGTGATGTTGAGAGTGAATGGGAAAATGACGATACTGTTGCAGCTCGAAATCAATTATGTAAAGGTAAATTTTCGCCA  
TGGAGATTAATCTCAGGCTAACCTGTGGAGAAGTTTCTCTACTCGAACGTGGCCCTGTACCTGCCCGACTCCTACAAGTACA  
CGCCGACCAACGTACGCTGCCGACCAACCAACACCTACGATTACATGAATGGCAGAGTGACACCTCCCTCGCTGGTAGAC

**Fig. 21E**

GCTACCTCAACATCGGGGCGCGCTGGTCGTGGACCCATGGACAACAGTCAACCCCTTCAACCAACCAACGCAACGCGGGGCT  
GCGCTACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCAAAAGTTTTTCGCCATCAAGAG  
CCTCCTGCTCCTGCCCGGTCTACACCTACGAGTGGAACCTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCCTAGGC  
CGACCTGCGCAGCGGACGGGGCCTCCATCGCCTTACCAGCATCAACCTCTACGCCACCTTCTTCCCATGGCGCACAAACCCGC  
CTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAAGTCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCC  
CATCCCGGCCAACGCCACCAACGTGCCATCTCCATCCCCTCGCGCAACTGGGCGCGCTTCCGCGGATGGTCTTACGCGCCT  
GAAGACCCGCGAGACGCCCTCGCTCGGCTCCGGTTGACCCCTACTTCGTCTACTCGGGCTCCATCCCCTACCTAGACGGCAC  
CTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTACGTGGCCCGGCAACGACCGCCTCTGACG  
CCCAACGAGTTCGAAATCAAGCGCACCGTCGACGGAGAGGGATACAACGTGGCCAGTGCAACATGACCAAGGACTGGTTCT  
TGGTCCAGATGCTGGCCACTACAACATCGGCTACCAGGGCTTCTACGTGCCCGAGGGGTACAAGGACCGCATGTACTCCTTCT  
TCCGCAACTTCCAGCCCATGAGCCGCCAGGTCGTGGACGAGGTCAACTACAAGGACTACCAGGCCGTACCTTGGCCTACCAG  
CACAACAACTCGGGCTTCGTGCGGTACCTCGCGCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAACTACCCCTACCCGCTC  
ATCGGCAAGAGCGCCGTCGCCAGCGTCACCCAGAAAAAGTTCTCTGCGACCGGGTCATGTGGCGCATCCCCTTCTCCAGCAA  
CTTCATGTCCATGGGCGCGCTACCGACCTCGGCCAGAACATGCTCTACGCCAACTCCGCCACGCGCTAGACATGAATTTG  
AGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTTGAAGTCTTCGACGTCGTCCGAGTGACCCAGCCCAACCGCGG  
CGTCATCGAAGCCGTCTACCTGCGCACGCCCTTCTCGGCCGCAACGCCACCACCTAAGCCGCTCTTGCTTCTTGAAGATGAC  
GGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATCTCCGCGACCTGGGCTGCGGGCCCTGCTTCTGGGCACCTTCGACAAG  
CGTTCCCTGGATTATGGCCCCGACAAGCTGGCTGCGCCATCGTGAACACGGCCGCGCGAGACCGGGGCGAGCACT  
GGCTGGCCTTCGCTGGAACCCGCGCTCCACACATGTACTCTTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGA  
TCTACCAGTTTCGAGTACGAGGGCCTGCTGCGTCGACGCGCCTGGCCACCGAGGACCGCTGCGTCACCTTGAAAAAGTCCACC  
CAGACCGTGCAGGGTCCGCGCTCGGCCGCTGCGGGCTCTTCTGCTGCATGTTCTCTGCACGCCTTCGTGCACTGGCCCGACCG  
CCCCATGGACAAGAACCCACCATGAACCTTACTGACGGGGGTGCCAACGGCATGCTCCAGTCGCCCCAGGTGGAACCCACCC  
TGCGCCGCAACCAGGAAGCGCTTACCGCTTCTCAATGCCACTCCGCCTACTTTCGCTCCACCGCGCGCGCATCGAGAAGG  
CCACCGCCTTCGACCGCATGAATCAAGACATGTAAAAAACCGGTGTGTGTATGTGAATGCTTTATTATAATAAACAGCACATG  
TTTATGCCACCTTCTCTGAGGCTCTGACTTTATTTAGAAATCGAAGGGGTTCTGCCGGTCTCGGCATGGCCCGCGGGCAGGG  
ATACGTTGCGGAACTGGTACTTGGGCAGCCACTTGAACCTCGGGGATCAGCAGCTTGGGCACGGGGAGGTGCGGGGAACGAGT  
CGCTCCACAGCTTGC GCGTGAGTTGCAGGGGCGCCAGCAGGTGGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTT  
CTGCGCGCGAGAGTTGCGGTACACGGGGTTGCAGCACTGGAACACCATCAGGGCCGGGTGCTTACGCTTGCCAGCACCGTC  
GCGTCGGTGATGCCCTCCACGTCCAGATCCTCGGCGTTGGCCATCCCGAAGGGGGTTCATCTTGAGGTCTGCCGCCCATGCT  
GGGCACGACGCCGGGCTTGTTGTTGCAATCGCAGTGACGGGGGATCAGCATCATCTGGGCTGCTCGGAGCTCATGCCCGGG  
TACATGGCCTTCATGAAAGCCTCAGCTGGCGGAAGGCCTGCTGCGCCTTGCCGCCCTCGGTGAAGAAGACCCCGCAGGACTT  
GCTAGAGAACTGGTTGGTGCGCAGCCGGCGTCTGTCACGCAGCAGCGCGCTGTTGTTGGCAGCTGCACCACGCTGCGC  
CCCCAGCGGTTCTGGGTGATCTTGCCCGGTTGGGGTTCTCTTCAGCGCGCGCTGCCGTTCTCGCTGCCACATCCATCTCG  
ATAGTGTGCTCCTTCTGGATCATCACGGTCCCGTGCAGGCACCGCAGCTTGCCTCGGCTTCGGTGACGCCGTGCAGCCAG  
CGCGCAGCCGGTGCACTCCAGTTCTTGTTGGGCGATCTGGGAGTGCGAGTGACGAAGCCCTGCAGGAAGCGGCCCATCATC  
GCGGTACGGGTCTTGTTGCTGTTGAAGGTACGCGGATGCCGCGGTGCTCCTCGTTACATACAGGTGGCAGATGCGGCGGT  
ACACCTCGCCCTGCTCGGCATCAGCTGGAAGCGGACTTCAGGTGCTCTCCACGCGGTACCGGTCCATCAGCAGCGTCATC  
ACTTCATGCCCTTCTCCAGGCCGAAACGATCGGCAGGCTCAGGGGGTTCTTCACCGCCATTGTCATCTTAGTCGCCGCCGCC  
GAGGTACAGGGGGTCTTCTCGTCCAGGGTCTCAAACTCGCTTCCGCTCCTTCTCGATGATGCGCACGGGGGGAAAGCTGA  
AGCCACGCGCCGACGCTCCTCCTCGGCTGCCTTTCGCTCTCGCTGTCTGGTGATGCTTGCAAAAGGCACATGCTTGGTCTT  
GCGGGGTTTCTTTTGGGCGGCAGAGGCGGCGCGCATGTGCTGGGAGAGCGCGAGTTCTCGTTACACGACTATTTCTTCTT  
CTTGGCCGTGCTCCGAGACCACGCGGCGGTAGGCATGCCTCTTCTGGGGCAGAGGCGGAGGCGACGGGCTCTCGCGGTTCC  
GCGGGCGGCTGGCAGAGCCCTTCCGCGTTCGGGGGTGCGCTCCTGGCGGCGCTGCTCTGACTGACTTCTCCGCGGCGCGG  
CATTGTGTTCTCCTAGGGAGCAACAACAAGCATGGAGACTCAGCCATCGTCGCCAACATCGCCATCTGCCCCCGCGGCCACCGC  
CGACGAGAACCAGCAGCAGAATGAAAGCTTAACCGCCCCGCGGCCAGCCCCACCTCCGACGCCGCGGCCCCAGACATGCAA  
GAGATGGAGGAATCCATCGAGATTGACCTGGGCTACGTGACGCCCGCGGAGCACGAGGAGGAGCTGGCAGCGCGCTTTTCA  
GCCCCGGAAGAGAACCACCAAGAGCAGCCAGAGCAGGAAGCAGAGAACGAGCAGAAACAGGCTGGGCACGAGCATGGCGA  
CTACCTGAGCGGGGCGAGGACGTGCTCATCAAGCATCTGGCCCGCCAATGCATCATCGTCAAGGACGCGCTGCTCGACCGC  
GCCGAGGTGCCCTCAGCGTGCGGGAGCTCAGCCGCGCTACGAGCGCAACCTTCTCGCCGCGCGTGCCCCCAAGCGCCA  
GCCCAACGGCACCTGTGAGCCCAACCCGCGCTCAACTTCTACCCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACCT

Fig. 21F

CTTTTTCAAGAACCAAAGGATCCCCGTCTCTGCCGCGCCAACCGCACCCGCGCCGACGCCCTGCTCAACCTGGGCCCCGGCGC  
CCGCCTACCTGATATCACCTCCTTGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGCGAACG  
CTCTGCAAGGAAGCGGAGAGGAGCATGAGCACCACAGCGCCTGCTGGAGTTGGAAGGCGACAACGCGCGCCTGGCGGTCC  
TCAAGCGCACGGTCGAGCTGACCCACTTCGCCTACCCGCGCTCAACCTGCCCCCAAGGTCATGAGCGCCGTCATGGACCAG  
GTGCTCATCAAGCGCGCCTCGCCCTCTCGGAGGAGGAGATGCAGGACCCCGAGAGTTCGGACGAGGGCAAGCCCGTGGTCA  
GCGACGAGCAGCTGGCGCGCTGGCTGGGAGCGAGTAGCACCCCCAGAGCCTGGAAGAGCGGCGCAAGCTCATGATGGCCG  
TGGTCTGCTGACCGTGGAGCTGGAGTGTCTGCGCCGCTTCTTGCCGACGCGGAGACCCTGCGCAAGGTCGAGGAGAACCT  
GCACTACCTCTTCAGGCACGGGTTCGTGCGCCAGGCCTGCAAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCCTACATGG  
GCATCCTGCACGAGAACCCTGGGGCAAACGTGCTGCACACCACCTGCGCGGGGAGGCCCGCCGCGACTACATCCGCGA  
CTGCGTCTACCTGTACCTCTGCCACACCTGGCAGACGGGCATGGGCGTGTGGCAGCAGTGCCTGGAGGAGCAGAACCTGAAA  
GAGCTCTGCAAGCTCCTGCAGAAGAACCTCAAGGCCCTGTGGACCGGTTTCGACGAGCGTACCACCGCCTCGGACCTGGCCG  
ACCTCATCTTCCCCGAGCGCCTGCGGCTGACGCTGCGCAACGGGCTGCCGACTTTATGAGCCAAAGCATGTTGCAAACTTTC  
GCTCTTTCATCCTCGAACGCTCCGGGATCTGCCCGCACCTGCTCCGCGCTGCCCTCGGACTTCGTGCCGTGACCTCCGCGA  
GTGCCCCCGCGCTCTGGAGCCACTGCTACTTGTGCGCCTGGCCAACTACCTGGCTACCACTCGGACGTGATCGAGGACG  
TCAGCGGCGAGGGTCTGCTGGAGTGCCACTGCCGTGCAACCTCTGCACGCCGACCCGCTCCCTGGCTGCAACCCCAAGCTG  
CTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGCCCGGCGACGCGGAGGGCAAGGGGGGTCTGAAACTCACC  
CCGGGGTGTGGACCTCGGCCTACTTGCAGTTCGTGCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCA  
ATCCAGCCGCCCAAGGCCGAGCTGTGCGCTGCGTCATACCCAGGGGGCCATCCTGGCCCAATTGCAAGCCATCCAGAAAT  
CCCGCCAAGAATTTCTGCTGAAAAAGGGCCACGGGGTCTACTTGGACCCCCAGACCGGAGAGGAGCTCAACCCAGCTTCCCC  
CAGGATGCCCGAGGAAGCAGCAAGAAGCTGAAAGTGGAGTCCCGCCGCGGAGGATTTGGAGGAAGACTGGGAGAGCA  
GTCAGGCAGAGGAGGAGGAGATGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAG  
GAAGACGAGGTGGAGGAGGCGAGGAAGAAGCAGCCGCCCGCCAGACCGTCTGCTCCTCGGCGGAGAAAGCAAGCAGCACGGA  
TACCATCTCCGCTCCGGGTCGGGTCGCGGCGGCCGGGCCACAGTAGGTGGGACGAGACCGGGCGCTTCCCGAACCCACC  
ACCCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCTGGCGGGGGCACAAAAACGCCATCGTCTCCTGCTTGAAGCCT  
GCGGGGGCAACATCTCCTTACCCGGCGCTACCTGCTTCCACCGCGGGGTGAATTTCCCCGCAACATCTTGCACTACTACC  
GTCACCTCCACAGCCCCCTACTACTGTTTCAAGAAGAGGCAGAAACCCAGCAGCAGCAGAAAACCGCGGCAGCAGCAGCTA  
GAAAAATCCACAGCGGCGGCAGGTGGACTGAGGATCGCGGCGAACGAGCCGCGCAGACCCGGGAGCTGAGGAACCGGATC  
TTTCCACCTCTATGCCATCTTCCAGCAGAGTCCGGGGCAGGAGCAGGAAGTCAAGAACCGTTCTCTGCGCTCGCT  
CACCCGAGTTGTCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACT  
GCGCGCTCACTCTAAAGAGTAGCCCGCGCCCGCCACACAGGAAAAAGGCGGGAATTACGTACCACCTGCGCCCTTCGCC  
CGACCATCATGAGCAAAGAGATTCCACGCTTACATGTGGAGCTACCAGCCCAGATGGGCTGGCCGCGCGCGCCGCCA  
GGACTACTCCACCCGATGAAGTGGCTCAGTGCCGGGCCCGCGATGATCTCACGGGTGAATGACATCCGCGCCACCGAAACC  
AGATACTCCTAGAACAGTCAGCGATCACCGCCACGCCCCGCCATCACCTTAATCCGCGTAATTGGCCCGCGCCCTGGTGTACC  
AGGAAATTTCCAGCCACGACCGTACTACTTCCGCGAGACGCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTG  
GCCGGCGGCGCGCCCTGTGTCGTACCGCCCCGCTCAGGGTATAAAGCGGCTGGTGATCCGAGGCAGAGGCACACAGCTCA  
ACGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCCAACCTCGCCGATCGGGGAGATCTTCTTCACG  
CCTCGTCAGGCGCTCCTGACTTTGGAGAGTTCGTCTCGACGCCCGCTCGGGCGGCATCGGCACTCTCCAGTTCTGTGGAGGA  
GTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCGGCCACTACCCGGACGAGTTCATCCGAACTTCGACGCCATC  
AGCGAGTCGGTGGACGGCTACGATTGAATGTCCATGGTGGCGCAGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCC  
GCCGTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGCTGCCCAGGAGCACCTCAGGGCCAGCCAC  
GGAGTGGGATCATCGTCAAGGGGGCCTCGACTCCACCTGCTTCGGATCTTCAGCCAGCGACCGATCCTGGTTCGAGCGCG  
AACAAGGACAGACCTTCTTACTTTGACTGCATCTGCAACACCCCGGCTGCATGAAAGTCTTTGTTGTCTGCTGTGACTGA  
GTATAATAAAAGCTGAGATCAGCGACTACTCCGGACTCGATTGTGGTGTCTCTGCTATCAACCGGTCCCTGTTCTTACCGGGA  
ACGAGACCGAGCTCCAGTCCAGTGTAAGCCCCACAAGAAGTACCTCACCTGGCTGTTCCAGGGTCCCCGATCGCGTTGTC  
AACCCTGCGACAACGACGGAGTCTGCTGAGCGGCCCTGCCAACCTTACTTTTTCCACCCGAGAAAGCAAGCTCCAGCTCTTC  
CAACCTTCTCCCCGGGACCTATCAGTGCGTCTCAGGACCCTGCCATCACACCTTCCACCTGATCCGAAATACCACAGCGCCG  
TCCCCGCTACTAACAACCAAACCTACCCACCAACGCCACCGTCGCGACCTTCTCTGAATCTAATACCACTACCGGAGGTGAGC  
TCCGAGGTGACCAACCTCTGGGATTTACTACGGCCCTGGGAGGTGGTGGGGTTAATAGCAAATAAAAAAATAATCATTTG  
ATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTAAACAAAATAAAGAATCACTTACTTGAAATCTGATACCAGGTCTC  
TGTCATGTTTTCTGCCAACACCACTCACTCCCTCTTCCAGCTCTGGTACTGCAGGCCCGCGGGCTGCAAACTTCTCCA

Fig. 21G

CACGCTGAAGGGGATGTCAAATTCCTCTGTCCCTCAATCTTCATTTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGG  
ATGATGACTTCGACCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCCTTCATCAACCCCCCTTCGTCTCTTCAGA  
TGGATTCCAAGAGAAGCCCTGGGGGTGTTGTCCTGCGACTGGCTGACCCCGTCACCACCAAGAACGGGGAAATCACCCTCA  
AGCTGGGAGAGGGGGTGGACCTCGACTCGTCGGGAAAACTCATCTCCAACACGGCCACCAAGGCCGCCCTCTCAGTAT  
TTCAAACAACACCATTTCCTTAAAACTGCTGCCCTTTCTACAACAACATGGAACCTTAAGCCTCAATGTCTCCACACCATTAG  
CAGTATTTCCACATTTAACACTTTAGGCATAAGTCTTGAAAACGGTCTTCAGACTTCAAATAAGTTGTTGACTGTACAACTAAC  
TCATCCTCTTACATTAGCTCAAATAGCATCACAGTAAAAACAGACAAAGGGCTATATATTAAGTCCAGTGGAACAGAGGACT  
TGAGGCTAATATAAGCCTAAAAAGAGGACTAGTTTTTGACGGTAATGCTATTGCAACATATATTGAAATGGCTTAGACTATG  
GATCTTATGATAGTGATGGAACAAAGACCCGTAATTACCAAAATTGGAGCAGGATTAATTTTGATGCTAACAAAGCAATA  
GCTGTCAAAGTACAGGTTAAGTTTGAAGTCCGCTGGTGCCTTGACAGCTGGAACAAACAGGATGACAAGCTAACACT  
TTGGACTACCCCTGACCAAGCCCTAATTGTCAATTACTTTCAGACAGAGATGCCAAATTTACTCTGTCTTACAAAATGCGGT  
AGTCAAATACTAGGCACTGTGGCAGTGGCGGTGTTACTGTAGGATCAGCACTAAATCCAATTAATGACACAGTCAAAAGCGC  
CATAGTTTTCCTTAGATTTGATTCCGATGGTGTACTCATGTCAAAGTCAATGGTAGGTGATTACTGGAACCTTAGGGAGGG  
ACAGACCACTCAAAGTGTAGCCTATACAAATGCTGTGGGATTGATGCCAAATATAGGTGCATATCCAAAAACCAAGTAAAA  
CACCTAAAAATAGCATAGTCAGTCAGGTATATTTAACTGGAGAACTACTATGCCAATGACACTAACCATAACTTTCAATGGCA  
CTGATGAAAAAGACACAACCCAGTTAGCACCTACTCTATGACTTTTACATGGCAGTGGACTGGAGACTATAAGGACAAAAAT  
ATTACCTTTGCTACCAACTCATTCTTTTTCTACATCGCCAGGAATAATCCACCCAGCAAGCCAACCCCTTTTCCACCACC  
TTTGTCTATATGAAACTCTGAAACAGAAAAATAAAGTTCAAGTGTTTTATTGAATCAACAGTTTACAGGACTCGAGCAGTTA  
TTTTCTCCACCCTCCAGGACATGGAATACACCACCTCTCCCCCGCACAGCCTGAACATCTGAATGCCATTGGTGATGGA  
CATGCTTTTGGTCTCCAGTTCCACACAGTTTCAGAGCGAGCCAGTCTCGGATCGGTGAGGAGATGAAACCTCCGGGCACT  
CCCGCATCTGCACCTCACAGCTCAACAGCTGAGGATTGTCTCGTGGTGGTGGGATCACGTTATCTGGAAGAAGCAGAAGAGC  
GGCGGTGGGAATCATAGTCCGGAACGGGATCGGCCGGTGGTGTGCGATCAGGCCCCGAGCAGTCTGCGCCGCCGCTC  
CGTCAAGCTGCTGCTCAGGGGGTTCGGGTCCAGGACTCCCTCAGCATGATGCCACGGCCCTCAGCATCAGTCGTCTGGTGC  
GGCGGGCGCAGCAGCGCATGCGAATCTCGCTCAGGTCACTGCAGTACGTGCAACACAGGACCACAGGTTGTTCAACAGTCC  
ATAGTTCAACACGCTCCAGCCGAAACTCATCGCGGGAAGGATGCTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAAATCA  
AGTGGCGCTCCCTCCAGAAGACGCTGCCATGTACATGATCTCTTTGGGCATGTGGCGGTTACCCACCTCCCGGTACCACATCA  
CCCTCTGGTTGAACATGCAGCCCCGGATGATCCTGCGGAACACAGGGCCAGCACCGCCCCGCCGCCATGCAGCGAAGAGA  
CCCCGGATCCCGGCAATGACAATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCAC  
AGCACAGGCATATGCTCATGATCTCTCAGCACTCTCAGCTCCTCGGGGGTCAAAACCATATCCAGGGCAGCGGGAACCTCTT  
GCAGGACAGCGAACCCCGCAGAACAGGGCAATCCTCGACATAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAG  
CACCGGGTGATCCTCCACCAGAGAAGCGCGGGTCTCGGTCTCTCAGCGTGTTAAGGGGGCCGGCCGATACGGGTGATGG  
CGGGACGCGGTGATCGTGTCTCGACCGTGTATGATGCAGTTGCTTTGCGACATTTTCTGACTTGCTGTAGCAGAACCTGGT  
CCGGGCGCTGCACACCGATCGCCGGCGGGCGGTCTCGGCGCTTGAACGCTCGGTGTTAAAGTTGTAACAGCCACTCTCTCA  
GACCGTGACGAGATCTAGGGCCTCAGGAGTGATGAAGATCCCATCATGCCTGATAGCTCTGATCAGTACGACACCGTGGAA  
TGGGCCAGGCCCAGCCAGATGATGCAATTTTGTGGGTTTGGTGACGGCGGGGGAGGGAAGAAGCAGGAAGAACCATGATT  
AACTTTTAAATCCAAACGGTCTCGGAGCACTTCAAATGAAGGTACGGAGATGGCACCTCTCGCCCCGCTGTGTTGGTGGAA  
AATAACAGCCAGGTCAAAGGTGATACGGTCTCGAGATGTTCCACGGTGGCTCCAGCAAAGCCTCCACGCGCACATCCAGAA  
ACAAGACAATAGCGAAAGCGGGAGGGTCTCTAATCTCAACCATCATGTTACACTCCTGCACCATCCCAAGATAATTTTCATT  
TTTCCAGCCTTGAATGATTGAACTAGTTCTGAGGTAAATCCAAGCCAGCCATGATAAAAAGCTCGCGCAGAGCACCTCCAC  
CGGCATTCTTAAGCACACCCTCATAATTCCAAGATATTCTGCTCCTGGTTCACCTGCAGCAGATTGACAAGCGGAATATCAAAA  
TCTCTGCCGCGATCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTTTTCATATCGTCTCCGAAATTTTAGCCATAGGACC  
CCAGGAATAAGAGAAGGGCAAGCCACATTACAGATAAACCGAAGTCCCCCAGTGAGCATTGCCAAATGTAAGATTGAAA  
TAAGCATGCTGGCTAGACCCGGTGATATCTCCAGATAAAGTGGACAGAAAAATCGGGTAAGCAATTTTAAAGAAAATCAACAAA  
AGAAAAATCTTCCAGGTGCACGTTTAGGGCTCGGGAACAACGATGGAGTAAGTGCAAGGGGTGCGTTCCAGCATGGTTAGT  
TAGCTGATCTGTAAAAAACAACAAAAATAAAAATTAAACCATGCTAGCCTGGCGAACAGGTGGGTAATCGTTCTCTCCAGCA  
CCAGGCAGGCCACGGGTCTCCGGCGCGACCCTCGTAAAAATTGTCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCG  
GTGGCCGGCGTGAATGATTCGAGAAGAAGCATACCCCCGGAACATTGGAGTCCGTGAGTGAACAAAAAGCGGCCGAGGAA  
GCAATGAGGCACTACAACGCTCACTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATTTTCAAGTGCGTAAA  
AAATGTAATTACTCCCCTCTGCACAGGCAGCGAAGCTCCCGATCCCTCCAGATACACATACAAAGCCTCAGCGTCCATAGCTT  
ACCGAGCGGCAGCAGCAGCGGCACACAACAGGCGCAAGAGTCAGAGAAAAAGTCTGAGCTTAACCTGTCCGCCGCTCTCTG  
CTCAATATATAGCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCAGCACAC  
GCCAGAAACCGGTGACACACTCAGAAAAATACGCGCACTTCTCAAACGGCCAAACTGCCGTCAATTTCCGGGTTCCACGCTA  
CGTCATCAAAACACGACTTTCAAATTCCGTCGACCGTTAAAAACATACCCGCCCGCCCTAACGGTCGCGCTCCCGCAGCC  
AATCACCTTCTCCTCCCAAAATCAAACAGCTCATTTGCATATTAACGCGCACCAAAAGTTGAGGTATATTATGATGATG

Fig. 21H

**AdC6 010-HIVgag (E1026) Amino acids – SEQ ID NO: 10****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVICGSGDR\*GRGG\*RFDDVAMRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFL  
 GGCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDLRGGFDYRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RLRS  
 PDPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMKNLLRVRRFALLRDVRARYTR\*H\*LLTSY\*\*\*SITGSLV  
 HSPYMEFRVT\*LTVNGPPG\*PPNDPRPLTSIMTYPIVTPIGTFH\*RQWVEYLR\*TAHLAVHQVYHMPSTPPIDVNDGKWPAAWHY  
 AQYMTLWDFPTWQYIYVLVIAITMVMRFWQYINGRG\*RFDSRGFSLHPIDVNGSLFWHQNRDFPKCRNNSAPLTQMGGRRV  
 RWEVYISRARLVNRQITRSFIADVYHS\*IANAVSASDITVSNLSCRWS\*GTGQVSIKVTRQV\*GDQ\*KLGLSRQRRLLRF\*\*APIGLT  
 DIHFALSTGVHSQFNYSS\*G\*ST\*YDSL\*ASATMGARASVLSGGELDRWEKIRLPGGKKKYKLKHIVWASRELERFAVNPGLET  
 EGCRQILGQLQPSLQGTSEELRSLYNTVATLYCVHQRIEVKDTKEALEKIEEQNKSKKKAQAAAADTGNSSQVSQNYPIVQNLQGG  
 MVHQAISPTLNWVVKVVEKAFAFSEVIMFSALEGATPQDLNMLNTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIA  
 PGQMREPRGSDIAGTTSTLQEQIGWMTNPPPIVGEIYKRWIILGNKIVRMYSPSILDIRQGPKEPFRDYVDRFYKTLRAEQASQE  
 VKNWMTETLLVQANPDCKTILKALGPAATLEEMMTACQGVGGPGHKARVLAEMSQVTNSATIMMQRGNFRNRKRTVKCFN  
 CGKEGHIAKNCRAPRKGCWKCGKEGHQMKDCTERQANFLGKIWPSHKGRPGNFLQSRPEPTAPPEESFRFGEETTPSQKQEP  
 DKELYPLASRLSFGNDPSSQ\*\*SSV\*TGPLESTRAAKPLISLDCAF\*LPAICCLPLPRAFLDPGRCHSHCPFLIK\*GNICALSE\*VSFYSG  
 GWGGAGQQGGGLGRQ\*QACWGCGLGYGF\*GGKNQICRSEFIYVGCGERGNEMVLWVLWVCINESVRYRHMLATVHVASHP  
 RKTWPEFEHNMTRCNVHLGSRRGFMFMPYQCNMQFVKVLEPDAMSRVSLTGVDNMNVELWKILRYDESKTRCRACECGGKH  
 ARLQPVCEVEDLDPDHLVLSNGTEFGSSGEESD\*SE\*CLGLGVSLHEGQND\*NWFSVCCSSMSGASFEAGGVSPYLTGRLPS  
 WAGVRQNVMGSTVDGRPVQANSTLTATLSSSSVDAASAAAAASAASAVRGMALGAGYSSLVANSSSTNNPASLNEEKLLLL  
 MAQLEALTQRLGELTQQVAQLQAETRAAVATVTK\*KMNQ\*INGDGC\*F\*HRVLNLYLIFRAR\*ALDHRSRLSTRWIFSRTR\*RW  
 AWMLRYMGMSPSRGWR\*LHCRASCSCGMVL\*ITQS\*QGRRAWCCTMSLRRLMATGSPLV\*VLTNLLSWEGCMRGEMRCILA  
 WILRLAMFPFRRRGFMLCRTTSTVYPVHLGNLSCNLEGKA\*KNLETP\*PPRFSMHSSMMMAMGPWAAAWAKTFRGSDTS\*L  
 WSWVSSS\*AILMNLGRRVPDWGTVKPSIPGA\*LPSQICISQALSSEGGIMSTCGAMKKTVSGAGEMSWAESFRSSWDLPQVGP  
 \*MTPMTGCRW\*LRRQLPSSRRRGATSFIIISRTCMFSRTSSARRRSPSERSSCEAKFFSGLSPSAMGILERVCCSSRRSSQSSVMCS  
 RASRRSPPRFAGWDCGSRAPGDGRPARPGSGPSRAAGSASAWSPSR\*RGARRAGRLRGCSGSSGWSRTAPGRRPARRPGS  
 N\*A\*VRS\*APRPRGPWRGAYLWKVRRDRGGT\*GRRAWGRGRRTGRRRPRRSWRRSRTPRAR\*GRGGWGQKRGFLRAF\*  
 CVSYLWSP\*ARVPAG\*QRCPCPRRPTLWAGPRAGCRGPRRRGTPTPRRRPGSRPARRRPRGRSGRCPPAGPPSPGYASTCPP  
 RHPHGR\*LACKCRPRDRGSRPGGYKRGAPARPHCLPDRCPGAPAVGVGIPSRRRA\*PRHSGCQFLETRRI\*Y\*RCRWRRLS\*APR  
 PFGQKRRSFCCRAWWRRSRGRWRRAAWRWSAWSGSFPCRRAPWRR\*AAARTRAPRTSIRGRW\*ARRARF\*PASRGAC\*\*G  
 PRWWPPRRAGARWSSRGARPCASRRGAAGPA\*ARRGRRPR\*RCRAGARGRSS\*CRCPDCPAPLASRARPARARRG\*GACPR  
 WGA\*ARRRTRCRRRRRGAPRGRRCRWGSSAPRGWCWRARSRTARARARGAPCRGWSVAAFRRGRRSGGRWRGSRWWRAF  
 GRC\*SGRGAGRPS\*SGRRSPAARRARR\*RGPRGRSSRGLG\*CHT\*AGPSASTARG\*EGTLRGPSTLRGGTRPDRHGKSPPC  
 RTG\*RPCRRSSPSRGRKLARPCAGRCG\*GRRCRAP\*P\*GTGA\*SRGRRSRPAPRVGSPCASCRRG\*AKRK\*HR\*RGSCPRGA\*S  
 CE\*CGKAGAPRPGC\*PGRGRSRRSR\*CCARRCRVPRIAGGP\*RGAA\*ARRR\*ARRGR\*ARAARGPSRRRGGR\*GRKSRDPR  
 PGRSASGPGTDGTGPRPFRRG\*RSRRCGRRRASGPT\*AGGRGRGRARRAAGPRRV\*PA\*RGRAACRRTPSRCRFPHRR\*GRAF  
 RCEDASRWGRTGSPATSWRNGC\*CDGSRNADGAPSTRACVYTSVRSARNAARDARAARAVPGFLWRGISVSGSALAAASRAVL  
 LGHRRGHRLPRWWSC\*RARAGGRSRPRLGRVGERGRGRAGRSCPGS\*DAESGQWAAAARG\*LAGAFPRAGGPDGT\*SPRR  
 RWWLRPRLAGCRAPGAPPCPVSSWALLPCRSEAAARTRAGRQGRLGARRQGRQGHVGAARGQVLVLRPEKTGVSDATVDV  
 DLTPLEGHGTREFEPEREFDRINLIVDGGLPQDLHVARVVLVGLDGLHLLDLLLLKVSAGALDGGREVVGDAAHELREGVHAG  
 LVPDAAVDHGSVGVARAHDHLGEVELDVAREDRVVAEALVEVVERGGDVLGDEEVHDPAAERHLADVAQGFQAFHGLVEVHGE  
 VEKLGVARRDGQLLLQKTDELGDGGAHLAELGPGGLLHLLHLL\*HLFYLLRRRWRGRGPASPAAHGQTVDEALDGLPAPATH  
 GLGDGAPVLAPQHEDAAHLQVAAGGVSVGGEGGADDASYQLTRDASAQPERLEIHGIRKPLNEGFEPAVAR\*AEPGLFFG  
 YLVGRRAGDAAGDEVEVGGPETADGGEEHQVLGPGLLDAQTVGHAPGVVLTPEVLVVLHEPLHGHLLARAABHAREPEPALR  
 LDERQVGDDALGEDGLLDLGEGLLEVVEDEAVVGSVDGVGAVGHDGPDVGLVAGSHELVLVLEARVGARVEDVVVAGAHEVL  
 VSDEEVRRRLAVERPSLGGGGAGREVLEHEAVVAVDPVGHGPDAGGGGGGARELADAVPDVAQRQEVVHGGRLAREARAVD  
 ALDIRAKTAVSGSTPWPGG\*ANGLGCACTPVRISNQAGAAANVVALPSRPKANETSRIIRRVVFWPWSLVMKN\*\*ARKAAAR  
 DGS\*SGERARVALRCAPVRASALGAGRIPRLTAWLPRRFQDPLASRLQLRSEPLFFLVFLPDASRTAADAPPPSTTTAPTAAA  
 ATAGASAPAPAAASHYRGRRRERSRRSV\*PGLGRGRGAGAAGGVVAGAAPARADEKGRSRLRAQAEPVQRQERRGARGDARL  
 PLPRGAGAAARPGPKAGAEGRGFRGGRADGDQPRARARGRGQPGHGVRADEGGEQLPKILQQPRAHLDRARGGDPGPDAPV  
 GPAGGHRAEPHEQAADGAAVSGGAAQSGQRDVQGGAAEYHRARGPLAPGPGEHFAEHRGAGARAAAVREAGGHQLLGAESG



Fig. 211

QVLR\*EDLQDPVRAHRQGGEDRRVLHAHDPESADPERRSGGVPQRQDAPRGERQPPARAERPGADAQPAAGPDRGRDRGGELL  
 \*HGRGPALAAQPPGLGSCRRFPLRGGGGGR\*GGGGRVPGRLMARPYFC\*MQQQPPPPPPDPAMRAALQSQPSGINSSDDWTQA  
 MQRIMALTTRNPEAFRQQPQANRLSAILEAVVPSRSNPHEKVLAINVALVENKAIRGDEAGLVYNALLERVARYNSTNVQTNLDR  
 MVTDVREAVSQRRERFHRESNLGSMVALNAFLSTQPANVPRGQEDYTNFISALRLMVAEVPQSEVYQSGPDYFFQTSRQGLQTVNL  
 SQAFKNLQGLWGVQAPVGDRA TVSSLLTPNSRLLLLLVAPFTDSGSVSRDYLGYLLNLYREAIGQAHVDEQTYQEITHVSRALGQE  
 DPGNLEATLNFLLTNRSQKIPQYALSTEEERILRYVQSVGLFLMQEGATPSAALDMTARNMEPSMYARNRPFINKLMDYLHRAA  
 AMNSDYFTNAILNPHWLPPPGFYTGEYDMPDPNDGFLWDDVDSSVFSRPGTNAVWKKEGGDRRPSALSGRAGAAA VPEAA  
 SPFSLPFSLSNVRSSSELGRLTRPRLLGEEYLNDSLLRPEREKNFPNNGIESLVDKMSRWKTYAHEHRDEPRASSAGTRRRQRHRRQ  
 RGLVWDDSDADDSSVLDLGGSGGNPFALHRPRIGRLM\*ESEKIKDGT HQHGDQRAFFSVVCSMMRRVYPEGPPPSYESVMQ  
 QAVAAAMQPPLEAPYVPPRYLAPTEGRNSIRYSELAPLYDTTRLYLVNKSADIASLNYQNDHSNFLT TVVQNNDFTPTEASTQTINF  
 DERSRWGGQLKTIMHTNMPNVNEFMYSNKFARVMVSRKTPNGVDDDYDGSQDELTYEWVEFELPEGNFVSMTIDLMMNNAI  
 DNYLAVGRQNGVLES DIGVKFDTRNFRLGWDPVTELVMGPVYTNEAFHPDIVLLPGCGVDFTESRLSNLLGIRKRPQFQEGFQILYE  
 DLEGGNIPALLDVEAYEKSKEDSTAAATAAVATASTEVRGDNFASAAAAAEAAETESKIVIQPVEKDSKDRSYNVLADKNTAYRSW  
 YLAYNYGDPEKGVRSWTLTSDVTCGVEQVYWSLPDMMQDPVTFRSTRQVS NYPVVGAE LLPVYSKFFNEQAVYSQQLRAFTS  
 LTHVFNRFENQILVRPPAPTITTVSENVPALTDHGTLPLRSSIRGVQRTVTDARRRTPCYVYKALGVVAPRVLSSRTF\*KMSILISPS  
 NNTGWGLRAPSKMYGGARQSTQHPVRVRGHFRAPWGALKGRVRSRTTVDDVIDQVADARNYTPAAAPVSTVDAVIDSVVAD  
 ARRYARTKSRRRIARRHRSTPAMRAARALLRRARRTGRRAMLRAARRAASGSSSAGTRRRRAATAAAAAIASMSRPRRGNVYVW  
 RDAATGVRVPVTRPRPT\*RC\*LRD VDSQRRGGCPSANTRKRCSSRLSTAPRRR\*RRKESPAN\*SGSKRTKRRRKMTDWWWS  
 LCASSPPGGACSGAGGK\*NRCCGPAPRWSSRPASVPAPPPSAPTTRCTGTRTSSSRSSVWASLRTASAAAPR\*KRRRCPSRWTT  
 ATPRRA\*SR\*PCSRCYRARRRAGASSARAARICTRPCS\*WCPSARSWRTCWST\*RWTPRCSPRSRCGPSSRWPRAWACRPWTSRS  
 PRSPWKRRPSP\*SPAPAPWRCRRIPGCQHQLPPALAEASTARPAC\*CPTTRCILPSSPRRATAARASTAATPAAAAARPPPAAVVA  
 AAAAAAPRLPPWCGECIAAGASL\*PCRARATTRASPFNYRLLADMALTCRLRVPTGYRGRKPRRRRLTGNGLRHHHRRRRRAISK  
 LGGGFLPALIPAAAAIGAIPGIASVAVQASQRH\*DTKKHGFVIKKMD\*RSWSCDVCF\*MEDINFSSLAPRHGTRPFMGWTS DIGN  
 SQLNGGAFNWSSLWSGLKNFGSTLKYGNKAWNSSTGQALREKLEQNFQKQVVDGLASGINGVVDLANQAVQKQINSRLDAV  
 PPAGSVEMPQVEEELPLDKRGDKRPRDAEETLLHTDEPPPYEEAVKLGLPTTRPVAPLATGVLPKSSSQPATLDLPPPRPSTVAK  
 PLPPVAVASRAPRGRPQANWQSTLNSIVGLGVQSVKRRRCY\*KTL\*RLTCLSVICMSADQKEECEARRRVARWPPHRCPPSGRT  
 CTSPDRTLST\*VRVWCSSPAPQTPTSVWGTS LGTPRWRPRTM\*PPTAASG\*RCASCPWTARTTPTRTKCATRWPWATTACWT  
 WPAPLTSAACWTGALASNP TLAPPTA\*LPRELPIPASGSKQKQAMGELWKHTHMVWPQWAERILQKMFVKLELT LQRIRINQF  
 MPTKHFNQNRK\*EKKIGKCLKTFMAVELLKKQT\*NLAMAPMLDPPMKKEVKLNKLEMMEFQPKNST\*TWLSLILPVAP\*TVKTS  
 IKQTLSCIPKTRIWK LQTRM WYTQARMMQVLKLTWFSSLCPTDPTTLGSGTTL SVLCTTALAIWVCLLVPPS\*MLWLICKTETP  
 SCPTSSCLTLWVTEPGISVCGTRRWVTMPMCASSKTMVWRMNCQTIASPW TALALTPHTKV\*K\*KMVKMVMLRVNGKMTILL  
 QLEINYVKVTFSPWRLISRLTCGEVSSTRTWPCPTPTSTRRPTSRCRPTPTIT\*MAE\*HLPRW\*TPTSTSGRAGRWTWPWTSTP  
 STTTATRACATAPCSWATGATCPSTSRCPKSFSPSRASCSCPGPTPTSGTSARTST\*SCRAP\*ATTCARTGPPSPSPASTSTPPSPWR  
 TTPPPSRPCCATPTTSPSTTSRRPTCSTPSRPTPPTCPSPSRATGPPSADGPSRA\*RPARRPRSAGSTPTSSTRAPSPT\*TAPSTS  
 TTPSRSPSPSTPPSAGPATTAS\*RPTSSKSSAPSTERDTTWPSAT\*PRTGWSRCPWPTTTSATRASTCPRATRTACTPSSATSSP\*AA  
 RSWTRSTTRTPSPWPTSTTTRASSATSRPPCARASPTPTTPTRSSARAPSPASPRKSSSATGSCGASPPATSCPWARSPTSARTC  
 STPTPPTR\*T\*ISKSTPWSMPPFMSLSSKSTSECTSPTAASSKPSTCARPSRPATPPPKPLLLAR\*RRAPASRSSGPSSATWAAGPA  
 SWAPSTSASLDSWPRTSWPAPS\*TRPAARPGASTGWSPGTRAPTHATSSTPSGSRTSASSRSTSSSTRACCAAPWPPRTAASP  
 WKSPPRPCRVRARPPAGSSAACSTPCTGPTAPWTRTPP\*TY\*RGCTACSSRPWNPPCAATRKRSTASSMPTPTFAPTARAS  
 RRPPPSTA\*IKTCKKPVCECFIHNKQHMFMPPSRL\*LYLEIEGVL PALGMARGQGYVAELVLGQPLELGDQQLGHGEVGERVAP  
 QLARELQGAQQVGRGDLEIAVGTRVLRARVAHVHGAALAEHQGRVLHACQHRRVGDALHVQILGVGHPEGGHLAGLPPHAGHA  
 AGLVVAIAVQGDQHHLGLGAHARVHGLHESLQAEGLRLAALGEEDPAGLARELVGGAAGVVHAAARVVVGQLHHAAPPAVL  
 GDLGPVGVLQRALPVLARHIHLDVLLDHHGPVQAPQALGFGAAVQPQRAAGALPVLVGD LGVRVHEALQEAHHRGQGLV  
 AGEQQRDAAVLLVHIQVADA AVHLALLGHQLEGLQVALHAVPVHQQRHFFHALLPGRNDRQAQGV LHRHCHLSRRRRGQGVV  
 LVQGLKHS LAVLLDDAHGGKAEAHGRQLLLGLPFVLAVLADVLQRHMLGLAGFLGRQRRRRRCAGRARVLVHHDYFFFLAVVRDH  
 AAVGMPLLGQRRRRRALAVRRAAGRAPSAFGGALLAALL\*LTSSAAGHCVLLGSNNKHGDSAIVANIAICPRRHRRREPAAE\*KLNR  
 PAAQPHLRRRGPRHARDGGIHRD\*PGLRDARGARGGAGSALFSPGREPPRAARAGSRERAEPGWARAWRLPERGRGRAHQASG  
 PPMHHRQGRAARPRRGAPQRGGAQPLRAQPLLAARAPQAPAQRHL\*APAPQLLPGLRGARGPGHLPPLFQEPKDPRLPRQP  
 HPRRRPAQPGRRPPT\*YHLLGRGSQDLRSGGQRRDSGRERSARKRGA\*APQRPGGVGRRQRAPGGPQAHGRADPLRLPGAQ  
 PAPQGHERRHGPAGHARLAPLGGGDAGPREFGRGQARGQRRRAAGALAGSE\*HPPEPGRAAQAHDRGPGDRGAGVSAPLLC  
 RRGDPAQGRGEPALPLQARVRAPGLQDLQRGADQPGLLHGHAPAREPPGAKRAAHPARGGPPRLHPRLPLVPLPHLADGHGRV

Fig. 21J

AAVPGGAEPERALQAPAEPPQGPVDRVRRAYHRLGPRPHLPAPAAADAAQRAARLYEPKHVAKLSLFHPRTLDRPARHLLRAALG  
 LRAADLPRVPPAALEPLLLAAPGQLPGLPLGRDRGRQRRGSAGVPLPLQLHAAPLPLQPPAAERDPDRHRLRVARPRRRRGQG  
 GSETHPGAVDLGLLAQVRARGPLSLRDQVLRGPIAAQGRAVGLRHHPGGHPGPIASHPEIPPRISAEKGPRGLLGPPDRRGAQPQ  
 LPPGCPEEAARS\*KWSCRRRIWRKTGRAVRQRRRWKTGTALRQRTACKTVWRRKTRWRRQRKKQPPDRRPRRRKQAARIP  
 SPLRVGVAAAGPTVGGTRPGASRTPPRPVRRSGRDTSPGGGKTTPSSPACKPAGATSPSPGATCSSTAG\*TSPATSCITTVTSTAPT  
 TVSKKRQKPSSSRKPAAAAARKSTAAAGGLRIAANEPAQTRELNRIFPTLYAIFQQSRGQEQELKVKNRSLRSLTRSCLYHKSEDLQ  
 RTLEDAEALFNKYCALTLKE\*PAPAHTRKAGITSPAPFARPS\*AKRFRLTCGATSPRWAWPPAPPRTTPPA\*TGSPVGPGR\*SHG\*  
 MTSAPTETRYS\*NSQRSPRPAILIRVIGPPPWCTRKFSPRPYFRETPRPKSS\*LTQVSSWPAAPPCVVTAPLRV\*SGW\*SEAE  
 HSSTTRW\*ALRWVCDLTESSNSPDRGDLPSRLVRPS\*LWRVRPRSPARAASALSSSWRSSLPRSTSTPSPAPPATTRTSSRTSTPSAS  
 RWTATIECPMVAQLT\*LGFDTWTTAAASAASLGISPLTLSCPRSTLRAQPTCEGSSSKGASTPTCFGSSASDRSWSSANKDRPFL  
 CTASATTPACMKVFFVCCVLSIIKAEISDYSGLDCGVPAINRSLFFTNETELQLQCKPHKKYLTWLFQGSPIAVVNHCDNDGVLLSGP  
 ANLTFSTRSKLQLFQPFPGTYQCVSGPCHHTFHLPNTTAPLPATNNQTTHQRHRRDLSSSENTTTGGELRGRPTSGIYYPWEVV  
 GLIANKNNHLLI\*NKDTIILMI\*V\*QK\*RITYLKSDTRSLMFSANTTSLPSSQLWYCRPRAANFLHTLKGMSNSSCPSIFILSSIRCPKS  
 ASGWMMTSTPSTPTMQTTHRPCSSTPPSSLQMDSKRSPWGCCPCDWLTPSPRTGKSPSSWERGWTSTRRENSSPTRPPRPP  
 LSVFQTTFPFLKLLPLSTTTMEL\*ASMSPHH\*QYFPHLT\*A\*VLETVFRQLQISC\*LYN\*LILLHSAQIASQ\*KQTKGYILTPVETEDLRLI\*  
 A\*KED\*FLTVMLLQHILEMA\*TMDLMIVMEKQDP\*LPKLEQD\*ILMLTKQ\*LSN\*AQV\*VLTPLPV\*QLETNRMTS\*HFGPLTQA  
 LIVNYFQTEMPNLLSVLQNAVVKY\*ALWQWRLL\*DKH\*IQMLTQSKAP\*FSLDLIPMVYSCQTHQW\*VITGTGRDRPLKV\*PIQ  
 MLWDSCQI\*VHIQKPKVKHLKIA\*SVRYI\*LEKLLCQ\*H\*P\*LSMALMCKKTQPQLAPTL\*LLHGSGLTIRTILPLPTHSLFPTSPRN  
 NPTQQANPFSHHLCYGNSETEK\*SSSVLLNQFYRTRAVIFPPPSQDMEYTTLSPTALNI\*MPLVMDMLLVSTFHTVSEASLGS  
 VREMKPSGHSRICTSQLNS\*GLSSVVGITVIWKKQKSGGGNHSPTGSAGGVASGPAAVAAAAAPSSCCSGGSGPGTPSA\*CPRPS  
 ASVVWCGGRSSACESRSGHCSTCNTGPPGCSTVHSSTRSSRNSSREGCYPRGRTRSSGKSSGAPSRRRCPCT\*SPWACGGSPPPG  
 TTSPSG\*TCSPG\*SCGTTGPAPPRPPCSEETPDGNDNGGPTARTRGSSGS\*TSLCWHSTGICSCISSALSAPRGSKPYPRARGTLA  
 QRTPQNRILAHNLHCAWTGYRNQAAPGDPPPEKGRSRSRPHSVVRGPADTGDGGTRLIVFSTVS\*CSCFRFTSYLL\*QNLVRLHT  
 DRRRRSRRLERSVLKL\*NSHSLRPCSRASGVMKIPSCIALITSTTVEWARPSQMMQFCWVSVTAGEGRTGRTMINF\*SKRSRST  
 SK\*RSRRWHLSPPLCWWKITARSKVIRFSRCSTVASSKASTRTSRNKTIKAGGFSNSSTIMLHSCITIP\*FSFFQP\*MIRTSS\*GKSKP  
 AMIKSSRRAPSTGILKHTLIIPRYSAPGSPAAD\*QAEYQNLCDP\*APPSAITVSTLSYRLRNF\*P\*DPQE\*EKGKPHYR\*TEVPPSEHC  
 QM\*D\*NKHAG\*TR\*YLPDNWTEENRVSNF\*ENQQKKNLPGARLGPREQRWSKCKGCVPAWLVS\*SVKKQKIKH\*TMLAWRTGG  
 \*IVLSSTRQATGSPARPS\*KLSL\*LKTITERRSRWPA\*MIREEAYTPGTLESVSEKKRPRKQ\*GTTTLTKSSKAMPCG\*STKFSGA\*KM  
 \*LLPSCTGSEAPDPSRYTYKASASIAAAAAAHNRKRSQRKD\*ALTCPPALCSIYSPRSTLT\*RPKSKNTRQIITHAQHTPRNR\*HTQ  
 KNTRTSSNGQTAVISGFPRYVIKTRLSNSVDR\*KHHPPRP\*RSPLQPITFLPPQIQTALHINAHQKFEVYY\*\*

Fig. 22A

**AdC7 010-HIVgp140(E1469) Nucleic Acids – SEQ ID NO: 3**

CATCATCAATAATATACCTCAAACCTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCCGAGAGACGGGGCGACCGTTAGGGGCGGGGCGGGTGACGTTTTGATGACGTGGCCGTGAGGCGGAGCCGGTTTGCAA  
GTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTCCCGCGCTCTCTGACAGGAAAT  
GAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAAAACCTGAATGAGGAAGTGAAAATCTGAGTAATTT  
CGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTT  
CACCTAAATTTCCGCGTACGGTGTCAAAGTCCGGTGTTTTACGTACGATATCATTTCCCCGAAAGTGCCACCTGACCGTAACTA  
TAACGGTCCTAAGGTAGCGAAAGCTCAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGT  
TAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTGCGTGAGTAGTGCGCGAGCAAATTTAAGCTACAACAAGGCAAGGC  
TTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTG  
ACATTGATTATTGACTAGTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCCCTGGCATTATGCCCAGTA  
CATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTAC  
ATCAATGGGCGTGATAGCGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTGGCA  
CCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCATTGACGCAAATGGGCGGTAGGCGTGACGGTGGGAG  
GTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAAC  
GCAGTCAGTGCTTCTGACACAACAGTCTCGAACTTAAGGCTAGAGTACTTAATACGACTCACTATAGGCTAGTTAAGGCTAGA  
GTTTCGACGCCACCATGCGCGTGATGGGCATCCTGCGCTCTACCAGCAGTGGTGATCTGGGGCATCCTGGGCTTCTGGATGC  
TGATGATCTGCAACGTGTGGGGCAACCTGTGGGTGACCGTGTAACGCGTGCCCGTGGAAGGAGGCCAAGACCACCT  
GTTCTGCGCTCCGACGCCAAGGCCACAAGGAGGAGGTGCACAACATCTGGGCCACCCACGCCTGCGTGCCACCGACCCCA  
ACCCCCAGGAGATCGTGCTGAAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGAACAGATGCACGAGG  
ACATCATCTCCCTGTGGGACCAGTCCCTGAAGCCCTGCGTGGAAGCTGACCCCCCTGTGCGTGACCTGAACTGCTCCGACGTGA  
AGATCAAGGGCACCAACGCCACCTACAACAACGCCACCTACAACAACAACAACACCATCTCCGACATGAAGAAGTCTCCTTCA  
ACACCACCACCGAGATCACCGACAAGAAGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGGCCCTGGACGGCAA  
GGAGACCAACTCCACCAACTCTCCGAGTACCGCCTGATCAACTGCAACACCTCCGCCGTGACCCAGGCCTGCCCAAGGTGTC  
CTTCGACCCCATCCCATCCACTACTGCGCCCCCGCCGGCTACGCCATCTGAAGTGCAACAACAAGACCTTCAACGGCACCGG  
CCCCTGCAACAACGTGTCCACCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGTCCACCCAGCTGCTGTGAACGGCTCCCT  
GGCCGAGGAGGAGGTGGTGATCCGCTTCGAGAACCTGACCAACAACGCCAAGATCATCATCGTGACCTGAACGAGTCCGTG  
GAGATCAACTGCACCCGCCCCCTCCAACAACACCCGCAAGTCCGTGCGCATCGGCCCGGCCAGACCTTCTTCGCCACCGGCCA  
CATCATCGGCGACATCCGCCAGGCCCACTGCAACATCTCCGCAAGAAGTGGAACACCACCCTGCAGCGGTGAAGGAGAAG  
CTGAAGGAGAAGTTCCCAACAAGACCATCCAGTTCGCCCCCTCTCCGGCGGCGACCTGGAGATCACCAACCACTCTTCAAC  
TGCCGCGGCGAGTTCCTTACTGCTACACCTCCGACCTGTTCAACTCCACCTACATGTCCAACAACACCGGCGGCGCAACATC  
ACCTGCAGTGCCGCATCAAGCAGATCATCCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCGCCGGCA  
ACATCACCTGCAAGTCCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGAGAAGAACGACACCGAGACCTTCG  
CCCCGGCGGCGGCGACATGCGCGACAACCTGGCGCTCCGAGCTGTACAAGTACAAGGTGGTGGAGATCAAGCCCCCTGGGCATC  
GCCCCGACAAGGCCAAGCTGACCGTGACGGCCCGCCAGCTGCTGTCCGGCATCGTGACGACGAGTCCAACCTGCTGCGCG  
CCATCGAGGCCCAGCAGCATGCTGCAGCTGACCGTGTTGGGGCATCAAGCAGCTGCAGACCCGCGTGTGGCCATCGAGCG  
CTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCTCCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACGCCT  
CCTGGTCCAACAAGTCTACGAGGAGATCTGGGGCAACATGACCTGGATGCAGTGGGACCGCGAGATCAACAACACCAAA  
CACCATCTACTCCCTGCTGGAGGAGTCCAGAACAGCAGGAGAAGAACGAGAAGGACCTGCTGGCCCTGGACTCCTGGGAG  
TCCCTGTGGTCTGTTCAACATCACCAACTGGCTGTGGTAAGGTACCTCTAGAGTCGACCCGGGCGGCCAAACCGCTGATCA  
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCCGTGCTTCTTGACCCTGGAAGGTGCCACTCCCA  
CTGTCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAG  
GACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAG  
AACCAGCAGATCTGCAGATCTGAATTCATCTATGTCGGGTGCGGAGAAAGAGGTAATGAAATGGCATTATGGGTATTATGGG  
TCTGCATTAATGAATCGGCCAGATATCGATATGCTGGCCACCGTGATGTGACCTCGACCCCCGCAAGACATGGCCCGAGTTC  
GAGCACAACGTCATGACCCGATGCAATGTGCACCTGGGGTCCGCCGAGGCATGTTTCATGCCCTACCAAGTGAACATGCAATT  
TGTGAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGCTGTGAAAA  
ATTCTGAGATATGATGAATCCAAGACCAGGTGCCGGGCTGCGAATGCGGAGGCAAGCACGCCAGGCTTCAGCCCGTGTGTG  
TGGAGGTGACGGAGGACCTGCGACCCGATCATTTGGTGTGCTGCAACGGGACGGAGTTCGGCTCCAGCGGGGAAGAATC

Fig. 22B

TGACTAGAGTGAGTAGTGTTTGGGGGAGGTGGAGGGCTTGATGAGGGGCAGAATGACTAAAATCTGTGTTTTCTGTGTGT  
TGCAGCAGCATGAGCGGAAGCGCCTCCTTTGAGGGAGGGGTATTACGCCCTTATCTGACGGGGCGTCTCCCTCCTGGGCGG  
GAGTGCCTCAGAATGTGATGGGATCCACGGTGGACGGCCGCCGTGACGCCCGCAACTCTCAACCCTGACCTACGCGAC  
CCTGAGCTCCTCGTCCGTGGACGCAGCTGCCGCCGAGCTGCTGCTCCGCCGCCAGCGCCGTGCGCGGAATGGCCCTGGG  
GCCGGCTACTACAGCTCTCTGGTGGCCAACTCGACTTCCACCAATAATCCCGCCAGCCTGAACGAGGAGAAGCTGCTGCTGCT  
GATGGCCAGCTCGAGGCCCTGACCCAGCGCCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGCAGGCGGAGACGCGGGC  
CGCGTTTGCCACGGTGAAAAACCAATAAAAAATGAATCAATAATAAACGAGACGGTTGTTGATTTTAACACAGAGTCTTGA  
ATCTTTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATTTTTTCAGGACCC  
GGTAGAGGTGGGCTTGGATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGT  
GCTCGGGGTGGTGTGTAATCACCCAGTCATAGCAGGGGCGCAGGGCGTGGTGTGTCACGATGTCCTTGAGGAGGAGAC  
TGATGGCCACGGGCAGCCCTTGGTGTAGGTGTTGACGAACCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGAT  
GCATCTTGGCCTGGATCTTGAGATTGGCGATGTTCCCGCCAGATCCCGCCGGGGTTCATGTTGTGCAGGACCACAGCAG  
GTGTATCCGGCGCACTTGGGGAATTTGTATGCAACTTGAAGGGAAGGCGTGAAAGAATTTGGAGACGCCCTTGTGACCGC  
CCAGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCCGTGGGCGGCGGCTGGGCAAAGACGTTTCGGGGGTCCGA  
CACATCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAATGAATTTGGGGCGGAGGGTGCCCGACTGGGGGACG  
AAGGTGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGCATCTCCAGGCCCTTGAGCTCGGAGGGGGGGATCATGT  
CCACCTGCGGGGCGATGAAAAAACGGTTTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAGGTTCCGGAGCAGCTGG  
GACTTGCCGCAGCCGGTGGGGCCGTAGATGACCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCC  
TCGCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACATGCATGTTCTCGCGCACGAGTCCGCCAGGAGGCGCTCGCC  
CCCCAGCAGAGAGGAGCTCTTGACGCGAGGCGAAGTTTTTCAGCGGCTTGAGYCCGTGCGCCATGGGCATTTTGAGAGGGT  
TGTTGCAAGAGTTCAGACGGTCCAGAGCTCGGTGATGTGCTTAGGGCATCTCGATCCAGCAGACCTCCTCGTTTCGCGGG  
TTGGGGCGACTGCGGGAGTAGGGACAGGCGATGGGCGTCCAGCGAGGCCAGGGTCCGGTCTTCAGGGTCGACGGGTC  
CGCGTCAGCGTGGTCTCCGTCACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCGGC  
TGGTCGAGAACCGTCCCGGTGCGCGCCCTGCGCGTGGCCAGGTAGCAATTGAGCATGAGTTCGTAGTTGAGCGCCTCGGC  
CGCGTGGCCCTTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGACAGCGGGACAGAGGAGGGACTTGAGGGCGTAGAGCTT  
GGGGGCGAGGAAGACGGACTCGGGGGCGTAGGCGTCCGCGCCGAGCTGGCGCAGACGGTCTCGCACTCCACGAGCCAGG  
TGAGGTGCGGGCCGGTTGGGGTCAAAAACGAGGTTTCTCCGTGCTTTTTGATGCGTTTCTTACCTCTGGTCTCCATGAGCTCGT  
GTCCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACTTTATGGGCCGGTCTCGAGCGGGGTGCCGCGGTC  
CTCGTCGTAGAGGAACCCCGCCACTCCGAGACGAAGGCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGAGGGGTA  
GCGGTGTTGTCCACCAGCGGGTCCACCTTCTCCAGGGTATGCAAGCACATGTCCCTCTGTCCACATCCAGGAAGGTGATTG  
GCTTGTAAGTGTAGGCCAGTGACCGGGGTCCCGGCCGGGGGGTATAAAGGGGGCGGGCCCTGCTGCTCCTCACTGTC  
TTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTCAAGGCTGGCATAACCTCGGCACTCAGGTTGT  
CAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTGGAGACGCCCTTCATGAGCCCTCGTCCATCTGGTCAGAA  
AAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCCGTAGAGGGCGTTGGAGAGGAGCTTGGCGATGGAGCGCATG  
GTCTGTTCTTTTCTTGTGCGCGCGCTCCTTGGCGCGATGTTGAGCTGCACGTACTCGCGCGCCACGCACTTCCATTGGGG  
AAGACGGTGGTGAGCTCGTCGGGCACGATTCTGACCCGCCAGCCGCGTTGTGCAGGGTGATGAGGTCCACGCTGGTGCCA  
CCTCGCCGCGCAGGGGCTCGTTGGTCCAGCAGAGGCGCCCGCCCTTGCGCGAGCAGAAGGGGGGCGAGCGGGTCCAGCATGA  
GCTCGTCGGGGGGGTGCGCGTCCACGGTGAAGATGCCGGGCAGAAGCTCGGGGTGCAAGTAGCTGATGCAGGTGTCCAGAT  
CGTCCAGCGCCGCTTGCCAGTCCGCGCAGGCCAGCGCGCGCTCGTAGGGGCTGAGGGGCGTGCCCAAGGCATGGGGTGCG  
TGAGCGCGGAGGCGTACATGCCGAGATGTCTGATAGCTAGAGGGGCTCCTCGAGGACGCCGATGTAGGTGGGGTAGCAGC  
GCCCCCGCGGATGCTGGCGCGCACGTAGTCGTACAGCTCGTGCAGGGGCGCGAGGAGCCCCGTGCCAGGTTGGAGCGTT  
GCGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAGTTGGAGGAGATGGTGGGCCTTGGAAGATGTTGA  
AGTGGGCGTGGGGCAGGCCGACGAGTCCCTGATGAAGTGGGCGTAGGAGTCTGCAGCTTGGCGACGAGCTCGGCGGTGA  
CGAGGACGTCCAGGGCGCAGTAGTCGAGGGTCTCTTGGATGATGTCTGTAAGTGGGCTTCTGCTTCCACAGCTCGCGG  
TTGAGAAGGAACTTTCGCGTCTTCCAGTACTCTTCAAGGGGGAACCGTCTGATCGGCACGGTAAGAGCCACCATGTA  
GAACTGGTTGACGGCCTTGATAGGCGCAGCAGCCCTTCTCCAGGGGAGGGCGTAAGCTTGTGCGGCCCTTGCGCAGGGAGGTG  
TGGGTGAGGGCGAAGGTGTGCGCACCATGACCTTGAGGAACTGGTGCTTGAAGTCGAGGTGTCGACGCCGCCCTGCTCCC  
AGAGCTGGAAGTCCGTGCGCTTCTTGTAGGCGGGGTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGCG  
GGGATGAAGTTGCGAGTGATGCGGAAAGGCTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGGACGATCTC  
GTCGAAGCCGTTGATGTTGTGCCGACGATGTAGAGTTCCACGAATCGCGGGCGGCCCTAACGTGGGGCAGCTTCTGAGCT  
CGTCGTAGGTGAGCTCGGCGGGGTGCTGAGCCCGTGTCTGCTGAGGGGCCAGTCGGCGACGTGGGGGTGGCGCTGAGGA

Fig. 22C

AGGAAGTCCAGAGATCCACGGCCAGGGCGGTCTGCAAGCGGTCCCGGTACTGACGGAACTGCTGGCCCCACGGCCATTTTTTC  
GGGGGTGACGCAGTAGAAGGTGCGGGGGTCCCGTGCACGCGGTCCCACTTGAGCTGGAGGGCGAGGTCGTGGGCGAGCT  
CGACGAGCGCGGGTCCCGGAGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGT  
AGGTTTCCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCGATGGGAAGAAGTGGATCTCTGCCACCA  
GTTGGAGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGCGCCGAGCACTCGTGCTTGTGTTTATACAAGCGT  
CCGCAGTGCTCGAACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGGGTTCCTTTGACGAGGAATTTCACTGGGCA  
GTGGAGCGCTGGCGGCTGCATCTGGTGCTGTAACGTCCTGGCCATCGGCGTGGCCATCGTCTGCCTCGATGGTGTCATGC  
TGACGAGCCCGCGCGGGAGGCAGGTCCAGACTTCGGCTCGGACGGGTGCGAGAGCGAGGACGAGGGCGCGCAGGCCGAG  
CTGTCCAGGGTCTGAGACGCTGCGGAGTCAGGTCACTGGGCGAGCGGGCGCGCGGTTGACTTGACGAGCTTTTCCAGG  
GCGCGCGGGAGGTCCAGATGGTACTTGATCTCCAGGCGCGGTTGGTGCGACGTCCACGGCTTGACGGGTCCCGTGCCCT  
GGGGCGCCACACCGTGCCCGTTTCTTGGGCGCTGCTTCCATGCCGTCAGAAGCGGCGGCGAGGACGCGCGCGGGC  
GGCAGGGGCGGCTCGGGACCGGAGGCAGGGGCGGCAGGGGCACGTGCGCGCGCGCGCGGGCAGGTTCTGGTACTGCGC  
CCGGAGAAGACTGGCGTGAGCGACGACGCGACGGTTGACGTCTGGATCTGACGCTCTGGGTGAAGGCCACGGGACCCGT  
GAGTTTGAACCTGAAAGAGAGTTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCTGCCGAGGATCTCTGACGTGCG  
CCGAGTTGCTCTGGTAGGCGATCTCGGTCACTGCTGATCTCTCTCTGAAGGTCTCCGCGCCGCGCGCTGACG  
GTGGCCGCGAGGTCGTTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTTCATGCCGCTCGTTCCAGACGCGGCTGAGA  
CCACGGCTCCGTCGGGGTTCGCGCGCGCATGACCACCTGGGCGAGGTTGAGCTGACGTGGCGCGTGAAGACCGGTAGT  
GCAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGCGATGTGCTCGGTGACGAAGAAGTACATGATCCAGCGCGGAGCG  
GCATCTCGTGACGTGCGCCAGGGCTTCAAGCGCTCCATGGCTCGTAGAAGTCCACGGCGAAGTTGAAAACTGGGAGTTG  
CGCGCCGAGACGGTCAACTCTCTCCAGAAGACGGATGAGCTCAGCGATGGTGCGCGCACCTCGCGCTCGAAGGCCCGG  
GGGGCTCTCTCTTCCATCTCTCTCTCCACTAACATCTCTTCTACTTCTCTCAGGAGGCGGCGGGGGAGGGGCCCT  
GCGTCGCCGCGCGCACGGGACAGCGGTGATGAAGCGCTGATGGTCTCCCGCGCGCGGACGCATGGTCTCGGTGAC  
GGCGCGCCGCTCTCGCGGGGCCGACGTGAAGACGCGCGCATCTCAGGTGGCGCGGGGGGTTCTCGGTTGGG  
CAGGGAGAGGGCGCTGACGATGCATCTTCAATTGGCCGTAGGACTCCGCGCAAGGACCTGAGCGTCTCGAGATCCACG  
GGATCCGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGAGTCGCAAGGTAGGCTGAGCCCGGTTTCTGTTCTTCGGGGA  
TTTCGGGAGGCGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAGTAGGCGGTCTGAGACGGCGGATGGTGCGAGGAGC  
ACCAGGTCTTGGGCCGGCTTGTGGATGCGCAGACGGTCGGCCATGCCAGGCGTGGTCTGACACCTGGCGAGGTCT  
TGAGTAGTCTGATGAGCCGCTCCACGGGACCTCTCTCGCCGCGCGGCGGTCATGCGCGTGAGCCGAACCCGCGC  
TGGGGCTGGACGAGCGCCAGGTGCGCGACGACGCGCTCGGCGAGGATGGCTGCTGTATCTGGGTGAGGGTGGTCTGGAAG  
TCGTGCAAGTCGACGAAGCGGTGGTAGGCTCCGGTGTGATGGTATAGGAGCAGTTGGCCATGACGGACCAATTGACGGTCT  
GGTGCGCGGTGCGACGAGCTCGTGGTACTTGAGGCGCGAGTAGGCGCGGTGTCGAAGATGTAGTCGTTGAGGTGCGCA  
CGAGGTACTGGTATCCGACGAGGAAGTGCAGCGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGCGCGGGC  
GCGAGGTCTCGAGCATGAGGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGCGCGGCTGGTGAGGCG  
CGCGGAACTCGCGACGCGGTTCCAGATGTTGCGCAGCGGACAGGAAGTAGTTCATGGTGCGCGGCTTGCGCCGTGAGG  
CGCGCGAGTCGTGGATGCTCTAGACATACGGGCAAAACGAAAGCGGTGAGCGGCTCGACTCCGTGGCCTGGAGGCTAAGC  
GAACGGGTTGGGCTGCGCGTGTACCCCGTTTCAATCTCGAATCAGGCTGGAGCCGAGCTAACGTGGTACTGGCACTCCCG  
TCTCGACCAAGCTGCTAACGAAACCTCCAGGATACGGAGGCGGGTGGTTTTTGGCCTTGGTCTGGTCTGATGAAAACTA  
GTAAGCGCGAAAGCGACCGCCCGGATGGCTCGTGCCGTAGTCTGGAGAAAGAATCGCCAGGGTGGCTGCGGTGCGGTGCC  
CCGGTTTCAGGCCTCAGCGCTCGGCGCGCGGCGGATTCCGCGGCTAACGTGGGCGTGGCTGCCCCGTCGTTTCAAGACCCCTT  
AGCCAGCCGACTTCTCAGTTACGAGCGAGCCCTCTTTTCTGTGTTTTTCCAGATGCATCCCGTACTGCGGCAGATGCG  
CCCCACCTCCACCTAACCGCCCCCTACCGCGCAGCAGCAACAGCCGCGCTTCTGCCCCGCCCCAGCAGACGACG  
CACTACCGCGCGCGCGCGGTGAGCGGAGCGCGGTTAGTATGACCTGGCCTTGAAGAGGGCGAGGGGCTGGCGCGGCT  
GGGGGCGTCTGCGCGGAGCGGCACCGCGCGTGCAGATGAAAAGGACGCTCGCGAGGCTACGTGCCAAGCAGAACCT  
GTTAGAGACAGGAGCGGCGAGGAGCCGAGGAGATGCGCGCCTCCCGCTTCCACGCGGGGCGGGAGCTGCGCGCGGCGCT  
GGACCGAAAGCGGGTGTGAGGGACGAGGATTTTCAGAGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCACGTGG  
CCGCGGCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCAAAAATCTTCAACAACCACGTGCG  
CACGTGATCGCGCGGAGGAGGTGACCCTGGGCTGATGCACCTGTGGGACCTGCTGGAGGCCATCGTGACAGAACCCACG  
AGCAAGCCGCTGACGGCGCAGCTGTTTCTGGTGGTGACGACAGTCGGGACAACGAGACGTTACGGGAGGCGCTGCTGAAT  
ATCACGAGCCCGAGGGCGGCTGGCTCTGGACCTGGTGAACATTCTGACAGCATCGTGGTGAGGAGCGCGGGCTGCCGC  
TGTCGAGAAAGCTGGCGGCTATCAACTTCTGGTGCTGAGCCTGGGCAAGTACTACGCTAGGAAGATCAAGAACCCCGTAC  
GTGCCATAGACAAGGAGGTGAAGATCGACGGTTTTACATGCGCATGACCCTGAAAGTGTGACCTGAGCGACGATCTGG

Fig. 22D

GGGTGTACCGCAACGACAGGATGCACCGCGCGGTGAGCGCCAGCCGCCGGCGGAGCTGAGCGACCAGGAGCTGATGCACA  
GCCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCGCTGGCAGCCCA  
GCCGCCGGGCCCTTGGAAGCTGCCGGCGGTTCCCTACGTGGAGGAGGTGGACGATGAGGAGGAGGAGGGCGAGTACCTG  
GAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAGCAACAGCCACCGCCTCTGATCCCGCGATGCGGGCGGCGCTGCA  
GAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAATCCCG  
AAGCCTTTAGACAGCAGCCTCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTGGTGCCTCGCGCTCGAACCCACGCAC  
GAGAAGGTGCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCATCCGCGGCGACGAGGCCGGGCTGGTGTACAACGCG  
CTGCTGGAGCGCGTGGCCCGCTACAACAGCACCAACGTGCAGACGAACTGGACCGCATGGTGACCGACGTGCGCGAGGCG  
GTGTGCGAGCGGAGCGGTTCCACCGCGAGTCGAACCTGGGCTCCATGGTGGCGCTGAACGCCTTCTGAGCACGCAGCCCG  
CCAACGTGCCCCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCGCTGCGGCTGATGGTGGCCGAGGTGCCCCAGAGCGA  
GGTGTACCAAGTCGGGGCCGACTACTTCTTCCAGACAGTCGCCAGGGCTTGACAGCCGTGAACCTGAGCCAGGCTTTCAAGA  
ACTTGAGGGACTGTGGGGCGTGCAGGCCCGGTGCGGGACCGCGCGACGGTGTGAGCCTGCTGACGCCGAACTCGCGCC  
TGCTGCTGCTGCTGGTGGCGCCCTTACGAGACGCGGCAGCGTGAGCCGCGACTCGTACCTGGGCTACCTGCTTAACCTGTAC  
CGCGAGGCCATCGGGCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCACGTGAGCCGCGCGCTGGGCCAGGAG  
GACCCGGGCAACCTGGAGGCCACCCTGAACCTTCTGCTGACCAACCGGTGCGAGAAGATCCCGCCCCAGTACGCGCTGAGCAC  
CGAGGAGGAGCGCATCTGCGCTACGTGCAGCAGAGCGTGGGGCTGTTCTGATGCAGGAGGGGGCCACGCCAGCGCCGC  
GCTCGACATGACCGCGCGCAACATGGAGCCAGCATGTACGCTCGAACCGCCGTTTCATCAATAAGCTGATGGACTACTTGC  
ATCGGGCGGCGCCATGAACTCGGACTACTTTACCAACGCCATCTTGAACCCGCACTGGCTCCCGCGCGCCGGTTCTACACG  
GGCGAGTACGACATGCCCGACCCCAACGACGGGTTCTGTGGGACGACGTGGACAGCAGCGTGTCTCGCGCGCGCCGCCA  
CCACCGTGTGGAAGAAAGAGGGCGGGGACCGCGGCCGTCTCGCGCTGTCCGGTGTGCGCGGGTGCTGCCGCGCGGTGTC  
CTGAGGCCGCCAGCCCTTCCGAGCCTGCCCTTTGCTGAACAGCGTGCAGCAGCAGAGCTGGGTGCGGTGACGCGGCC  
GCGCCTGCTGGGCGAGGAGGAGTACCTGAACGACTCCTGTTGAGGCCGAGCGCGAGAAGAACTTCCCAATAACGGGATA  
GAGAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTACGCGCAGCAGACAGGGACGAGCCCCGAGCTAGCAGCAGCGC  
AGGCAACCGTAGACGCCAGCGACACGACAGGACGCGGGTCTGGTGTGGGACGATGAGGATTCGCGCGACGACAGCAGCGT  
GTTGGACTTGGGTGGGAGTGGTGGTGAACCGTTGCTCACTTGCGCCCCGTATCGGGCGCCTGATGTAAGAATCTGAAA  
AAATAAAAAACGGTACTACCAAGGCCATGGCGACCAGCGTGCGTCTTCTCTGTTGTTGTAGTAGTATGATGAGGCGCGTG  
TACCCGGAGGGTCTCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGGTGGCGGCGGCGATGCAGCCCCGCTGGAGGCG  
CCTTACGTGCCCCGCGGTACCTGCGCCTACGGAGGGGGCGGAACAGCATTGTTACTCGGAGCTGGCACCTTGTACGATAC  
CACCCGGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCTCGTGAACCTACCAGAACGACCACAGCAACTTCTGACCA  
CCGTGGTGCAGAACAAACGATTTACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTGACGAGCGCTGCGGTGGGGCGG  
CCAGCTGAAAACCATCATGCACACCAACATGCCCAACGTGAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGGGTGATG  
GTCTCGCGAAGACCCCCAATGGGGTTCGCGGTGGATGAGAATTATGATGGTAGTCAGGACGAGCTGACTTACGAGTGGGTGG  
AGTTTGAGCTGCCCCGAGGGCAACTTCTCGGTGACCATGACCATCGATCTGATGAACAACGCCATCATCGACAACCTACTTGGCG  
GTGGGGCGTCAGAACGGGGTGTGGAGAGCGACATCGGCGTGAAGTTCGACACGCGCAACTTCCGGCTGGGCTGGGACCCC  
GTGACCGAGCTGGTGATGCCGGGCGGTGTACCAACGAGGCGCTTCAACCCGACATCGTCTGCTGCCCCGCTGCGGCGTGG  
ACTTACCGAGAGCCGCTCAGCAACCTGCTGGGCATCCGCAAGCGGCAGCCCTTCCAGGAGGGCTTCCAGATCTGTACGAG  
GACCTGGAGGGGGGCAACATCCCCGCGCTCTTGATGTGCAAGCCTATGAGAAAAGCAAGGAGGAGGCCGCGCGAGCGGCG  
ACCGCAGCCGTGGCCACCGCCTTACCGAGGTGCGGGGCGATAATTTTGCTAGCGCCGCGGCGAGTGCCGAGGCGGCTGAAA  
CCGAAAGTAAGATAGTCATCCAGCCGGTGGAGAAGGACAGCAAGGACAGGAGCTACAACGTGCTCGCGGACAAGAAAAACA  
CCGCTACCGCAGCTGGTACCTGGCCTACAACCTACGGCGACCCCGAGAAGGGCGTGCGCTCTGGACGCTGCTACCACTCG  
GACGTCACTGCGGCTGGAGCAAGTCTACTGGTGCCTGCCGACATGATGCAAGACCCGGTCACTTCCGCTCCACGCGTCA  
AGTTAGCAACTACCCGGTGGTGGGCGCCGAGTCTGCCCCGTTACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGC  
AGCAGCTGCGCGCCTTCACTCGCTCACGCACGTCTTAAACCGCTTCCCGAGAACAGATCCTCGTCCGCCCGCCGCGCCCA  
CCATTACCACCGTCAGTGAACCGTTCTGCTCTACAGATCACGGGACCTGCGGCTGCGCAGCAGTATCCGGGGAGTCCAG  
CGCGTGACCGTCACTGACGCCAGACGCCGACCTGCCCCACGTCTACAAGGCCCTGGGCGTAGTGTGCGCGCGCGCTCTCTC  
GAGCCGACCTTCTAAAAATGTCCATTCTCATCTCGCCAGTAATAACACCGGTTGGGGCTGCGCGCGCCAGCAAGATGT  
ACGGAGGCGCTCGCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCACTTCCGCGCTCCCTGGGGCGCCCTCAAGGG  
CCGCGTGCGCTCGCGCACCAACGTCGACGACGTGATCGACAGGTGGTGGCCGACGCGCGCAACTACACGCCCGCGCGCG  
CCCGCCTCCACCGTGGACGCCGTATCGACAGCGTGGTGGCCGATGCGCGCGGTACGCCCGCGCCAAGAGCCGGCGCGGC  
GCATCGCCCGCGGCGCACCGGAGCACCCCGCATGCGCGCGGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCA  
GGGCCATGCTCAGGGCGGCCAGACGCGCGGCCCTCCGGCAGCAGCAGCGCCGGCAGGACCCGAGACGCGCGGCCACGGCG

Fig. 22E

GCGGCGGCGGCCATCGCCAGCATGTCCCGCCCGCGGCGCGGCAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGC  
GTGCCGTGCGCACCCGCCCCCTCGCACTTGAAGATGCTGACTTCGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCC  
AAGCGCAAATACAAGGAAGAGATGCTCCAGGTCATCGCGCTGAGATCTACGGCCCCGCGGTGAAGGAGGAAAGAAAGCCC  
CGCAAACCTGAAGCGGGTCAAAAAGGACAAAAAGGAGGAGGAAGATGTGGACGGACTGGTGGAGTTTGTGCGCGAGTTTCGC  
CCCCGGCGGCGCGTGCAGTGGCGCGGGCGGAAAGTGAAACCGGTGCTGCGGCCGGCACCACGGTGGTCTTCACGCCCGG  
CGAGCGTTCCGGCTCCGCCTCAAGCGCTCCTACGACGAGGTGTACGGGACGAGGACATCCTCGAGCAGGCGGTGCGAGCGT  
CTGGGCGAGTTTGCTTACGCAAGCGCAGCCGCCCGCGCCCTTGAAAGAGGAGGCGGTGTCCATCCCGTGGACCACGGCA  
ACCCACGCCGAGCCTGAAGCCGGTGACCCTGCAGCAGGTGCTGCCGAGCGCGGCGCGCGCCGGGGCTTCAAGCGCGAGG  
GCGGCGAGGATCTGTACCCGACCATGCAGCTGATGGTGCCCAAGCGCCAGAAGCTGGAGGACGTGCTGGAGCACATGAAGG  
TGACCCCGAGGTGCAGCCCGAGGTCAAGGTGCGGCCATCAAGCAGGTGGCCCCGGGCGTGGCGTGCAGACCGTGGACA  
TCAAGATCCCCACGGAGCCCATGGAACGCAGACCGAGCCCGTGAAGCCAGCACACAGCCATGGAGGTGCAGACGGATCC  
CTGGATGCCGGCGCGGCTTCCACCACTCGCCGAAGACGCAAGTACGGCGCGGCCAGCCTGCTGATGCCAACTACGCGCTG  
CATCCTTCCATCATCCCCACGCCGGGCTACCGCGGCACGCGCTTCTACCGCGGCTACACCAGCAGCCGCCGCAAGACCACCAC  
CGCGCGCGCGTCTGTCGACCCGCCGACGACACCGCGACTTCCGCCCGCGCCTGGTGCGGAGAGTGTACCGCAGCGGGC  
GCGAGCCTCTGACCCTGCCGCGCGCGCTACCACCCGAGCATCGCCATTTAACTCTGCCGTGCGCTCTACTTGCAGATATGG  
CCCTCACATGCCGCTCCGCTCCCCATTACGGGCTACCGAGGAAGAAAGCCGCGCGTAGAAGGCTACGGGGAACGGGCT  
GCGTCGCCATCACACCGGCGGCGGCGGCCATCAGCAAGCGGTTGGGGGAGGCTTCTGCCGCGCTGATCCCCATCATC  
GCCGCGCGATCGGGGCGATCCCCGGCATAGCTTCGTGGCGGTGCAGGCCTCTCAGCGCCACTGAGACACAGTTGAAAAA  
TTTGTAATAAAAAAATGGAAGTACGCTCCTGGTCTGTGATGTGTGTTTTAGATGGAAGACATCAATTTTTCTGCCCTGGCAC  
CGCGACACGGCACGCGGCCGTTTATGGGCACCTGGAGCGACATCGGCAACAGCCAACTGAACGGGGGCGCCTTCAATTGGAG  
CAGTCTCTGGAGCGGGCTTAAGAATTTCCGGTCCACGCTCAAAACCTATGGCAACAAGGCGTGGAAACAGCAGCACAGGGCAG  
GCGCTGAGGGAAAAAGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTCGATGGCCTGGCCTCGGGCATCAACGGGGTGGTG  
GACCTGGCCAACAGGCCGTGCAGAAACAGATCAACAGCCGCTGGACGCGGTCCC GCCCGCGGGGTCCGTGGAGATGCCCC  
AGGTGGAGGAGGAGCTGCCTCCCTGGACAAGCGCGGCGACAAGCGACCGCGTCCCAGCGGAGGAGACGCTGCTGACGC  
ACACGGACGAGCCGCCCCGTACGAGGAGGCGGTGAACTGGGTCTGCCACCACGCGGCCGTGGCGCCTCTGGCCACCGG  
GGTGTGAAACCCAGCAGCAGCAGCCAGCCGCGACCTGGACTTGCTCCGCTGCTTCCCGCCCCTCCACAGTGGCTAAGC  
CCCTGCCGCCGGTGGCGTGCCTGCGCGCGCCCCGAGGCCGCCCCAGGCGAACTGGCAGAGCACTCTGAACAGCATCGT  
GGGTCTGGGAGTGAGAGTGTGAAGCGCGCGCTGCTATTAAGACACTGTAGCGCTTAACTTGCTTGTGTGTATAT  
GTATGTCCGCCACCAGAAGGAGGAAGAGGCGCGTCCCGAGTTGCAAGATGGCCACCCATCGATGCTGCCCACTGGGC  
GTACATGCACATCGCCGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTGCCCCGCGCCACAGACCTACT  
TCAGTCTGGGAACAAGTTAGGAACCCACGGTGGCGCCACGCACGATGTGACCACCGACCGCAGCCAGCGGCTGACGCT  
GCGCTTCTGCCCCGTGGACCGCAGGACAACCTACTCTGTAAGTGCCTACACGCTGGCGTGGGCGACAACCGCGTG  
CTGGACATGGCCAGCACCTACTTTGACATCCGCGCGTGTGGATCGGGGGCCAGCTTCAAACCTACTCCGGCACCGCTA  
CAACAGCCTGGCTCCCAAGGGAGCGCCCAACACTTGCCAGTGGACATATAAGCTGGTGATACTGATACAGAAAAACCTATA  
CATATGGAATGCACCTGTGCAAGGCATTAGCATTACAAAGGATGGTATTCAACTTGGAAGTACAGCGATGGTCAGGCAATC  
TATGCAGACGAACTTATCAACCAGAGCCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAATATGG  
AGGCAGAGCTCTTAAGCTGACACCAAAATGAAGCCTTGCTATGGTTCTTTGCCAAGCCTACCAATAAAGAAGGAGGCCAGG  
CAAATGTGAAAACCGAAACAGGCGGTACCAAGAATATGACATTGACATGGCATTCTTCGATAATCGAAGTGCAGCTGCCGCC  
GGCCTAGCCCCAGAAATTGTTTTGTATACTGAGAATGTGGATCTGGAACTCCAGATACCCATATTGTATACAAGGCAGGTAC  
AGATGACAGTAGCTCTTCTATCAATTTGGGTGAGCAGTCCATGCCAACAGACCCAACTACATTGGCTTCAGAGACAACCTTAT  
CGGTCTGATGTACTACAACAGCACTGGCAATATGGGTGACTGGCTGGACAGGCCTCCAGCTGAATGCTGTGGTGGACTTGC  
AGGACAGAAAACCGAACTGTCTACCAGCTCTTGCTGACTCTGGGTGACAGAACCAGGTATTTAGTATGTGGAATCAG  
GCGGTGGACAGTTATGACCCGATGTGCGCATTATTGAAATCACGGTGTGGAGGATGAACTTCTAACTATTGCTTCCCCCTG  
GATGCTGTGGGTAGAAGTATACTTACCAGGGAATTAAGGCCAATGGTGATAATCAAACCACTGGACCAAAGATGATACTGT  
TAATGATGCTAATGAATTGGGCAAGGGCAATCCTTTGCCATGGAGATCAACATCCAGGCCAACCTGTGGCGGAACTTCTCT  
ACGCGAACGTGGCGCTGTACCTGCCGACTCCTACAAGTACACGCCGGCCAAACATCACGCTGCCACCAACACCAACACCTAC  
GATTACATGAACGGCCGCGTGGTGGCGCCCTCGTGGTGGACGCTACATCAACATCGGGGCGCGTGGTCTGCTGGACCCCA  
TGGAACAACGTCAACCCCTTCAACCACACCGCAACGCGGGCCTGCGATACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTG  
CCCTTCCACATCCAGGTGCCCCAAAAGTTTTTCGCCATCAAGAGCCTCCTGCTCCTGCCGGGTCTACACCTACGAGTGGAACT  
TCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCCTCGGCAACGACCTGCGCACGGACGGGGCCTCCATCGCTTACCAGC  
ATCAACCTCTACGCCACCTTCTTCCCATGGCGCACAAACACCGCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGAC

Fig. 22F

CAGTCCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCATCTCCATCCCT  
CGCGAACTGGGCCGCTTCCGCGGCTGGTCTTACGCGCCTCAAGACCCGCGAGACGCCCTCGCTCGGCTCCGGTTTCGAC  
CCCTACTTCTGCTACTCGGGCTCCATCCCTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTT  
CGACTCCTCCGTGAGCTGGCCCGGCAACGACCGCCTCTGACGCCAACGAGTTCGAAATCAAGCGCACCGTCGACGGAGAG  
GGGTACAACGTGGCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCACTACAACATCGGCTACCAGG  
GCTTCTACGTGCCCCGAGGGCTACAAGGACCGCATGTACTCTTCTCCGCAACTTCCAGCCCATGAGCCGCCAGGTCTGGAC  
GAGGTCAACTACAAGGACTACCAGGCCGTACCCCTGGCTACCAGCACAACAACCTCGGGCTTCTCGGCTACCTCGCGCCAC  
CATGCGCCAGGGCCAGCCCTACCCGCCAACTACCCCTACCCGCTCATCGGCAAGAGCGCGCTCGCCAGCGTACCCAGAAAA  
AGTTCCTCTGCGACCGGGTCATGTGGCGCATCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGA  
ACATGCTCTACGCCAACTCCGCCACGCGCTAGACATGAATTCGAAGTCGACCCCATGGATGAGTCCACCTTCTCTATGTTGT  
CTTCGAAGTCTTCGACGTCTCGAGTGCACAGCCCCACCGCGGCTCATCGAGGCCGTCTACCTGCGCACGCCCTTCTCGGC  
CGGCAACGCCACCACCTAAGCCTCTTGCTTCTTGCAAGATGACGGCTGCGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATC  
CTCCGCGACCTGGGCTGCGGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCCCGGGATTATGCCCCGCAAGCTGGC  
CTGCGCCATCGTCAACACGGCCGGCCGCGAGACCGGGGGCGAGCACTGGCTGGCCTTCGCCTGGAACCCGCGCTCCACACC  
TGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACCAGTTCGAGTACGAGGGCTGCTGCGTCG  
AGCGCCTGGCCACCGAGGACCGCTGCGTACCCTGAAAAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCTGCG  
GGCTCTTCTGCTGCATGTTCTGACGCTTCTGTCACCTGGCCGACCGCCCCATGGACAAGAACCCACCATGAACCTGCTGA  
CGGGGTGCCAACGGCATGCTCCAGTCGCCCAGGTGGAACCCACCTGCGCCGAACAGGAGGCGCTTACCGCTTCTC  
AACGCCCACTCCGCTACTTTCGCTCCACCGCGCGCATCGAGAAGGCCACCGCTTCGACCGCATGAATCAAGACATGTAA  
TCCGGTGTGTATGTGAATGCTTTATTCATCATAATAAACAGCACATGTTTATGCCACCTTCTCTGAGGCTCTGACTTTATTA  
GAAATCGAAGGGGTTCTGCCGCTCTCGGCATGCCCCGCGGGCAGGGATACGTTGCGGAACCTGGTACTTGGGCAGCCACTTG  
AACTCGGGGATCAGCAGCTTCGGCACGGGGAGGTGCGGGAACGAGTCGCTCCACAGCTTGCCTGAGTTGCAGGGCGCCC  
AGCAGGTCGGGCGCGGAGATCTTGAATCGCAGTTGGGACCCGCGTTCGCGCGGAGAGTTACGGTACAGGGGTTGCAG  
CACTGGAACACCATCAGGGCCGGGTGCTTACGCTCGCCAGCACCGTCGCGTCGGTGATGCCCTCCAGTCCAGATCCTCGGC  
GTTGGCCATCCGAAGGGGGTCATCTTGACGGTCTGCGCCCCATGCTGGGCACGCAGCCGGGCTTGTTGTTGCAATCGCAGT  
GCAGGGGGATCAGCATCATCTGGGCTGCTCGGAGCTCATGCCCGGTACATGGCCTTCATGAAAGCCTCCAGCTGGCGGAA  
GGCCTGCTGCGCTTGCCGCCCTCGGTGAAGAAGACCCGCGAGGACTTGCTAGAGAACTGGTTGGTGGCGCAGCCAGCGTCG  
TGACGCAGCAGCGCGCGTCTGTTGGCCAGCTGCACACGCTGCGCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTGCG  
GGTCTCTCTCAGCGCGCGTCCCCGTTCTGCTCGCCACATCCATCTCGATCGTGTGCTCCTTCTGGATCATCAGGTCCCGTG  
CAGGCACCGCAGCTTGCCCTCGGCTCGGTGCACCCGTGCAGCCACAGCGCGCAGCCGGTGCTCTCCAGTTCTTGTGGGCGA  
TCTGGGAGTGCGAGTGACGAAGCCCTGCAGGAAGCGGCCATCATCGTGGTCAGGGTCTTGTGCTGGTGAAGGTGACGCG  
AATGCCGCGGTGCTCTCGTTACATACAGGTGGCAGATACGGCGGTACACCTCGCCCTGCTCGGGCATCAGCTGGAAGGCG  
GACTTCAGGTGCTCTCCACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCCATGCCCTTCTCCAGGCCGAAACGATCGGC  
AGGCTCAGGGGGTTCTTACCGTTGTCTTAGTCGCGCCGCCGAAAGTCAGGGGGTCTTCTCGTCCAGGGTCTCAAACAC  
TCGCTTGCCGTCCTTCTCGGTGATGCGCACGGGGGAAAGCTGAAGCCACGGCCGCCAGCTCCTCCTCGGCTGCTTTTCTGT  
CCTCGTGTCTGGCTGATGTCTTGAAGGCACATGCTTGGTCTTGCGGGGTTTCTTTTGGGCGGCAGAGGCGGCGGCGGA  
GACGTGCTGGGCGAGCGGAGTTCTCGCTACCACGACTATTTCTTCTCTTGGCCGTCGTCGAGACCACGCGGCGGTAGGC  
ATGCCTCTTCTGGGGCAGAGGCGGAGGCGACGGGCTCTCGCGTTCCGGCGGGCGGTGGCAGAGCCCTTCCGCGTTCGGG  
GGTGGCTCTTGGCGGCGCTGCTCTGACTGACTTCTCCGCGGCCGCGCCATTGTGTTCTCCTAGGGAGCAAGCATGGAGACTC  
AGCCATCGTCGCCAACATCGCCATCTGCCCCCGCGCCGCGACGAGAACCAGCAGCAGCAGAATGAAAGCTTAACCGCCCCG  
CCGCCAGCCCCACCTCCGACGCCGAGCCCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTACCTGGGCTACGTGA  
CGCCCGCGGAGCACGAGGAGGAGCTGGCAGCGCGCTTTTCAGCCCCGGAAGAGAACCACCAAGAGCAGCCAGAGCAGGAAG  
CAGAGAGCGAGCAGAACCAGGCTGGGCTCGAGCATGGCGACTACCTGAGCGGGCAGAGGACGTGCTCATCAAGCATCTGG  
CCCGCCAATGCATCATCGTCAAGGACGCGCTGCTGACCGCGCCGAGGTGCCCTCAGCGTGGCGGAGCTCAGCCGCGCTAC  
GAGCGCAACCTCTTCTCGCCGCGGTGCCCCCCAAGCGCCAGCCAAACGGCACCTGCGAGCCCAACCCGCGCTCAACTTCTAC  
CCGGTCTTCCGCGGTGCCCCGAGGCCCTGGCCACCTACCACCTCTTTTCAAGAACCAAGGATCCCCGTCTCCTGCGCGCCAAC  
CGACCCGCGCCGACGCCCTGCTCAACCTGGGCCCCGGCGCCGCTACCTGATATCGCCTCCTTGAAGAGGTTCCCAAGAT  
CTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGGAACGCTCTGCAAGGAAGCGGAGAGGAGCATGAGCACCACAGCGC  
CCTGGTGGAGTTGGAAGGCGACAACGCGCGCTGGCGGTCTCAAGCGCACGGTCGAGCTGACCACTTCGCTACCCGGCG  
CTCAACCTGCCCCCAAGGTCTGAGCGCCGTATGGACCAGGTGCTCATCAAGCGCGCCTCGCCCTCTCGGAGGAGGAGAT  
GCAGGACCCCGAGAGCTCGGACGAGGGCAAGCCCGTGGTACGCGACGAGCAGCTGGCGCGCTGGCTGGGAGCGAGTAGCA



Fig. 22G

CCCCCAGAGCCTGGAAGAGCGGCGCAAGCTCATGATGGCCGTGGTCTGGTGACCGTGGAGCTGGAGTGTCTGCGCCGCTT  
CTTCGCGGACGCGGAGACCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGACACGGGTTCTGTGCGCCAGGCCTGC  
AAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTGCACGAGAACCCTGGGGCAGAACGTGTGCA  
CACCACCCTGCGCGGGGAGGCCCGCGGACTACATCCGCGACTGCGTCTACCTGTACCTTGCCACACCTGGCAGACGGGCA  
TGGGCGTGTGGCAGCAGTGCCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAACCTCAAGGCCCTGTG  
GACCGGGTTTCGACGAGCGCACACCACCGCGCGGACCTGGCCGACCTCATCTTCCCCGAGCGCCTGCGGCTGACGCTGCGCAAC  
GGGCTGCCCCGACTTTATGAGCCAAAGCATGTTGAAAACCTTTCGCTCTTTCATCCTCGAACGCTCCGGGATCCTGCCCCCACC  
TGCTCCGCGCTGCCCTCGGACTTCGTGCCGCTGACCTTCGCGAGTGCCCCCGCGCTCTGGAGCCACTGCTACCTGCTGCGC  
CTGGCCAACTACCTGGCCTACCACTCGGACGTGATCGAGGACGTGACGGCGAGGGCCTGCTCGAGTGCCACTGCCGCTGCA  
ACCTCTGCACGCCGACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAA  
GGCCCCGGCGAGGGCAAGGGGGGTCTGAACTCACCCGGGGTGTGGACCTCGGCCTACTTGCGCAAGTTCGTGCCCGAG  
GACTACCATCCCTTCGAGATCAGTTTCTACGAGGACCAATCCAGCCGCCAAGGCCGAGCTGTCGGCCTGCGTCATACCCA  
GGGGGCCATCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTTCTGCTGAAAAAGGGCCACGGGGTCTACTTGG  
ACCCCCAGACCGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCCGAGGAAGCAGCAAGAAGCTGAAAGTGAGGCTGC  
CGCCGCCGCGGAGGATTTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGGAGGAGGAGATGGAAGACTGGGACAGCACT  
CAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAGGAAGACGAGGTGGAGGAGGCAGAGGAAGAAGCAGCCGCCG  
CCAGACCGTCTGCTCGGCGGAGGAGGAGAAAGCAAGCAGCAGGATACCATCTCCGCTCCGGGTGCGGGTCTGCGCGGCC  
GGGCCACAGTAGATGGGACGAGACCGGGCGCTTCCGAACCCACCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACA  
AGTCTGGCGGGGGCACAAAAACGCCATCGTCTCCTGCTTGAAGCCTGCGGGGGCAACATCTCCTTCACCGGGCGCTACCTG  
CTCTTCCACCGCGGGGTGAACCTCCCCGCAACATCTTGCACTTACTACCGTCACCTCCACAGCCCCCTACTACTGTTTCAAGAAG  
AGGCAGAAACCCAGCAGCAGCAGCAGCAGCAGCAAAAACAGCGGCAGCAGCTAGAAAATCCACAGCGGCGGCAGGTGGACT  
GAGGATCGCGGCGAACGAGCCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTTCCACCCCTATGCCATCTTCAGCAG  
AGTCGGGGGCAAGAGCAGGAACCTGAAAGTCAAGAACCGTTCTGCGCTCGCTACCCGAGTTGTCTGTATCACAAGAGCG  
AAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCGCG  
CCCGCCACACACGGAAAAAGGCGGGAATTACGTACCACTGCGCCCTTCGCCCCGACCATCATGAGCAAAGAGATTCCC  
ACGCTTACATGTGGAGCTACCAGCCCCAGATGGGCCTGGCCGCCGGCGCCGCCCAGGACTACTCCACCCGCATGAAGTGGCT  
CAGTGCCGGGCCCCGCGATGATCTACGGGTGAATGACATCCGCGCCACCGAAACAGATACTCCTAGAACAGTCAGCGATCA  
CCGCCACGCCCCGCCATCACCTTAATCCGCGTAATTGGCCGCCGCCCTGGTGTACCAGGAAATCCCCAGCCACGACCGTAC  
TACTTCCGCGAGACGCCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCCGGCGGCGCCGCCCTGTGTCTCAC  
CGCCCCGCTCAGGGTATAAGCGGCTGGTGTATCCGAGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAGCTCTTCGCTGG  
GTCTGCGACCTGACGGAGTCTTCCAACCTCGCCGATCGGGGAGATCTTCTTACGCCTCGTCAGGCCGTCTGACTTTGGAG  
AGTTCGTCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAGTTCGTGGAGGAGTTCACTCCCTCGGTCTACTTCAACCCC  
TTCTCGGCTCCCCCGGCCACTACCCGACGAGTTCATCCGAACTTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTG  
AATGTCCATGGTGGCGCGGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCCGCTTCGCTGCTTCGCTCGGGATCT  
CGCCGAGTTTGCTACTTTGAGCTGCCCCGAGGAGACCCCTCAGGGCCCCGGCCACGGAGTGCGGATCGTCGTGCAAGGGGGT  
CTCGACTCCACCTGCTTCGGATCTTCAGCCAGCGTCCGATCCTGGCCGAGCGCGAGCAAGGACAGACCCTTCTGACCCTGTAC  
TGCATCTGCAACCAACCCCGCCCTGCATGAAAGTCTTTGTTGTCTGCTGTGTACTGAGTATAATAAAAGCTGAGATCAGCGACTA  
CTCCGGACTTCCGTGTGTTCTGTATCAACAGTCCCTGTTCTTACCCGGAACGAGACCGAGCTCCAGCTCCAGTGTAAGCC  
CCACAAGAAGTACCTCACCTGGCTGTTCCAGGGCTCTCCGATCGCCGTTGTCAACCACTGCGACAACGACGGAGTCTGTGTA  
GCGGCCCTGCCAACCTTACTTTTCCACCCGAGAAGCAAGCTCCAGCTCTTCCAACCTTCTCCCCGGGACCTATCAGTGCGT  
CTCGGGACCTGCCATCACACCTCCACCTGATCCCGAATACCACAGCGTGCCTCCCCGCTACTAACAACCAAACTACCCACCA  
CGCCACCGTCGCGACCGCGGACATGTACAGAGCTCGAGAAGTACTAGGCCACAATACATGCCATATTAGACTATGAGGCCGA  
GCCACAGCGACCCATGCTCCCCGCTATTAGTTACTTCAATCTAACCGCGGAGATGACTGACCACTGGCCAACAACAACGTCA  
ACGACCTTCTCTGGACATGGACGGCCGCGCCTCGGAGCAGCGACTCGCCAACTTCGATTTCGCCAGCAGCAGGAGAGAGC  
CGTCAAGGAGCTGCAGGACGGCATAGCCATCCACAGTGCAAGAAAGGCATCTTCTGCCTGGTGAAACAGGCCAAGATCTCC  
TACGAGGTACCCCCGACCGACCATCGCCTCTCCTACGAGCTCCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTGGAGTCAA  
CCCCATCGTCATACCCAGCAGTCGGGCGATACCAAGGGGTGCATCCACTGCTCCTGCGACTCCCCGACTGCGTCCACACTCT  
GATCAAGACCTCTGCGGCCTCCGCGACCTCTCCCCATGAACTAATCACCCCTTATCCAGTGAAATAAATATCATATTGATGA  
TGATTTAAATAAAAAATAATCATTTGATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTTAAAAAATAAAGAATCACT  
TACTTGAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACCAACCTCACTCCCCTTCCAGCTCTGGTACTGCAGACC  
CCGGCGGGCTGCAAACTTCTCCACACGCTGAAGGGGATGTCAAATTCCTCTGTCCCTCAATCTTCATTTTATCTTATCAGA

Fig. 22H

TGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCTTC  
 ATCAACCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCTGGGGGTGCTGTCCTGCGACTGGCTGACCCCGTCACC  
 ACCAAGAACGGGGAATCACCTCAAGCTGGGAGAGGGGGTGGACCTCGACTCCTCGGGAAAACTCATCTCCAACACGGCCA  
 CCAAGGCCGCCGCCCTCTCAGTTTTTCCAACAACACCATTTCCCTTAACATGGATACCCCTCTTTATACCAAAGATGGAAAAAT  
 ATCCTTACAAGTTTCTCCACCGTTAAACATATTTAAATCAACCATTCTGAACACATTAGCTGTAGCTTATGGATCAGGTTTAGGA  
 CTGAGTGGTGGCACTGCTCTTGCAGTACAGTTGGCCTCTCCACTCACTTTTGATGAAAAAGGAAATATTTAAATTAACCTAGCC  
 AGTGGTCCATTAAACAGTTGATGCAAGTCGACTTAGTATCAACTGCAAAAGAGGGGTCACTGTCACTACCTCAGGAGATGCAAT  
 TGAAGCAACATAAGCTGGCCTAAAGGTATAAGATTTGAAGGTAATGGCATAGCTGCAAAACATTGGCAGAGGATTGGAATTT  
 GGAACCACTAGTACAGAGACTGATGTCACAGATGCATACCCAATTCAAGTTAAATGGGTACTGGCCTTACCTTTGACAGTACA  
 GGCGCCATTGTTGCTTGGAAACAAAGAGGATGATAAACTTACATTATGGACCACAGCCGACCCCTCGCCAAATTGCAAAATATA  
 CTCTGAAAAAGATGCCAACTCACACTTTGCTTGACAAAGTGGAAGTCAAATTCTGGGTACTGTGACTGTATTGGCAGTGA  
 ATAATGGAAGTCTCAACCAATCACAACACAGTAAGCACTGCACTCGTCTCCCTCAAGTTTGATGCAAGTGGAGTTTGTCTAA  
 GCAGTCCACATTAGACAAAGAATATTGGAACCTCAGAAAGGGAGATGTTACACCTGCTGAGCCCTATACTAATGCTATAGGT  
 TTTATGCCTAACATAAAGGCTATCCTAAAAACACATCTGCAGCTTCAAAAAGCCATATTGTCAGTCAAGTTTATCTCAATGGG  
 GATGAGGCCAAACCACTGATGCTGATTATTACTTTTAACTGAACTGAGGATGCAACTGCACTACAGTATCACTTTTCAATGG  
 AAATGGGATAGTACTAAGTACACAGGTGAAACACTTGCTACCAGCTCCTTACCTTCTCTACATCGCCCAAGAATGAACACTG  
 TATCCACCTGCGATGCCAACCTTCCACCCCACTCTGTCTATGGAAAACTCTGAAGCAGCAAAATAAAATAAAGTTCAAGT  
 GTTTTATTGATTCAACAGTTTACAGGATTGAGCAGTTATTTTCTCCACCTCCAGGACATGGAATACACCACCTCTCCCC  
 CCGCACAGCCTTGAACATCTGAATGCCATTGGTGTGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAG  
 TCTCGGGTGGTCAGGGAGATGAAACCTCCGGGCACTCCGCGATCTGCACCTCACAGCTCAACAGCTGAGGATTGTCTCGG  
 TGGTCCGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGCGGTGGGAATCATAGTCCGCGAACGGGATCGGCCGGTGGTG  
 TCGCATCAGGCCCCGAGCAGTCGCTGCCGCCGCGCTCGTCAAGCTGCTGCTCAGGGGGTCCGGGTCCAGGGACTCCCTCA  
 GCATGATGCCACGGCCCTCAGCATCAGTCGTCTGGTGGCGGGCGCAGCAGCGCATGCGGATCTCGCTCAGGTGCTGCA  
 GTACGTGCAACACAGGACCACAGGTTGTTCAACAGTCCATAGTTCAACACGCTCCAGCCGAACTCATCGCGGGAAGGATGC  
 TACCCACGTGGCCGTCTGATCAGATCCTCAGGTAATCAAGTGGCGCTCCCTCCAGAACACGCTGCCACGTACATGATCTCT  
 TGGGCATGTGGCGGTTACACACTCCCGGTACCACATCACCTCTGGTTGAACATGCAGCCCCGGATGATCTGCGGAACCAC  
 AGGGCCAGCACCGCCCCGCCGATGCAGCGAAGAGACCCCGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGTACC  
 CGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCTCTTTCAGCACTCTCAGTCTCT  
 CGGGGGTCAAAACCATATCCAGGGCACGGGGAATCTTGACAGGACAGCGAACCCCGCAGAACAGGGCAATCTCGCACATA  
 ACTTACATTGTGATGGACAGGGTATCGCAATCAGGCAGCACCGGGTATCTCCACCAGAGAAGCGCGGGTCTCGGTCTCT  
 CACAGCGTGGAAGGGGGCGCGGATACGGGTGATGGCGGGACGCGGTGATCGTGTTCGCGACCGGTGTCATGATGCAGT  
 TGCTTTCGGACATTTTCGTAAGTGTAGCAGAACCTGGTCCGGGCGCTGCACACCGATCGCGGGCGGGTCCCGGCGCTT  
 GGAACGCTCGGTGTTGAAATGTAAACAGCCACTCTCTCAGACCGTGCAGCAGATCTAGGGCCTCAGGAGTGATGAAGATCC  
 CATCATGCCTGATAGCTCTGATCAGATCGACACCGTGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTGGTTTCG  
 GTGACGGCGGGGAGGGAAGAAGCAAGGAAGCAATGATTAACTTTTAACTCAAAACGGTCTCGGAGCACTTCAAAATGAAGGT  
 CGCGGAGATGGCACCTCTCGCCCCGCTGTGTTGGTGGAAATAACAGCCAGGTCAAAGGTGATACGGTTCTCGAGATGTTCC  
 ACGGTGGCTTCAGCAAAAGCCTCCACGCGCATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTTCTCTAATTCCTCAAT  
 CATCATGTTACACTCTGCACCATCCCCAGATAATTTTCAATTTTCCAGCCTTGAATGATTGCAACTAGTTCCTGAGGTAATCCA  
 AGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCATTCTTAAGCACACCCCTCATAATTCGAAGATATTCTGCTC  
 CTGGTTACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGATCCCTAAGCTCCTCCCTCAGCAATAACTGTAA  
 GACTCTTTCATATCCTCTCCGAAATTTTAGCCATAGGACCACAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCG  
 AAGTCCCTCCCACTGAGCATTGCCAAATGCAAGACTGCTATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAAAGTGG  
 ACAGAAAATCACCCAGGCAATTTTAAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGCAGGTTTAGAGCCTCGGGAACAACG  
 ATGAAGTAAATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAAAAAACAAAAATAAAAATTAACCATGCT  
 AGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCAGCACACAGGCAGGCCACGGGGTCTCCGGCGCGACCCCTCGTAAAAATG  
 TCGCTATGATTGAAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTGACAAGATGAATACACCCCGGAAC  
 ATTGGCGTCCGCGAGTGAAAAAAGCGCCCGAGGAAGCAATAAGGCACTACAATGCTCAGTCTCAAGTCCAGCAAGCGCATG  
 CCATGCGGATGAAGCACAAAATCTCAGGTGCGTACAAAATGTAATTACTCCCTCTGCACAGGCAGCGAAGCCCCGATCC  
 CTCCAGATACACATAAAAGCCTCAGCGTCCATAGCTTACCGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCT  
 GAGCTCTAACCTGTCCACCGCTCTCTGCTCAATATATAGCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCG  
 CCAATAATCACACACGCCAGCACACGCCAGAAACCGGTGACACACTCAAAAAATACGCGCACTTCTCAACGCCCAAA  
 CTGCCGTCAATTCGGGTTCCACGCTACGTATCGGAATTCGACTTTCAAATTCGTCGACCGTTAAAAACGTACCCGCCCCG  
 CCCCTAACGGTCGCCGCTCTCTCGCCAATCACCTTCTCCCTCCCAAAATCAACAGCTCATTTGCATATTAACGCGACCAA  
 AAGTTTGAGGTATATTATTGATGATG

Fig. 22I

**AdC7 010-HIVgp140(E1469) Amino acids – SEQ ID NO: 11****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVGRETGDR\*GRGG\*RFDDVAVRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFLG  
GCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDLRGGFDIRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RKLRS  
DPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMKNLLRVRRFALLRDVRARYTR\*H\*LLTSMPTPPIDVND  
GKWPAWHYAQYMTLWDFPTWQYIYVLIAITMVMRFWQYINGRG\*RFDSRGFSPSLHPIDVNGSLFWHQNRDQDFPKCRNNSAP  
LTQMGGRRVRWEVYISRARLVNRQITRSFIADVYHS\*IANAVSASDTTVSNLRLEYLIRLTIG\*LRLEFDATMRVMGILRSYQQWWI  
WGILGFWMMLMNCVWGNLWVTVYGVVWKEAKTTLFCASDAKAHKEEVHNIWATHACVPTDPNPQEIVLKNVTENFNMWK  
NDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLNCSVDKIKGTATYNNATYNNNNNTISDMKNCSFNNTTEITDKKKKEYALFYKLDV  
VALDGKETNSTNSSEYRLINCNTSAVTQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCNNVSTVQCTHGKIPVSTQLLNG  
SLAEVEVIRFENLTNNAKIIIVHLNESVEINCTRPSNNTRKSVRIGPGQTFATGDIIGDIRQAHCNISRKKNWNTTLQRVKEKLEKFPN  
KTIQFAPSSGGDLEITTHSFNCRGEFFCYTSDLFNSTYMSNNTGGANITLQCRIKQIIRMWQGVQAMYPPIAGNITCKSNITGLL  
LTRDGGKEKNDTETFRPGGDMRDNRSELYKYKVEIKPLGIAPDKAKLTQARQLLSGIVQQSNLLRAIEAQQHMLQLTVWG  
IKQLQTRVLAIERYLKDQQLGIWGCSGKLICTTAVPWNASWSNKSYYEIWGNMTWMQWDREINNYNTIYSLLEESQNNQKEKNE  
KDLLALDSWESLWSWFNITNWLW\*GTSRVDPGGQTADQPRCLLVASHLLFAPPPCLP\*PWKVPLPSFPNKMRLHRIV\*VGVIL  
FWGVGWGRTARGRIGKTIAGMLGMRWALWLLRRKEPADLQ\*IHLRVRRRK\*\*NGIMGIMGLH\*\*IGQISICWPPCM\*PRTPA  
RHGPSSTTS\*PDAMCTWGPAEACSCPTSATCNL\*RCCWSPMPCE\*A\*RGCLT\*MWSCGKF\*DMMNPRPGAGPANAEASTP  
GFSPCVWR\*RRCDPIIWCCPATGRSSAPAGKNLTVSSVWGRWRACMRGRMTKICVFLCVA\*\*AEAPLREGYSALI\*RGVSPP  
GRECVRM\*WDPRTAGPCSPRTLQ\*PTRP\*APRPWTQLPPQLLPPAPCAEWPAWATTALWWPTRLPPIPPA\*TRRSSCC  
\*WPSSRP\*PSAWAS\*PSRWLSCRRRRGRPLRP\*KPNKK\*INK\*TETVDFNTES\*IFI\*FFARGRPWTGLDH\*APGGFFPGPRGG  
LGC\*GTWA\*ARPGGGSSAGPRARGWCCCKSPSHSRGAGRGAAARCP\*GGD\*WPRAAPWCRC\*RTC\*AGRDACGGR\*DASWP  
GS\*DWRCRPPDPAGGSCCAGPPARCIRRTWGICHATWKGRRIWRPPCDRPGFCTHP\*\*WRWARGRRPGQRRFGRTHRSC  
GPG\*ARHRPF\*\*IWGGGCPTGGRRCPRSRGRSCPRRSASPR\*ARRGGSCPPAGR\*KKRFPGRGR\*AGPKAGSGAAGTCRSRWG  
RR\*PR\*PAAGGS\*GRDSCRPRGGGPPRSSRAHACSRARVPPGARPPARGALAARRSFAA\*XRRPWAFWRGVARVPDGP  
AR\*CALGHLDPADLLVSRVGATAGVGHQAMGVQRGQGPVLPQSQGPQRGLRHGEGVRAGLGACEGALQHPAGREPLVGA  
LRVGQVAIEHEFVVERLGRVALGAELTFGSVSADGTEGLEGVGGEEDGLGGVGVRAAAGADGLALHEPGEVGPVGVKNEVSSV  
LFDALFTSLGHELVSPDGKEAVRVPVDRLYGPVLERGA AVLVEEPRPLRDEGPGPGQHEGGHVGGVAVVHQRVHLLQGMQA  
HVPLVHIQEGDWLVS VGHVTGGPGRGGIKGGGPLLVLTVFRIAVQERQLLG\*VFPLEGWHNLGTQVVSF\*KRGGFDIDGAVGDAF  
HEPLVHLVRKDDLFVVELGGEGAVEGVGEELGDGAHGLVLFLVGLLGGDVELHVLARHALPFGEDGGELVGHDSPPAAVVQGD  
EVHAGGHAAQGLVGPAEAPALARAEGGQRVQHELVGGVGVHGEDAGQKLGEVADAGVQIVQRRLPVAHGQRLVGAEGRA  
PGHGVRERGVHAADVVDVEGLLEDADVGGVAAPPADAGAHVVVQLVRGREETRAEVGALRLFGAVDDLAEDGVGVGGDGGP  
LEDVEGVGQADRPDEVGVVLQLGDELGGDEDVQGA VVEGLLDDVLELALLPQLAVEKELFAVLPVLFEGEPVLIGTVRAHH  
VELVDGLVGAAALLHGEVSLCGLAQGGVGEGEVGAHHDLEELVLEVEVVAALLPELEVRALLVGGVGQSESNIVEEDLARAGHE  
VASDAERLGHLPVDDLGGEDDLVEADVVPDDVEFHESRAALNVGQLELVVVGELGGVAEPVLEGPVGDVGVGAEEGSPEIH  
GQGGQLQAVPVLTELLAHGHFFGGDAVEGAGVAVPAVPLELEGEVVGELDERRPVGEFHDQHEGDELLAEGPHPGVGFHIVGEEEP  
FGARMRADGEELDLLPVGGMAVDVMEVEMPTARRALVLFIQASAVLATLHGMHVLHLYLGSFDEEFQWAVRWRLHLVLY  
VLAIGVAIVCLDGGHADEPAREAGPDFGSDGSESEDEGAQAGAVQGPETLRSQVSGQRRRAVDLQELFQGAREVQMVLDLHGA  
GGDVHGLQGPVPLGRHHRAPFLGRCFHAGQKRRRGRAPGGRGSGPGRGGRGTSAPRAGRFWYCARRLA\*ATTRLTSWI  
\*RLWVKATGPVSLNLKESSTESISVSLTAACRRISCTSPELSW\*AISVMNCSSISS\*RSRPARSTVAARSLEMRPMSCEKAFMPASFQ  
TRL\*TTAPSGSRARMTTWARLSSTWRVKTA\*LQRRW\*R\*LSVVAMCSVTKKYMIQRRSGISLTSPRASKRSMAS\*KSTAKLKNWEL  
RAETVNSSSSRRRMSAMVARTSRKAPGGSSSSSSSTNISSTSSSGGGGGGGALRRRRRTGRRSMKRSMSVPRRRRMVSVTARP  
SSRGRSVKTPPRISRWPPGGSPLGRERALTMHLINWPVGTPRKDLVSRSSTGSENR\*TKASSQSQSGRLSPVSCSSGISGGGRAML  
LVMKLK\*AVLRRRMVARSTRSLGPACWMRRRSAMPQAWS\*HLARSL\*\*SCMSRSTGTSSSPARPCMRVSPNPRWGWSARSAT  
TRSARMACCIWVRVWVWSSKSTKRW\*APVLMV\*EQLAMTDQLTVWWPGRTSSWYLRRE\*ARVSKM\*SLQVRTRYWYPTKCG  
GGWR\*SGHRSVAGAPGARSSSMRRW\*P\*MYLDIQVMPAAVVEARGNSRTRFQMLRSGRK\*FMVAAVWPVRAQSWML\*TY  
GQKRKRSAARLRGLEAKRTGWAARVPRFESRIRLEPQLTWYWSRLDPSLLTKPPGYGGGSFFGLGRWS\*KTSKRGRKPPAMARC  
RSLEKESPLRRCGVPRFEPQRSAPAGFRG\*RGRCGPVSKTP\*PADFSSYGASPSFSCVFARCIPYCGRCAPTLLNRPYRSSNSRR  
FCPRPSSSQPLRRPP\*AEPAFSMTWPWKRARGWRGWGRRRRSGTRACR\*KGTARPTCPSTCSETGAARSPRRCAPASTRG  
GSCGAAWTESGC\*GTRISRRTS\*RGSA PRARTWPRPTWSRRTSRP\*RRRATSKNPSTTTCAR\*SRARR\*PWA\*CTCGTCWRPSCR  
TPRASR\*RRSCFWWCSTVGTTRRSGRRC\*ISPSRAAGSWTW\*TFCRASWCRSAGCRCPSRWRLSTSRC\*AWASTTLGRSTRPRT

Fig. 22J

CP\*TRR\*STGFTCA\*P\*KC\*P\*ATIWGCTATTGCTAR\*APAAGAS\*ATRS\*CTACSGP\*PGPGPRGRATLTWARTCAGSPAAGPW  
 KLPVPPPTWRRWTMRRRRRASTWKTGATVFLDDAATATAS\*SRDAGGAAEPAVRH\*LLGRLDPGHATHHGADDPQSRSL\*TAAS  
 GQPALGHPGGRGALALEPHAREGAGHRERAGGEQGHPRRRRGRAGVQRAAGARGPLQQHQRADEPGPHGDRRARGGVAARAV  
 PPRVEPLHGGAERLPEHAARQAPGPGGLHQLHQRAADGGRGAPERGVVAGALLPDQSPGLADREPEPGFQELAGTVGRA  
 GPGRGPRDGVPEADAEAPAAAAGGALHGQRQREPRVLPLPA\*PVPRGHRAGARGRADLPGDHPREPRAGPGGPGQPGGHP  
 ELPADQPVAEDPAPVRAEHRGGAHPALRAAERGAVPDAGGHAQRRARHDRAQHGAAHVRSQPPVHQ\*ADGLLASGGRHEL  
 LLYQRHLEPALAPAAARVLHGRVRHARPQRRVPVGRGQQRVLAAPRHHRVEERGRGPAAVLGAVRSRGCGRGA\*GRQPLPEPA  
 LFAEQRAQQRAGSADAAAPAGRGVPERLLVEARAREELPQ\*RDREPGGQDEPLEDVRARAQGRAPS\*QQRHRP\*TPATRQAAG  
 SGVGR\*GFRRRQQRVGLGWEWWW\*PVRSLAPPYRAPDVRI\*KNKKRYSRPPWRPACVLLCCL\*\*YDEARVPGSSSLVRERDAA  
 GGGGGDAAPAGGALRAPAVPGAYGGAEQHSLLGAGTLVRYHPVVPGGQVVGHRLAELPERPQQLPDHRGAEQRFHPHGGQH  
 PDHQL\*RALAVGRPAENHHAHQHAQREVRHVQQVQVQAGDGLAQDPQWGRGG\*EL\*W\*SGRADLRVGGV\*AARGQLGDH  
 DHRSDEQRHHRQLLGGGASERGAGERHRRREVRAHQLPAGLGRPRDRAGDAGRVHQRLPPRRHPAARLRRLHREPPQQPAGHP  
 QAAALPGGLPDPVRGPGGGQHPRALGCRSL\*EKQGGGRRSGDRSRGHRLYRGAGR\*FC\*RRGSGRGG\*NRK\*DSHPAGGEGQQ  
 GQELQRRARGQEKHRLPQLVPLQLRRPREGRALLDAAHHLGRHLRRGASLLVAARHDARPGHLPLHASS\*QLPGGGRRAPARLLQ  
 ELLQRAGRLLAAARLHLAHLRLQLPREPDPRPPARAHYHRQ\*KRSCSHSRDPAAAQQYPGSPARDRH\*RQTPHLRLQLGP  
 GRSRAARPLEPHLLKNVHSHLAQ\*\*HRLGPARAQDVRRRSPTLHATPRARARALPRSLGRPQGRALAHRRRRDRPGGGRAQ  
 LHARRRRLHRRRRHRQRGGRCAPVRPRQEPAAHRPAPEHPRHARGASLAAQGAHQGTQGHAGGGQTRGLRQQRRQDP  
 QTRGHGGGGGHRQHVPAAARQRLVGARRRHRCARARAHPPPSHLKMLTSLC\*CVPAARRMSKRKYKEMLQVIAPEIYGPVAVKE  
 ERKPRKLKRVKKDKKEEDVDGLVEFVREFAPRRRVQWRGRKVKPVLPRGTTVFTPGERSGSASKRSYDEVYGEDILEQAVERLG  
 EFAYGKRSRPAPLKEEAVSIPLDHGNPTPSLKPVTLLQVLPSPAAPRRGFKREGGEDLYPTMQLMVPKRQKLEDVLEHMKVDPEVQP  
 EVKVRPIKQVAPGLGVQTVDIKIPTMETQTEPVKPTSTMEVQTDPMWMPAPASTRRRRKYGAASLLMPNYALHPSIPTPGYRG  
 TRFYRGYTSSRRKTTTTRRRRRRTRRSSTATSAAALVRRVYRSGREPLTLPRARYHPSIAI\*LCRRLLADMALTCRLRVITGYRGRKPRR  
 RRLTGNGLRHHHRRRRRAISKRLGGGFLPALIPIIAAIGAIPGASVAVQASQRH\*DTAWKICNKKMD\*RSWSCDVCF\*MEDINFSS  
 LAPRHGTRPFMTGWSIDIGNSQLNGGAFNWSSLSWGLKNFGSTLKTGYNKAWNSSTGQALREKLKEQNFQKQVVDGLASINGV  
 VDLANQAVQKQINSRLDAVPPAGSVEMPQVEELPLDKRGDKRPRDAEETLLTHTDEPPPYEEAVKGLPPTTRPVAPLATGVLPK  
 SSSSQPATLDLPPASRPSTVAKPLPPVAVASRAPRGRPQANWQSTLNSIVGLGVQSVKRRRCY\*CTL\*RLTCLSVICIMSDAQKEE  
 ARRRVARWPPHRCPSGRCTSPDRTLRST\*VRVWCSSPAPQTPTSVWGTSLGTPRWRPRTM\*PPTAASG\*RCASCPWTARTTP  
 TRTKCATRWPWATTACWTWPAPTLSAACWIGGPASNPTAPPTTAWLPRERPTLASGHIKLILIQKKPIHMEMHLCALALQR  
 MVFNLELTAMVRQSMQTKLINQSLKWWMLNGMTSLVLMKNMEALLSLTPK\*SLAMVLLPSLPKKEARQM\*PKQAVPKNMTL  
 TWHSSIEVLPPA\*PQKLFILRMWIKLQIPILYTRQVQMTVALLSIWVSSPCPTDPTTLASETTLV\*CTTALAIWVYWLDRPPS  
 \*MLWWTCRTETPNCPTSSCLTLVWTEPGISVCGIRRWVMTMPMCKLITVWRMNFILTIASPMWMLWVELITRELPMVIKPPGP  
 KMILLMLLMNWARAILSPWRSTSRPTCGGTSSTRTWRCTCPTPTSTRPTSRCPPTPTIT\*TAAWWRPRWWTPTSTSGRAGR  
 WTPWTTSTPTTTATACDTPCWSATGATCPSTSRCPKSFSPSRASCSCPGPTPTSGTSARTST\*SCRAPSATTARTGPPSPSPAS  
 TSTPPSSPWRTTPPPSRPCCATPTTSTPTTSSRRPTCSTPSRPTPTCPSPRATGPPSAAGPSRASRPARRPRAPGSTPTSSTRA  
 PSPTSTAPSTSTPSRRSPSTPPSAGPATTAS\*RPTSSKSSAPSTERGTTWPSAT\*PRTGWSRCWPTTTSATRASTCPRATRTACT  
 PSSATSSP\*AARSWTRSTTRTRPSPWPTSTTRASSATSRRPCARASPTPTPTRSSARAPSPASPRKSSATGSCGASPSPATSCP  
 WARSPTSARTCTPTPTR\*T\*ISKSTPWMSPFMSLSKSSSTSECTSPTAASSRPSTCARPSRPATPPKPLASCKMTACAGSGEQE  
 LRAILRDLGCGPCFLGTDFKRFPGFMAPHKLACAIVNTAGRETGGEHWLAFAWNPRSHTCYLFDPFGFSDERLKQIYQFEYEGLLRR  
 SALATEDRCVTLEKSTQTVQGPRSAACGLFCCMFHLHAFVHWPDRPMDKNPTMNLTLGVPNGMLQSPQVEPTLRRNQEALYRFLN  
 AHSAYFRSHRARIKATAFDRMNQDM\*SGVCM\*MLYSS\*\*TAHVYATFSEALTFRNRRGSAGSRHGPRAGIRCGTGTWAAT\*TR  
 GSAASARGGRGTSRSTACA\*VAGRPAGRARRS\*NRWDPRSARESYGTRGCTGTPSGPGASRSPAPSRR\*CPRPDPRRWPSRR  
 GSSCRSAAPCWARSACGCNRSAGGSASSGPARSSCPGTWPS\*KPPAGGRPAAPCRPR\*RRPRRTC\*RTGWWRSQRRARSSARR  
 CWPAAPRCAPSGSG\*SWPGRGSPSARAARSRSPHPSRSCAPSGSSRSRAGTAACPRPRCTRAATARSRCSPSSCGRSGSASARPA  
 GSGPSSWSGSCCW\*RSAECRGAPRSHTGGRYGGTPRPARASAGRRTSGRSPRGTPSAASSLPCSPRPRKRSAGSGGSSPLSS\*SPP  
 PKSGGRSRPGSQTACRPSR\*CARGES\*SPRPAPPRAFRPRCPG\*CLAKAHAWSCGVSWAAEAAAETCWASASSRPRLL  
 GRRPRPRGRHASSGAEAEATGSRGSAGGWQSPFRVRGCAPGGAALTDFLRGRPLCSPREQAWRLSHRRQHRHLPPPPPTRTSSS  
 RMKA\*PPRRPAPPPTPQPQTCKRWRNPSRLTWT\*RPSTRRSWQRAFPQRKRTTKSSQSRKQASRTRLGSSMATT\*AGQRTC  
 SSSIWPANASSRTRCSTAPRCPSAWRSSAAPTSSRRACPPSASPTAPASPTRASTSTRSSRCPRWPPTTSFSRTKGSPSPAAPT  
 APAPTPCSTWAPAPAYLISPPWKRFPRSSRVWAATRLGPRTLCKEAERSMSTTAPWWSWKATTRAWRSSARSS\*PTSPTRRSTCP  
 PRS\*APSWTRCSSAPRPSRRRCRTPRARTRASPWSATSSWRAGWERVAPPRAWKSGASS\*WPWSW\*PWSWSVCAASSPTR  
 RPCARSRTCTTSSDTGSCARPARSPTWS\*PTWSPTWASCTRTAWGRTCTTPCAGRPAATTSATASTCTSATPGRRRAWACGSSA

Fig. 22K

WRSRT\*KSSASSCRRTSRPCPGSTSAAPPRTWPTSSSPSACG\*RCATGCPTL\*AKACCKTFALSSSNAPGSCPPAPRCPRTSCR\*P  
 SASAPRRSGATATCCAWPTTWPTTRT\*SRTSAARACSSATAAATSARRTAPWPATPSC\*ARPRSSAPSSCKAPARARGV\*NSPRGC  
 GPRPTCASSCPRTTIPSRSGSTRTNPSRPRPSCRPAASSPRGPSWPNCCKPSRNPKNFC\*KRATGSTWTPRERSSTPASPRMPRGSS  
 KKLKVELPPPPEDLEEDWESSQAEEEEMEDWDSTQAEEDSLQDSLEEEDEVEEAEEEEAAARPSSSAEEEEKASSTDTISAPGRGRGG  
 RAHSRWDETRGFNPPTQTGKKERQGYKSWRGHKNAIVSCLQACGGNISFTRRYLLFHRGVNFPRNHLHYRHLHSPYYCFQEEAE  
 TQQQQQQQKTSGSS\*KIHSGGRWTEDRGERAGADPGAEPDLSHPLCHLPAESGARAGTESQEPFSALAHPLSVSQERRPTSAH  
 SRGRRGSLQQVLAHS\*RVARARPHTEKGGNYVTTALRPTIIMSKEIPTPYMWSYQPMGLAAGAAQDYSTRMNWLSAGPAMI  
 SRVNDIRAHNRNQLLEQSAITATPRHHLNPRNWPAALVYQEIQQPTTVLLPRDAQAEVQLTNSGVQLAGGAALCRHRPAQGIKRLVI  
 RGRGTQLNDEVSSSLGLRPDGVFQLAGSGRSSFTPRQAVLTLESSSSQPRSGGIGTLQFVEEFTPSVYFNPFSGSPGHYPDEFIPNFD  
 AISEVDGYD\*MSHGGAADLARLRHLDHCRFRFCFARDLAEFAYFELPEEHPOGPAHGVRIVVEGGDLSHLLRIFSQRPIAEREQG  
 QTLTLYCICNHPGLHESLCCLLCTEYNKS\*DQRLRTSVCSYQPVVHLRERDRAPAPV\*APQEVPHLAVPGLSDRRCQPLRQRRS  
 PAERPCQPYFFHPQKQAPALPTLPPRDLVRLGTLPSHLPPDEYHSAVAPRY\*QPNYPPTPPSRPRTCTELEKY\*ATIHAIHRL\*GRAT  
 ATHAPRY\*LLQSNRRR\*LTHWPTTTSTTFSWTWTAAPRSSDSPNFAFASSRREPSRSCRTA\*PSTSARKASSAW\*NRPRSPTRSPRP  
 TIASPTSSCSSARSSPAWSESTPSSSPSRAIRPGASTAPATPPTASTL\*SRPSAASATSSP\*TNHPLIQ\*NKYHIDDDLNNK\*SFDLK\*R  
 YNHIDDLSEFK\*RITYLKSOTRSLMSFANTTSLPSSQLWYCRPRRAANFLHTLKGMSSNSCPSIFILSIRCPKASGWMMTSTPSTPT  
 MQTTHRPCSSSTPPSSLQMDSKRSPWGCPDCLTSPSPRTGKSPSSWERTSTPRENSSPTRPPRPPPLSVFPTTFFPLTWIPLF  
 IPKMENYPYKFLHR\*TY\*NQPF\*TH\*L\*LMDQV\*D\*VVALLQYSWPLHSLMKKEILKLT\*PVVH\*QLMQVDLVSTAKEGSLSLPQ  
 EMQLKAT\*AGLKV\*DLKVMA\*LQTLAEDWNLEPLVQRLMSQMHTQFKNLWVLAALPLTVQAPLLGTRKMINLHYGPQPTPRQIA  
 KYTLKKMPNSHFA\*QSVEVKFWVL\*LYWQ\*IMEVSTQSQTQ\*ALHSSPSSLMQVEFC\*AAPH\*TKNIGTSEREMLHLLSPILML\*VL  
 CLT\*RPILKTHLQLQKAILSVKFISMGMRPNH\*C\*LLLLMKLRMLQAPTIVSLFNGNGIVLSTQVKHLLPAPSPSPSPKNEHCIPPCMP  
 TLPTPLCLWKKL\*STK\*NKVQVYF\*FNSFTGFEQLFFLHPRTWNTPPSPPAQ\*P\*TSECHW\*WTCFWSPRSTQFQSEPVSGRSGR\*  
 NPPGTPASAPHSSTAEDCPRWSGSRSLSGRSRAAVGIIVRERDRPVVSHQAPQQSLPPLRQAAAQGVVRVQGLPQHDHAGPQH  
 SSGAAGAAAHADLAQVA AVRATQDHQVQQSIVQHAPAETHRGKDATHVAVVPDPQVNQVALPPEHAAHVHDLGHVAVVHLL  
 PVPHHPLVEHAAPDDPAEPQGGHRRPARHAARKPRVPAMAMEDPPLVPVDHLGAEQVYVGTAAQAYAHASLQHSQLLGGQNHIP  
 GHGELLQDSEPRRTGQSSHITYIVHGQGIARQHRVILHQRSAGLGLTAW\*GGRPIRVMAGRG\*SCSRPCHDAVAFGHFRTCCSRT  
 WSGRCTPIAGGGPGAWNARC\*NCKTATLSDRAADLGPQE\*\*RSHHA\*\*L\*SHRPPWNGPDPAR\*CNFVGFR\*RRGREEQEEP\*L  
 TFNPNGLGALQNEGRGDGTSRPRCVGGK\*QPGQR\*YGRSDVPRWLPKPPRAHPETRQ\*RKREGSLIPQSSCYTPAPSPDNFHS  
 SLE\*FELVPEVNPSQP\*\*RARAERPPPAFLSTPS\*FQDILLVHLQQIDKRNKISAAIPKLLPQQ\*L\*VLFHILSEIFSHRTTRNKIRASHS  
 TDKPKSSPVSIKCKTAISMLARPGDIFQITGQKITQAIKKINKRKILQVHV\*SLGNNDVNASGAFQHG\*LADL\*KTKNKTNLHASL  
 ANRWVNRLQHQAGHGVSGATLVKIVAMIENHHRETFPVAGVNDSTR\*IHPRNIGVRE\*KKAPEEAI RHNAQSQVQQSDAMR  
 MKHKILRCVQNVITPLLHRQRSRSLQIHQSLSVHSLPSSSTQQAQSEK\*ALTCPPALCSIYSPDLH\*RKGQSLKIPAK\*SHTPSTRP  
 ETGDTLKKIRALPQTPKLPSFPGSHATSSEFDFQIPSTVKNVTRPAPNGRPSLGQSPSSLPKFKQLICILTRTKSLRYIID

Fig. 23A

**AdC7 010-HIVgag(E1048) Nucleic Acids – SEQ ID NO: 4**

CATCATCAATAATATACCTCAAACCTTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCCGAGAGACGGGCGACCGTTAGGGGCGGGGCGGGTGACGTTTTGATGACGTGGCCGTGAGGCGGAGCCGGTTTGCAA  
GTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTCCCGCGCTCTCTGACAGGAAAT  
GAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAAAACTGAATGAGGAAGTAAAAATCTGAGTAATTT  
CGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTT  
CACCTAAATTTCCGCGTACGGTGTCAAAGTCCGGTGTTTTTACGTACGATATCATTTCCCCGAAAGTGCCACCTGACCGTAACTA  
TAACGGTCCTAAGGTAGCGAAAGCTCAGATCTCCCGATCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGT  
TAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTAAGCTACAACAAGGCAAGGC  
TTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTG  
ACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAA  
CTTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACG  
CCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAACTGCCACTTGGCAGTACATCAAGTGTATCATATG  
CCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCT  
ACTTGGCAGTACATCTACGTATTAGTCATCGTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCG  
GTTTGACTCACGGGGATTTCGAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGGCACCAAAATCAACGGGACTTTCC  
AAAATGTCGTAACAACTCCGCCCATTTGACGCAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTCGT  
TTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGTGCTTCTGACACA  
ACAGTCTCGAAGCTTAAGCTGCAGAAGTTGGTCGTGAGGCACTGGGCAGGTAAGTATCAAGGTTACAAGACAGGTTTAAGGAG  
ACCAATAGAACTGGGCTTGTGAGACAGAGAAGACTCTTGCGTTTCTGATAGGCACCTATTGGTCTTACTGACATCCACTTTG  
CCTTTCTCTCCACAGGTGTCCACTCCAGTTCAATTACAGCTCTTAAGGCTAGAGTACTTAATACGACTCACTATAGGCTAGCGC  
CACCATGGGCGCCAGAGCCAGCGTGCTGAGCGGGGAGAGCTGGATCGCTGGGAAAAGATTAGACTGAGGCCCGGAGGGA  
AGAAAAAGTACAAGCTGAAACACATCGTGTGGGCCAGCAGGGAGCTGGAGCGCTTCGCGTGAACCCCGGACTGCTGGAGA  
CCTCCGAAGGCTGTGCGCAGATCCTGGGGCAGCTGCAGCCTTCCTGCAGACAGGCTCCGAGGAGCTGCGGTCTCTGTATAAT  
ACAGTGGCCACACTGTACTGTGTGCACCAGCGGATTGAGGTGAAGGATACAAAAGAGGCCCTGGAGAAGATTGAGGAGGAG  
CAGAACAAAGAGCAAGAAGAAAGCCAGCAGGCCGCGCCGACACCGGCAATAGCTCCAGGTGAGCCAGAACTATCCAATTG  
TGCAGAATCTGCAGGGCCAGATGGTGACCAGGCCATTTCCCAACGGACACTGAACGCCTGGGTGAAGGTGGTGGAGGAGA  
AGGCCTTCAGCCCCGAAGTGATCCCTATGTTTCCGCCCTGTCCGAAGGCGCCACCCCTCAGGACCTGAACACCATGCTGAACA  
CAGTGGGGGGACACCAGGCCCATGCGAGATGCTGAAGGAAACCATCAACGAGGAGGCCGCCGAGTGGGATCGGCTGCACC  
CCGTGCACGCCGGGCCAATCGCCCCTGGCCAGATGAGGGAGCCAGAGGCTCTGACATCGCCGGCACCACATCTACCCTGCA  
GGAACAGATCGGGTGGATGACCAATAACCCACCAATCCAGTGGGCGAGATCTACAAGAGGTGGATTATTCTGGGACTGAAC  
AAAATTGTGCGCATGTATTCCCTACATCCATCCTGGACATCAGGCAGGGCCCTAAGGAACCTTTCCGCGACTACGTGGATCGG  
TTCTACAAAACCTGCGCGCCGAGCAGGCCAGCCAGGAAGTGAAGAATTGGATGACAGAGACCTGCTGGTGCAGAACGCCA  
ATCCTGACTGTAAAACCATCTGAAGGCCCTGGGCCCTGCCGCCACTGGAGGAAATGATGACCGCTGCCAGGGCGTGGG  
CGGCCCTGGCCACAAAGCCAGGGTGTGGCCGAGGCCATGTCTCAGGTGACCAACTCTGCCACAATTATGATGCAGCGGGG  
AACTTTCCGAACAGAGGAAGACCGTGAAGTGCTTCAACTGTGGCAAGGAGGGACACATCGCCAAGAATTGCCGCGCCCCAC  
GGAAGAAGGGGTGTTGGAAATGCGGGAAGGAGGGCCACCAGATGAAAGACTGCACAGAGCGGCAGGCCAACTTTCTGGGC  
AAGATTTGGCCAGCCACAAGGGCCGCCCGGAACTTTCTGCAGTCCAGGCCTGAGCCTACCGCCCCCTGAGGAATCCTT  
CCGGTTCGCGGAGGAGACAACACCCCAAGCCAGAAGCAGGAACCCATCGACAAAGAGCTGTACCCCTGGCCAGCCTGAGA  
TCCCTGTTCCGGAATGACCCAGCTCTCAGTGATGATCTAGCGTTAAACGGGCCCTTAGAGTCGACCCGGGCGGCCAAACC  
GCTGATCAGCCTCGACTGTGCCTCTAGTTGCCAGCCATCTGTTGTTGCCCTCCCCGTCCTTCTTACCTGGAAGGTGC  
CACTCCCACTGTCCTTCTAATAAAATGAGGAAATGCATCGCATTGTCTGAGTAGGTGTATTCTATTCTGGGGGTGGGGT  
GGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGG  
CGGAAAGAACCAGCAGATCTGCAGATCTGAATTCATCTATGTCGGGTGCGGAGAAAGAGGTAATGAAATGGCATTATGGGTA  
TTATGGGTCTGCATTAATGAATCGGCCAGATATGCTGGCCACCGTGCATGTGACCTCGACCCCCGCAAGACATGGCCCGAGT  
TCGAGCACAACGTCATGACCCGATGCAATGTGCACCTGGGGTCCCGCCGAGGCATGTTTCATGCCCTACCAAGTGAACATGCAA  
TTTGTGAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGCTGTGGA  
AAATTCTGAGATATGATGAATCCAAGACCAGGTGCCGGGCCCTGCGAATGCGGAGGCAAGCACGCCAGGCTTCAGCCCGTGTG  
TGTGGAGGTGACGGAGGACCTGCGACCCGATCATTTGGTGTTGTCTGCAACGGGACGGAGTTCGGCTCCAGCGGGGAAGA  
ATCTGACTAGAGTGAGTAGTGTGGGGGAGGTGGAGGGCTGTATGAGGGGCAGAATGACTAAAATCTGTGTTTTCTGTG

Fig. 23B

TGTTGCAGCAGCATGAGCGGAAGCGCCTCCTTTGAGGGAGGGGTATTGAGCCCTTATCTGACGGGGCGTCTCCCCTCCTGGGC  
GGGAGTGCCTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCCGTGACGCCCGGAACTCTCAACCCTGACCTACGCG  
ACCCTGAGCTCCTCGTCCGTGGACGAGCTGCCGCCGAGCTGCTGCTCCGCCGCCAGCGCCGTGCGCGGAATGGCCCTGGG  
CGCCGGCTACTACAGCTCTCTGGTGGCCAACTCGACTTCCACCAATAATCCCGCCAGCCTGAACGAGGAGAAGCTGCTGCTGC  
TGATGGCCCAGCTCGAGGCCCTGACCCAGCGCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGACGGCGGAGACGCGGG  
CCGCGGTTGCCACGGTGAACCAATAAAAAATGAATCAATAAATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTTG  
AATCTTTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGATTITTTCCAGGACC  
CGGTAGAGGTGGGCTTGATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGGTGAGGTAGCTCCATTGCAGGGCCTCG  
TGCTCGGGGGTGGTGTGTAATCACCCAGTCATAGCAGGGGCGCAGGGCGTGGTGCTGCACGATGTCCTTGAGGAGGAGA  
CTGATGGCCACGGGACGCCCTTGGTGTAGGTGTTGACGAACCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGA  
TGCATCTTGCCCTGGATCTTGAGATTGGCGATGTTCCCGCCAGATCCCGCCGGGGTTCATGTTGTGCAGGACCACAGCAC  
GGTGTATCCGGCGCACTTGGGAATTTGTATGCAACTTGAAGGGAAGGCGTGAAAGAATTTGGAGACGCCCTTGTGACCG  
CCCAGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCGTGGGCGGCGCCTGGGCAAAGACGTTTCGGGGGTGCG  
ACACATCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAATGAATTTGGGGCGGAGGGTGCCCGACTGGGGGAC  
GAAGGTGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGCATCTCCAGGCCTTGAGCTCGGAGGGGGGGATCATG  
TCCACCTGCGGGGCGATGAAAAAACGGTTTCCGGGGCGGGGAGATGAGCTGGGCCGAAAGCAGGTTCCGGAGCAGCTG  
GGACTTGCCGAGCCGGTGGGGCCGTAGATGACCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTC  
CTCGCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGACATGCATGTTCTCGCGACAGAGTCCGCCAGGAGGCGCTCGC  
CCCCAGCGAGAGGAGCTTTGACGCGAGGCGAAGTTTTTACGCGCTTGAGCCCGTGGCCATGGGCATTTTGAGAGGGT  
CTGTTGCAAGAGTTCAGACGGTCCAGAGCTCGGTGATGTGCTCTAGGGCATCTCGATCCAGCAGACCTCCTCGTTTCGCGG  
GTTGGGGCGACTGCGGGAGTAGGGCACAGGCGATGGGCGTCCAGCGAGGCCAGGGTCCGGTCTTCCAGGGTCCGAGGGT  
CCGCGTCAGCGTGGTCTCCGTACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGCAGGGTGCGCTTCAGGCTCATCCGG  
CTGGTCGAGAACCGCTCCCGTCCGGCGCCTGCGCGTCCGCCAGGTAGCAATTGAGCATGAGTTCGTAGTTGAGCGCCTCGG  
CCGCGTGGCCCTTGGCGCGGAGCTTACCTTTGGAAGTGTGTCGCGAGACGGGACAGAGGAGGGACTTGAGGGCGTAGAGCT  
TGGGGGCGAGGAAGACGGACTCGGGGGCGTAGGCGTCCGCGCCGAGCTGGCGCAGACGGTCTCGCACTCCACGAGCCAG  
GTGAGGTGCGGGCCGTTGGGGTCAAAACGAGGTTTCTCCGTGCTTTTGATGCGTTTCTTACCTCTGGTCTCCATGAGCTCG  
TGTCCTCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACTTATGGGCCGGTCTCGAGCGGGGTGCCGCGGT  
CCTCGTCGTAGAGGAACCCGCCACTCCGAGACGAAGGCCCGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGAGGGGT  
AGCGGTGTTGTCCACGAGCGGGTCCACCTTCTCCAGGGTATGCAAGCACATGTCCCCTCGTCCACATCCAGGAAGGTGATT  
GGCTTGTAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAGGGGGCGGGCCCTGCTCGTCTCACTG  
TCTTCCGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCCTCTGAAGGCTGGCATAACCTCGGCACTCAGGTT  
GTCAGTTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTTGGAGACGCCTTTCATGAGCCCTCGTCCATCTGGTCAG  
AAAAGACGATCTTTTTGTTGTGAGCTTGGTGGCGAAGGAGCCGTAGAGGGCGTGGAGAGGAGCTTGGCGATGGAGCGCA  
TGGTCTGGTTCTTTCTTGTGCGCGCGCTCCTTGGCGGCGATGTTGAGCTGCACGTAAGTTCGCGCGCCACGCACTTCCATTGCG  
GGAAGACGGTGGTGTGAGCTCGTCGGGCACGATTCTGACCCGCCAGCCGCGTGTGTCAGGGTGATGAGGTCCACGCTGGTGG  
CCACCTCGCCGCGCAGGGGCTCGTTGGTCCAGCAGAGGCGCCGCCCTTGCAGCAGCAGAGGGGGGACGCGGGTCCAGCA  
TGAGCTCGTCGGGGGGGTGCGCGTCCACGGTGAAGATGCCGGGCGAGAAGCTCGGGGTGCAAGTAGCTGATGCAGGTGTCCA  
GATCGTCCAGCGCCGCTTGCCAGTCGCGCACGGCCAGCGCGCTCGTAGGGGTGAGGGGCGTGCCCCAGGGCATGGGGT  
GCGTGAGCGCGGAGGCGTACATGCCGCAGATGTGCTAGACGTAGAGGGGCTCCTCGAGGACGCCGATGTAGGTGGGGTAGC  
AGCGCCCCCGCGGATGCTGGCGCGCACGTAGTGTACAGCTCGTGCAGGGGCGGAGGAGCCCCGTGCCGAGGTTGGAGC  
GTTGCGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAGTTGGAGGAGATGGTGGGCCTCTGGAAGATGT  
TGAAGTGGGCGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTAGGAGTCTGACGCTTGGCGACGAGCTCGGCGG  
TGACGAGGACGTCCAGGGCGCAGTAGTCGAGGGTCTCTGGATGATGTGTAAGTGGGCTGAGCTGGCCCTTCTGCTTCCACAGCTCG  
CGGTTGAGAAGGAACTCTTCGCGTCTTCCAGTACTCTTCGAGGGGGAACCCGTCTGATCGGCACGGTAAGAGCCACCAT  
GTAGAAGTGGTTGACGGCCTTGAGGCGCAGACGCCCTTCTCCAGGGGAGGGCGTAAGCTTGTGCGGCCTTGCAGGGGAG  
GTGTGGGTGAGGGCGAAGGTGTGCGGCACCATGACCTTGAGGAACTGGTGCTTGAAGTCGAGGTGCTGCGAGCCGCCCTGCT  
CCCAGAGCTGGAAGTCCGTGCGCTTCTGTAGGCGGGGTTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGC  
GCGGGGCATGAAGTTCGAGTGATGCGGAAAGGTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGGACGAT  
CTCGTCGAAGCCGTTGATGTTGTGCCCCACGATGTAGAGTTCCACGAATCGCGGGCGGCCCTTAACGTGGGGCAGCTTCTTGA  
GCTCGTCGTAGGTGAGCTCGGCGGGGTCGTGAGCCCGTGTGCTCGAGGGGCCAGTCGGCGACGTGGGGGTTGGCGCTGA  
GGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTCTGCAAGCGGTCCCGGTACTGACGGAAGTGTGGCCACGGCCATTTT

**Fig. 23C**

TCGGGGGGTGACGACAGTGAAGGTGCGGGGTCGCCGTGCCAGCGCTCCACTTGAAGCTGGAGGGCGAGGTCGTGGGCGA  
 GCTCGACGAGCGGCGGGTCCCCGAGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGT  
 GTAGGTTTTCCACATCGTAGGTGAGGAAGAGCCTTTGCGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCCTGCCAC  
 CAGTTGGAGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGCGCCGAGCACTCGTGCTTGTTTATACAAGC  
 GTCCGCAGTGCTCGCAACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGGGTTCCTTTGACGAGGAATTTCACTGGG  
 CAGTGGAGCGCTGGCGGCTGCATCTGGTGCTGTACTACGTCTGGCCATCGGCGTGGCCATCGTCTGCCTCGATGGTGGTCAT  
 GCTGACGAGCCCGCGCGGGAGGCAGGTCCAGACTTCGGCTCGGACGGGTCGGAGAGCGAGGACGAGGGGCGCGCAGGCCGG  
 AGCTGTCCAGGGTCTGAGACGCTGCGGAGTCAGGTCACTGGGCGAGCGGCGCGCGGTTGACTTGACGAGAGCTTTCCAG  
 GGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACGGCGCCGTTGGTGGCGACGTCCACGGCTTGACAGGGTCCCGTGCCCC  
 TGGGGCGCCACCACCGTGCCCCGTTTCTTCTTGGGCGCTGCTTCCATGCCGGTCAGAAGCGGCGGCGAGGACGCGCGCCGGG  
 CGGCAGGGGCGGCTCGGGACCCGGAGGCGAGGGGCGGCAGGGGACGTCGGCGCCGCGCGCGGGCAGGTTCTGGTACTGCG  
 CCGGAGAAGACTGGCGTGAGCGACGACGCGACGGTTGACGTCTGGATCTGACGCTCTGGGTGAAGGCCACGGGACCCG  
 TGAGTTTGAACCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCTGCGCGAGGATCTCTGACGTCG  
 CCCGAGTTGTCTGGTAGGCGATCTCGGTGATGAAGTCTCGATCTCTCTCTGAAGGTCTCCGCGGCGGCGCGCTCGAC  
 GGTGGCCGCGAGGTCTTGGAGATGCGGCCATGAGCTGCGAGAAGGCGTTCATGCCGGCCTCGTTCCAGACGCGGCTGTA  
 GACCACGGCTCCGTGCGGGTGCAGCGCGCGCATGACCACCTGGGCGAGGTTGAGCTCGACGTGGCGCGTGAAGACCGCGTA  
 GTTGACAGAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTGACGAAGAAGTACATGATCCAGCGCGGAG  
 CGGCATCTCGTGACGTGCGCCAGGGCTTCAAGCGCTCCATGGCCTCGTAGAAGTCCACGGCGAAGTTGAAAACTGGGAG  
 TTGCGCGCGGAGACGGTCAACTCTCTCCAGAAGACGGATGAGCTCAGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCC  
 CGGGGGGCTCCTCTTCTCCATCTCTCTCTCCACTAACATCTCTTCTACTTCTCTCAGGAGGCGGCGGGGGGAGGGG  
 CCTGCGTGCAGCGGCGGCGCACGGGCGAGCGGTGATGAAGCGCTCGATGGTCTCCCGCGCGGCGGCGACGCATGGTCTCGGT  
 GACGGCGCGCCCCGTCTCGCGGGGCGCAGCGTGAAGACGCGCGCGCATCTCCAGGTGGCCGCGGGGGGGTCTCCGTT  
 GGGCAGGGAGAGGGCGCTGACGATGCATCTTATCAATTGCCCCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAGATCC  
 ACGGATCCGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGAGTCGCAAGGTAGGCTGAGCCCCGTTTCTGTTCTTCGG  
 GGATTTGGGAGGCGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAGTAGGCGGTCTGAGACGGCGGATGGTGGCGAGG  
 AGCACCAGGTCTTGGGCCCGGCTTGTGGATGCGCAGACGGTCGGCCATGCCCAGGCGTGGTCTGACACCTGGCGAGGT  
 CTTGTAGTAGTCTCGATGAGCCGCTCCACGGGCACCTCTCTCGCCGCGCGGCGCGTGCATGCGCGTGAGCCGAACCCG  
 CGCTGGGGCTGGACGAGCGCCAGGTGCGCGACGACGCGCTCGGCGAGGATGGCCTGCTGTATCTGGGTGAGGGTGGTCTGG  
 AAGTCGTGCAAGTCGACGAAGCGGTGGTAGGCTCCGGTGTGATGGTATAGGAGCAGTTGGCCATGACGGACCAAGTTGACG  
 GTCTGGTGGCCGGTTCGACGAGCTCGTGGTACTTGAGGCGCGAGTAGGCGCGCGTGTGCAAGATGTAGTCGTTGACGGTG  
 CGCACGAGGTACTGGTATCCGACGAGGAAGTGCAGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCC  
 GGGCGCGAGGTCTCGAGCATGAGGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGGCGGCGGTGGTGG  
 GGCGCGCGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTTCATGGTGGCCGCGGTCTGGCCGT  
 GAGGCGCGCGCAGTCGTGGATGCTCTAGACATACGGGCAAAAACGAAAGCGGTGAGCGGCTGACTCCGTGGCTGGAGGC  
 TAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGGTTCAATCTCGAATCAGGCTGGAGCCGCGAGCTAACGTGGTACTGGC  
 TCCCGTCTGACCCAAGCCTGCTAACGAACCTCCAGGATACGGAGGCGGGTCTTTTTTGGCCTTGGTGGTGGTATGAAA  
 AACTAGTAAGCGCGGAAAGCGACCGCCCGCATGGCTCGCTGCCGTAGTCTGGAGAAAGAAATCGCCAGGGTTGCGTTGCGGT  
 GTGCCCCGGTTTCGAGCTCAGCGCTCGGCGCGGCGCGGATTCCGCGGCTAACGTGGGCGTGGCTGCCCCGTCGTTTCAAGAC  
 CCTTAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCTCTTTTTCTGTGTTTTTGCAGATGCATCCCGTACTGCGGCAGA  
 TCGCCCCCACCCTCCACCTCAACCGCCCCCTACCGCCGCGAGCAGCAGCAACAGCCGCGCTTCTGCCCCGCCCCAGCAGCAGC  
 CAGCCACTACCGCGGCGGCGCCGTGAGCGGAGCCGGCGTTCAATGACCTGGCCTTGAAGAGGGCGAGGGGCTGGCGC  
 GGCTGGGGGCGTCTGCGCGGAGCGGCACCCGCGCGTGCAGATGAAAAGGGACGCTCGCGAGGCCTACGTGCCAAGCAGA  
 ACCTGTTTCAGAGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGCGCCTCCCGCTTCCACGCGGGGCGGGAGCTGCGGCGCG  
 GCCTGGACCGAAAGCGGGTGCTGAGGGACGAGGATTTGAGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCGCAC  
 GTGGCCGCGGCCAACCTGGTACGCGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCAAAAATCTTCAACAACCACG  
 TCGCACGCTGATCGCGCGGAGGAGGTGACCCTGGGCTGATGCACCTGTGGGACCTGCTGGAGGCCATCGTGAGAACC  
 CAGGACGAAGCCGCTGACGGCGCAGCTGTTTCTGGTGGTGCAGCACAGTCGGGACAACGAGACGTTACAGGAGGCGCTGCT  
 GAATATCACCGAGCCCGAGGGCGGCTGGCTCTGGACCTGGTGAACATTCTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTG  
 CCGCTGTCCGAGAAGCTGGCGGCTATCAACTTCTCGGTGCTGAGCCTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCC  
 GTACGTGCCATAGACAAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGACCCTGAAAGTGTGACCCTGAGCGACGAT  
 CTGGGGGTGTACCGCAACGACAGGATGCACCGCGGGTGAGCGCCAGCCGCGGCGCGAGCTGAGCGACCAAGGAGCTGATG



Fig. 23D

CACAGCCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCGCTGGCAG  
CCCAGCCGCCGGGCTTGGAAGCTGCCGGCGGTTCCCCCTACGTGGAGGAGGTGGACGATGAGGAGGAGGAGGGCGAGTAC  
CTGGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAGCAACAGCCACCGCCTCTGATCCCGCGATGCGGGCGGCGCTG  
CAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAATCC  
CGAAGCCTTTAGACAGCAGCCTCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTGGTGCCCTCGCGCTCGAACCCACGC  
ACGAGAAGGTGCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCATCCGCGGCGACGAGGCCGGGCTGGTGTACAACG  
CGTGCTGGAGCGCGTGCCCGCTACAACAGCACCAACGTGCAGACGAACCTGGACCGCATGGTGACCGACGTGCGCGAGG  
CGGTGTGCGAGCGCGAGCGGTTCCACCGCGAGTGAACCTGGGCTCCATGGTGGCGCTGAACGCCTTCTGAGCACGCAGCC  
CGCCAACGTGCCCCGGGGCCAGGAGGACTACACCACTTCATCAGCGCGCTGCGGCTGATGGTGGCCGAGGTGCCCCAGAGC  
GAGGTGTACCACTCGGGGCCGACTACTTCTCCAGACAGTCGCCAGGGCTTCAGACCGTGAACCTGAGCCAGGCTTTCAA  
GAACCTGCAGGGACTGTGGGCGTGACAGGCCCGGTGCGGGACCGCGCGACGGTGTGAGCCTGCTGACGCCGAACCTCGCG  
CCTGCTGCTGCTGGTGGCGCCCTTACGGACAGCGGCAGCGTGAGCCGCGACTCGTACCTGGGCTACCTGCTTAACCTGT  
ACCGCGAGGGCCATCGGGCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATACCCACGTGAGCCGCGCGCTGGGCCAGG  
AGGACCCGGGCAACCTGGAGGGCCACCTGAACCTTCTGCTGACCAACCGGTGCGAGAAGATCCCGCCCCAGTACGCGCTGAG  
CACCGAGGAGGAGCGCATCCTGCGCTACGTGCAGCAGAGCGTGGGGCTGTTCTGATGCAGGAGGGGGCCACGCCAGCGC  
CGCGCTCGACATGACCGCGCGCAACATGGAGCCAGCATGTACGCTCGCAACCGCCGTTTCATCAATAAGCTGATGGACTACT  
TGCATCGGGCGGCCCATGAACCTGGACTACTTTACCAACGCCATCTTGAACCCGCACTGGCTCCCGCCGCCGGGTTCTACA  
CGGGCGAGTACGACATGCCGACCCCAACGACGGGTTCTGTGGGACGACGTGGACAGCAGCGTGTCTCGCCGCGCCCCGC  
CACCAACGTGTGGAAGAAAGAGGGCGGGGACCGCGCGCCGTCTCGCGCTGTCCGGTTCGCGCGGGTGCTGCCGCGCGCGT  
GCCTGAGGCCGCCAGCCCTTCCCGAGCCTGCCCTTTGCTGAACAGCGTGCGCAGCAGCGAGCTGGGTGCGCTGACGCGG  
CCGCGCTGCTGGGCGAGGAGGAGTACCTGAACGACTCCTTGTGAGGCCCGAGCGCGAGAAGAACTTCCCAATAACGGGA  
TAGAGAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTACGCGCACGAGCACAGGGACGAGCCCCGAGCTAGCAGCAGCG  
CAGGCACCCGTAGACGCCAGCGACACGACAGGCAGCGGGGTCTGGTGTGGGACGATGAGGATTCCGCCGACGACAGCAGCG  
TGTTGGACTTGGGTGGGAGTGGTGGTGAACCGTTGCTCACTTGCGCCCCGTATCGGGCGCCTGATGTAAGAATCTGAA  
AAAATAAAAAACGGTACTCACCAAGGCCATGGCGACACGCGTGCGTTCTTCTGTTGTTGTAGTAGTATGATGAGGCGCGT  
GTACCCCGAGGGTCTCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGGTGGCGGCGCGCATGCAGCCCCGCTGGAGGC  
GCCTTACGTGCCCCCGCGGTACCTGGCGCTACGGAGGGGCGGAACAGCATTGTTACTCGGAGCTGGCACCTTGTACGATA  
CCACCCGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGAACCTACCAGAACGACCACAGCAACTTCTGACC  
ACCGTGGTGCAGAACAACGATTTACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCG  
GCCAGCTGAAAACCATCATGCACACCAACATGCCAACGTGAACGAGTTATGTACAGCAACAAGTTCAAGGCGCGGGTGAT  
GGTCTCGCGCAAGACCCCAATGGGGTCGCGGTGGATGAGAATTATGATGGTAGTCAGGACGAGCTGACTTACGAGTGGGTG  
GAGTTTGAGCTGCCGAGGGGCAACTTCTCGGTGACCATGACCATCGATCTGATGAACAACGCCATCATCGACAATACTTGGC  
GGTGGGGCGTCAAGACGGGGTGCTGGAGAGCGACATCGGCGTGAAGTTCGACACGCGCAACTTCCGGCTGGGCTGGGACCC  
CGTGACCGAGCTGGTGTGCGGGCGGTGTACACCAACGAGGCCTTCCACCCCGACATCGTCTGCTGCCCCGCTGCGGCGTG  
GACTTACCGAGAGCCGCTCAGCAACCTGCTGGGCATCCGCAAGCGGCAGCCCTTCCAGGAGGGCTTCCAGATCCTGTACGA  
GGACCTGGAGGGGGGCAACATCCCCGCGCTCTTGATGTGGAAGCCTATGAGAAAAGCAAGGAGGAGGCCGCCGAGCGGC  
GACCGCAGCCGTGGCCACCGCCTTACCGAGGTGCGGGGCGATAATTTTGCTAGCGCCGCGGCACTGGCCGAGGCGGTGAA  
ACCGAAAGTAAGATAGTCATCCAGCCGGTGGAGAAGGACAGCAAGGACAGGAGCTACAACGTGCTCGCGGACAAGAAAAAC  
ACCGCCTACCGCAGCTGGTACCTGGCTACAACCTACGGCGACCCCGAGAAGGGCGTGCGCTCCTGGACGTGCTCACCACCTC  
GGACGTACCTGCGGCGTGGAGCAAGTCTACTGGTCTGCTGCCCACATGATGCAAGACCCGGTCACTTCCGCTCCACGCGTC  
AAGTTAGCAACTACCCGGTGGTGGGCGCCGAGCTCCTGCCGCTACTCCAAGAGCTTCTTAACGAGCAGGCCGTCTACTCG  
CAGCAGCTGCGCGCTTACCTCGTCAACGACGTCTTCAACCGCTTCCCGAGAACCAGATCCTCGTCCGCCCCCGCGCGCC  
ACCATTACCACCGTCAGTGAACGTTCTGCTCTACAGATCACGGGACCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCA  
GCGCGTGACCGTCACTGACGCCAGACGCCGACCTGCCCTACGTCTACAAGGCCCTGGGCGTAGTCGCGCGCGCGCTCTCT  
CGAGCCGCACCTTCTAAAAAATGTCCATTCTCATCTCGCCAGTAATAACACCGGTTGGGGCCTGCGCGCGCCAGCAAGATGT  
ACGGAGGCGCTCGCAACGCTCCACGCAACACCCCGTGCGCGTGCGCGGGCACTTCCGCGCTCCCTGGGGCGCCCTCAAGGG  
CCGCGTGCGCTCGCGCACCAACGTCGACGACGTGATCGACAGGTGGTGGCCGACGCGCGCAACTACACGCCCGCCGCGCG  
CCCGCCTCCACCGTGGACGCCGTATCGACAGCGTGGTGGCCGATGCGCGCGCGGTACGCCCGCGCCAAGAGCCGGCGCGGC  
GCATCGCCCCGCGGACCCGAGCACCCCGCCATGCGCGCGGCGCGAGCCTTGTGCGCAGGGCCAGGCGCACGGGACGCA  
GGGCCATGCTCAGGGCGGCCAGACGCGCGGCCCTCCGGCAGCAGCAGCGCGGCGAGGACCCGAGACGCGCGGCCACGGCG  
GCGGCGGCGGCCATCGCCAGCATGTCCCGCCCGCGGCGCGGCAACGTGTACTGGGTGCGCGACGCGGCCACCGGTGTGCGC

Fig. 23E

GTGCCCCGTGCGCACCCGCCCCCTCGCACTTGAAGATGCTGACTTCGCGATGTTGATGTGTCCCAGCGGCGAGGAGGATGTCC  
AAGCGCAAATACAAGGAAGAGATGCTCCAGGTCATCGCGCTGAGATCTACGGCCCCGCGTGAAGGAGGAAAGAAAGCCC  
CGCAAACCTGAAGCGGGTCAAAAAGGACAAAAAGGAGGAGGAAGATGTGGACGGAAGTGGTGGAGTTTGTGCGCGAGTTTCG  
CCCCGGCGGCGCGTGCAGTGGCGCGGGCGGAAAGTGAAACCGGTGCTGCGGCCGCGCACCGGTGGTCTTACGCCCGG  
CGAGCGTTCCGGCTCCGCTCCAAGCGCTCCTACGACGAGGTGTACGGGGACGAGGACATCCTCGAGCAGGCGGTGCGAGCGT  
CTGGGCGAGTTTGTCTACGGCAAGCGCAGCCGCCCCGCGCCCTTGAAGAGGAGGCGGTGTCCATCCCGCTGGACCACGGCA  
ACCCACGCGGAGCCTGAAGCGGTGACCTGACGAGGTGCTGCCGAGCGCGGCGCGCGCGGGGCTTCAAGCGCGAGG  
GCGGCGAGGATCTGTACCCGACCATGCAGCTGATGGTGCCCAAGCGCCAGAAGCTGGAGGACGTGCTGGAGCACATGAAGG  
TGGACCCCGAGGTGCAGCCGAGGTCAAGGTGCGGCCATCAAGCAGGTGGCCCCGGGCTGGGCGTGCAGACCGTGGACA  
TCAAGATCCCCACGGAGCCCATGGAACGCAGACCGAGCCCGTGAAGCCAGCACCAGCACCATGGAGGTGCAGACGGATCC  
CTGGATGCCGCGCGCGCTTCCACCACTCGCCGAAGACGCAAGTACGGCGCGGCCAGCCTGCTGATGCCAACTACGCGCTG  
CATCCTTCCATCATCCCCACGCGGGGTACCGCGGCACGCGCTTCTACCGCGGTACACCAGCAGCCGCGCAAGACCACCAC  
CGCCGCGCGCTGCTGCGACCCGCGCGCAGCAGCACCAGCGACTTCCGCGCGCGCCTGGTGCGGAGAGTGTACCGCAGCGGGC  
GCGAGCCTCTGACCTGCGCGCGCGCGCTACCACCCGAGCATCGCCATTAACTCTGCCGTCGCTCCTACTTGCAGATATGG  
CCCTCACATGCCGCTCCGCTCCCCATTACGGGCTACCGAGGAAGAAAGCCGCGCGTAGAAGGCTGACGGGGAACGGGCT  
GCGTCGCCATCACACCGGCGGCGGCGGCCATCAGCAAGCGGTTGGGGGAGGCTTCTGCCGCGCTGATCCCCATCATC  
GCCGCGCGATCGGGCGATCCCCGCATAGCTTCGTGGCGGTGCAGGCCTCTCAGCGCCACTGAGACACAGTTGAAAA  
TTTGTAAATAAAAAATGGAAGTACGCTCCTGGTCTGTGATGTGTGTTTTAGATGGAAGACATCAATTTTTCTGCCCTGGCAC  
CGCGACACGGCAGCGGCGCTTATGGGCACCTGGAGCGACATCGGCAACAGCCAAGTGAACGGGGCGCCTTCAATTGGAG  
CAGTCTCTGGAGCGGGCTTAAGAATTCGGGTCCACGCTCAAAACCTATGGCAACAAGGCGTGAACAGCAGCACAGGGCAG  
GCGCTGAGGAAAAAGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTCGATGGCCTGGCCTCGGCATCAACGGGGTGGTG  
GACCTGGCAACCAGGCGCTGCAGAAACAGATCAACAGCCGCTGGACGCGGTCCCGCCGCGGGGTCCGTGGAGATGCCCC  
AGGTGGAGGAGGAGTGCCTCCCTGGACAAGCGCGGCGACAAGCGACCGCGTCCCGACGCGGAGGAGACGCTGCTGACGC  
ACACGGACGAGCCGCCCCGTACGAGGAGGCGGTGAACTGGGTCTGCCACCACGCGGCCGTGGCGCCTCTGGCCACCGG  
GGTGTGAAACCCAGCAGCAGCAGCCAGCCGCGACCTGGACTTGCTCCGCTGCTTCCCGCCCTCCACAGTGGCTAAGC  
CCCTGCCGCGGTGGCGTGCCTGCGCGCGCCCCGAGGCGCCCCAGGCGAACTGGCAGAGCACTCTGAACAGCATCGT  
GGGTCTGGGAGTGAGAGTGTGAAGCGCGCGCTGCTATTAAGACACTGTAGCGCTTAACTTGCTTGTCTGTGTATAT  
GTATGTCGCGGACCAAGAAGGAGGAAGAGGCGCGTGCAGGTTGCAAGATGGCCACCCATCGATGCTGCCCCAGTGGG  
GTACATGCACATCGCCGACAGGACGCTTCGAGTACCTGAGTCCGGGTCTGGTGAGTTTCCCGCGCCACAGACACCTACT  
TCAGTCTGGGGAACAAGTTAGGAACCCACGGTGGCGCCACGCACGATGTGACCACCGACCGCAGCCAGCGGCTGACGCT  
GCGCTTCTGTCGGTGGAACGCGAGGACAACCTACTCTGTAAGAGTGCCTACACGCTGGCGTGGGCGACAACCGCTG  
CTGGACATGGCCAGCACTACTTTGACATCCGCGCGTGTGGATCGGGGGCCAGCTTCAAACTACTCCGGCACCGCTA  
CAACAGCCTGGCTCCAAGGGAGCGCCCAACACTTGCCAGTGGACATATAAGCTGGTGATACTGATACAGAAAAACCTATA  
CATATGGAATGCACCTGTGCAAGGCATTAGCATTACAAAGGATGGTATTCAACTTGGAAGTACAGCGATGGTCAGGCAATC  
TATGCAGACGAACTTATCAACCAGAGCCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAATATGG  
AGGCAGAGCTCTTAAGCTGACACCAAAATGAAGCCTTGTATGTTCTTTGCCAAGCTACCAATAAAGAAGGAGGCCAGG  
CAAATGTGAAAACCGAAACAGGCGGTACCAAGAATATGACATTGACATGGCATTCTTCGATAATCGAAGTGCAGCTGCCGCC  
GGCCTAGCCCCAGAAATTGTTTTGTATACTGAGAATGTGGATCTGGAAGTCCAGATACCCATATTGTATAAAGGAGGTAC  
AGATGACAGTAGCTCTTATCAATTTGGGTGAGCAGTCCATGCCAACAGACCCAACTACATTGGCTTCAGAGACAACCTTAT  
CGGTCTGATGTACTACAACAGCACTGGCAATATGGGTGACTGGCTGGACAGGCCTCCAGCTGAATGCTGTGGTGGACTTGC  
AGGACAGAAACACCGAAGTGTCTACAGCTCTTGTGACTCTGGGTGACAGAACCAGGTATTTAGTATGTGGAATCAG  
GCGGTGGACAGTTATGACCCGATGTGCGCATTATTGAAAATCACGGTGTGGAGGATGAACTTCTAACTATTGCTTCCCCCTG  
GATGCTGTGGGTAGAAGTACTTACCAGGGAATTAAGGCCAATGGTGATAATCAAACCACTGGACCAAGATGATACTGT  
TAATGATGCTAATGAATTGGGCAAGGGCAATCTTTGCCATGGAGATCAACATCCAGGCCAACCTGTGGCGGAACCTCCTCT  
ACGCGAACGTGGCGCTGTACCTGCCGACTCCTACAAGTACACGCGCGCAACATCACGCTGCCACCAACACCAACCTAC  
GATTACATGAACGGCGCGTGGTGGCGCCCTCGCTGGTGGACGCTACATCAACATCGGGGCGCGTGGTGGTGGACCCCA  
TGGACAACGTCAACCCCTTCAACCACACCGCAACGCGGCCCTGCGATACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTG  
CCCTTCCACATCCAGGTGCCCCAAAAGTTTTCGCCATCAAGAGCCTCCTGCTCCTGCCGCGTCTACACCTACGAGTGGAACT  
TCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCTCGGCAACGACCTGCGCACGGACGGGGCTCCATCGCCTTACCAGC  
ATCAACCTCTACGCCACCTTCTCCCATGGCGCACAAACCGCCTCCACGCTCGAGGCCATGCTGCGCAACGACCAACGAC  
CAGTCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCATCCCGGCCAACGCCAACAGTGGCCATCTCCATCCCT

Fig. 23F

CGCGCAACTGGGCCGCTTCCGCGGCTGGTCCTTACGCGCCTCAAGACCCGCGAGACGCCCTCGCTCGGCTCCGGGTTCGAC  
CCCTACTTCGTCTACTCGGGCTCCATCCCCTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTT  
CGACTCCTCCGTAGCTGGCCCCGCAACGACCGCCTCTGACGCCAACGAGTTTCAAATCAAGCGCACCGTCGACGGAGAG  
GGGTACAACGTGGCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCCACTACAACATCGGCTACCAGG  
GCTTCTACGTGCCCCGAGGGCTACAAGGACCGCATGTACTCTTCTCCGCAACTTCCAGCCCATGAGCCGCCAGGTCTGGAC  
GAGGTCAACTACAAGGACTACCAGGCCGTACCCTGGCTACCAGCACAACAACCTCGGGCTTCGTGGCTACCTCGCGCCAC  
CATGCGCCAGGGCCAGCCCTACCCGCGCAACTACCCCTACCCGCTCATCGGCAAGAGCGCGCTCGCCAGCGTCACCCAGAAAA  
AGTTCCTCTGCGACCGGGTCATGTGGCGCATCCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGA  
ACATGCTCTACGCCAACTCCGCCACGCGCTAGACATGAATTCGAAGTCGACCCCATGGATGAGTCCACCTTCTCTATGTTGT  
CTTCGAAGTCTTCGACGTCTGCGAGTGCACAGCCCCACGCGGCGTCATCGAGGCGCTTACCTGCGCACGCCCTTCTCGGC  
CGGCAACGCCACCACCTAAGCCTCTTGCTTCTTGAAGATGACGGCTGCGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATC  
CTCCGCGACCTGGGCTGCGGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCCGGGATTATGCCCCGCAAGCTGGC  
CTGCGCCATCGTCAACACGGCCGGCCGCGAGACCGGGGCGAGCACTGGCTGGCCTTCGCTGGAACCCGCGCTCCACACC  
TGCTACCTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACCAGTTCGAGTACGAGGGCTGCTGCGTCGC  
AGCGCCTGGCCACCGAGGACCGCTGCGTACCCTGGAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCTGCG  
GGCTCTTCTGCTGCATGTTCTGACGCCTTCGTGCACTGGCCGACCGCCCCATGGACAAGAACCCACCATGAAGTCTGTA  
CGGGGTGCCAACGGCATGCTCCAGTCGCCCAGGTGGAACCCACCTGCGCCGAACAGGAGGCGCTTACCGCTTCTC  
AACGCCCACTCCGCTACTTTCGCTCCACCGCGCGCATCGAGAAGGCCACCGCTTCGACCGCATGAATCAAGACATGTAA  
TCCGGTGTGTATGTGAATGCTTTATTCATATAATAAACAGCACATGTTTATGCCACCTTCTCTGAGGCTCTGACTTTATTA  
GAAATCGAAGGGGTTCTGCCGGCTCTCGGCATGGCCCCGCGGCGAGGATACGTTGCGGAAGTGGTACTTGGGCAGCCACTTG  
AACTCGGGGATCAGCAGCTTCGGCACGGGGAGGTGCGGGAACGAGTCGCTCCACAGCTTGCAGCTGAGTTGCAGGGCGCCC  
AGCAGGTCGGGCGCGGAGATCTTGAATCGCAGTTGGGACCCGCGTTCGCGCGGAGAGTTACGGTACACGGGGTTGCAG  
CACTGGAACACCATCAGGGCCGGGTGCTTCACGCTCGCCAGACCGTCGCGTCGGTGATGCCCTCCAGTCCAGATCCTCGGC  
GTTGGCCATCCGAAGGGGGTCATCTTGCAAGTCTGCCGCCCATGCTGGGCACGCAGCCGGGCTTGTGGTTGCAATCGCAGT  
GCAGGGGGATCAGCATCATCTGGGCTGCTCGGAGCTCATGCCCGGTACATGGCCTTCATGAAAGCTCCAGCTGGCGGAA  
GGCCTGCTGCGCCTTGCCGCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGAGAACTGGTTGGTGGCGCAGCCAGCGTCG  
TGACGCAGCAGCGCGCGTCTGTTGGCCAGCTGCACCACGCTGCGCCCCCAGCGTTCTGGGTGATCTTGGCCCGGTGCG  
GGTCTCTCTCAGCGCGCTGCCGTTCTCGCTCGCCACATCCATCTCGATCGTGTGCTCCTTCTGGATCATCAGGTCCCGTG  
CAGGCACCGCAGCTTGCCCTCGGCTCGGTGACCCGTGACGCCACAGCGCGCAGCCGGTGCTCTCCAGTTCTTGTGGGCGA  
TCTGGGAGTGCGAGTGCAGGAAGCCCTGCAGGAAGCGGCCCATCATCGTGGTCAGGGTCTTGTGCTGGTGAAGGTGAGCGG  
AATGCCGCGGTGCTCCTGTTACATACAGGTGGCAGATACGGCGGTACACCTCGCCCTGCTCGGGCATCAGCTGGAAGGCG  
GACTTCAGGTGCTCTCCACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCATGCCCTTCTCCAGGCCGAACGATCGGC  
AGGCTCAGGGGGTTCTTACCGTTGTCATCTTAGTCGCGCGCGCCGAAGTCAGGGGGTCTTCTCGTCCAGGGTCTCAAACAC  
TCGCTTGCCGTCCTTCTCGGTGATGCGCACGGGGGAAAGCTGAAGCCACGGCCGCAAGCTCCTCCTCGGCCTGCCTTTCGT  
CCTCGTGTCTGGCTGATGTCTTCAAAGGCACATGCTTGGTCTTGCGGGGTTTCTTTTGGGCGGCAGAGGCGCGCGCGGA  
GACGTGCTGGGCGAGCGCGAGTTCTCGCTCACCACGACTATTTCTTCTCCTTGGCCGTCGTCGAGACCACGCGCGGTAGGC  
ATGCTCTTCTGGGGCAGAGGCGGAGGCGACGGGCTCTCGCGGTTGCGGGGCGGCTGGCAGAGCCCTTCCGCGTTCGGG  
GGTGGCTCTGGCGGCGCTGCTCTGACTGACTTCTCCGCGGCGGCCATTGTGTTCTCTAGGGAGCAAGCATGGAGACTC  
AGCCATCGTCGCCAACATCGCCATCTGCCCCCGCCCGCCGACGAGAACCAGCAGCAGCAGAATGAAAGCTTAACCGCCCCG  
CCGCCAGCCCCACCTCCGACGCCGACGCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGACCTGGGCTACGTGA  
CGCCCGCGGAGCACGAGGAGGAGCTGGCAGCGCTTTTTCAGCCCCGAAGAGAACCACCAAGAGCAGCCAGAGCAGGAAG  
CAGAGAGCGAGCAGAACCAGGCTGGGCTCGAGCATGGCGACTACCTGAGCGGGGCGAGGACGTGCTCATCAAGCATCTGG  
CCCGCAATGCATCATCGTCAAGGACGCGCTGCTGACCGCGCGGAGGTGCCCTCAGCGTGGCGGAGCTCAGCCGCGCTAC  
GAGCGCAACCTCTTCTCGCGCGCTGCCCCCAAGCGCCAGCCCAACGGCACCTGCGAGCCCAACCCGCGCTCAACTTCTAC  
CCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACCTTTTTTCAAAGAACCAAGGATCCCGTCTCCTGCCGCGCAAC  
CGACCCCGCGCGACGCCCTGCTAACCTGGGCCCGCGCGCCGCTACCTGATATCGCCTCCTTGAAGAGGTTCCCAAGAT  
CTTCGAGGGTCTGGGACGACGAGACTCGGGCCGCAACGCTCTGCAAGGAAGCGGAGAGGAGCATGAGCACCACAGCGC  
CCTGGTGGAGTTGGAAGGCGACAACGCGCGCTGGCGGTCTCAAGCGCACGGTCGAGCTGACCACTTCGCTACCCGGCG  
CTAACCTGCCCCCAAGGTGATGAGCGCGTATGGACAGGTGCTCATCAAGCGCGCTCGCCCTCTCGGAGGAGGAGAT  
GCAGGACCCCGAGAGCTCGGACGAGGGCAAGCCCGTGGTACGCGACGAGCAGCTGGCGCGCTGGCTGGGAGCGAGTAGCA  
CCCCCAGAGCCTGGAAGAGCGGCGCAAGCTCATGATGGCGTGGTCTGGTGACCGTGGAGCTGGAGTGTCTGCGCGCTT

Fig. 23G

CTTCGCCGACGCGGAGACCCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGACACGGGTTCTGCGCCAGGCCTGC  
AAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTGCACGAGAACCCTGGGGCAGAACGTGCTGCA  
CACCACCCTGCGCGGGGAGGCCCGCCGCGACTACATCCGCGACTGCGTCTACCTGTACCTTGCCACACCTGGCAGACGGGCA  
TGGGCGTGTGGCAGCAGTGCCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAACCTCAAGGCCCTGTG  
GACCGGGTTCGACGAGCGCACACCACCGCCGCGGACCTGGCCGACCTCATCTTCCCCGAGCGCCTGCGGCTGACGCTGCGCAAC  
GGGCTGCCCCGACTTTATGAGCCAAAGCATGTTGCAAACTTTGCTCTTTTCATCCTCGAACGCTCCGGGATCTGCCCCCACC  
TGCTCCGCGCTGCCCTCGACTTCGTGCCGCTGACCTTCCGCGAGTGCCCCCGCCGCTCTGGAGCCACTGCTACCTGCTGCGC  
CTGGCCAACCTACCTGGCCTACCACTCGGACGTGATCGAGGACGTGACGGGCGAGGGCCTGCTCGAGTGCCACTGCCGCTGCA  
ACCTCTGCACGCCGACCGCTCCCTGGCCTGCAACCCCGAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAA  
GGCCCCGCGAGGGCAAGGGGGGTCTGAACTCACCCGGGGCTGTGGACCTCGGCCTACTTCGCGCAAGTTCGTGCCCGAG  
GACTACCATCCCTTCGAGATCAGTTCTACGAGGACCAATCCAGCCGCCAAGGCCGAGCTGTCGGCCTGCGTCATCACCCA  
GGGGGCCATCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTTCTGCTGAAAAAGGGCCACGGGGTCTACTTGG  
ACCCCCAGACCGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCCGAGGAAGCAGCAAGAAGCTGAAAGTGGAGCTGC  
CGCGCCCGCCGGAGGATTTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGGAGGAGGAGATGGAAGACTGGGACAGCACT  
CAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAGGAAGACGAGGTGGAGGAGGCAGAGGAAGAAGCAGCCGCCG  
CCAGACCGTCGTCCTCGCGGAGGAGGAGAAAGCAAGCAGCAGGATACCATCTCGCTCCGGGTGGGGTTCGCGCGGCC  
GGGCCACAGTAGATGGGACGAGACCGGGCGCTTCCCGAACCCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACA  
AGTCTGGCGGGGGCACAAAAACGCCATCGTCTCCTGCTTGAAGCCTGCGGGGGCAACATCTCTTCACCGGGCGTACCTG  
CTCTTCCACCGCGGGGTGAACCTTCCCCGCAACATCTTGCTTACTACCGTCACCTCCACAGCCCCCTACTACTGTTTCAAGAAG  
AGGCAGAAACCCAGCAGCAGCAGCAGCAGCAGCAAAACCAGCGGCAGCAGCTAGAAAATCCACAGCGCGGCAGGTGGACT  
GAGGATCGCGGCGAACGAGCCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTTCCACCCTCTATGCCATCTTCAGCAG  
AGTCGGGGGCAAGAGCAGGAACCTGAAAGTCAAGAACCGTTCTCTGCGCTCGCTCACCCGAGTTGTCTGTATCACAAGAGCG  
AAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCCGC  
CCCGCCACACAGGAAAAAGGCGGGAATTACGTACACACCTGCGCCCTTCGCCCCGACCATCATGAGCAAAGAGATTCCC  
ACGCTTACATGTGGAGCTACCAGCCCCAGATGGGCCTGGCCGCCGGCGCCGCCCCAGGACTACTCCACCCGCATGAACTGGCT  
CAGTGCCGGGCCCCGCGATGATCTACGGGTGAATGACATCCGCGCCACCGAAACCAGATACTCTAGAACAGTCAGCGATCA  
CCGCCACGCCCCGCCATCACCTTAATCCGCGTAATTGGCCCGCCGCTGGTGTACCAGGAAATTCCCCAGCCACGACCGTAC  
TACTTCCGCGAGACGCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCCGGCGGCGCCGCTGTGTCTGTAC  
CGCCCCGCTCAGGGTATAAGCGGCTGGTGTATCCGAGGCAGAGGCACACAGCTCAACGACGAGGTGGTGTGAGCTCTTCGCTGG  
GTCTGCGACCTGACGGAGTCTTCAACTCGCCGATCGGGGAGATCTTCTTACGCCTCGTCAGGCCGTCTGACTTTGGAG  
AGTTCGTCTCGCAGCCCCGCTCGGGTGGCATCGGCACTCTCCAGTTCGTGGAGGAGTTCACTCCCTCGGTCTACTTCAACCCC  
TTCTCCGGCTCCCCCGCCACTACCCGACGAGTTCATCCGAACTTCGACGCCATCAGCGAGTCGGTGACGGCTACGATTG  
AATGTCCATGGTGGCGCGGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTCGCTCGGGATCT  
CGCCGAGTTTGCCTACTTTGAGCTGCCCCGAGGAGCACCTCAGGGCCCCGCCACGGAGTGCGGATCGTCGTGCAAGGGGGT  
CTCGACTCCACCTGCTTCGATCTTCAGCCAGCGTCCGATCCTGGCCGAGCGGAGCAAGGACAGACCCTTCTGACCTGTAC  
TGCATCTGCAACCAACCCGGCCTGCATGAAAGTCTTTGTTGTCTGTGTACTGAGTATAATAAAAGCTGAGATCAGCGACTA  
CTCCGGACTTCGCTGTGTTCTGTATCAACCAAGTCCCTGTTCTTACCCGGGAACGAGACCGAGCTCCAGCTCCAGTGTAAGCC  
CCACAAGAAGTACCTCACCTGGCTGTTCCAGGGCTCTCCGATCGCGTTGTCAACCACTGCGACAACGACGGAGTCTGTGTA  
GCGGCCCTGCCAACCTTACTTTTCCACCCGAGAAAGCAAGCTCCAGCTCTTCAACCCCTCTCCCCGGGACCTATCAGTGCGT  
CTCGGGACCTGCCATCACACCTTCCACCTGATCCGAATACCACAGCGTCGCTCCCCGCTACTAACAACCAAACTACCCACCAA  
CGCCACCGTCGCGACCGCGGACATGTACAGAGCTCGAGAAGTACTAGGCCACAATACATGCCATATTAGACTATGAGGCCGA  
GCCACAGCGACCCATGCTCCCCGCTATTAGTTACTTCAATTAACCGCGGAGATGACTGACCACTGGCCAACAACAACGTCA  
ACGACCTTCTCTGGACATGGACGGCCGCGCCTCGGAGCAGCGACTCGCCAACTTCGATTTCGCCAGCAGCAGGAGAGAGC  
CGTCAAGGAGCTGAGGACGGCATAGCCATCCACAGTGCAAGAAAGGCATCTTCTGCTGGTGAACAGGCCAAGATCTCC  
TACGAGGTACCCCCGACCGACCATCGCTCTCTACGAGCTCCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTGGAGTCAA  
CCCCATCGTCATCACCCAGCAGTCGGGCGGATACCAAGGGGTGCATCCACTGCTCCTGCGACTCCCCGACTGCGTCCACACTCT  
GATCAAGACCCTCTGCGGCCTCCGCGACCTCTCCCCATGAACTAATCACCCCTTATCCAGTGAAATAAATATCATATTGATGA  
TGATTTAAATAAAAAATAATCATTTGATTTGAAATAAAGATACAATCATATTGATGATTTGAGTTTTAAAAATAAAGAATCACT  
TACTTGAAATCTGATACCAGGTCTGTGTCATGTTTTCTGCCAACACCACTCACTCCCCTCTCCAGCTCTGGTACTGCAGACC  
CCGGCGGGCTGCAAACTTCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGTCCCTCAATCTTCATTTATCTTATCAGA  
TGTCAAAAAGCGCGTCCGGGTGGATGATGACTTCGACCCGCTACCCCTACGATGCAGACAACGCACCGACCGTGCCTTC

Fig. 23H

ATCAACCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCCTGGGGGTGCTGTCCCTGCGACTGGCTGACCCCGTCACC  
ACCAAGAACGGGGAAATCACCTCAAGCTGGGAGAGGGGGTGGACCTCGACTCCTCGGGAAAACATCTCCAACACGGCCA  
CCAAGGCCGCCGCCCTCTCAGTTTTTCCAACAACACCATTTCCCTTAACATGGATACCCCTCTTTATACCAAAGATGGAAAATT  
ATCCTTACAAGTTTCTCCACCGTTAAACATATTTAAATCAACCATTTCTGAACACATTAGCTGTAGCTTATGGATCAGGTTTAGGA  
CTGAGTGGTGGCACTGCTCTTGCAGTACAGTTGGCCTCTCCACTCACTTTTGATGAAAAAGGAAATATTTAAATTAACCTAGCC  
AGTGGTCCATTAAACAGTTGATGCAAGTCGACTTAGTATCAACTGCAAAAGAGGGGTCACTGTCACTACCTCAGGAGATGCAAT  
TGAAAGCAACATAAGCTGGCCTAAAGGTATAAGATTTGAAGGTAATGGCATAGCTGCAAAACATTGGCAGAGGATTGGAATTT  
GGAACCACTAGTACAGAGACTGATGTACAGATGCATACCAATTAAGTTAAATTGGGTACTGGCCTTACCTTTGACAGTACA  
GGCGCCATTGTTGCTTGGAACAAAGAGGATGATAAACTTACATTATGGACCACAGCCGACCCCTCGCCAAATTGCAAAATATA  
CTCTGAAAAAGATGCCAACTCACACTTTGCTTGACAAAGTGTGGAAGTCAAATTCTGGGTACTGTGACTGTATTGGCAGTGA  
ATAATGGAAGTCTCAACCAATCACAACACAGTAAGCACTGCACTCGTCTCCCTCAAGTTTGATGCAAGTGGAGTTTTGCTAA  
GCAGTCCACATTAGACAAAGAATATTGGAACCTCAGAAAGGGAGATGTTACACCTGCTGAGCCCTATACTAATGCTATAGGT  
TTTATGCCTAACATAAAGGCCTATCCTAAAAACACATCTGCAGCTTCAAAAAGCCATATTGTCACTCAAGTTTATCTCAATGGG  
GATGAGGCCAAACCACTGATGCTGATTATTACTTTAATGAACTGAGGATGCAACTGCACCTACAGTATCACTTTTCAATGG  
AAATGGGATAGTACTAAGTACACAGGTGAAACACTTGCTACCAGCTCCTTACCTTCTCTACATCGCCCAAGAATGAACACTG  
TATCCACCTGCGATGCCAACCTTCCACCCCACTCTGTCTATGGAAAAACTCTGAAGCACAATAAAATAAAGTTCAAGT  
GTTTTATTGATTCAACAGTTTTACAGGATTGAGCAGTTATTTTCTCCACCTCCAGGACATGGAATACACCACCTCTCCCC  
CCGCACAGCCTTGAACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAG  
TCTCGGGTCGGTCAGGGAGATGAAACCTCCGGGCACTCCGCGATCTGCACCTCACAGCTCAACAGCTGAGGATTGCTCTCGG  
TGGTCCGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGCGGTGGGAATCATAGTCCGCGAACGGGATCGGCCGGTGGTG  
TCGCATCAGGCCCGCAGCAGTCGCTGCCGCCGCTCGTCAAGCTGCTGCTCAGGGGGTCCGGGTCCAGGGACTCCCTCA  
GCATGATGCCACGGCCCTCAGCATCAGTCGTCTGGTGGCGGGGCGCAGCAGCGCATGCGGATCTCGCTCAGGTGCTGCA  
GTACGTGCAACACAGGACCACAGGTTGTTCAACAGTCCATAGTTCAACACGCTCCAGCCGAACTCATCGCGGAAGGATGC  
TACCCACGTGGCCGTCGTACCAGATCCTCAGGTAATCAAGTGGCGTCCCTCCAGAACACGCTGCCACGTACATGATCTCT  
TGGGCATGTGGCGTTTACCACCTCCCGTACCACATACCCTCTGGTTGAACATGCAGCCCCGGATGATCCTGCGGAACCAC  
AGGGCCAGCACCGCCCCGCCGCCATGCAGCGAAGAGACCCCGGTCCCGCAATGGCAATGGAGGACCAACCGCTCGTACC  
CGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTCTCAGCACTCTCAGCTCCT  
CGGGGGTCAAACCATATCCAGGGCACGGGGAATCTTGACAGACAGCGAACCCCGCAGAACAGGGCAATCCTCGCACATA  
ACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCAGAGAAGCGCGGGTCTCGGTCTCT  
CACAGCGTGTAAGGGGGCCGGCGGATACGGGTGATGGCGGGACGCGGTGATCGTGTTCGCGACCGTGTGATGAGT  
TGCTTTCCGACATTTTCGTAATTGCTGTAGCAGAACCTGGTCCGGGCGCTGCACACCGATCGCCGGCGGGTCCCGGCGCTT  
GGAACGCTCGGTGTTGAAATTGTAACACAGCACTCTCTCAGACCGTGCAGCAGATCTAGGGCCTCAGGAGTGATGAAGATCC  
CATCATGCCTGATAGCTCTGATCACATCGACCACCGTGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTGGGTTTCG  
GTGACGGCGGGGGAGGGGAAGAACAGGAAGAACCATGATTAACTTTAAATCCAAACGGTCTCGGAGCACTTCAAATGAAGGT  
CGCGGAGATGGCACCTCTCGCCCCGCTGTGTTGGTGGAAAAAATACAGCCAGGTCAAAGGTGATACGGTTCTCGAGATGTTCC  
ACGGTGGCTTCCAGCAAAGCCTCCACGCGCATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTTCTCTAATTCCTCAAT  
CATCATGTTACACTCCTGCACCATCCCCAGATAATTTTCATTTTCCAGCCTTGAATGATTGCAACTAGTTCCTGAGGTAATCCA  
AGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCTCCACCGGCATTCTTAAGCACACCTCATAATCCAAGATATTCTGCTC  
CTGGTTACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGATCCCTAAGCTCCTCCCTCAGCAATAACTGTAA  
GTACTCTTTCATATCTCTCCGAAATTTTAGCCATAGGACCACAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCG  
AAGTCTCCCCAGTGAGCATTGCCAAATGCAAGACTGCTATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAACTGG  
ACAGAAAATCACCCAGGCAATTTTAAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGCACGTTTAGAGCCTCGGGAACAACG  
ATGAAGTAAATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAAAAAACAAAAATAAACATTAAACCATGCT  
AGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCAGCACAGGACAGGCCAGGGGTCTCCGGCGCGACCCCTGTAAAAATTG  
TCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTGACAAGATGAATACACCCCGGAAC  
ATTGGCGTCCGCGAGTGAAAAAAGCGCCGAGGAGCAATAAGGCACTACAATGCTCAGTCTCAAGTCCAGCAAAAGCGATG  
CCATGCGGATGAAGCACAAAATCCTCAGGTGCGGTACAAAATGTAATTACTCCCTCCTGCACAGGCAGCGAAGCCCGGATCC  
CTCCAGATACACATACAAAGCCTCAGCGTCCATAGCTTACCGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCT  
GAGCTCTAACCTGTCCACCGCTCTCTGCTCAATATATAGCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCG  
CCAAATAATCACACACGCCAGCACACGCCAGAAACCGGTGACACACTCAAAAAAATACGCGCACTTCTCAAACGCCCAA  
CTGCCGTCAATTCGGGTTCCACGCTACGTATCGGAATTCGACTTTCAAATTCGTCGACCGTTAAAAACGTACCCGCCCG  
CCCCTAACGGTCGCCCGTCTCTCGGCAATCACCTTCTCCCTCCCAAAATCAAACAGCTCATTTGCATATTAACGCGACCAA  
AAGTTTGAGGTATATTATTGATGATG

Fig. 23I

**AdC7 010-HIVgag(E1048) Amino acids – SEQ ID NO: 12****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVVIGRETGDR\*GRGG\*RFDDVAVRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFLG  
GCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDLRGGFDIRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RLRSP  
DPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCKMKNLLRVRRFALLRDVARYTR\*H\*LLTSY\*\*\*SITGSLVH  
SPYMEFRVT\*LTVNGPPG\*PPNDPRPLTSIMTYVPIVPIGTFH\*RQWVEYLR\*TAHLAVHQVYHMPSTPPIDVNDGKWPAPWHYA  
QYMTLWDFPTWQYIYVLVIAITMVMRFWQYINGRG\*RFDSRGFPSLHPIDVNGSLFWHQNRDQFPCRNNAPLTQMGGRRVR  
WEVYISRARLVNRQITRSFIADVYHS\*IANAVSASDTTVSNLSCRSWS\*GTGQVSIKVTQV\*GDQ\*KLGLSRQRRLLRF\*\*APIGLTD  
IHFAFLSTGVHSQFNYS\*G\*ST\*YDSL\*ASATMGARASVLSGGELDRWEKIRLPGGKKYKLVKHIWASRELERFAVNPGLLETSE  
GCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEVKDTKEALEKIEEENKSKKKAQQAADTGNSQVSQNYPIVQNLQGG  
MVHQAIPTLNNAWVKVVEKAFAFSEVPMFSALEGATPQDLNMLNTVGGHQAAMQMLKETINEEAAEWDRHPVHAGPIA  
PGQMREPRGSDIAGTTSTLQEQIGWMTNPPPIVGEIYKRWIILGLNKIVRMYSPSILDIRQGPKEFRDYVDRFYKTLRAEQASQE  
VKNWMTETLLVQANPDCKTILKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVTNSATIMMQRGNFRNRKTKVCFN  
CGKEGHIAKNCRAPRKGCWKCGKEGHQMKDCTERQANFLGKIWPSHKGRPGNLFQSRPEPTAPPEESFRFGEETTPSQKQEP  
DKELYPLASRLSFGNDPSSQ\*\*SSV\*TGPLESTRAAKPLISLDCAF\*LPAICCLPLPRAFLDPGRCHSHCPFLIK\*GNICALSE\*VSFYSG  
GWGGAGQQGGGLGRQ\*QACWGCGLYGF\*GGKNQICRSEFIYVGCGERGNEMALWVLWVCINESARYAGHRACDLAPPQD  
MARVRAQRHDPMQCAPGVPPRHVHALPVQHAICEGAAGARCHVQSEPDGGV\*HECGAVENSEI\*\*IQDQVPGLRMRRQARQA  
SARVCGGDGGPATRSFGVVLQRDGVRLQRGRI\*LE\*VVFGGGGGLV\*GAE\*LKSVFFCVLQQHERKRL\*GRGIQPLSDGASPLLG  
GSASECDGIHGGPARAAELFNPDLRDELLVGRSCRRSCCFRRQRARNGPGRRLQLSGGQLDFHQ\*SRQPERGEAAAADG  
PARGPDPAPGRADPAGGSAAGGDAGRCHGENQJKNESINKRRRLILTSLESFDFSRVAVGPGPPVSIIEHPVDFQDPVEVGLD  
VEVHGHEPVPGEVAPLQGLVLGGGVVNHPIAGAQQVVLHVDLEEEDGHGQPLGVGVDEPVELGGMHAGGDEMHLGLDLEI  
GDVPAQIPPGVHVVDHGHGVSGALGEFVMQLGREGVKEFGDALVTAQVFHALIHDDGDGPVGGGLGKDVSGVGHIVVVLGE  
LVIGHFNEFGAEGARLGDEGALDPGGVVALADLHPLGLELGGGDHVLHRLGDEKNGRGGGDELGRKQVPEQLGLAAAGGAVDDP  
DDRQVVEGETAAVLAEEGGHLVHHLAHMHVLAHEFRQALAPQREELLQRGEVFQRLEPVGHGHFGEGLLEFQTVPELGDVL  
\*GISIQQTSSFRGLRLRE\*GTRRWASSEARVRSFQGRVRVSVSVTVKGCAPGWALARVFRILRLVENRSRSPACASAR\*QLSM  
SS\*LSASAAWPLARSLPLEVCPQTGQRDLRA\*SLGARKTDSGA\*ASAPQLAQTVSHSTSQVRSGLGSKTRFPFCFLMRFLPLVSM  
SSCPRWVTKRLSVSP\*TDFMGRSSSGVPRSS\*RNPAHSETKARVQASTKEATWEG\*RLSTSGSTFSRVCKHMSPSSTSRKIVGL\*V  
\*AT\*PGVPAGGV\*KGAGPCSSSLSSGSLRSASCWGRYLSKAGITSALRLSVSRNEEDLITVPLETFMSPSSIWSEKTIFFLLSLVAK  
EP\*RALERSLAMERMVWFFSLSARSLAAMLSCYSTRATHFHSGKTVSSSGTILTRQPRLCRVMRSTLVATSPRRGSLVQQRPPPLR  
EQKGGSGSSMSSSGSASTVKMPGRSSGSK\*LMQVSRSSAACQSRTASARS\*GLRGVPQGMGCVSAEAYMPQMS\*T\*RGSSRT  
PM\*VG\*QRPPRMLART\*SYSSCEGARSPVPRLERCGFSAR\*TIWRKMAWELEEMVGLWKMLKWAUWGRPTESLMKWA\*ESCSL  
ATSSAVTRTSRAQ\*SRVSWMMSYLSWPFCHSSRLRRNSSRSFYSSRGNPS\*SAR\*EPTM\*NWLTAL\*AAQPFSTGRA\*ACAAL  
RREVWVRKVSRTMTLRNWCLKSRSSQPPCSQSWKSVRF\*AGLGKAKVTSKRLPARGMKLRVMRKGWGTSARLLMTWAAR  
TISSKPLMLCPTM\*SSTNRGRPLTWGSFLSSS\*VSSAGSLSPCCSRAQSATWGLALRKEVQRSTARAVCKRSRY\*NCNWPTAIFSGVT  
Q\*KVRGSPCQRSHLSWRARSWASSTSGGSPESFMTSMKGTSCLPKDIQV\*VSTS\*VRKSLSVRGCEPMGKNWISCHQLEEWLLM  
\*WK\*KCRRRAEHSCCLYKRPQCSQRCTGCTCCTCTWVPLTRNFSGQWSAGGCIWCCTTSWPSAWPSSASMVVMILTSRGRQ  
VQTSARTGRRARTRARRPELSRVLRRCGVRSVSGGARLTCSRFSRARGRSRWYLISTAPLVATSTACRVPCPWGATTVPFFLGAA  
SMPVRSGGEDARRAAGAARDPEAGAAGARRRRARAGSGTAPGEDWRERRRDG\*RPGSASG\*RPRDP\*V\*T\*KRVQRNQSRYR  
\*RRPAAGSLARRPSCPGRRRSR\*TARSPPEGLRGRARRWRPRGRWRCGP\*AARRRSCRPRSRRCRPLRRGRARA\*PPGRG\*A  
RRGA\*RPRSCRAGGRGS\*AWWRCAR\*RRST\*SSGGAASR\*RRPLSAPWPRRSPRRS\*KTGSCAPRRSTPPPEDG\*AQRWWRA  
PRARRPRGAPLLPSLPPPLTSLLLPPQEAAGEGPCVAGGARADGR\*SARWSPRAGDAWSR\*RRARPRGAAA\*RRRRASPGGRRG  
GLRWAGRGR\*RCILSIGP\*GLRART\*ASRDPRDPKTAERRLRASRSKVG\*ARFLVLRGFREAGGRCCW\*\*S\*SRRS\*DGGWWRG  
APGPWARLAGCADGRPCRRGPDTRWGPCSSPA\*AAPRAPPPRPRGRACA\*ARTRAGAGRAPGRRRRARRRGPVAVSG\*GWSG  
SRRSRRSGGLRLC\*WYRSSWP\*RTS\*SGGRVARARGT\*GASRRACRRCSRCRCARGTGIRRGSAAGGAAIARWRGRARRGP  
RA\*GGGSRCTWTSR\*CRRRWRRRAGTRGRGSRCCAAAGSSWWPRSGP\*GARSRGCSRHTGKNESGQRLDSVAWRLSERVG  
LRVYPGSNLESGWSRS\*RTGTGPVSTQAC\*RNLQDTEAGRFLALVAGHEKLVSAESDRPRWLAADVWRKNRQGCVAVCPGSSLSA  
RRRPDSAAANVGVAAPSFRPLSQPTSPVTERAPFLVFLPDASRTAADAPPPSTSTAPTAATAAAGASAPAAASHYRGGRRRS  
RRSV\*PGLGRGRGAGAAGGVVAGAAPARADEKGRSRLRAQAEVQRQERRGARGDARLPLRGAGAAARPGPKAGAEGRGFR  
GGRADGDQPRARARGRGQPGHGVADREGGEQLPKILQQPRAHADRRARGDGPDPAPVGPAGGHRAEPHEQAADGAAVSGG  
AAQSGQRDVQGGAAEYHRARGPLAPGGEHSAEHRGAGARAAAVREAGGYQLLGAEPGQVLR\*EDLQDPVRAHRQGGEDRRV

Fig. 23J

LHAHPESADPERRSGGVPQRQDAPRGERQPPARAERPGADAQPAAGPDRGRDRGGELL\*HGRGPALAAQPPGLGSCRRFPLRG  
GGGR\*GGGGRVPGRLMARPYFC\*MQQQPPPPDAMPRAALQSQPSGINSSDDWTQAMQRMALTRNPEAFRQQPQANRLSA  
ILEAVVPSRSNPHEKVLAINNALVENKAIRGDEAGLVYNALLERVARYNSTNVQTNLDRMVTDVREAVSQRERFHRESNLGSMVAL  
NAFLSTQPANVPRGQEDYTNFISALRLMVAEVPQSEVYQSGPDYFFQTSRQGLQTVNLSQAFKNLQGLWGVQAPVGDRAVSSLL  
TPNSRLLLLLVAPFTDSGSVSRDSYLGILLNLYREAIGQAHVDEQTYQEITHVSALGQEDPGNLEATNLFLLTNRSQKIPQYALSTEE  
ERILRYVQQSVGLFLMQEGATPSAALDMTARNMEPSMYARNRPFINKLMDYLHRAAAMNSDYFTNAILNPHWLPPPGFYTGEYD  
MPDPNDGFLWDDVDSSVFSRPATTVWKKEGGDRRPSALSGRAGAAAAPPEASPFPSLPFSLNSVRSELGRLTRPRLLGEEEYL  
NDSLLRPEREKNFPNNGIESLVDKMSRWKTYAHEHRDEPRASSAGTRRRQRHQRGLVWDDDESDADDSSVLDLGGSGGGNPF  
AHLRPRIGRLM\*ESEKINGTHQGHGDQRAFFSVVCSSMMRRVYPEGPPSYESVMQQAVAAAMQPPLEAPVPPRYLAPTEGR  
NSIRYSELAPLYDTRRLYLDNKSADIASLNYQNDHSNFLTTVQNNDFTPTEASTQTINFDESRWGGQLKIMHTNMPNVNEFM  
YSNKFARVMVSRKTPNGVAVDENYDGSQDELTYEWVEFELPEGNFSVTMTIDLNNAIIDNYLAVGRQNGVLESIGVKFDTRN  
FRLGWDVPTELVMPGVYTNEAFHPDIVLLPGCGVDFTESRLSNLLGIRKRPQFQEGFQILYEDLEGGNIPALLDVEAYESKEEAAAA  
ATAAVATASTEVRGDNFASAAVAEAAETESKIVIQPEVKDSKDRSYNVLADKNTAYRSWYLAYNYGDPEKGVRSWTLTSDVTC  
GVEQVYWSLPDMMQDPVTRSTRQVSNYPVVGAE LLPVYSKSFNEQAVYSQQLRAFTSLTHVFNRFENQILVRPPAPTITTVSE  
NVPALTDHGTLP LRRSSIRGVQRTVTDAARRTCPYVYKALGVVAPRVLSSRTF\*KMSILISPSNNTGWGLRAPSKMYGGARQSTQH  
PVRVRGHFRAPWGALKGRVRSRTTVDDVIDQVADARNYTPAAAPASTVDAVIDSVVADARRYARAKSRRRIARRHRSTPAMRA  
ARALLRRARRTGRRAMLRAARRAASGSSSAGRTRRRAATAAAAAIASMSRPRRGNVYVVRDAATGVRVPVTRPPRT\*RC\*LRDV  
DVSQRRGGCPSANTRKRCSSRLRSTAPR\*RRKESPA\*SGSKRTKRRRKMWTDWWSLCASSPPGGACSGAGGK\*NRCCGPAP  
RWSSRPASVPAPPSAPTTRCTGTRTSSRRSSVWASLLTASAAAPR\*KRRRCPSRWTTATPRRA\*SR\*PCSRCCRARRRAGASSA  
RAARICTRPCS\*WCPSARSWRTCWST\*RWTPRCSPSRRCGPSSRWPRAWACRPWTSRSPSPWKRRPSP\*SPAPAPWRCRPIG  
CRRRLPLAEDASTARPAC\*CPTRCIPSSPRRATAARASTAATPAAAAARPPAAAVVAPAAAAPRLPPPPWCGECTAAGASL\*PC  
RARATTRASPFNSAVASYLQIWPSHAASASPLRATEEESRAVEG\*RTGCVAITTGGGAPSASGWGEASCP\*SPSSPRRSGRSPA\*  
LPWRCRPLSATETQLGKFVIKKWTDAPGPVMCVRWKSIFRPWHRDTARGRLWAPGATSATAN\*TGAPSIGAVSGAGLRISGPR  
SKPMATRRTGTAQGR\*GKS\*KSRTSSRRWSMAWPRASTGWWTWTPRCPNRNSTAAWTSRPRGPWRCPWRWRSCLPWTSA  
ATSDRVPTRRRR\*RTRTSRPTRRR\*NWVCPPRGPWRLWPPGC\*NPAASASPRPWTCLRLPAPPQWLSPCRRWPSRRAPPEA  
APRRTGRAL\*TASWVWECEV\*SAASAIKRHCSA\*LACLCVYVCPTRRRKRRVAELQDGHPIAAPVGVHAHRTGRFGVPESGS  
GAVRPRHRHLLQSSEQV\*EPHGGAHARC DHRPQPAADAALRARGPRGQHLLVQSALHAGRGRQPRAGHGQHL\*HPRRAGSG  
AQLQTLRHRLLQPGSQGSAQHLPVDI\*SW\*Y\*YRKNLYWKCTCARH\*HYKGWYSTWN\*QRWSGNLCRRNLSTRASSG\*C\*M  
A\*HHWY\*KIWRQSS\*A\*HQNEALLWFFCQAYQ\*RRRPGKCNENRRYQRI\*H\*HGILR\*SKCSCRRSPRNCVFY\*ECGSGNSRY  
PYCIQGRYR\*Q\*LFYQFGSAVHAQQTQLHLWLQRQLYRSDVLQQHWQYGTGTGLPAECCGGLAGQKHRTVLPALA\*LSG\*QN  
QVFQYVESGGGQL\*PRCAHY\*KSRCGG\*TS\*LLPPGCCG\*N\*YLPGN\*GW\*SNHLDQR\*YC\*C\*IGQGQSFHGDQHPG  
QPVAELPLRERGAVPARLLQVHAGQHHAHQHQLRLHERPRGGALAGGRLHQHARGALVAGPHGQRQPLQPPQRGPAIPLHA  
PGQRALRALPHGAPKVRHQPAPARVLHLRVELPQGRQHDPALPRQRPAGHRLHRLHQLRLHLLPHGAQHRLHARGH  
AAQRHQRVPLQRLPLGGQHALPHPGQRHQRHHLPLAQLGLRPLVLHAPQDPRDALARLRVRPLRLGLHPLPRRHLLPQPHL  
QEGHLHLRLRLQARQRPDPDAQRVRNQAHRRRRGVQRGPVQHDQGLVPGPDAGPLQHRLPGLLRARGLQGPVHLLPLQPLAH  
EPPGRGRGQLQGLPRHPLPAQQLGLRRLPRAHHPAGPALPRQLPLPAHRQERRRQRHPEKVLPRPGHVAHPLLQQLHVHGRA  
HRPRPEHALRQLRPRARHEFRSRPHG\*VHPSLCLRLRRLRPSAPAPRRHRGRLPAHALLGRQRHLSLLLAR\*RPAPASRSSG  
PSSATWAAGPASWAPSTSASRDSWPRTSWPAPSSTRPAARPGASTGWPSPGTRAPTATSSSTPSGSRSSASSRSTSSSTRACCVAA  
PWPPRTAASPWKSPRRPCRVRARPPAGSSAACCTPSCTGPTAPWTRTPP\*TC\*RGCTACSSRPRWNPPCAATRRRSTASSTPTP  
PTFAPTARASRRPPSTA\*IKTCNPVCCECFIHHNKQHMFMPPSLRL\*LYLEIEGVLPAALGMARGQGYVAELVLGQPLELDGQQLR  
HGEVGERVAPQLARELQGAQQVGRGDLEIAVGTRVLARVTVHGVALEHHQGRVLHARQHRRVGDALHVQILGVGHPEGGHL  
AGLPFHAGHAAGLVVAIVQGDQHHLGLLGAHARVHGLHESLQLAEGLLRLAALGEEDPAGLARELVGGAASVVHAAARVVVGQ  
LHHAAPPVAVLGLDGPVGVLLQRALPVLARHIHLDRVLLDHHGVPVQAPQLALGLGAPVQPQRAAGALPVVLDLGVVHEALQEA  
AHRGQGLVAGEGQRNAAVLLVHIQVADTAVHLALLGHQLEGGQLQVALHAVPVHQQRHFFHALLPGRNDRQAQGVLRHCHLSR  
RRRSQGVVLVQGLKHSVLAVLLGDAHGGKAEAHGRQLLLGLPFVLAVLADVLRHMLGLAGFLFRQRRRRRRRAGRARVLAHHDYF  
FSLAVVRDHAAGVGMPLLGQRRRRRALAVRRAAGRAPSAFGGALLAALL\*LTSSAAGHCVLLGSKHGDSAIVANIAICPRRRRRREPAA  
AE\*KLNRPAAQPHLRRRSPRHARDGGIHRD\*PGLRDARGARGGAGSALFSPGREPPRAARAGSRERAEPGWARAWRLPERGRGR  
AHQASGPPMHHRQGRAARPRRGAPQRGGAQPLRAQPLLAARAPQAPAQRHLRAQAPQLLPGLRGARGPGHLPPLFQEPKDP  
RLLPRQPHPRRRPAQPGRRPPT\*YRLLGRGSQDLRGSGQRRDSGRERSARKRRGA\*APQRPGGVGRRQRAPGGPQAHRADPL  
RLPGAQAPQGHERRHGPAGAHQARLAPLGGGDAGPRELGRGQARGQRRRAAGALAGSE\*HPPEPGRAAQAHDRGPGDRGAG  
VSAPLLRRRGDPAQGRGEPALPLQTRVRAPGLQDLQRGADQPLHGHAPAREPPGAERAAHHPARGGPPRLHPLRLPVPLPLHA

Fig. 23K

DGHGRVAAVPGGAEPERALQAPAEPPQGPVDRVRAHHRRGPRPHLPAPAAADAAQRAARLYEPKHVAKLSLFHPRTLDPAR  
HLLRAALGLRAADLPRVPPAALEPLLPAAPGQLPGLPLGRDRGRQRRGPARVPLPLQLHAAPLPGLQPPAAERDPDRHLRVARP  
RRGQGGSETHPGAVDLGLLAQVRARGLPSLRDQVLRGPIAAQGRAVGLRHHPGGHPGPIASHPEIPPRISAEKGPRGLLGPDRR  
GAQPQLPPGCPPEEAARS\*KWSCRRRRRIWRKTGRAVRQRRRRWKTGTALRQRTACKTVWRRKTRWRRQRKKQPPDRRPRRR  
RRKQAAARIPSLRVGVAAAGPTVDGTRPGASRTPPRPVRRSGRDTSPGGGKTTPSSPACKPAGATSPSPGATCSSTAG\*TSPATSCI  
TTVTSTAPTTVSKKRQKPSSSSSRKPAAARKSTAAAGGLRIAANEPAQTRERNRIFPTLYAIFQQSRGQEQLKVKNRSLRSLTRSC  
LYHKSEDQLQRTLEDAEALFNKYCALTLKE\*PAPAHTRKKAGITSPAPFARPS\*AKRFPRLTCGATSPRWAWPPAPRTPPA\*TG  
SVPGPR\*SHG\*MTSAPTETRY\*NSQRSPRPAILIRVIGPPPWCTRKFPSPRPYFRETPRPKSS\*LTQVSSWPAAPPCVVTAPLRV  
\*SGW\*SEAEHSSSTRW\*ALRWVCDLLESSNSPDRGDLPSRLVRPS\*LWVRPRSPARVASALSSSWRSSLPSTSTPSPAPPATTR  
TSSRTSTPSASRWATIECPMVARLT\*LGFDTWTTAAASAASLGISPLPTLSCPRSTLRARPTECGSSSKGVSTPTCFGSSASVRSWP  
SASKDRPF\*PCTASATTPACMKVFFVCCVLSIIKAEISDYSGLPCVPAINQSLFFTGNELQLQCKPHKKYLTWLFQGSPIAVVNHCD  
NDGVLLSGPANLTFSTRSKLQLFQPFPGTYQCVSGPCHHTFHLPNTTASLPATNNQTHQRHRRDRGHVQSSRSTRPQYMPILD  
YEAEPQRPMPLPAISYFNLTGGDD\*PTGQQQRQPSPGHGRPRLGAATRPTSHSPAAGESRQGAAGRSHPPVQERHLLPGETGQ  
DLLRGHPDRPSLLRAPAAAEVHLPGRSQPHRHHPAVGRYQGVHPLLLRLPRLPHSDQDPLRPPPPHELITLPSSEINIILMMI\*  
IKNNHLI\*NKDTIILMI\*VLKNKESLT\*NLIPGLCPCLPTPPHSPLPSSGTADPGGLQTSSTR\*RGCIQPPVPQSSFYLLSDVQKARPGG  
\*\*LRPRLPLRCRQRTDRALHQPPLRLFRWIPREAPGGAVPATG\*PRHHQERGNHPQAGRGGGPRLLGKTHLQHGHHQGRRPSQFF  
QQHHFP\*HGYPQLYQWIKILTSFSTVKHIKINHSEHISCSLWIRFTEWWHCSCSTVGLSTHF\*\*KRKY\*N\*PSQWSINS\*CKST\*YQ  
LQKRGHCHYLRCN\*KQHKLA\*RYKI\*R\*WHSCKHWWQIRIGIWNH\*YRD\*CHRCIPNSS\*IGYWPYL\*QYRRHCCLEQRG\*\*TYIMD  
HSRPLAKLQNIL\*KRCQTHLLDKVWKSNSGYCDCIGSE\*WKSQPNHKKHCHCTRLPQV\*CKWSFAKQLHIRQRILELQKGRCYTC\*  
ALY\*CYRFYA\*HKGLS\*KHICSFKKPYCQSSLSQWG\*GQTTDADYF\*\*N\*GCNLHLQYHFSMEMG\*Y\*VHR\*NTCYQLLHLLHRP  
RMNTVSHPACQPFPPHSVYGKNSEAQNKIKFCIDSTVLQDSSSYFSSTLPGHGIHPLPPHSLEHLNAIGDGHAFGLHVPHSFRAS  
QSRVGQGDETLRALPHLHLTAQQLRIVLGGRDHGYLEAEERRWES\*SANGIGRWCRIRPRSSRCRRRSVKLLLRGSGSRDLSMM  
PTALSISRLVRRQQRMRLSLRSLQYVQHRTTFLNSP\*FNTLQPKLIAGRMPLTPWPSYQILR\*IKWRSQNTLPTYMISLGMWRFTT  
SRYHITLWLNMQPRMILNRHRASTAPPAMQRRDPGSRQWQWRTHRSYPWIIWELNKSMLAQHRHMLMHLFSTLSSSGVKTSIQ  
GTGNSCRTANPAEQGNPRT\*LTLCMDRVSQSGSTG\*SSTREARVSQSRGKGAGRYG\*WRDAADRVRDRVMMQLLSDIFVLAV  
AEPGPGAAHRSPAAVPAALGTLGVEIVKQPLSQTVQI\*GLRDEDPIMPDSDDHIDHRGMGQTQPDAILLFGDGGGGKNRKN  
HD\*LLIQTVESEHFKMKVEMAPLAPAVLVENNSQVKGDTVLEMFHGGFQQSLHAHIQKQDNSESGRVL\*FLNHHVTLHHPQIIFI  
FPALNDSN\*FLR\*IQASHDKELAQSALHRHS\*APHNKIFCSWFTCSRLTSGISKSLPRSLSSSLNNCKYSFISSPKFLAIGPPGIRLGQ  
ATVQINRSPQ\*ALPNARLL\*ACWLDPVISSR\*LDRKSPRQFLRKSTKEKSSRCTFRASGTTMK\*MQAVRSSMVS\*LICKKQKIKH\*T  
MLAWRTGG\*IVLSSTRQATGSPARPS\*KLSL\*LKTITERRSRWPA\*MIRQDEYTPGTLASASEKKRPRKQ\*GTTMLSLKSSKAMP  
CG\*STKSSGAYKM\*LLPSCGTSEAPDSRYTYKASASIAYRAAAHNRRKSQRKAE\*PVHPLSAQYIAQIYTDVKAKV\*KYPPNNHTRPA  
HAQKPVTHSKKYAHFLKRPNCRHRVPTLRHNSTFKFRPLKTSAPPLTVARLSANHLPPSPNSNSSFAY\*RAPKV\*GILLMM



Fig. 24A

**AdC6 020-DU172gp160(E1620) Nucleic Acids – SEQ ID NO: 5**

CATCATCAATAATATACCTCAAACCTTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCTGCGGGAGCGGCGACCGTTAGGGGCGGGGCGGGTGACGTTTTGATGACGTGGCTATGAGGCGGAGCCGGTTTGCAAG  
TTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTGAACACGGAAATACTCAATTTCCCGCGCTCTCTGACAGGAAATG  
AGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAAAACCTGAATGAGGAAGTGAAAATCTGAGTAATTTT  
GCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTTC  
ACCTAAATTTCCGCGTACGGTGTCAAAGTCCGGTGTTTTACGTACGATATCATTTCCCGAAAAGTGCCACCTGACCGTAACTAT  
AACGGTCCTAAGGTAGCGAAAAGCTCAGATCTCCCGATCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT  
AAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCT  
TGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGA  
CATTGATTATTGACTAGTATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTAC  
ATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACA  
TCAATGGGCGTGGATAGCGGTTTGAATCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTGGCACC  
AAAATCAACGGGACTTTCCAAAATGTCGAACAACCTCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGT  
CTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAACGC  
AGTCAGTGCTTCTGACACAACAGTCTCGAACTTAAGGCTAGAGTACTTAATACGACTCACTATAGGCTAGTTAAGGCTAGAGTT  
CGACGCCACCATGCGCGTGATGGGCATCTGCGCTCTACCAGCAGTGGTGGATCTGGGGCATCTGGGCTTCTGGATGCTGA  
TGATCTGCAACGTGTGGGCAACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCTGTT  
CTGCGCTCCGACGCCAAGGCCACAAGGAGGAGGTGCACAACATCTGGGCCACCCACGCTGCGTGCCACCGACCCCAAC  
CCCCAGGAGATCGTGCTGAAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGACCAGATGCACGAGGAC  
ATCATCTCCCTGTGGGACCACTCCCTGAAGCCCTGCGTGAAGCTGACCCCTGTGCGTGACCTGAACTGCTCCGACGTGAA  
GATCAAGGGCACCAACGCCACCTACAACAACGCCACCTACAACAACAACAACACCATCTCCGACATGAAGAACTGCTCCTCAA  
CACCACCACCGAGATCACCGACAAGAAGAAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGCCCTGGACGGCAAG  
GAGACCAACTCCACCAACTCCTCCGAGTACCGCCTGATCAACTGCAACACCTCCGCCGTGACCCAGGCTGCCCAAGGTGTCC  
TTCGACCCCATCCCATCCACTACTGCGCCCCCGCGGCTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGC  
CCCTGCAACAACGTGTCCACCGTGAGTGCAACCCACGGCATCAAGCCCGTGGTGTCACCCAGCTGCTGCTGAACGGCTCCCT  
GGCCGAGGAGGAGGTGGTGATCCGCTTCGAGAACCTGACCAACAACGCCAAGATCATCATCGTGACCTGAACGAGTCCGTG  
GAGATCAACTGACCCGCCCCCTCCAACAACACCCGCAAGTCCGTGCGCATCGGCCCGGCCAGACCTTCTCGCCACCGGCGA  
CATCATCGGCGACATCCGCCAGGCCACTGCAACATCTCCGCAAGAAGTGGAACACCACCTGCAGCGCGTGAAGGAGAAG  
CTGAAGGAGAAGTTCCCCAACAAGACCATCCAGTTCGCCCCCTCCTCCGGCGGCGACCTGGAGATCACCAACCACTCCTTCAAC  
TGCCGCGGCGAGTTCTTCTACTGCTACACCTCCGACCTGTTCAACTCCACCTACATGTCCAACAACACCGGCGGCGCAACATC  
ACCCTGCAGTGCCGCATCAAGCAGATCATCCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCGCCGCA  
ACATCACCTGCAAGTCCAACATACCCGGCCTGCTGCTGACCCGCGACGGCGGCAAGGAGAAGAACGACACCGAGACCTTCCG  
CCCCGGCGGCGGCGACATGCGCGCAACTGGCGCTCCGAGCTGTACAAGTACAAGGTGGTGGAGATCAAGCCCTGGGCATC  
GCCCCGACAAGGCCAAGCGCCGCTGGTGAGCGCGAGAAGCGCGCCGTGGGCATCGGCGCCGTGTTCTGGGCTTCTGTG  
GGCGCCCGGCGAGCACCATGGGCGCCGCGCAGCATGACCCTGACCGTGCAAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAAGC  
AGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCACATGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGAC  
CCGCGTGCTGGCCATCGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACC  
ACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCTACGAGGAGATCTGGGGCAACATGACCTGGATGCAGTGGGAC  
CGCGAGATCAACAACCTACCAACACCATCTACAGCTGCTGGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGAAGGAC  
CTGCTGGCCCTGGACAGCTGGGAGAGCCTGTGGAGCTGGTTCAACATCAACAACTGGCTGTGGTACATCCGCATCTTCATCAT  
CATCGTGGGCGGCTGATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCC  
TGAGCTTCCAGACCTGACCCCCAGCCCCGCGAGCCGACCGCCTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACC  
GCGCCCGCAGCGTGCGCCTGGTGAACGGCTTCTGGCCCTGGCCTGGGAGGACCTGCGCAGCCTGTGCTGTTTACGCTACCAC  
CGCTGCGCGACCTGATCCTGATCGCCGCCGCGCCGCCCTGCTGGGCCGAGCAGCCTGTGGGGCTGCAGAAGGGCT  
GGGAGGCCCTGAAGTACCTGGGACGCTGGTGCACTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCTGTTTCGACG  
CCATCGCCATCACCGTGGCCGAGGGCACCGACCGCATCATCAACATCGTGACGCGCATCAGCCGCGCTTCTACAACATCCCCC  
GCCGCATCCGCCAGGGCTTCGAGGCCACCTGCAAGTAAGGTACCTCTAGAGTCGACCCGGGCGGCCAAACCGCTGATCAGCCT  
CGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCGTGCTTCTTGACCTGGAAGGTGCCACTCCCACTGT  
CCTTCTCAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGTGGGGTGGGCGAGGACA

Fig. 24B

GCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACC  
AGCAGATCTGCAGATCTGAATTCATCTATGTGCGGTGCGGAGAAAGAGGTAATGAAATGGCATTATGGGTATTATGGGTCTGC  
ATTAATGAATCGGTCAGATATCGACATATGCTGGCCACCGTGCATGTGGCTCGCACCCCGCAAGACATGGCCCGAGTTCTGA  
GCACAACGTCATGACCCGCTGCAATGTGCACCTGGGCTCCGCGGAGGCATGTTTCATGCCCTACAGTGCAACATGCAATTTGT  
GAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGCTGTGGAAAATT  
CTGAGATATGATGAATCCAAGACCAGGTGCCGGGCTGCGAATGCGGAGGCAAGCACGCCAGGCTTCAGCCCGTGTGTGTGG  
AGGTGACGGAGGACCTGCGACCCGATCATTGGTGTGTCTGCAACGGGACGGAGTTCGGCTCCAGCGGGGAAGAATCTGA  
CTAGAGTGAGTAGTGTGGGGCTGGGTGTGAGCCTGCATGAGGGGCGAGAATGACTAAAATCTGTGGTTTTCTGTGTGTGTC  
AGCAGCATGAGCGGAAGCGCTCCTTTGAGGGAGGGGTATTCAGCCCTTATCTGACGGGGCGTCTCCCTCTGGGCGGGAG  
TGCGTCAGAAATGTATGGGATCCACGGTGGACGGCGGGCGGTGCAGCCCGCAACTCTCAACCTGACCTACGCGACCCCTG  
AGCTCCTCGTCCGTGGACGCAGCTGCCGCCGAGCTGCTGCTCCGCCGACGCGCGTGCAGGAAATGGCCCTGGGCGCCG  
GCTACTACAGCTCTGCTGTGGCCAACTCGAGTTCCACCAATAATCCGCCAGCTGAACGAGGAGAAGCTGCTGCTGCTGATG  
GCCAGCTCGAGGCCCTGACCCAGCGCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGCAGGCGGAGACGCGGGCCGCG  
GTTGCCACGGTGAAAACCAAATAAAAAATGAATCAATAAATAAACGGAGACGGTTGTTGATTTTAACACAGAGTCTTGAATCT  
TTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATCTTTTCCAGGACCCGGTA  
GAGGTGGGCTTGGATGTTGAGGTACATGGGCATGAGCCGTCCCGGGGGTGGAGGTAGCTCCATTGACGGGCCCTCGTGCTC  
GGGGATGGTGTGTAATCACCCAGTCATAGCAGGGGCGCAGGGCGTGGTGCTGCACGATGCTCTTGAGGAGGAGACTGAT  
GGCCACGGGCGAGCCCTTGGTGTAGGTGTTGACGAACCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGATGCAT  
CTTGGCCTGGATCTTGAGATTGGCGATGTTCCGCCAGATCCGCCGGGGGTTTCATGTTGTGCAGGACCACAGCACGGTGT  
ATCCGGTGCATTTGGGGAATTTGTATGCAACTTGGAAAGGAAGGCGTGAAAGAATTTGGAGACGCCCTTGTGACGCCCCAG  
GTTTTTCATGCACTCATCCATGATGATGGCGATGGGCCCTGGGCGGCGGCTGGGCAAAGACGTTTTCGGGGTGCGACACA  
TCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAATGAATTTGGGGCGGAGGGTGCCGACTGGGGGACGAAGG  
TGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGCATCTCCAGGCCTTGAGCTCGGAGGGGGGGATCATGTCCACC  
TGCGGGGCGATGAAAAAACGGTTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAGGTTCCGGAGCAGCTGGGACTT  
GCCGCAACCGGTGGGGCCGTAGATGACCCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCCTCGCG  
GAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACATGCATGTTCTCGCGCACGAGTTCGCCAGGAGGCGCTCGCCCCCA  
GCGAGAGGAGCTCTTGACGCGAGGCGAAGTTTTTCAGCGGCTTGAGTCCGTGCGCCATGGGCATTTTGGAGAGGGTCTGTTG  
CAAGAGTTCCAGACGGTCCAGAGCTCGGTGATGTGCTCTAGGGCATCTCGATCCAGCAGACCTCTGTTTCGCGGGTGGG  
GCGACTGCGGGAGTAGGGCACCAGGCGATGGGCGTCCAGCGAGGCCAGGGTCCGGTCTTCCAGGGCCGAGGGTCCGCGT  
CAGCGTGGTCTCCGTACGGTGAAGGGGTGCGCGCGGGGCTGGGCGCTTGCGAGGGTGCGCTTACGGCTCATCCGGCTGGTC  
GAGAACCCTCCGGTGGGCGCCCTGCGCGTGGGCCAGGTAGCAATTGAGCATGAGTTCGTAGTTGAGCGCCTCGGCCGCGT  
GGCCCTTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGACAGCGGGACAGAGGAGGAGCTTGGGGCGTAGAGCTTGGGGG  
CGAGGAAGACGGAAGTCCGGGGCGTAGGCGTCCGCGCCGAGCTGGCGCAGACGGTCTCGCACTCCACGAGCCAGGTGAGGT  
CGGGGCGGTTGGGGTCAAAAACGAGGTTTCTCCGTGCTTTTATGATGCGTTTCTTACCTCTGGTCTCCATGAGCTCGTGCCCC  
GCTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACTTATGGGCCGTCTCGAGCGGGGTGCCGCGTCTCGTC  
GTAGAGGAACCCCGCCACTCCGAGACGAAGGCCCGGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGAGGGGTAGCGGT  
CGTTGTCCACAGCGGGTCCACCTTCTCAGGGTATGCAAGCACATGTCCCCCTCGTCCACATCCAGGAAGGTGATTGGCTTGT  
AAGGTAGGCCACGTGACCGGGGTCCCGCGCGGGGGGTATAAAGGGGGCGGGCCCTGCTCGTCTCACTGTCTTCCG  
GATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCTCTCGAAGGCGGGCATGACCTCGGCACTCAGGTTGTCAATT  
TCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTTGGAGACGCTTTTCATGAGCCCTCGTCCATTTGGTCAGAAAAGAC  
GATCTTTTGTGTGCGAGCTTGGTGCGAAGGAGCCGTAGAGGGCGTTGGAGAGCAGCTTGGCGATGGAGCGCATGGTCTGG  
TTCTTTTCTTGTGCGCGCGCTCCTTGGCGCGCATGTTGAGCTGCAGTACTCGCGCGCCACGCACTTCCATTGCGGGAAGACG  
GTGGTGAGCTCGTGGGCGACGATTCTGACCCGCCAGCGCGGTTGTGCAGGGTATGAGGTCCACGCTGGTGGCCACCTCGC  
CGCGCAGGGGCTGTTGGTCCAGCAGAGGCGCCCGCCTTGCAGGAGCAGAAGGGGGGACGCGGGTCCAGCATGAGCTCGT  
CGGGGGGGTGGCGTCCACGGTGAAGATGCCGGGCGAGGCTCGGGGTGGAAGTAGCTGATGCAGGTGCCAGATTGTCCA  
GCGCCGCTTGCAGTCGCGCACGGCCAGCGCGGCTCGTAGGGGCTGAGGGGCGTGCCCCAGGGCATGGGGTGCGTGAGCG  
CGGAGGCGTACATGCCGAGATGTCGTAGACGTAGAGGGGCTCCTCGAGGACGCCGATGTAGGTGGGGTAGCAGCGCCCC  
CGCGGATGCTGGCGCGCACGTAGTCGTACAGCTCGTGCAGGGGCGGAGGAGCCCGTGCCGAGGTTGGAGCGTTGCGGCT  
TTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAGTTGGAGGAGATGGTGGGCCTTTGGAAGATGTTGAAGTGGG  
CGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTAGGAGTCTGCAGCTTGGCGACGAGCTCGGCGGTGACGAGGA  
CGTCCAGGGCGCAGTAGTCGAGGGTCTCTTGGATGATGTCATACTTGAAGTGGCCCTTCTGCTTCCACAGCTCGCGGTTGAGA

Fig. 24C

AGGAACTCTTCGCGGTCTTCCAGTACTCTTCGAGGGGGAACCCGTCTGATCGGCACGGTAAGAGCCCACCATGTAGAACTG  
GTTGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGAGGGCGTAAGCTTGC GCGGCCCTTGC GCGAGGGAGGTGTGGGT  
GAGGGCGAAGGTGTCGCGCACCATGACCTTGAGGAACTGGTGCTTGAAGTCGAGGTCGTGCGAGCCGCCCTGCTCCAGAGT  
TGGAAGTCCGTGCGCTTCTGTAGGCGGGGTAGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGCGGGGCA  
TGAAGTTGCGAGTGATGCGGAAAGGCTGGGGCACCTCGGCCCGTTGTTGATGACCTGGGCGGCGAGGACGATCTCGTCGA  
AGCCGTTGATGTTGTGCCGACGATGTAGAGTTCCACGAATCGCGGGCGGCCCTTGACGTGGGGCAGCTTCTTGAGCTCGTCG  
TAGGTGAGCTCGGCGGGGTGCTGAGCCCGTGCTGCTGAGGGGCCAGTCGGCGACGTGGGGGTGGCGCTGAGGAAGGA  
AGTCCAGAGATCCACGGCCAGGGCGGTCTGCAAGCGTCCCGTACTGACGGAAGTGTGGCCACAGGCCATTTTTTCGGGG  
GTGACGCAGTAGAAGGTGCGGGGGTCCCGTGCCAGCGGTCCACTTGAGCTGGAGGGCGAGGTGCTGGGCGAGCTCGACG  
AGCGGCGGGTCCCCGAGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCATCCAGGTGTAGTTT  
CCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCCTGCCACAGTTGGA  
GGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGCGCCGAGCACTCGTGCTTGTGTTTATACAAGCGTCCGCAG  
TGCTCGAACGCTGCACGGGATGCACGTGCTGCACGAGCTGTACCTGGGTTCTTTGGCGAGGAATTTAGTGGGCAGTGGA  
GCGCTGGCGGCTGCATCTCGTGCTGTACTACGTCTTGCCATCGGCGTGGCCATCGTCTGCCTCGATGGTGGTCATGCTGACG  
AGCCCGCGCGGGAGGCGAGGTCCAGACCTCGGCTCGGACGGGTGCGAGAGCGAGGACGAGGGCGCGCAGGCCGAGCTGTC  
CAGGGTCTGAGACGCTGCGGAGTCAGGTGAGTGGGCGAGCGCGCGCGGTTGACTTGAGGAGCTTTTCAGGGCGCG  
CGGGAGGTCCAGATGGTACTTGATCTCCACGGCGCCGTTGGTGGCTACGTCCACGGCTTGACGGGTGCCGTGCCCTGGGGC  
GCCACCACCGTGCCCCGTTTCTTGGGCGTGCTTCCATGTCGTCAGAAAGCGGCGGCGAGGACGCGCGCGGGCGGCGAG  
GGGCGGCTCGGGGCGGAGGCGAGGGGCGGAGGGGCGGCGGCGCGGGGCGGAGTTCTGGTACTGCGCCCGGA  
GAAGACTGGCGTGAGCGACGACGCGAGGTTGACGTCTGGATCTGACGCTCTGGGTGAAGGCCACGGGACCCGTGAGTTT  
GAACCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGACGGCGGCTGCCGAGGATCTCTTGACGTGCCCCGAGT  
TGTCTGGTAGGCGATCTCGGTCATGAACTGCTCGATCTCTCTCTGAAGGTCTCCGCGGCCGCGCGCTCGACGGTGGCC  
GCGAGGTCGTTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTCATGCCGGCTCGTTCCAGACGCGGCTGTAGACCACGG  
CTCCGTCGGGTCGCGCGCGCATGACCACCTGGGCGAGGTTGAGCTCGACGTGGCGCGTGAAGACCGCGTAGTTGAGA  
GGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTGACGAAGAAGTACATGATCCAGCGGCGGAGCGGCATCT  
CGTGACGTGCCCCAGGGCTTCCAAGCGTTCATGGCCTCGTAGAAGTCCACGGCGAAGTTGAAAACTGGGAGTTGCGCGC  
CGAGACGGTCAACTCTCTCCAGAAGACGGATGAGCTCGGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCCCGGGGGG  
CTCTCTTCCATCTCTCTCTCTCTCTCCACTAACATCTCTTCTACTTCTCTCAGGAGGCGGTGGCGGGGAGGGGCCCTG  
CGTCGCCGCGGCGCACGGGCGAGCGGTGATGAAGCGCTCGATGGTCTCCCCGCGCGGCGACGCATGGTCTCGGTGACG  
GCGCGCCGTCCTCGCGGGGCGCAGCATGAAGACGCCGCGCGCATCTCCAGGTGGCCGCGGGGGGCTCCGTTGGG  
AGGGAGAGGGCGTGACGATGCATCTTATCAATTGACCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAGATCCACGG  
GATCCGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGAGTCGCAAGGTAGGCTGAGCCCGTTTCTGTTCTTGGGTATT  
TGGTGGGAGGCGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAGTAGGCGGTCTGAGACGGCGGATGGTGGCGAGGAG  
CACCAGGTCTTGGGCGGGCTTGGTGGATGCGCAGACGGTCGGCCATGCCCCAGGCGTGGTCTGACACCTGGCGAGGTCC  
TTGTAGTAGTCTGCATGAGCCGCTCCACGGGACCTCTCTCGCCGCGCGGCGTGCATGCGCGTGAGCCGAACCCGCG  
CTGCGGCTGGACGAGCGCCAGGTGCGCGACGACGCGCTCGGTGAGGATGGCCTGCTGGATCTGGGTGAGGGTGGTCTGGAA  
GTCGTGCAAGTCGACGAAGCGGTGGTAGGCTCCGTTGTTGATGGTGTAGGAGCAGTTGGCCATGACGGACCAAGTTGACGGT  
CTGGTGGCCGGGTGCGACGAGCTCGTGGTACTTGAGGCGCAGTAGGCGCGCTGTCGAAGATGTAGTCTGTCAGGCGCG  
CACGAGGTACTGGTATCCGACGAGGAAGTGCGGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCCGG  
GCGCGAGGTCTCGAGCATGAGGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGCGGCGGTTGGTGGAGG  
CGCGCGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTTCATGGTGGCCGCGTCTGGCCGTGA  
GGCGCGCGCAGTCGTGGATGCTTAGACATACGGGCAAAAACGAAAGCGGTACGCGGCTCGACTCCGTGGCCTGGAGGCTA  
AGCGAACGGGTTGGGCTGCGCGTGTACCCGGTTCGAATCTCGAATCAGGCTGGAGCCGACGTAACGTGGTACTGGCACTC  
CCGTCTGACCCAAGCCTGCTAACGAAACCTCCAGGATACGGAGGCGGGTCTTTTTGGCCTTGGTCTGCTGGTCATGAAAA  
CTAGTAAGCGCGGAAAGCGGCCCGCGCATGGCTCGCTGCCGTAGTCTGGAGAAAGAATCGCCAGGGTTGCGTTGCGGTGT  
GCCCCGTTTCGAGCCTCAGCGCTCGGCGCGGCGGATTCCGCGGCTAACGTGGGCGTGGCTGCCCCGCTGTTTCCAAGACCC  
CTAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCTCTTTTTTTCTTGTGTTTTGCCAGATGCATCCCGTACTGCGGCA  
GATGCGCCCCACCTCCACCACAACCGCCCCTACCGCAGCAGCAGCAACAGCCGCGCTTCTGCCCCGCCCGAGCAGCAGC  
CAGCCACTACCGCGGCGGCGCCGTGAGCGGAGCGGCGTTCAGTATGACCTGGCCTTGGAAAGAGGGCGAGGGGCTGGCGC  
GGCTGGGGGCGTCTGCGCGGAGCGGACCCGCGCGTGCAGATGAAAAGGGACGCTCGCGAGGCCTACGTGCCAAGCAGA  
ACCTGTTAGAGACAGGAGCGGCGAGGAGCCCCGAGGAGATGCGCGCTCCCGCTTCCACGCGGGGCGGGAGCTGCGGCGCG

Fig. 24D

GCCTGGACCGAAAGCGGGTGCTGAGGGACGAGGATTTGAGGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCAC  
GTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCAAAAAATCCTTCAACAACCACG  
TGCGCAGCTGATCGCGCGGAGGAGGTGACCCTGGGCTGATGCACCTGTGGGACCTGCTGGAGGCCATCGTGACAGAACCC  
CACGAGCAAGCCGCTGACGGCGCAGCTGTTTCTGGTGGTGCAGCACAGTCGGGACAACGAGACGTTTCAGGGAGGCGCTGCT  
GAATATCACCGAGCCCGAGGGGCCGCTGGCTCCTGGACCTGGTGAACATTTTGACAGCATCGTGGTGCAGGAGCGCGGGCTG  
CCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGCTGAGTCTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCC  
GTACGTGCCATAGACAAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGAT  
CTGGGGGTGTACCGCAACGACAGGATGCACCGCGCGGTGAGCGCCAGCCGCGCGGAGCTGAGCGACCAGGAGCTGATG  
CACAGCCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCGCTGGCAG  
CCCAGCCGCGGGCCCTTGAAGCTGCCGGCGGTTCCCCCTACGTGGAGGAGGTGGACGATGAGGAGGAGGAGGGCGAGTAC  
CTGGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAGCAACAGCCACCGCCGCGCTCTGATCCCGCGATGCGGGCG  
GCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCC  
GCAATCCCGAAGCCTTAGACAGCAGCCTCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTGGTGCCCTCGCGCTCGAAC  
CCCACGCACGAGAAGGTGCTGGCCATCGTGAACCGCTGGTGGAGAACAAGGCCATCCGCGGTGACGAGGCCGGGCTGGTG  
TACAACGCGCTGCTGGAGCGCTGGCCCCGCTACAACAGCACCAACGTGCAGACGAACCTGGACCGCATGGTGACCGACGTGC  
GCGAGGCGGTGTCGACGCGGAGCGGTTCCACCGGAGTGAACCTGGGCTCCATGGTGGCGCTGAACGCCTTCTGAGCAC  
GCAGCCCGCAACGTGCCCCGGGGCCAGGAGGACTACCAACTTCATCAGCGCGCTGCGGCTGATGGTGGCCGAGGTGCC  
CAGAGCGAGGTGTACAGTCGGGGCCGACTACTTCTTCAGACCAAGTCGCCAGGGCTTGACAGCCGTGAACCTGAGCCAGG  
CTTTCAAGAACTTGAGGGACTGTGGGGCGTGCAGGCCCGGTGCGGGACCGCGCAGCGGTGTCGAGCCTGCTGACGCCGA  
ACTCGCGCTGCTGCTGCTGGTGGCGCCCTTACCGACAGCGGCAGCGTGAGCCGCGACTCGTACCTGGGCTACCTGCTT  
AACCTGTACCGCGAGGCCATCGACAGGGCGACGTGGACGAGCAGACCTACCAGGAGATCACCCAGTGAGCCGCGCGCTG  
GGCCAGGAGGACCCGGGCAACCTGGAGGCCACCCTGAATTCCTGCTGACCAACCGGTGCGAGAAGATCCCGCCCCAGTACG  
CGTGAGCACCGAGGAGGAGCGCATCCTGCGCTACGTGCAGCAGAGCGTGGGGCTGTTCTGATGCAGGAGGGGGCCACGC  
CCAGCGCGGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCCCGCAACCGCCGTTTCATCAATAAGCTGATG  
GACTACTTGATCGGGCGGCCCGCATGAACTCGGACTACTTTACCAACGCCATCTTGAACCCGCACTGGCTCCCGCGCCCGG  
GTTCTACACGGGCGAGTACGACATGCCCCACCCCAACGACGGGTTCTGTGGGACGACGTGGACAGCAGCGTGTCTCGCCG  
CGTCCAGGAACCAATGCCGTGTGGAAGAAAGAGGGCGGGGACCGGCGGCCGTCTCGGCGCTGTCCGGTCGCGCGGGTGCT  
GCCGCGCGGTGCCGAGGGCCGACGCCCTTCCCGAGCCTGCCCTTTGCTGAACAGCGTGCGCAGCAGCGAGCTGGGTC  
GGCTGACGCGACCGCGCCTGCTGGGCGAGGAGGAGTACCTGAACGACTCCTTGTGAGGCCGAGCGCGAGAAGAACTTCCC  
CAATAACGGGATAGAGAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTACGCGCACGAGCACAGGGACGAGCCCCGAGC  
TAGCAGCGCAGGCACCCGTAGACGCCAGCGGCACGACAGGCAGCGGGGACTGGTGTGGGACGATGAGGATTCCGCCGACGA  
CAGCAGCGTGTGGACTTGGGTGGGAGTGGTGGTAACCCGTTGCTCACCTGCGCCCCGTATCGGGCGCTGATGTAAGAA  
TCTGAAAAAATAAAGACGGTACTACCAAGGCCATGGCGACCAGCGTGCGTTCTTCTGTTGTTGTAGTAGTATGATGAG  
GCGCGTGTACCCGGAGGGTCTCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGGTGGCGGCGCGATGCAGCCCCGCTG  
GAGGCGCCTTACGTGCCCCGCGGTACCTGGCGCTACGGAGGGGCGGAACAGCATTGTTACTCGGAGCTGGCACCTTGT  
ACGATACACCCGTTGTACCTGGTGGACAACAAGTCGGCAGACATCGCTCGCTGAACTACCAGAACGACCACAGCAACTTC  
CTGACCACCGTGGTGCAGAACAAACGATTTACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTG  
GGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCAACGTGAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGG  
GTGATGGTCTCGCGCAAGACCCCCAACGGGGTGGATGATGATTATGATGGTAGTCAGGACGAGCTGACCTACGAGTGGGTGG  
AGTTTGAGCTGCCCAGGGCAACTTCTCGGTGACCATGACCATCGATCTGATGAACAACGCCATCATCGACAACTACTTGGCG  
GTGGGGCGGCAGAACGGGGTGTGGAGAGCGACATCGGCGTGAAGTTCGACACGCGCAACTCCGGCTGGGCTGGGACCCC  
GTGACCGAGCTGGTGTGCCGGCGGTGTACCAACGAGGCGCTTCAACCCGACATCGTCTGCTGCCCGCTGCGGCGTGG  
ACTTCACCGAGAGCCGCTCAGCAACTGCTGGGCATCCGCAAGCGGCAGCCCTTCCAGGAGGGCTTCCAGATCCTGTACGAG  
GACCTGGAGGGGGCAACATCCCCGCGCTCTGGATGTGCAAGCCTACGAGAAAAGCAAGGAGGATAGCACCGCCGCGGCG  
ACCGCAGCCGTGGCCACCGCCTCTACCGAGGTGCGGGGCGATAATTTTGCTAGCGCTGCGGCAGCGGCCGAGGCGGTGAAA  
CCGAAAGTAAGATAGTATCCAGCCGGTGGAGAAGGACAGCAAGGACAGGAGCTACAACGTGCTCGCGGACAAGAAAAACA  
CCGCTACCGCAGCTGGTACCTGGCCTACAACTACGGCGACCCCGAGAAGGGCGTGCGCTCTGGACGCTGCTCACCACCTCG  
GACGTCACTGCGCGTGGAGCAAGTCTACTGGTGCCTGCCCCACATGATGCAAGACCCGGTCACTTCCGCTCCACGCGTCA  
AGTTAGCAACTACCCGGTGGTGGGCGCCGAGCTCTGCCGTCTACTCCAAGAGCTTCTTCAACGAGCAGGCGCTACTCGC  
AGCAGCTGCGCGCTTCACTCGCTACGCACGTCTTAACCGCTTCCCGAGAACAGATCCTCGTCCGCCGCGCCGCGCCA  
CCATTACCACCGTCAGTGAACAGTTCTGCTCTACAGATCACGGGACCTGCGCTGCGCAGCAGTATCCGGGGAGTCCAG

Fig. 24E

CGCGTGACCGTCACTGACGCCAGACGCCGACCTGCCCCCTACGTCTACAAGGCCCTGGGCGTAGTCGCGCCGCGCGTCCTCTC  
GAGCCGCACCTTCTAAAAAATGTCCATTCTCATCTCGCCAGTAATAACACCGGTTGGGGCTGCGCGCGCCAGCAAGATGT  
ACGGAGGCGCTCGCAACGCTCCACGCAACACCCCGTGC GCGTGC GCGGGCACTTCGCGCTCCCTGGGGCGCCCTCAAGGG  
CCGCGTGC GCTCGCGCACCAACGTCGACGACGTGATCGACCAGGTGGTGGCCGACGCGCGCAACTACACGCCCGCGCGCG  
CCCGTCTCCACCGTGAGCGCGTCACTGACAGCGTGGTGGCCGACGCGCGCGGTACGCCCCACCAAGAGCCGGCGCGCGC  
GCATCGCCCGCGCGCACCGGAGCACCCCGCCATGCGCGCGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCA  
GGGCCATGCTCAGGGCGGCCAGACGCGCGGCTCCGGCAGCAGCAGCGCCGGCAGGACCCGACAGCGCGGCCACGGCG  
GCGGCGGGCGCCATCGCCAGCATGTCCCGCCCGCGCGCGGCAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGC  
GTGCCCGTGC GCAACCGCCCCCTCGCACTTGAAGATGCTGACTTCGCGATGTTGATGTGTCAGCGGCGAGGAGGATGTCC  
AAGCGCAAATACAAGGAAGAGATGCTCCAGGTATCGCGCTGAGATCTACGGCCCCGCGCGCGGTGAAGGAGGAAAGA  
AAGCCCCGAACTGAAGCGGGTCAAAAAGGACAAAAAGGAGGAGGAAGATGACGGAAGTGGTGGAGTTTGTGCGCGAGTTC  
GCCCCCGCGCGCGGTGCACTGGCGCGGGCGGAAAGTGAAACCGGTGCTGCGGCCGCGCACACGGTGGTCTTACGCCC  
GGCGAGCGTTCCGGCTCCGCTCCAAGCGCTCTACGACGAGGTGTACGGGGACGAGGACATCCTCGAGCAGGCGGTGCGAGC  
GTCTGGGCGAGTTTGCCTACGGCAAGCGCAGCCGCCCCGCGCCCTTGAAAGAGGAGGCGGTGTCCATCCCGCTGGACACGG  
CAACCCACGCGGAGCCTGAAGCGGTGACCCTGCAGCAGGTGCTACCGAGCGCGGCGCGCGCGGGGCTTCAAGCGCGA  
GGGCGGCGAGGATCTGTACCGACCATGCAGCTGATGGTGC CCAAGCGCCAGAAGCTGGAGGACGTGCTGGAGCATGAA  
GGTGGACCCGAGGTGCAGCCGAGGTCAAGGTGCGGCCATCAAGCAGGTGGCCCCGGGCTGGGCGTGCAGACCGTGGA  
CATCAAGATCCCCACGAGGCCATGGAAACGAGACCGAGCCGTGAAGCCCAGCACCAGCACCATGGAGGTGCAGACGGAT  
CCCTGGATGCCAGCACCAGCTTCCACCAGCACTCGCCGAAGACGCAAGTACGGCGCGGCCAGCCTGCTGATGCCAACTACGC  
GCTGCATCCTTCCATCATCCCCACGCCGGGTACCGCGCACGCGCTTACCGCGGTACACCAGCAGCCGCCCGCGCAAGA  
CCACCACCCGCCGCGTCTGTCGAGCCGCCGAGCAGCACCAGCGACTTCCGCTTGGTGC GAGAGTGTATCGAGCGGGCG  
CGAGCCTCTGACCCTGCCGCGCGCGCTACACCCGAGCATCGCCATTAACTACCGCTCCTACTTGCAGATATGGCCCTCA  
CATGCCGCTCCGCGTCCCATACGGGCTACCGAGGAAGAAAGCCGCGCGTAGAAGGCTGACGGGGAACGGGCTGCGTC  
GCCATCACACCGCGCGCGCGGCCATCAGCAAGCGTTGGGGGAGGCTTCTGCCGCGTGTATCCCATCATCGCCG  
GGCGATCGGGGCGATCCCGGCATAGCTTCCGTGGCGGTGCAGGCCTCTACGCGCACTGAGACACAAAAAGCATGGATTT  
GTAATAAAAAAATGGACTGACGCTCCTGGTCTGTGATGTGTGTTTTAGATGGAAGACATCAATTTTTCTGTCCTGGCA  
CCGCGACACGGCACGCGGCCGTTTATGGGCACCTGGAGCGACATCGGCAACAGCCAAGTGAACGGGGCGCCTTCAATTGGA  
GCAGTCTCTGGAGCGGGTTAAGAATTCGGGTCCACGCTCAAACTATGGCAACAAGGCGTGAACAGCAGCACAGGGCA  
GGCGTGAAGGAAAAGCTGAAAGAACAGAACTTCCAGCAGAAGGTGGTTGATGGCCTGGCCTCAGGCATCAACGGGGTGGT  
TGACCTGGCCAACAGCCGTGCAGAAACAGATCAACAGCCGCTGGACGCGGTCCCGCCCGCGGGGTCCGTGGAGATGCC  
CAGGTGGAGGAGGAGTGCCTCCCTGGACAAGCGCGGCGACAAGCGACCGCTCCCGACGCGGAGGAGACGCTGCTGACG  
CACACGAGCAGCCGCCCCGTACGAGGAGGCGGTGAACTGGGCCTGCCACCACGCGGCCGCTGGCGCTCTGGCCACCG  
GAGTGTGAAACCCAGCAGCAGCCAGCCGCGACCTGGACTTGCTCCGCTCGCCCTCCACAGTGCTAAGCCCTGCCG  
CCGTTGGCGTGC GTCGCGCGCCCCGAGGCCGCCCCAGGCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGG  
GAGTGCAGAGTGTGAAGCGCCGCGCTGCTATTAAGACACTGTAGCGCTTAACTTGCTTGTGTGTATATGTATGCC  
GCCGACCAGAAGGAGGAGTGTGAAGAGCGCGTGC CCGAGTTGCAAGATGGCCACCCATCGATGCTGCCCAAGTGGCGT  
ACATGCACATCGCCGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTCGCCGCGCCACAGACACTTTC  
AGTCTGGGGAACAAGTTTAGGAACCCACGGTGGCGCCACGCAGATGTGACCACCGACCGCAGCCAGCGGTGACGCTGC  
GCTTCGTGCCGTTGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTACACGCTGGCCGTGGGCGACAACCGCGTGT  
GGACATGGCCAGCAGCTACTTTGACATCCGCGCGTGTGGACCGGGGCCCTAGCTTCAAACCTACTCTGGCACCGCCTACA  
ACAGCCTAGTCCCAAGGGAGCTCCCAATTCAGCCAGTGGGAGCAAGCAAAAACAGGCAATGGGGGAACTATGGAACACA  
CACATATGGTGTGGCCCCAATGGGCGGAGAGAATATTACAAAAGATGGTCTTCAAATTGGAAGTACGTTACAGCGAATCAG  
AATAAACCAATTTATGCCGACAAAACATTTCAACGAGAACCGCAAGTAGGAGAAGAAAATTGGCAAGAACTGAAAATTTTA  
TGGCGGTAGAGCTCTTA AAAAGACACAAACATGAAACCTTGCTATGGCTCTATGCTAGACCCACCAATGAAAAAGGAGGTC  
AAGCTAACTTAAAGTTGGAGATGATGGAGTTCACCAAGAAATTCGACATAGACCTGGCTTCTTTGATACTCCCGGTGGC  
ACCGTGAACGGTCAAGACGAGTATAAAGCAGACATTGTGATGTATACGAAAACAGTATTTGGAACTCCAGACACGCATGT  
GGTATACAAACCAGGCAAGGATGATGCAAGTTCTGAAATTAACCTGGTTGAGCAGTCTATGCCAACAGACCCAACTACATTG  
GGTTCAGGGACAATTTATCGGTCTTATGTACTACAACAGCACTGGCAATATGGGTGTGCTTGTGGTCAAGGCTCCAGCTGA  
ATGCTGTGGTTGATTTGCAAGACAGAAACACCGAGCTGTCTACAGCTCTTGCTGACTCTTGGGTGACAGAACCCGGTATT  
TCAGTATGTGGAACAGGCGGTGGACAGTTATGACCCGATGTGCGCATATCGAAAACCATGGTGTGGAGGATGAATTGCC  
AACTATTGCTTCCCTTGGACGGCTCTGGCACTAACCGCGCATACCAAGGTGTGAAAGTAAAGATGGTCAAGATGGTGATG

TTGAGAGTGAATGGGAAATGACGATACTGTTGCAGCTCGAAATCAATTATGTAAGAGTAACATTTTCGCCATGGAGATTAAT  
CTCCAGGCTAACCTGTGGAGAAGTTTCTCTACTCGAACGTGGCCCTGTACCTGCCGACTCTACAAGTACACGCCGACCAAC  
GTACAGCTGCCGACCAACACCAACACCTACGATTACATGAATGGCAGAGTGACACCTCCCTCGCTGGTAGACGCCTACCTCAAC  
ATCGGGGCGCGCTGGTTCGCTGGACCCCATGGACAACGTCAACCCCTTCAACCACCACCGCAACGCGGGCCTGCGCTACCGCTC  
CATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCAAAAGTTTTCGCCATCAAGAGCCTCTGCTCCT  
GCCCCGGTCTACACCTACGAGTGGAACCTCCGCAAGGACGTCAACATGATCCTGCAGAGCTCCTAGGCAACGACCTGCGCA  
CGGACGGGGCCTCCATCGCTTACCAGCATCAACCTCTACGCCACCTTCTTCCCATGGGCGACAACACCGCCTCCACGCTCG  
AGGCCATGCTGCGCAACGACACCAACGACCAAGTCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCA  
ACGCCACCAACGTGCCCATCTCCATCCCCTCGCGCAACTGGGCGCGCTTCCGCGGATGGTCTTACGCGCCTGAAGACCCGCG  
AGACGCCCTCGCTCGGCTCCGGGTTGACCCCTACTTCGTCTACTCGGGCTCCATCCCCTACCTAGACGGCACCTTCTACCTCAA  
CCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTGAGCTGGCCCGGCAACGACCGCCTCTGACGCCCAACGAGTT  
CGAAATCAAGCGCACCGTCGACGGAGAGGGATAACAACGTGGCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATG  
CTGGCCCACTACAACATCGGCTACCAGGGCTTCTACGTGCCGAGGGCTACAAGGACCGCATGTACTCCTTCTCCGCAACTTC  
CAGCCCATGAGCCGCCAGGTCTGGACGAGGTCAACTACAAGGACTACCAGGCCGTACCCCTGGCTACCAGCACAACAACCTC  
GGGCTTCGTGGCTACCTCGCGCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAATAACCCCTACCCGCTCATCGGCAAGA  
GCGCCGTGCGCAGCGTACCCAGAAAAAGTTCTCTGCGACCGGGTCATGTGGCGCATCCCTTCTCCAGCAACTTCATGTCCA  
TGGGCGCGCTCACCGACCTCGGCCAGAACATGCTCTACGCCAACTCCGCCACGCGCTAGACATGAATTCGAAGTCGACCCC  
ATGGATGAGTCCACCTTCTCTATGTTGTCTTGAAGTCTTCGACGTCGTCCGAGTGCAACGACCCACCGCGCGTCATCGAA  
GCCGTCTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACCACTAAGCCGCTTGTCTTCTGCAAGATGACGGCGGGCTCC  
GGCGAGCAGGAGCTCAGGGCCATCTCCGCGACCTGGGCTGCGGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCCCTG  
GATTCATGGCCCCGACAAGCTGGCCTGCGCCATCGTGAACACGCGCCGGCCGCGAGACCGGGGGCGAGCACTGGCTGGCCTT  
CGCTGGAACCCGCGCTCCACACATGCTACCTTCTGACCCCTTTCGGGTTCTCGGACGAGCGCTCAAGCAGATCTACCAGTT  
CGAGTACGAGGGCCTGCTGCGTCGACGCGCCCTGCCACCGAGGACCGCTGCGTCACCTGGAAAAGTCCACCCAGACCGTG  
CAGGGTCCGCGCTCGGCCGCTGCGGGCTTCTGCTGCATGTTCTGTCACGCTTCTGTCAGTGGCCGACCGCCCCATGGAC  
AAGAACCCACCATGAACTTACTGACGGGGTGCCCAACGGCATGCTCCAGTCGCCCCAGGTGGAACCCACCTGCGCCGCAA  
CCAGGAAGCGCTTACCCTTCTCAATGCCACTCCGCTACTTTCGCTCCACCGCGCGCATCGAGAAGGCCACCGCCTT  
TGACCGCATGAATCAAGACATGTAAAAAACCGTGTGTGTATGTGAATGCTTTATTATAATAAACAGCACATGTTTATGCCAC  
CTTCTCTGAGGCTCTGACTTTATTTAGAAATCGAAGGGGTTCTGCCGGCTCTCGGCATGGCCCGCGGGCAGGGATACGTTGCG  
GAACTGGTACTTGGGCAGCACTTGAACCTCGGGATCAGCAGCTTGGGCACGGGGAGGTTCGGGGAACGAGTCGCTCCACAG  
CTTGCGCGTGAGTTGCAGGGCGCCAGCAGGTGCGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCTGCGCGCGA  
GAGTTGCGGTACACGGGGTTCAGCACTGGAACACCATCAGGGCCGGGTGCTTACGCTTGCAGACACCGTCGCGTCGGTGA  
TGCCCTCCACGTCCAGATCCTCGGCGTTGGCCATCCCGAAGGGGGTCATCTGCAGGTCTGCCGCCCCATGCTGGGCACGCG  
CCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGGCCTGCTCGGAGCTCATGCCCGGGTACATGGCCTT  
CATGAAAGCCTCCAGCTGGCGGAAGGCCTGCTGCGCCTTGCCGCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGAGAAC  
TGTTGGTGGCGCAGCCGGCGTCTGTCACGCAGCAGCGCGCTGTTGTTGGCCAGCTGCACCACGCTGCGCCCCACGCGGT  
TCTGGGTGATCTTGGCCCGTTGGGGTTCTCTTACGCGCGCTGCCGTTCTCGCTGCCACATCCATCTCGATAGTGTGCT  
CCTTCTGGATCATCACGGTCCCGTGCAGGCACCGCAGCTTGCCCTCGGCTTCGGTGCAGCCGTGCAGCCACAGCGCGCAGCCG  
GTGCACTCCAGTTCTTGTGGGCGATCTGGGAGTGCAGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATCGGGTCAGGG  
TCTTGTGCTGGTGAAGGTGAGCGGGATGCCGCGGTGCTCCTCGTTACATACAGGTGGCAGATGCGGCGGTACACCTCGCCC  
TGCTCGGGCATCAGCTGGAAGGCGGACTTCAGGTGCTCTCCACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCCATGCC  
CTTCTCCAGGCCGAAACGATCGGCAGGCTCAGGGGGTTCTTACCGCCATTGTCATCTTAGTCGCCGCGCCGAGGTGAGGG  
GGTGTCTCGTCCAGGGTCTAAACACTCGCTTGCCGTCTTCTCGATGATGCGCACGGGGGGAAAGCTGAAGCCCACGGCC  
GCCAGTCTCCTCGGCTGCTTTCGTCTCGCTGTCTGGCTGATGCTTGCAAAAGGCACATGCTTGGTCTTGGGGGTTTCT  
TTTTGGGCGGCAGAGGCGGCGCGATGTGCTGGGAGAGCGGAGTTCTCGTTACCACGACTATTTCTTCTTGGCCGTGCG  
TCCGAGACCACGCGGCGGTAGGCATGCTTCTGGGGCAGAGGCGGAGGCGACGGGCTCTCGCGGTTGGGCGGGCGGCTG  
GCAGAGCCCTTCCGCGTTCCGGGGTGCGCTCTGGCGGCGCTGCTCTGACTGACTTCTCCGCGGCGCGCCATTGTGTTCTCC  
TAGGGAGCAACAACAAGCATGGAGACTCAGCCATCGTCGCCAACATCGCCATCTGCCCCCGCGCCACCGCCGACGAGAACCA  
GCAGCAGAATGAAAGCTTAACCGCCCCGCGCCACGCCACCTCCGACGCGCGGCCCCAGACATGCAAGAGATGGAGGAA  
TCCATCGAGATTGACCTGGGCTACGTGACGCGCGGAGCACGAGGAGGAGCTGGCAGCGCGCTTTTCAGCCCCGGAAGAGA  
ACCACCAAGAGCAGCCAGAGCAGGAAGCAGAGAACGAGCAGAACCAGGCTGGGCACGAGCATGGCGACTACCTGAGCGGG  
GCAGAGGACGTGCTCATCAAGCATCTGGCCCGCAATGCATCATCGTCAAGGACGCGCTGCTCGACCGCGCGGAGGTGCCCT

Fig. 24G

CAGCGTGGCGGAGCTCAGCCGCGCCTACGAGCGCAACCTCTTCTGCGCGCGTGCCCCCAAGCGCCAGCCCAACGGCACCT  
GTGAGCCCAACCCGCGCTCAACTTCTACCCGGTCTTTCGCGGTGCCCCGAGGCCCTGGCCACCTACCACCTCTTTTTCAAGAACC  
AAAGGATCCCCGTCTCTGCGCGCCAACCGCACCCGCGCGGACGCCCTGCTCAACCTGGGCCCCGGCGCCCCGCTACCTGAT  
ATCACCTCCTTGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGCAGCGACGAGACTCGGGCCGGAACGCTCTGCAAGGAA  
GCGGAGAGGAGCATGAGCACCACAGCGCCTGGTGGAGTTGGAAGGCGACAACGCGCGCCTGGCGGTCTCAAGCGCACGG  
TCGAGCTGACCCACTTCGCTACCCGGCGCTCAACCTGCCCCCAAGGTATGAGCGCGTCATGGACCAGGTGCTCATCAAG  
CGCGCCTCGCCCTCTCGGAGGAGGAGATGCAGGACCCCGAGAGTTCGGACGAGGGCAAGCCCGTGGTCAGCGACGAGCAG  
CTGGCGCGCTGGCTGGGAGCGAGTAGCACCCCCAGAGCCTGGAAGAGCGGCGCAAGCTCATGATGGCCGTGGTCTGGTG  
ACCGTGGAGCTGGAGTGTCTGCGCCGCTTCTTTCGCGACGCGGAGACCCTGCGCAAGGTGAGGAGAACCTGCACTACCTCTT  
CAGGCACGGGTTCTGTGCGCCAGGCCTGCAAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCCTACATGGGCATCTGCAAG  
AGAACCGCCTGGGGCAAAACGTGCTGCACACCACCTGCGCGGGGAGGCCCGCCGCGACTACATCCGCGACTGCGTCTACCT  
GTACCTCTGCCACACCTGGCAGACGGGCATGGGCGTGTGGCAGCAGTGCCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAA  
GCTCCTGCAGAAGAACCTCAAGGCCCTGTGGACCGGGTTCGACGAGCGTACCACCGCCTCGGACCTGGCCGACCTCATCTTCC  
CCGAGCGCCTGCGGCTGACGCTGCGCAACGGGTGCCCCGACTTATGAGCCAAAGCATGTTGCAAACTTTTCGCTCTTTCATCC  
TCGAACGCTCCGGGATCTGCCCCGACCTGCTCCGCGCTGCCCTCGGACTTCGTGCGCGTGACCTTCGCGAGTGCCCCCGC  
CGCTCTGGAGCCACTGCTACTTGTGCGCCTGGCCAACTACCTGGCCTACCACTCGGACGTGATCGAGGACGTGAGCGGCGAG  
GGTCTGCTGGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGAGCGAGAC  
CCAGATCATCGGCACCTTCGAGTTGCAAGGCCCGGCGACGCGGAGGGCAAGGGGGTCTGAAACTACCCCGGGGCTGTG  
GACCTCGGCCTACTTTCGCAAGTTCGTGCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCCAGCCGCC  
CAAGGCCGAGCTGTGGCCTGCGTCATCACCCAGGGGGCCATCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAAT  
TTCTGCTGAAAAAGGGCCACGGGTCTACTTGGACCCCCAGACCGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCGG  
AGGAAGCAGCAAGAAGCTGAAAGTGGAGCTGCCGCCCGGAGGATTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGG  
AGGAGGAGATGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAGGAAGACGAGGT  
GGAGGAGGAGAGGAAGAAGCAGCCGCCGAGACCGTCTGCTCCTGCGCGGAGAAAGCAAGCAGCAGGATACCATCTCCGC  
TCCGGGTGCGGGTTCGCGCGGCCGGGCCACAGTAGGTGGGACGAGACCGGGCGCTTCCCGAACCCACCCAGACCGG  
TAAGAAGGAGCGGCAGGGATACAAGTCTGGCGGGGGCACAAAACGCCATCGTCTCCTGCTTGAAGCCTGCGGGGGCAA  
CATCTCCTTACCCGGCGTACCTGCTTCCACCGCGGGGTGAACCTCCCCGCAACATCTTGCACTTACTACCGTCACCTCCAC  
AGCCCTACTACTGTTTCAAGAAGAGGCAGAAACCCAGCAGCAGCAGAAACCAGCGGCAGCAGCAGCTAGAAAAATCCACA  
GCGGCGGACAGTGGACTGAGGATCGCGGCGAACGAGCCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTTCCACCCCTC  
TATGCCATCTTCCAGCAGAGTCGGGGGACAGGAGCAGGAACTGAAAGTCAAGAACCGTTCTGCGCTCGCTACCCGCAAGTTG  
TCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTTCAACAAGTACTGCGCGTCACTCT  
TAAAGAGTAGCCCGCGCCGCCACACAGGAAAAAGGCGGAATTACGTACCCACCTGCGCCCTTCGCCGACCATCATGAG  
CAAAGAGATTCCACGCTTACATGTGGAGCTACCAGCCCCAGATGGGCTGGCCGCCGCGCGCCGAGGACTACTCCACCC  
GCATGAACTGGCTCAGTGCCGGGCCGCGATGATCTACGGGTGAATGACATCCGCGCCACCGAAACAGATACTCTAGAA  
CAGTCAGCGATACCGCCACGCCCGCATCACCTTAATCCGCGTAATTGGCCCGCGCCCTGGTGTACCAGGAAATCCCCAG  
CCCACGACCGTACTACTTCCGCGAGACGCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCCGGCGGCGCCG  
CCTGTGTCGTACCCGCCCGCTCAGGGTATAAAGCGGCTGGTGATCCGAGGCAGAGGCACACAGCTCAACGACGAGGTGGTG  
AGCTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCAACTCGCCGATCGGGGAGATCTTCCTTACGCCTCGTCAGGCCGTC  
CTGACTTTGGAGAGTTCGTCTCGCAGCCCCGCTCGGGCGGCATCGGCACTCTCCAGTTCGTGGAGGAGTTCACTCCCTCGGTC  
TACTTCAACCCCTTCTCCGGCTCCCCCGCCACTACCCGACGAGTTCATCCCGAACTTCGACGCCATCAGCGAGTCGGTGGAC  
GGCTACGATTGAATGTCCCATGGTGGCGCAGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTC  
GCTCGGGATCTCGCCGAGTTTGCTACTTTGAGCTGCCCGAGGAGCACCTCAGGGCCAGCCACGGAGTGCGGATCATCGT  
CGAAGGGGGCCTCGACTCCACCTGCTTCGGATCTTCAGCCAGCGACCGATCCTGGTCGAGCGCGAACAAGGACAGACCCTTC  
TTACTTTGACTGCATCTGCAACACCCCGCCTGCATGAAAGTCTTTGTTGTCTGCTGTGACTGAGTATAATAAAGCTGAGA  
TCAGCGACTACTCCGACTCGATTGTGGTGTCTGCTATCAACCGGTCCCTGTTCTTACCGGGAACGAGACCGAGCTCCAGC  
TCCAGTGTAAGCCCCACAAGAAGTACCTACCTGGTGTTCAGGGTCCCCGATCGCCGTTGTCAACCACTGCGACAACGAC  
GGAGTCTGCTGAGCGGCCCTGCCAACCTTACTTTTCCACCCGAGAAGCAAGCTCCAGCTCTTCAACCTTCTCCCCGGG  
ACCTATCAGTGCGTCTCAGGACCTGCCATCACACCTTCCACCTGATCCCGAATACCACAGCGCCGCTCCCCGCTACTAACAACC  
AACTACCCACCAACGCCACCGTCGCGACCTTCTCTGAATCTAATACCACTACCGGAGGTGGCTTCTGCTGTAGTGCTCCCC  
CGTCCCGTCGACCCCGGTCCCCACTCAGTCCCCGAGGAGGTTGCAAATGCAAATCCAAGAACCCTGGAAATTCCTCAAA  
TGCTACCGCCAAAAATCAGACATGCATCCAGCTGGATCATGATCATTGGGATCGTGAACATTCTGGCTGCACCTCATCTCC



Fig. 24H

TTTGTGATTACCCCTGCTTTGACTTTGGTTGGAACCTCGCCAGAGGCGCTCTATCTCCCGCTGAACCTGACACACCACCACAGC  
AGCAACCTCAGGCACACGCACTACCACCACCACAGCCTAGGCCACAATACATGCCCATATTAGACTATGAGGCCGAGCCACAG  
CGACCATGCTCCCGCTATTAGTTACTTCAATCTAACCGGCGGAGATGACTGACCACTGGCCAATAACAACGTCAACGACCT  
TCTCTGGACATGGACGGCCGCGCTCGGAGCAGCGACTCGCCCACTTCGCATTCTGTCAGCAGCAGGAGAGAGCCGTCAAG  
GAGCTGCAGGACGGCATAGCCATCCACCAGTGCAAGAGAGGCATCTTCTGCCTGGTGAACAGGCCAAGATCTCTACGAGG  
TCACCCAGACCGACCATCGCCTCTCTACGAGCTCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTGGAGTCAACCCCATCG  
TCATCACCAGCAGTGGGGGATACCAAGGGGTGCATCCACTGCTCTGCGACTCCCCGACTGCGTCCACACTCTGATCAAGA  
CCCTCTGCGGCTCCGCGACCTCTCCCATGAACATAACCCCCCTTATCCAGTGAAATAAAGATCATATTGATGATTGATTTAA  
ATAAAAAAATAATCATTGATTGAAATAAAGATACAATCATATTGATGATTGAGTTTAAACAAAAATAAAGAATCACTTACTT  
GAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACCTCACTCCCCTCTCCAGCTCTGGTACTGCAGGCCCGG  
CGGGTGCAAACTTCTCCACACGCTGAAGGGGATGTCAAATTCCTCTGTCCCTCAATCTTCATTTTATCTTATCAGATGTC  
CAAAAAGCGCTCCGGTGGATGATGACTTCGACCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCTTCATCA  
ACCCCTCTCGTCTCTCAGATGGATTCCAAGAGAAGCCCTGGGGGTGTTGTCCCTGCGACTGGTGCACCCGTCAACCCA  
AGAACGGGGAATCACCCTCAAGCTGGGAGAGGGGGTGGACCTCGACTCGTGGGAAAACTCATCTCAACACGGCCACCA  
GGCGGCGCCCTCCTCAGTATTTCAAACAACACCATTTCCCTTAAAACTGCTGCCCTTTCTACAACAACATGAACTTTAAAG  
CTCAATGTCTCCACAGTATAGCAGTATTTCCACATTTAACACTTTAGGCATAAGTCTTGGAAACGGTCTTGCAGACTTCAAATA  
AGTTGTTGACTGTACAATACTCATCTCTTACATTGAGTCAAAATGATCAGTAAACAGACAGAAAGGGCTATATATTA  
ACTCCAGTGGAACAGAGGACTTGAGGCTAATATAAGCCTAAAAAGAGGACTAGTTTTGACGGTAATGCTATTGCAACATAT  
ATTGGAATGGCTTAGACTATGGATCTTATGATAGTGATGGAACAAAGACCCGTAATTACCAAAATTGGAGCAGGATTAAA  
TTTTGATGCTAACAAAGCAATAGCTGTCAAACAGGACAGGTTTAAAGTTTGACTCCGCTGGTGCCTTGACAGCTGGAAACAA  
ACAGGATGACAAGCTAACACTTTGGACTACCCCTGACCAAGCCCTAATTGTCAATTACTTTCAGACAGAGATGCCAAATTTAC  
TCTGTCTTACAAAATGCGTAGTCAAATACTAGGCACTGTGGCAGTGGCGGCTGTTACTGTAGGATCAGCACTAAATCCAA  
TAATGACACAGTCAAAAGCGCCATAGTTTTCTTAGATTGATTCGATGGTGTACTCATGTCAAACATCATCAATGGTAGGTGA  
TTACTGGAATTTAGGGAGGGACAGACCACTCAAAGTGTAGCCTATACAAATGCTGTGGGATTCATGCCAAATATAGGTGCAT  
ATCAAAAACCCAAAGTAAACACCTAAAAATAGCATAGTCAGTCAGGTATATTTAACTGGAGAACTACTATGCCAATGACA  
CTAACCATAACTTTCAATGGCACTGATGAAAAAGACACAACCCCAAGTTAGCACCTACTCTATGACTTTTACATGGCAGTGGACT  
GGAGACTATAAGGACAAAAATATTACCTTTGCTACCAACTCATTTCTTTTCTACATCGCCAGGAATAATCCCACCCAGCAA  
GCCAACCCCTTTTCCACCACCTTTGCTATATGGAACCTGAAACAGAAAAATAAAGTTCAAGTGTATTATTGAATCAACAGT  
TTTACAGGACTCGAGCAGTTATTTTTCTCCACCCTCCAGGACATGGAATACACCACCCTCTCCCCCGCAGCAGCTTGAACAT  
CTGAATGCCATTGGTGATGACATGCTTTTGGTCTCCAGTTCCACAGTTTCAGAGCGAGCGTCTCGGATCGGTGATCGGTGAGG  
AGATGAAACCTCCGGGCACTCCGCTCTGCACCTCACAGCTCAACAGCTGAGGATTGTCTCGGTGGTGGGATCACGGTT  
ATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATCATAGTCCGCGAACGGGATCGGCGGCTGGTGTGCGATCAGGCCCGCA  
GCAGTCGCTGCCGCGCGCTCCGTCAAGCTGCTGCTCAGGGGTTTCGGGTCCAGGGACTCCCTCAGCATGATGCCACGGCC  
CTCAGCATAGTCGTCTGGTGGCGGGCGGCGCAGCAGCGCATGCGAATCTCGCTCAGGTCACTGCAGTACGTGCAACACAGGA  
CCACCAGGTTGTTCAACAGTCCATAGTTCAACACGCTCCAGCCGAACTCATCGCGGAAGGATGCTACCCACGTGGCGCTCG  
TACCAGATCTCAGTAAATCAAGTGGCGTCCCTCAGAAGACGTCGCCATGTACATGATCTCTTGGGCATGTCGCGGTTT  
ACCACCTCCCGGTACCACATCCCTCTGGTTGAACATGCAGCCCGGATGATCCTGCGGAACACAGGGCCAGCAGCCCTC  
GCCCGCATGCAGCGAAGAGACCCCGATCCCGCAATGACAATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAG  
CTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTCTCAGCACTCTCAGTCTCTCGGGGTCAAAACCAT  
TCCAGGGGCAGGGGAATCTTGCAGGACAGCGAACCCCGCAGAACAGGGCAATCCTCGCACATAACTTACATTGTGCATGG  
ACAGGGTATCGCAATCAGGCAGCACCGGGTATCTCCACCAGAGAAGCGCGGTCTCGGTCTCTCACAGCGTGGTAAGGG  
GGCGGGCGGATACGGGTGATGGCGGGACGCGGTGATCGTGTCTCGACCGTGTGATGATGCAAGTGTCTTCGGACATTTTCG  
TACTTGCTAGCAGAACTGTGTCGGGCGCTGCACACAGTATCGCGCGGCGGTCTCGGCGCTTGGAACGCTGAGTGTAA  
AGTTGTAAAACAGCCACTCTCTCAGACCGTGCAGCAGTCTAGGGCTCAGGAGTGATGAAGATCCCATGCTCATGCTGATGCT  
CTGATCAGATCGACCACTGGAATGGGCCAGGCCAGATGATGCAATTTTGTGGTTCGGTGACGGCGGGGAGG  
GAAGAACAGGAAGAACCATGATTAACCTTTAATCCAACGGTCTCGGAGCACTTCAAATGAAGGTACGGAGATGGCACCTC  
TCGCCCCGCTGTGTTGGTGGAAAAAAGCAGCCAGGTCAAAGGTGATACGGTCTCGAGATGTTCCACGGTGGCTCCAGCAA  
AGCCTCCACGCGCACATCCAGAAACAAGACAATAGCGAAAGCGGGAGGGTCTCTAATTCTCAACCATCATGTTACACTCTG  
CACCATCCCCAGATAATTTTCAATTTTCCAGCCTTGAATGATTCGAAGTCTCTGAGGTAATCCAAGCCAGCCATGATAAAA  
AGCTCGCGCAGAGCACCTCCACCGGCATTCTTAAGCACACCTCATAATTCAGATATTCTGCTCTGGTTACCTGCGCA  
GATTGACAAGCGGAATATCAAAATCTCTGCGCGATCCCTGACTCTCCCTCAGCAATAACTGTAAGTACTCTTTCATATCGTC  
TCCGAAATTTTATGCCATAGGACCCCAAGGAATAAGAGAAGGGCAAGCCACATTACAGATAAACCGAAGTCCCCCAGTGAG  
CATTGCCAAATGTAAGATTGAAATAAGCATGCTGGCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAAAATCGGGTAAG  
CAATTTTTAAGAAAATCAACAAAAGAAAAATCTTCCAGGTGCACGTTTAGGGCTCGGGAACAACGATGGAGTAAGTGAAG  
GGGTGCGTTCAGCATGTTAGTTAGCTGATCTGTAAAAAACAATAAATCAATTAACCATGCTAGCCTGGCGAACAGG  
TGGGTAAATCGTTCTCCAGCACAGGCAGGCCACGGGTCTCCGGCGCGACCTCGTAAAAATTGTGCTATGATTGAAAA  
CCATCAGAGAGAGACTTCCGGTGGCGGCGTGAATGATTGAGAAGAACATACACCCCGGAACATAGGAGTCCGTGAG  
TGAAAAAAGCGCGGAGGAAGCAATGAGGCATAACACGCTCACTCAAGTCCAGCAAGCGATGCCATGCGGATGAAGC  
ACAAAATTTTCAAGTGCGTAAAAAATGTAATTACTCCCCTCTGCACAGGCAGCGAAGCTCCCGATCCCTCCAGATACACATAC  
AAAGCCTCAGCGTCCATAGCTTACCAGCGGCAGCAGCAGCGGCACACAACAGGCGCAAGAGTCAGAGAAAAGACTGAGCT  
CTAACCTGTCCGCGCTCTCTGCTCAATATATAGCCCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAA  
ATAATCACACACGCCCAGCACACGCCCAGAAACCGGTGACACACTCAGAAAAATACGCGCACTTCTCAAACGGCCAACTGC  
CGTCAATTTCCGGGTCCACGCTACGTATCAAAACACGACTTTCAAATTCGTCGACCGTTAAAAACATACCCGCCCCGCCC  
TAACGGTCCGCGCTCCGCGAGCAATACCTTCTCCCTCCCAAAATCAAACAGCTCATTTGCATATTAACGCGCACCAAAAGT  
TTGAGGTATATTATTGATGATG



Fig. 24I

**AdC6 020-DU172gp160(E1620) Amino acids – SEQ ID NO: 13****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVICGSGDR\*GRGG\*RFDDVAMRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFL  
 GGCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDRLRGGFDYRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RLRS  
 PDPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMKNLLRVRRFALLRDVRARYTR\*H\*LLTSMPTPIDVN  
 DGKWPAPWHYAQYMTLWDFPTWQYIYVLVIAITMVMRWFQYINGRG\*RFDSRGFPSLHPIDVNGSLFWHQNRDFPKCRNNSA  
 PLTQMGGRRVRWEVYISRARLVNRQITRSFIADVYHS\*IANAVSASDTSVNLRLLEYLIRLTIG\*LRLEFDATMRVMGILRSYQQWWI  
 WGILGFWMMLICNVWGNLWVTVYGVVWKEAKTTLFCASDAKAHKEEVHNIWATHACVPTDPPNPQEIIVLKNVTENFNMWK  
 NDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLNCSVDKIKGTNATYNNATYNNNNNTISDMKNCSFNNTTEITDKKKKEYALFYKLDV  
 VALDGKETNSTNSSEYRLINCNTSAVTQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCNNVSTVQCTHGKPKVVSTQLLNG  
 SLAEVEVIRFENLTNNAKIIIVHLNESVEINCTRPSNTRKSVRIGPGQTFATGDIIGDIRQAHCNISRKKWNTTLQRVKEKLEKEFPN  
 KTIQFAPSSGGDLEITTHSFNCRGEFFCYTDLFNSTYMSNNTGGANITLQCRIKQIIRMWQGVQAMYPPIAGNITCKSNITGLL  
 LTRDGGKEKNDTETFRPGGDMRDNRSELYKYKVVEIKPLGIAPDKAKRRVVEREKRAVGIGAVFLGFLGAAGSTMGAASMTLT  
 VQARQLLSGIVQQSNLLRAIEAQQHMLQLTVWGIKQLQTRVLAIERLYKDDQLLGIWGCSGKLICTTAVPWNASWSNKSYYEIIW  
 GNMWTWMQWDREINNYNTIYSLLEESQNQKEKNEKDLLALDSWESLWSWFNITNWLWYIRIFIIIVGGGLIGLRIIFAVLSIVNRVRQ  
 GYSPLSFQTLTPSPREPDRLGRIEEEGGEQDRARSVRLVNGFLALAWEDLRSLCLFSYHRLRDLILIAARAAALLGRSSLWGLQKGWE  
 ALKYLGLSVQYWGLELKKSAISLDAITVAEGTDRIINIVQRISAFYNIPRRIRQGFEATLQ\*GTSRVDPPGGQTADQPRCLLVASHL  
 LFAPPPCLP\*PWKVPLPSFPNKMRLHRIV\*VGVILFWGVGWGRTARGRIGKTIAGMLGMRWALWLLRRKEPADLQI\*IHLCRVR  
 RKR\*\*NGIMGIMGLH\*\*IGQISTYAGHRACGLAPPQDMARVRAQRHDPLQCAPGLPPRHVHALPVQHAICEGAAGARCHVQSEP  
 DGGV\*HECGAVENSEI\*\*IQDQVPGLMRMRQARQASARVCGGDGGPATRSFGVVLQRDGVRLQRGRI\*LE\*VVFAGCEPA\*GA  
 E\*LKSVMFCVLQQHERKRL\*GRGIQPLSDGASPLLGSSASECDGIHGGPARAAARELFNPDLRDPELLVRGRSCRRSCCFRRQRAR  
 NGPGRRLQLSGGQLEFHQ\*SRQPERGEAAAADGPARGPDAPGRADPAGGSAAGGDAGRGCHGENQIKNESINKRRRLILTQS  
 LESLDFDSRAVGPVPPVSIIEHPVDLFQDPVEVGLDVEVHGHEPVPVGEVAPLQGLVLGDGVVNHPIAGAQQVVLHDVLEEETDG  
 HGQPLGVGVDEPVELGGMHAGGDEMHLGLDLEIGDVPQIPPGVHVVDQHQHGVSGALGEFVMQLGREGVKEFGDALVTAQV  
 FHAIHDDGDGPVGGGLGKDVSGVGHIVVVVLGELVIGHFNEFGAEGARLGDEGALDPGGVALADLHLPGLLEGGGDHVLHGRD  
 EKNGFRGGGDELGRKQVPEQLGLAATGGAVDDPDDRLQVVEGETAAVLAEEGGHLVHHLAHMHVLAHEFRQEALAPQRELL  
 QRGEVFQRLESVGHGHFGEGLLQEFQTVPELGDVL\*GISIQQTSSFRGLGRLE\*GTRRWASSEARVRSFQGRVRVSVSVTVKGC  
 APGWALARVRFRILRLVENRRSAPCASAR\*QLSMSS\*LSASAAWPLARSLPLEVCPQTGQRRDLRA\*SLGARKTDSGA\*ASAPQLA  
 QTVSHSTSQVRSRGLSGKTRFPFCFLMRFLPLVSMSSCPRWVTKRLSVSP\*TDFMGRSSSGVPRSSS\*RNPAHSETKARVQASTKEA  
 TWEG\*RLSTSGSTFSRVCKHMSPTSRSKVIQL\*V\*AT\*PGVPAGGV\*KGAGPCSSSLSSGSLRSASCWGYSLSKAGMTSALRLS  
 VSRNEEDLITVPLETFMSPSSIWSEKTIFLLSSLVAKEP\*RALESSLAMERMVWFFSLSARSLAAMLSCITYSRATHFHSKTVVSSSG  
 TILTRQPRLCRVMRSTLVATSPRRGSLVQRRPPLREKQGGSGSSMSSSGSASTVKMPGRSSGSK\*LMQVPRLSAACQSRTASA  
 RS\*GLRGVPQGMGCVSAEAYMPQMS\*T\*RGSSRTPM\*VG\*QRPPRMLART\*SYSSCEGARSPVRLERCGRFSAR\*TIWRKMAW  
 ELEEMVGLWKMMLKAWWGRPTESLMKWA\*ESCSLATSSAVTRTSRAQ\*SRVSWMMSYLSWPFCHSSRLRRNSSRSFQYSSRGN  
 PS\*SAR\*EPTM\*NWLTAL\*AQQPFSTGRA\*ACAALREVWVRKVSRTMTLRNWCLKSRSSQPPCSQSWKSVRLF\*AGLGKAKVT  
 SLKRILPARGMKLRVMRKGWGT SARLLMTWAARTISSKPLMLCPTM\*SSTNRGRPLTWGSFLSSS\*VSSAGSLSPCCSRAQSATW  
 GLALRKEVQRSTARAVCKRSRY\*RNCWPTAIFSGVTQ\*KVRGSPCQRSHLSWRARSWASSTSGGSPESFMTSMKGTSCLPKDPQIV  
 \*VSTS\*VRKSLSVRGCEPMGKNWISCHQLEEWLLM\*WK\*KCRRRAEHSCCLYKRPQCSQRTGCTCCTSTWVPLARNFSGQW  
 SAGGCISCCTTSWPSAWPSSASMVVMVLTSPRGRQVQTSARTGRRARTRARRPELSRVLRRCGVRSVSGGARLTCRSFSRARGRSR  
 WYLISTAPLVATSTACRVPCPWGATTVPFRFLGAASMSVRSGGEDARRAAGAARGPEAGAAGARRRRARAGSGTAPGEDWRERR  
 RDG\*RPGSDASG\*RPRDP\*V\*T\*KRVQRNQSRYSR\*RRPAAGSLARRPSCPGRRRSR\*TARSPPEGLRGRARRRWPRGRWRGCP\*  
 AARRRSCRPRSRRGCRPLRRGRARA\*PPGRG\*ARRGA\*RPRSCRAGAGRS\*AWWRCAR\*RRST\*SSGGAASR\*RRPGLPSVPW  
 PRRSPRRS\*KTGSCAPRRSTPPPEDG\*ARRWWRAPRARRPRGAPLPSPLPPPLTSLLLPPQEAVAGEGPCVAGGARADGR\*SAR  
 WSPRAGDAWSR\*RRARPRGAAA\*RRRRASPGGRRGGLRWAGRGR\*RCILSIDP\*GLRART\*ASRDPRDPKTAERRLRASRSKVG  
 \*ARFLVLRVFGREAGGCCW\*\*S\*SRRS\*DGGWWRGAPGPWARLAGCADGRPCPRRGPDTWRGPCSSPA\*AAPRAPPPRPRGR  
 ACA\*ARTAAAGRAPGRRRRAR\*GWPAAGSG\*GWSGSRSSRSRSGRLRC\*WCRSSWP\*RTS\*RSGRVARARGT\*GASRRACRR  
 CSRCRRARGTGIRRGSAAGGAAIARWRGRRRARGPRA\*GGGSRRCTWTSR\*CRRRWWRAGTRGRGRSCAAAGSSSWWP  
 RSGP\*GARSRGCSRHTGKNESGQRLDSVAWRLSERVGLRVYPGNSLESWSRS\*RGTTGPVSTQAC\*RNLDQTEAGRFLALVAGH  
 EKLVAESGRPRWLAAVWVRKNRQGCVAVCPGSSLSARRRPDAAANVGVAAPSFRPLSQPTSPVTERAPLFFSCVFARCIYCGRC  
 APTLHHRNPYRSSNSRRFCPRPSSSQPLRRPP\*AEPAFSMTWPWKRRARGWRGWGRRRRSGTRACR\*KGTLARPTCPSRTCSET

Fig. 24J

GAARSPRRCAPASTRGGSCGAAWTESGC\*GTRISRRTS\*RGSA PRARTWPRPTWSRRTSRP\*RRRATSKNPSTTT CAR\*SRARR\*  
PWA\*CTCGTCWRPSCRTPRASR\*RRSCFWWCSTVGTTRRSGRRC\*ISPSRAAGSWTW\*TFCRASWCRSAGCRCPSRWRPSTSR  
C\*VWASTTLGRSTRPTCP\*TRR\*STGFTCA\*P\*KC\*P\*ATIWGCTATTGCTAR\*APAAGAS\*ATRS\*CTACSGP\*PGPGPRGRAT  
LTWARTCAGSPAAGPWKLPVPPTWRRWTMRRRRASTWKTDGATVFLDAAATATAAAS\*SRDAGGAAEPAVRH\*LLGRDLP GH  
ATHHGADD PQSRL\*TAASGQPALGHPGGRGALALEPHAREGAGHRERAGGEQGHPR\*RGRAGVQRAAGARGPLQHQHRADE  
PGPHGD RRARGGVAARAVPPRVEPGLHGGAERLPEHAARQAPGPGGLHLHQRAAADGGRGAPERGVVPGAGLLLPDQSPGL  
ADREPEPGFQELAGTVGRAGPGRGPRDGV EPADAELAPAAAAGGALHGQRQREPRLPGLPA\*PVPRGHRTGARGRADLP GDH  
PREPRAGPGGPGQPGGHP ELPADQPVAEDPAPVRAEHRGGAHPALRAAERGAVPDAGGGHQAQRGARHDRAQHGAAQHV RPQP  
PVHQ\*ADGLLASGGRHELGLLYQRHLEPALAPAARVLHGRVRHARPQRRVPVGRRGQQRVLAASRNQCRVEERGRGPAAVLGAV  
RSRGCCRGGARGRQPLPEPALFAEQRAQQRAGSADATAPAGRGGVPERLLVEARAREELPQ\*RDREPGGQDEPLEDV RARAQGR  
APS\*QRRHP\*TPAARQAAGTGVR\*GFRRRQQRVGLGWEWW\*PVRSPAPPYRAPDVRI\*KNRRYSRPPWRPACVLLCCL\*\*YD  
EARVPGGSSSLVRERDAAGGGGGDAAPAGGALRAPAVPGAYGGAEQHSLGAGTLVRYHPVVP GGQVQVGRHRLAELPERPQQLP  
DHRGAEQRFHPHGGQHPDHQL\*RALAVGRPAENHHAHQHAQREVRHVQQVQVQAGDGLAQDPQRGG\*\*L\*W\*SGRADLRV  
GGV\*AARGQLLDGHDHRSDEQRHHRQLLGGGAAERGAGERHRREVRHAQLPAGLGRDRAGDAGR VHQRGLPPRHRPAARLR  
RGLHREPPQQPAGHPQAAALPGGLDPVRGPGGGQHPRALGCRSLREKQGG\*HRRGDRSRGHRLYRGAGR\*FC\*RCGSGRGG\*  
NRK\*DSHPAGGEGQQGQELQRARGQEKHRLPQLVPLQLRRPREGRALLDAAHHLGRHLRGASLLVAARHDARPGHLP LHASS  
\*QLPGGRRRAPARLLQELLQRAGRLAAAAARLHLAHLQPLPREDP RPPPARAHYHRQ\*KRSCSHRSRDPAAAQQYQGPSARD  
RH\*RQTPHLRLRQGPGRSRAARPLEPHLLKNVHSLAQ\*\*HRLGPARAQDVRRRSPTLHATPRARARALPRSLGRPQGP RALAH  
HRRRRDRPGGRRALHARRRRLHRGRRHRQRGGRRAPVRPHQEPAAAHRPAEHPRHARGASLAAQGAHQGTQGHQAQG  
GQTRGLRQQRRQDPQTRGHGGGGGHRQHVP PAARQVRLGARRRHRCARARAHPPPSHLKMLTSRC\*CVPAARRMSKRKYKE  
EMLQVIAPEIYGPA AAVKEERKPRKLKRVKKDKKEEEDDLGVEFVREFAPRRRVQWRGRKVKPVLPGTTVVFTPGERSGSASKRSY  
DEVYGGDEDILEQAVERLGEFAYGKRSRPAPLKEEAVSIPLDHGNPTPSLKPVTLQQVLPSAAPRRGFKREGGEDLYPTMQLMVPKRQ  
KLEDVLEHMKVDPEVQPEVKVRPIKQVAPGLGVQTVDIKIPTMETQTEPVK PSTSTMEVQTD PWPAPASTSTRRRRKYGAASL  
LMPNYALHPSIIPTPGYRGTRFYRGYTSSRRRKT TTTTTRRRRSRRSSTATSALVRRVYRSGREPLTPRARIYHPSIAI\*LPPPTCRYGPHM  
PPRPHYGLPRKKAAP\*KADGERAASPPPAARHQAVGGRLPARADPHRRGDRGDP RHSFRGGAGLSAPLRHKKAWICNKK  
KNGLTLLVL\*CVFLDGRHQFFVPGTATRHA AVYGHLEHRHQQPTERGLRQLEQSLERA\*EFRVHAQNLWQQGVEQQHRAGAEGK  
AERTELP AEGG\*WPGLRHQRGG\*PGQPGR AETDQPPGRGPARGVRGDAPGGGGAASPGQARRQATASRRGGDAADAHGRA  
APVRGGGETGPAHHAARGASGHRSAETQQQPARDPGLASASPLHSG\*APAAGRRVARPPRPPPGELAEHSEQHRGSGSAECEA  
PPLLLKDTVALNLLVCVYMYVRRPEGGV\*RGASPSCKMATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNP  
TVAPTHDVTTRDQRLLTRFVPVDREDNTYSYKVRYTLAVGDNVRLDMASTYFDIRGVLD RGPSPFKPYSGTAYNSLAPKGAPNSSQ  
WEQAKTGNGGTMETHTYGVAPMGENITKDGLQIGTDVTANQN KPIYADKTFQPEPQVGEENWQETENFYGGRALKKDTNMK  
PCYGSYARPTNEKGGQAKLKVGDGVP TKEFDIDLAFDTPGGTVNGQDEYKADIVMYTENTYLETPDTHVVYKPGKDDASSEINL  
VQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTYFSMWNQAVDSYDPDV  
RIIENHGVEDELPNYCFPLDGS GTNAAYQGVKVDGQDGDVESEWENDDTVAARNQLCKGNIFAMEINLQANLWRSFLYSNVALY  
LPDSYKYPTNTVLTNTNTYDYMNGRVT PPSLVDAYLNIGARWSLDPMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQ  
KFFAIKSLLLPGSYTYEWNFRKDVNMILQSSLGNDLR TDGASIAFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSFNDYLSAAN  
MLYPIPANATNVPISIPSRNWA AFRGWSFTRLKTRETPSLGSGFD PPFVYSGSIPYLDGTFFLNHTFKKVSITFDSSVSWPGNDRLLTP  
NEFEIKRTVDGEGYNVAQCNMTKDWFLVQMLAHYNIQYQGFYVPEGYKDRMYSFERNFQPM SRQVVDENVYKDYQAVTLAYQH  
NNSGFVGYLAPTMRQQGPYPANYPYPLIGKSAVASVTQKKFLCDRVMWRIPSSNFMSMGALTDLGQNMLYANSAHALDMNFE  
VDPMDSTLLYVVFVFDVVRVHQPHRGVIEAVYL RTPFSAGNATT\*AALASCKMTAGSGEQELRAILRDLGCGPCFLGTDFDKRFPG  
FMAPHKLACAIVNTAGRETGGEHWLAFAWNPRSHTCYLDFPFGFSDERLQIYQFEYEGLLRRSALATEDRCVTLKSTQTVQGRS  
AACGLFCCMFLHAFVHWPDRPMDKNPTM NLLTGVPNGMLQSPQVEPTLRNQEALYRFLNAHSAYFRSHRARIEKATAFDRMN  
QDM\*KTGVC M\*MLYS\*\*TAHVYATFSEALTFRNRRGSAGSRHGPRAGIRCGTGTWAAT\*TRGSAAWARGGRGTSRSTACA\*VA  
GRPAGRARRS\*NRSWDPRSARESCGTRGCSTGTSPGPGASRLPAPSRR\*CPPRPDPRRWP SRRGSSCRSAAPCWARSACGCNRS  
AGGSASSGPARRSSCPGTWPS\*KPPAGGRPAAPCRPR\*RRPRRTC\*RTGWWRSRRRARSSARRC WPAAPRCAPSGSG\*SWPGWG  
SPSARAARSRSHP SR\*CAPSGSSRSRAGTAACPRLRCSRAATARSCTPSSCGRSGSASARSAPAGSGPSSRSGSCCW\*RSAGCRGA  
PRSHTGGRCGGTPRPARASAGRTSGRSPRG TGPSAASSLPCSPRPKR SAGSGGSSPPLSS\*SPPPRS GGRSRPGSQTACRPSR\*C  
ARGES\*SPRPAPP RPAFRPRCPG\*CLAKAHAWSCGVSWAAEAAA MCWESASSRPRLLFLLGRPRPRGGRHASSGAEAEATG  
SRGSAGGWQSPFRVRGCAPGGAALTDFLRGRPLCSPREQQQAWRLSHRRQHRHLPPPPPTRTSSRMKA\*PPRRPAPPPTPRPQ  
TCKRWRNPSRLTWAT\*RPRSTRRSWQRA FQPRKRTTKSSQSRKQRTSRTLGTSMATT\*AGQRTCSSSIWPANASSSRTRCSTAPR  
CPSAWRSSAAPT SATSSRRACPPSASPTAPVSPTRASTSTRSSRCPRWPPTTSF SRTKGSPSPAAPTAPAPT PCSTWAPAPAYLISP

Fig. 24K

WKRFRSSRVWAATRLGPRTLCKEAERSMSTTAPWWSWKATTRAWRSSARSS\*PTSPTRRSTCPPRS\*APSWTRCSSAPRPSR  
 RRRCRTPRVRTRASPWSATSSWRAGWERVAPPAWWSGASS\*WPWSW\*PWSWSVCAASLPTRRPCARSRRCTTSSGTGSCAR  
 PARSPTWS\*PTWSPTWASCTRTAWGKTCCTPPCAGRPAATTSATASTCTSATPGRRRAWACGSSAWRSRT\*KSSASSCRRTSRPCG  
 PGSTSVPPPTWPTSSSPSACG\*RCATGCPTL\*AKACCKTFALSSSNAPGSCPPAPRCPRTSR\*PSASAPRRSGATATCCAWPTT  
 WPTTTRT\*SRTSAARVCWSATAAATSARRTAPWPATPSC\*ARPRSSAPSSCKAPATARARGV\*NSPRGCGPRPTCASSCPRTTIPSR  
 GSTRTNPSRPRPSCRPAASSPRGPSWPNCPSRNPACNFC\*KRATGSTWTPRPERSTPASPRMPRGSSKKLVLPPEDEEDWES  
 SQAEEMEDWDSTQAEEDSLQDSLEEEDVEEAEAEAAARPSSSAEKASSTDTISAPGRGRGGRHRSRWDETGRFPNPTTQTGK  
 KERQGYKSWRGHKNIVSCLQACGGNISFTRRYLLFHRGVNFPRNLIHYRHLHSPYYCFQEEAETQQQKQTSGSS\*KIHSGGRWT  
 EDGERAGADPGAEPDLSHPLCHLPAESGAGAGTESQEPFSALAHPLSVSQERRPTSAHSRGRGSLQQLRAHS\*RVARARPH  
 TEKGGNYVTTCALRPTIMSKEIPTYMWSYQPMGLAAGAAQDYSTRMNWLSAGPAMISRVDIRAHNRNQLLEQSAITATPRHH  
 LNPRNWPAAALVYQEIPTTPTVLLPRDAQAEVQLTNSGVQLAGGAALCRHRPAQGIKRLVIRGRGTQLNDEVVSSSLGLRDPGVFQL  
 AGSGRSSFTPRQAVLTLESSSQPRSGGIGTLQFVEEFTPSVYFNPFGSGPGHYDEFIPNFDaisesVDGYD\*MSHGGAADLARLRLH  
 DHCRRFRFCFARDLAEFAYFELPEEHPQGAHVRIIEGGDLSHLLRIFSQRPIVEREQQTLLTYCICNHPGLHESLCCLLCTEYNKS  
 \*DQRLRLRLWCSCYQPVPLHRERDRAPAV\*APQEVPHLAVPGLPDRRCQPLRQRSPAERPCQPYFFHPQKQAPALPTLPPRD  
 LSVRLRLPSHLPPDPEYHSAAPRY\*QPNYPPTPPSRPFL\*I\*YHYRRWLLLLVLRPVDPRSPTQSPEVRKCKFQEPWFKLCYRQK  
 SDMHPSWIMIIIVNIIACTLISFVIYPCFDFGWNSPEALYLPPEPTPPQQPQAHALPPPQPRPQYMPILDYEAEPQRPMLPAISY  
 FNLTGGDD\*PTGQ\*QRQRPSPGHGRPRLGAATRPTSHSSAAGESRQGAAGRHSPPVQERHLLPGETGQDLLRGHPDRPSPLRA  
 PAAAEVHLPGRSQPHRHHPAVGRYQGVHPLLLRLPRLPHSDQDPLRPPRPPHELITPLSSEIKIILMMI\*IKKII\*FEIKIQSY\*\*FEF  
 NKNKESLT\*NLIPLGLCPCLPTPPHSPSSGTAGPGLQTSSTR\*RGCIQPPVPQSSFYLLSDVQKARPGG\*\*LRPLRLRCRQRTDR  
 ALHQPLRLFRWIPREAPGGVVPATG\*PRHHQERGNHPQAGRGGRPLVGKTHLQHGHHQGRRPSQYFKQHHP\*NCPCFLQQQ  
 WNFKPQCLHTISSISHI\*HFRHKSWKRSSDFK\*VVDCTTNSSSYIQLK\*HHSKNRQRAIY\*LQWKQRT\*G\*YKPKKRTSF\*R\*CYCNIY  
 WKWLRLWIL\*\*\*WKNKTRNYQNWRIKF\*C\*QSNQCQTRHRFKF\*LRWCLDSWKQGT\*QANTLDYP\*PKP\*LSITFRQRCQIYSL  
 YKMR\*SNTRHCGSGGCYCRISTKSN\*\*HSQKRHSFP\*I\*FRWCTHVKLINGR\*LLEL\*GGTDHSCSLYKCCGIHAKYRCISKNP\*NT  
 \*K\*HSQSGIFNWRNYANDTNHNFQWH\*\*KRHNPS\*HLLYDFYMAVDWRL\*GQKYLYCQLILFFLHRPGIIPPSKPTPFPTTFVY  
 METLKQKNKVQVY\*INSFTGLEQLFFLHPRTWNTPPSPPAQ\*PTSECHW\*WTCFWSRSTQFQSEPVSDRSGR\*NPPGTPASA  
 PHSTAEDCPRWSGSRLSGRSRAAVGIIVRERDRPVVSHQAPQQLPPLRQAAAQGVVQGLPQHDHAGPQHQSAGAAGAAA  
 HANLAQVTAVRATQDQHVQVQSSIVQHAPAETHRGKDATHVAVVDPQVNQVALPPEDAHHVHDLGHVAVHPLVPHPHPLVE  
 HAAPDDPAEPQGQHRPARHAARKPRIPAMTMEDPPLVPVDHLGAEQVYVGTAAQAYAHASLQHSQLLGGQNHIPGHGELLQDSE  
 PRRTGQSSHITYIVHGQGIARQHRVILHQRSAGLGLTAW\*GGRPIRVMAGRG\*SCSRPCHDAVAFGHFRTCCSRTWSGRCTPIA  
 GGGGLGAWNARC\*SCKTATLSDRAADLGPOE\*\*RSHHA\*L\*SHRPPWNGPGPAR\*CNFVGFR\*RRGREEQEEP\*LTFNPNGLGAL  
 QNEGHGDGTSRPRCVGGK\*QPGQR\*YGSRDVPRWLPAKPPRAHPETRQ\*RKREGSLIPQPSCTYPAPSPDNFHFSSLE\*FELVPEV  
 NPSQP\*\*KARAEHPPAFLSTPS\*FQDILLVHLQQLDKRNIKISAAIPELLPQQ\*L\*VLFHIVSEIFSHRTPRNKRASHITDKPKSPVSI  
 AKCKIEISMLARPGDIFQITGQKIG\*AIFKKINKRKIFQVHV\*GLGNNDGVSARGAFQHG\*LADL\*KNKK\*NIKPC\*PGEQVGSFSPA  
 PGRPRGLRRDPRKNCRYD\*KPSQRDVPGGRR\*FEKKHTPPEHWSP\*VKKSGRGSNEALQRLSSPAKRCHADEAQNFQVRKKCN  
 YSPPAQAAKLPIPDTHTKPRP\*LTERQQQRHTTGARVREKTEL\*PVRPLSAQYIAPDLH\*RKGQSLKIPAK\*SHTPSTRPETGDTLR  
 KIRALPQTAKLPSPFGSHATSSKHDFQIPSTVKNITRAPNGRRRSQSPSSLPKFKQLICILTRTKSLRYIIDD

Fig. 25A

**AdC6 020-DU422gp160(E1621) Nucleic Acids – SEQ ID NO: 6**

CATCATCAATAATATACCTCAAACCTTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCTGCGGGAGCGGGGACCGTTAGGGGCGGGGCGGGTGACGTTTTGATGACGTGGCTATGAGGCGGAGCCGGTTTGCAAG  
TTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTTCCCGCGCTCTCTGACAGGAAATG  
AGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAAAATGAATGAGGAAGTGAAAATCTGAGTAATTTT  
GCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTTC  
ACCTAAATTTCCGCGTACGGTGTCAAAGTCCGGTGTTTTACGTACGATATCATTTCCCGGAAAGTGCCACCTGACCGTAACTAT  
AACGGTCCTAAGGTAGCGAAAGCTCAGATCTCCGATCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT  
AAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCT  
TGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGA  
CATTGATTATTGACTAGTATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTAC  
ATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACA  
TCAATGGGCGTGGATAGCGGTTTGAATCACGGGGATTTCAAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTGGCACC  
AAAATCAACGGGACTTTCAAATGTCTGAACAACCTCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGT  
CTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAACGC  
AGTCAGTGCTTCTGACACAACAGTCTGAACTTAAGGCTAGAGTTCGACGCCACCATGCGCGTGCGCGGCATCCCCGCAACT  
GGCCCCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATGATCATCATCTGCCGCGTGGTGGGCAACCTGGACCTGTGGGT  
GACCGTGTAACGCGGTGCCCGTGTGGAAGGAGGCCAAGACCACCTGTTCTGCGCTCCGACGCCAAGGCCTACGACAAG  
GAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCAAGGAGATCGTGCTGGAGAACGTGACCG  
AGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACGAGGACATCATCTCCCTGTGGGACCACTCCCTGAAGCC  
CTGCGTGAAGCTGACCCCCCTGTGCGTGACCCCTGAAGTGAAGAACGTGAACATCTCCGCCAACGCCAACGCCACCGCCACCC  
TGAAGTCTCCATGAACGGCGAGATCAAGAACTGCTCCTTCAACACCACCCAGAGCTGCGCGACAAGAAGCAGAAGGTGTAC  
GCCCTGTTCTACAAGCCCCGACGTGGTGCCCTGAACGGCGGCGAGCACAACGAGACCGGCGAGTACATCCTGATCAACTGCA  
ACTCCTCCACCATCACCCAGGCTGCCCAAGGTGTCCTTCGACCCCATCCCATCCACTACTGCGCCCCCGCGGCTACGCCAT  
CCTGAAGTGCAACAACAGACCTTCAACGGCACCGGCCCTGCAACAACGTGTCCACCGTGCAAGTGACCCACGGCATCAAGC  
CCGTGGTGTCCACCCAGCTGCTGCTGAACGGCTCCTGGCCGAGGAGGAGATCATCTGCGCTCCGAGAACCTGACCAACAAC  
ATCAAGACCATCATCTGTCACCTGAACAAGTCCGTGGAGATCAAGTGACCCGCCCCAACACAACACCCGCAAGTCCGTGCG  
CATCGGCCCGGCCAGACCTTCTACGCCACCGGCGAGATCATCGCGACATCCGCGAGGGCCACTGCAACATCTCCGCGAGA  
CCTGGAAGTCCACCCTGATCCAGGTGAAGGAGAAGCTGCGCGAGCACTACAACAAGACCATCAAGTTCGAGCCCTCCTCCGGC  
GGCGACCTGGAGGTGACCACCACTCCTTCAACTGCCGCGGCGAGTTCTTCTACTGCGACACCACCAAGCTGTTCAACGAGAC  
CAAGCTGTTCAACGAGTCCGAGTACGTGGACAACAAGACCATCATCCTGCCCTGCCGATCAAGCAGATCATCAACATGTGGC  
AGGAGGTGGGCCGCGCCATGTACGCCCCCCCCATCGAGGGCAACATCACTGCAAGTCCAACATACCGGCCTGCTGCTGACC  
TGGGACGGCGGCGAGAACTCCACCGAGGGCGTGTTCGCCCCGCGGCGGCAACATGAAGGACAAGTGGCGCTCCGAGCTG  
TACAAGTACAAGGTGGTGGAGATCAAGCCCCTGGGCGTGCCCCCACCAGAGCAAGCGCAAGGTGGTGGGCCGCGAGAAG  
CGCGCCGTGGGCTGGGCGCGGTGCTGCTGGGCTTCTGGGCGCGCCGCGGAGCACCATGGGCGCGGCCAGCATCACCTGA  
CCGTGCAGGCCCCGACGTGCTGAGCGGCATCGTGACGAGCAGAGCAACCTGCTGCGCGCATCGAGGCCAGCAGCACCT  
GCTGCAGCTGACCGTGTGGGCATCAAGCAGCTGCAGACCCGCGTGTGGCCATCGAGCGCTACCTGAAGGACCAGCAGCTG  
CTGGGCTGTGGGGCTGCAGCGGCAAGCTGATCTGCGCCACCGCCGTGCCCTGGAACAGCAGCTGGAGCAACAAGAGCCTG  
GGCGACATCTGGGACAACATGACCTGGATGCAAGTGGGACCGCGAGATCAGCAACTACACCAACACCATCTCCGCTGCTGG  
AGGACAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGCCCTGGACAGCTGGAAGAACCTGTGGAAGTGGTTG  
ACATACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCTGATCGGCCTGCGCATCATCTCGGCGTGC  
TGGCCATCGTGAAGCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCAGACCCTGATCCCCAACCCCCGCGGCCCGACCGC  
CTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACAAGGACCGCAGCATCCGCTGGTGAGCGGCTTCTGGCCCTGGCC  
TGGGACGACCTGCGCAGCCTGTGCTGTTTACGTACCAACAGCTGCGCGACTTCATCCTGACCGCCGCCCGCGCCGAGCT  
GCTGGGCCGAGCAGCCTGCGCGGCTGCAGCGCGCTGGGAGGTGCTGAAGTACCTGGGCAACCTGGTGCACTACTGGG  
CCTGGAGCTGAAGCGCAGCGCCATCAACCTGTTTCGACACCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAG  
GTGATCCAGCGCATCTGCCGCGCATCCGCTACATCCCCACCCGATCCGCCAGGGCTTCGAGGGCGCCCTGCTGTAAGGTACC  
TCTAGAGTCGACCCGGGCGGCCAAACCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTCCCCCTCC  
CCGTGCCCTTCTTGACCCTGGAAGGTGCCACTCCCACTGTCTTTCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA  
GGTGTCAATTCTATTCTGGGGGTGGGGTGGGGCAGGACGACAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGG

Fig. 25B

GATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCAGATCTGCAGATCTGAATTCATCTATGTCGGGTGCGGAGA  
 AAGAGGTAATGAAATGGCATTATGGGTATTATGGGTCTGCATTAATGAATCGGTGAGATATCGACATATGCTGGCCACCGTGC  
 ATGTGGCCTCGCACCCCCGCAAGACATGGCCGAGTTCGAGCACAACGTCATGACCCGCTGCAATGTGCACCTGGGCTCCCGC  
 CGAGGCATGTTTATGCCCTACAGTGCAACATGCAATTTGTGAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCCT  
 GACGGGGGTGTTTGACATGAATGTGGAGCTGTGGAAAATTTCTGAGATATGATGAATCCAAGACCAGGTGCCGGGCTGCGAA  
 TGGGAGGCAAGCACGCCAGGCTTCAGCCCGTGTGTGTGGAGGTGACGGAGGACCTGCGACCCGATCATTGGTGTGTCTCT  
 GCAACGGGACGGAGTTCCGGCTCCAGCGGGGAAGAATCTGACTAGAGTGAGTAGTGTGGGGCTGGGTGTGAGCCTGCATG  
 AGGGGCAGAATGACTAAAATCTGTGGTTTTCTGTGTGTTCGAGCAGCATGAGCGGAAGCGCCTCCTTTGAGGGAGGGGTATT  
 CAGCCCTTATCTGACGGGGCGTCTCCCTCCTGGGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGACGGCCGGCCC  
 GTGACGCCCGCAACTCTTCAACCTGACCTACGCGACCCTGAGCTCCTCGTCCGTGGACGCAGCTGCCGCCGAGCTGTGCT  
 TCCGCCGCCAGCGCGGTGCGCGGAATGGCCCTGGGCGCCGGCTACTACAGCTCTCTGGTGGCCAACCTGAGTTCCACCAATA  
 TCCCGCCAGCCTGAACGAGGAGAAGCTGTGCTGTGATGGCCAGCTCGAGGCCCTGACCCAGCGCCTGGGCGAGCTGACC  
 CAGCAGGTGGCTCAGCTGCAGGCGGAGACGCGGGCCGCGGTGCCACGGTGAACCAATAAAAAATGAATCAATAAATA  
 AACGGAGACGGTTGTTGATTTTAACACAGAGTCTTGAATCTTTATTTGATTTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCT  
 CGATCATTGAGCACCCGGTGGATCTTTCCAGGACCCGGTAGAGGTGGGCTTGGATGTTGAGGTACATGGGCATGAGCCCGT  
 CCCGGGGGTGGAGGTAGCTCCATTGACGGGCTCGTGTGCGGGATGGTGTGTAATCACCAGTCATAGCAGGGGCGCAG  
 GGCCTGGTGTGACGATGTCTTGAGGAGGAGACTGATGGCCACGGGACGCCCTTGGTGTAGGTGTTGACGAACCTGTTG  
 AGCTGGGAGGGATGCATGCGGGGGGAGATGAGATGCATCTTGGCTGGATCTTGAGATTGGCGATGTTCCGCCAGATCCC  
 GCCGGGGGTTCATGTTGTGACGAGACCACAGCACGGTGTATCCGGTCACTTGGGGAATTTGTATGCAACTTGAAGGGAA  
 GGCCTGAAAGAATTTGGAGACGCCCTTGACCGCCAGGTTTTTCATGCACTCATCCATGATGATGGCGATGGGCCGTGGG  
 CGGCGCCTGGGCAAAGACGTTTCGGGGGTGCGACACATCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAAT  
 GAATTTGGGGCGGAGGGTGCCGACTGGGGGACGAAGGTGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGCAT  
 CTCCAGGCCTTGAGCTCGGAGGGGGGGATCATGTCCACCTGCGGGCGATGAAAAAACGGTTCCGGGGCGGGGGAGAT  
 GAGCTGGGCCGAAAGCAGGTTCCGGAGCAGCTGGGACTTGCCGCAACCGGTGGGGCCGTAGATGACCCCGATGACCGGTG  
 CAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCTCGCGGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACATGCATG  
 TTCTCGCGCACGAGTTCCGCCAGGAGGCGCTCGCCCCCAGCGAGAGGAGCTCTTGACGCGAGGCGAAGTTTTTCAGCGGCTT  
 GAGTCCGTGCGCCATGGGCATTTTGGAGAGGGTCTGTTGCAAGAGTTCAGACGGTCCAGAGCTCGGTGATGTGCTCTAGG  
 GCATCTCGATCCAGCAGACCTCCTCGTTTCGCGGTTGGGGCGACTGCGGGAGTAGGGACACGAGCGATGGGCGTCCAGCGA  
 GGCCAGGGTCCGGTCTTCCAGGGCCGAGGGTCCGCGTCAGCGTGGTCTCGTCACGGTGAAGGGGTGCGCGCCGGGCTG  
 GCGCTTGCGAGGGTGCGCTTCAGGCTCATCCGGTGGTTCGAGAACCCTCCGGTCCGCGCCCTGCGCGTCCGCCAGGTAG  
 CAATTGAGCATGAGTTCGTAGTTGAGCGCTCGGCCGCTGGCCCTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGCAGAC  
 GGGACAGAGGAGGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGAAGTCCGGGGCGTAGGCGTCCGCGCCGAG  
 CTGGCGCAGACGGTCTCGCACTCCAGAGCCAGGTGAGGTGCGGGGCGGTTGGGGTCAAAAACGAGGTTTCTCCGTGCTTTT  
 TGATGCGTTTCTTACCTCTGGTCTCCATGAGCTCGTGTCCCGCTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACT  
 TTATGGGCCGGTCTCGAGCGGGGTGCCGCGTCTCGTGTAGAGGAACCCGCCACTCCGAGACGAAGGCCCGGGTCCA  
 GGCCAGCACGAAGGAGGCCACGTGGGAGGGGTAGCGGTGTTGTCCACAGCGGGTCCACCTTCTCCAGGGTATGCAAGCA  
 CATGTCCCCCTCGTCCACATCCAGGAAGGTGATTGGCTTGAAGTGTAGGCCACGTGACCGGGGTCCCGGCCGGGGGGTA  
 TAAAGGGGGCGGGGCCCTGCTCGTCTCACTGTCTTCCGGATCGTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATCCCT  
 CTCGAAGGCGGGCATGACCTCGGCACTCAGGTTGTGAGTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTTGGAG  
 ACGCCTTTCATGAGCCCTCGTCCATTTGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCCGTAGAG  
 GCGTTGGAGAGCAGCTTGGCGATGGAGCGCATGTTGTTCTTTCTTGTGCGCGCTCCTTGGCGGCGATGTTGAGCT  
 GCACGTACTCGCGGCCACGCACTTCCATTGGGGGAAGACGGTGGTGTGAGCTGTCGCGGCACGATTCTGACCCGCCAGCCGCG  
 GTTGTGACGGGTGATGAGGTCCACGCTGGTGGCCACCTCGCCGCGCAGGGGCTGTTGGTCCAGCAGAGGCGCCGCCCTTG  
 CGCGAGCAGAAGGGGGGCGAGCGGGTCCAGCATGAGCTGTCGCGGGGGTGGCGTCCACGGTGAAGATGCCGGGCGAGGAG  
 CTCGGGGTCAAGTAGCTGATGCAGGTGCCAGATTGTCCAGCGCCGCTTGCAGTCCGCGACGGCCAGCGCGCTCGTAG  
 GGGCTGAGGGGCGTGCCCCAGGGCATGGGGTGGTGTGAGCGCGGAGGCGTACATGCCGCGATGTCTGAGACGTAGAGGGG  
 CTCCTCGAGGACGCCGATGTAGGTGGGGTAGCAGCGCCCCCGCGGATGCTGGCGCGCACGTAGTCGTACAGCTCGTGCAG  
 GCGCGAGGAGCCCCGTGCCGAGTTGGAGCGTTGCGGCTTTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAG  
 TTGGAGGAGATGGTGGGCCTTTGGAAGATGTTGAAGTGGGCGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTAG  
 GAGTCTGACGCTTGGCGACGAGCTCGGCGGTGACGAGGACGTCCAGGGCGCAGTAGTCGAGGGTCTTGGATGATGTCAT  
 ACTTGAGCTGGCCCTTCTGCTCCACAGCTCGCGGTTGAGAAGGAACCTTTCGCGGTCTTCCAGTACTCTTCGAGGGGGAACC

**Fig. 25C**

GCGCTGATCGGCACGGTAAGAGGCCACCATGTAGAACTGGTTGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGAG  
 GCGCTAAGCTTGC CGCGCCTTGC CGCAGGGAGGTGTGGGTGAGGGCGAAGGTGTGCGCACCATTGACCTTGAGGAACTGGTG  
 CTTGAAGTCGAGGTCTGTCGACGCCCTGCTCCAGAGTTGGAAGTCCGTGCGCTTCTTGTAGGCGGGGTTAGGCAAAGCG  
 AAAGTAACATCGTTGAAGAGGATCTTGCCCGCGCGGGGCATGAAGTTGCGAGTGATGCGGAAAGGCTGGGGCACCTCGGCC  
 CGGTTGTTGATGACCTGGGCGGCGAGGACGATCTCGTCGAAGCCGTTGATGTTGTGCCCGACGATGTAGAGTTCCACGAATC  
 GCGGGCGGCCCTTGACGTGGGGCAGCTTCTTGAGCTCGTCGTAGGTGAGCTCGGCGGGGTGCTGAGCCCGTGTCTGCTCGAG  
 GGCCAGTCGCGCAGCTGGGGGTGGCGCTGAGGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTCTGCAAGCGGTCCCG  
 GTAGTGACGGAAGTGTGGCCACGGCCATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGGTGC CGGTGCCAGCGGTCC  
 CACTTGAGCTGGAGGGCGAGGTCTGGGCGAGCTCGACGAGCGGCGGGTCCCCGGAGAGTTTCATGACCAGCATGAAGGGG  
 ACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCG  
 AGCCGATGGGGAAGAACTGGATCTCTGCCACAGTTGGAGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGC  
 GCGCCGAGCACTGTGCTTGTTTATAACAAGCGTCCGAGTGCTCGCAACGCTGCACGGGATGCACGTGCTGCACGAGCTGT  
 ACCTGGGTTCTTTGGCGAGGAATTTCACTGGGCGAGTGGAGCGTGCGCGGTGCATCTGTGCTGTACTACGTCTTGCCATC  
 GCGGTGGCCATCGTCTGCTCGATGGTGGTCATGCTGACGAGCCCGCGGGGAGGCAAGTCCAGACCTCGGCTCGGACGGGT  
 CGGAGAGCGAGGACGAGGGCGCGCAGGCCGAGCTGTCCAGGTCCTGAGACGCTGCGGAGTCAGGTGAGTGGGCGAGCGG  
 CGCGCGCGGTTGACTTGACAGGAGCTTTTCCAGGGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACGGCGCCGTTGGTG  
 GCTACGTCCACGGCTTGACGGGTGCCGTGCCCTGGGGCGCCACCACCGTGCCCGTTTCTTCTGGGCGCTGCTTCCATGTCG  
 GTCAGAAAGCGGCGGCGAGGACGCGCGCGGGCGGCGAGGGCGGCTCGGGGCCCGGAGGCAAGGGCGGCGAGGGGCACGTC  
 GCGCGCGCGCGCGGGCAGGTTCTGGTACTGCGCCCGGAGAAGACTGGCGTGAGCGACGACGCGACGGTTGACGTCTGGAT  
 CTGACGCTCTGGGTGAAGGCCACGGGACCCGTGAGTTTGAACCTGAAAGAGAGTTTCAGACAGAATCAATCTCGGTATCGTTG  
 ACGGCGGCCTGCCGAGGATCTTTCACGTGCGCCGAGTTGTCCTGGTAGGCGATCTCGGTATGAAGTCTCGATCTCCTCC  
 TCCTGAAGGTCTCCGCGGCCGCGCGCTCGACGGTGGCCGCGAGGTGCTTGGAGATGCGGCCCATGAGCTGCGAGAAGGGC  
 TTCATGCCGCGCTCGTTCCAGACGCGGCTGTAGACCACGGCTCCGTGCGGGTGC GCGCGCGCATGACCACCTGGGCGAGGT  
 TGAGCTCGACGTGGCGGTGAAGACCGGTAGTTGACAGAGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGG  
 TGACGAAGAAGTACATGATCCAGCGGCGAGCGGCATCTGCTGACGTGCGCCAGGGCTTCAAGCGTTCCATGGCTCGTA  
 GAAGTCCACGGCGAAGTTGAAAACTGGGAGTTGCGCGCCGAGACGCTAACTCCTCCTCCAGAAGACGGATGAGCTCGGCG  
 ATGGTGGCGCGCACCTCGCGCTCGAAGGCCCGGGGGGCTCCTCTTCATCTCCTCCTCCTCCTCCTCCTCACTAACATCTCTTCTA  
 CTTCTCCTCAGGAGGCGGTGGCGGGGAGGGGCCCTGCGTGC CGGCGGCGCACGGGCAGACGGTCGATGAAGCGCTCGA  
 TGGTCTCCCCGCGCGGCGACGATGGTCTCGGTGACGGCGCGCCGTCCTCGCGGGGCCGACGATGAAGACGCCGCCGCG  
 CATCTCCAGGTGGCCGCGGGGGGGTCTCCGTTGGGCAGGGAGAGGGCGCTGACGATGCATCTTATCAATTGACCCGTAGGG  
 ACTCCGCGCAAGGACCTGAGCGTCTCGAGATCCACGGGATCCGAAAACCGTGAACGAAGGCTTCGAGCCAGTCGAGTCGC  
 AAGGTAGGCTGAGCCCGGTTTCTTGTTCTTCGGGTATTTGGTCGGGAGGCGGGCGGGCGATGCTGCTGGTGATGAAGTTGAA  
 GTAGGCGGTCTGAGACGGCGGATGGTGGCGAGGAGCACAGGTCTTGGGCCCGGCTTGCTGGATGCGCAGACGGTCGCG  
 CATGCCACAGCGGTGGTCTGACACCTGGCGAGGTCTTGTAGTAGTCTGATGAGCCGCTCCACGGGCACCTCCTCCTCGCC  
 CGCGCGGCCGTGCATGCGCGTGAGCCCGAACCCGCGCTGCGGCTGGACGAGCGCCAGGTGCGCGACGACGCGCTCGGTGAG  
 GATGGCCTGCTGGATCTGGGTGAGGGTGGTCTGGAAGTCGTGAAGTCGACGAAGCGGTGGTAGGCTCCGGTGTGATGGT  
 GTAGGAGCAGTTGGCCATGACGGACAGTTGACGGTCTGGTGGCGGGTGCACGAGCTCGTGGTACTTGAGGCGCGAGTA  
 GCGCGCGGTGTCGAAGATGTAGTCGTTGAGGCGCGCACGAGGTACTGGTATCCGACGAGGAAGTGCGGCGGCGGCTGGCG  
 GTAGAGCGGCCATCGCTCGGTGGCGGGGGCGCCGGGCGGAGGTCTCGAGCATGAGGCGGTGGTAGCCGTAGATGTACCT  
 GGACATCCAGGTGATGCCGGCGGCGGTGGTGGAGGCGCGCGGGAACCTCGCGACGCGGTTCCAGATGTTGCGCAGCGGCA  
 GGAAGTAGTTGATGGTGCCGCGGTCTGGCCCGTGAGGCGCGCGCAGTCGTGGATGCTCTAGACATACGGGCAAAAACGAA  
 AGCGGTGAGCGGCTGACTCCGTGGCCTGGAGGCTAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGTTCAATCTCGAAT  
 CAGGCTGGAGCCGACGTAACGTGGTACTGGCACTCCCGTCTCGACCAAGCCTGCTAACGAAACCTCCAGGATACGGAGGC  
 GGGTCGTTTTTTGGCCTTGGTGCCTGGTCATGAAAACTAGTAAGCGCGGAAAGCGGCCGCCCGCGATGGCTCGCTGCCGTA  
 GTCTGGAGAAAGAATCGCCAGGGTTGCGTTGCGGTGTGCCCCGGTTGAGCCTCAGCGCTCGGCGCGGCGGATCCGCGG  
 CTAACGTGGGCGTGCTGCCCGTCGTTTCCAAGACCCCTTAGCCAGCCGACTTCTCAGTTACGGAGCGAGCCCTCTTTTTTT  
 TTCTTGTTTTTGGCAGATGCATCCCGTACTGCGGCAGATGCGCCCCACCTCCACCACAACCGCCCTACCGCAGCAGCAG  
 CAACAGCCGGCGCTTCTGCCCCGCCCCAGCAGCAGCCAGCCACTACCGCGGCGGCGCGCTGAGCGGAGCCGCGTTCAGT  
 ATGACCTGGCCTTGAAGAGGGCGAGGGGCTGGCGCGGCTGGGGCGTGTGCGCGGAGCGGCACCCGCGCGTGCAGATG  
 AAAAGGGACGCTCGCGAGGCCTACGTGCCAAGCAGAACCTGTTAGAGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGC  
 GCCTCCCGCTTCCACGCGGGGCGGGAGCTGCGGCGCGGCTGGACCGAAAGCGGGTGTGAGGGACGAGGATTCGAGGGC

Fig. 25D

GACGAGCTGACGGGGATCAGCCCCGCGCGCGCACGTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAG  
GAGGAGAGCAACTTCAAAAAATCCTTCAACAACACGTGCGCACGCTGATCGCGCGGAGGAGGTGACCTGGGCTGATGC  
ACCTGTGGGACCTGCTGGAGGCCATCGTGCAGAACCCACGAGCAAGCCGCTGACGGCGCAGCTGTTTCTGGTGGTGCAGCA  
CAGTCGGGACAACGAGACGTTAGGGAGGCGCTGCTGAATATCACCGAGCCCGAGGGCCGCTGGCTCCTGGACCTGGTGAAC  
ATTTTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTGCCGCTGTCCGAGAAGCTGGCGGCCATCAACTTCTCGGTGCTGAGTC  
TGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTGCCCATAGACAAGGAGGTGAAGATCGACGGGTTTACAT  
GCGCATGACCCTGAAAGTCTGACCCTGAGCGACGATCTGGGGGTGTACCGCAACGACAGGATGACCGCGCGGTGAGCGC  
CAGCCCGCGCGCGAGCTGAGCGACCAGGAGCTGATGCACAGCCTGCAGCGGGCCCTGACCGGGGCCGGGACCGAGGGGG  
AGAGCTACTTTGACATGGGCGCGGACCTGCGCTGGCAGCCAGCCCGGGCCTTGGAAGCTGCCGGCGGTTCCCTACGT  
GGAGGAGGTGGACGATGAGGAGGAGGAGGGCGAGTACCTGGAAGACTGATGGCGCGACCGTATTTTGTAGATGCAGCA  
ACAGCCACCGCGCCGCTCTGATCCCGCGATGCGGGCGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGGACGATT  
GGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAATCCCGAAGCCTTAGACAGCAGCCTCAGGCCAACGGGCTC  
TCGGCCATCCTGGAGGCCGTGGTGCCTCGCGCTCGAACCCACGCACGAGAAGGTGCTGGCCATCGTGAACGCGCTGGTGG  
AGAACAAGGCCATCCGCGGTGACGAGGCCGGGCTGGTGTACAACGCGCTGCTGGAGCGCTGGCCCGCTACAACAGCACCA  
ACGTGCAGACGAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCGGTGTGCGAGCGCGAGCGGTTCCACCGCGAGTCGA  
ACCTGGGCTCCATGGTGGCGCTGAACGCCTTCTGAGCAGCAGCCCGCAACGTGCCCCGGGGCCAGGAGGACTACACCAA  
CTTCATCAGCGCGCTGCGGCTGATGGTGGCCGAGGTGCCCGAGCGAGGTGTACCAGTCGGGGCCGACTACTTCTTCAG  
ACCACTGCCAGGGCTTGACAGCCGTGAACCTGAGCCAGGCTTTCAAGAACTGCAGGGACTGTGGGGCGTGCAGGCCCGG  
TCGGGGACCGCGCAGCGGTGTCGAGCCTGCTGACGCCGAACCTCGCGCTGCTGCTGCTGCTGGTGGCGCCCTTCAGGACAG  
CGGCAGCGTGAGCCGCGACTCGTACCTGGGCTACCTGCTTAACCTGTACCGCGAGGCCATCGGACAGGCGCACGTGGACGAG  
CAGACCTACCAGGAGATCACCCACGTGAGCCGCGCGCTGGGCCAGGAGGACCCGGGCAACCTGGAGGCCACCTGAATTCC  
TGCTGACCAACCGGTCGAGAAGATCCCGCCCCAGTACGCGCTGAGCACCGAGGAGGAGCGCATCCTGCGCTACGTGCAGCA  
GAGCGTGGGGCTGTTCTGATGCAGGAGGGGGCCACGCCAGCGCGGCGCTCGACATGACCGCGCGCAACATGGAGCCCAG  
CATGTACGCCCGCAACCGCCGTTTCATCAATAAGCTGATGGACTACTTGCATCGGGCGGCCGCCATGAACTCGGACTACTTTAC  
CAACGCCATCTTGAACCCGCACTGGCTCCCGCCGCCCGGGTCTACACGGGCGAGTACGACATGCCCGACCCCAACGACGGGT  
TCCTGTGGGACGACGTGGACAGCAGCGTGTCTCGCCGCGTCCAGGAACCAATGCCGTGTGGAAGAAAGAGGGCGGGGACC  
GGCGGCCGCTCCTGGCGCTGTCCGGTGCAGCGGGTGTGCGCGGGCGGTGCCGAGGCGGCCAGCCCTTCCGAGCCTGCC  
CTTTTCGCTGAACAGCGTGCGCAGCAGCGAGCTGGGTGGGTGACGCGACCGCGCCTGCTGGGCGAGGAGGAGTACCTGAAC  
GACTCCTTGTGAGGCCCCGAGCGCGAGAAGAACTTCCCAATAACGGGATAGAGAGCCTGGTGACAAGATGAGCCGCTGGA  
AGACGTACGCGCACGAGCACAGGGACGAGCCCCGAGCTAGCAGCGCAGGCACCCGTAGACGCCAGCGGCACGACAGGCAGC  
GGGGACTGGTGTGGGACGATGAGGATTCCGCCGACGACAGCAGCGTGTGGACTTGGGTGGGAGTGGTGGTAACCCGTTTCG  
CTCACCTGCGCCCCGATCGGGCGCTGATGTAAGAACTGAAAAAATAAAAGACGGTACTACCAAGGCCATGGCGACCAG  
CGTGCGTTCTTCTCTGTTGTTGTAGTAGTATGATGAGGCGCGTGTACCCGAGGGTCTCCTCCTCGTACGAGAGCGTGATG  
CAGCAGGCGGTGGCGGGCGGATGCAGCCCCGCTGGAGGCGCCTTACGTGCCCCGCGGTACCTGGCGCCTACGGAGGGG  
CGAACAGCATTCTTACTCGGAGCTGGCACCCCTTGTACGATACCACCGGTTGTACCTGGTGACAACAAGTCGGCAGACAT  
CGCCTCGCTGAACTACCAGAACGACCACAGCAATTCCTGACCACCGTGGTGCAGAACAAACGATTTCACCCCCACGGAGGCCA  
GCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCAACGT  
GAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGGGTGTGTTCTCGCGCAAGACCCCCAACGGGGTGGATGATGATTAT  
GATGGTAGTCAGGACGAGCTGACCTACGAGTGGGTGGAGTTTGTGCTGCCGAGGGCAACTTCTCGGTGACCATGACCATCG  
ATCTGATGAACAACGCCATCATCGACAACCTTGGCGGTGGGGCGGCAGAACGGGGTGTGAGAGCGACATCGGCGTGA  
AGTTCGACACGCGCAACTTCCGGCTGGGTGGGACCCCGTGACCGAGCTGGTGTGATGCCGGGCGGTGACACCAACGAGGCCCT  
CCACCCCGACATCGTCTGCTGCCGGCTGCGGCGTGGACTTCACCGAGAGCCGCTCAGCAACCTGCTGGGCATCCGCAAGC  
GGCAGCCCTTCAGGAGGGCTTCAGATCCTGTACGAGGACCTGGAGGGGGGCAACATCCCGCGCTCTTGATGTGGAAGC  
CTACGAGAAAAGCAAGGAGGATAGCACCGCGCGGCGACCGCAGCCGTGGCCACCGCCTTACCGAGGTGCGGGGCGATAA  
TTTTGCTAGCGCTGCGGCAGCGGCCGAGGCGGTGAAACCGAAAGTAAGATAGTCATCCAGCCGTTGGAGAAGGACAGCAA  
GGACAGGAGCTACAACGTGCTCGCGGACAAGAAAAACACCGCCTACCGCAGCTGGTACCTGGCCTACAACCTACGGCGACCCC  
GAGAAGGGCGTGCGCTCCTGGACGCTGCTACCACTCGGACGTACCTGCGGCGTGAGCAAGTCTACTGGTGCCTGCCCG  
ACATGATGCAAGACCCGTCACCTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGGCGCGGAGCTCCTGCCCGTC  
TACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTACCTCGCTCACGCAGCTTCAACCGC  
TTCCCCGAGAACCAGATCCTCGTCCGCCCGCCGCGCCACCATACCACCGTCAGTGAACCGTTCCTGCTCTCACAGATCAC  
GGGACCTGCGCGTGCAGCAGATATCCGGGGAGTCCAGCGCGTGACCGTCACTGACGCCAGACGCCGACCTGCCCCACG

Fig. 25E

TCTACAAGGCCCTGGGCGTAGTCGCGCCGCGCGTCTCTCGAGCCGCACCTTCTAAAAATGTCCATTCTCATCTCGCCAGTA  
ATAACACCGGTTGGGGCTGCGCGCGCCAGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGCGCGT  
GCGCGGGCACTTCCGCGTCCCTGGGGCGCCCTCAAGGGCGCGTGCCTCGCGACCACCGTCGACGACGTGATCGACCAG  
GTGGTGGCCGACGCGCGCAACTACACGCCCGCCGCGCGCCGTCTCCACCGTGACGCGGTATCGACAGCGTGGTGCCG  
ACGCGCGCCGTACGCCCGACCAAGAGCCGGCGGCGCGCATCGCCGGCGGCACCGGAGCACCCCGCCATGCGCGCGG  
CGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCATGCTCAGGGCGGCCAGACGCGCGCCTCCGGCAGCA  
GCAGCGCCGGCAGGACCCGAGACGCGCGGCCACGGCGGCGGCGGCGGCCATCGCCAGCATGTCCCGCCGCGCGCGGCA  
ACGTGTAAGTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCGTGCGCACCCGCCCCCTCGCACTTGAAGATGCTGACTT  
CGCGATGTTGATGTGTCCAGCGGCGAGGAGGATGTCCAAGCGCAAATACAAGGAAGAGATGCTCCAGGTCATCGCGCCTGA  
GATCTACGGCCCCGCGGCGCGGTGAAGGAGGAAAGAAAGCCCCGAACTGAAGCGGGTCAAAAAGGACAAAAGGAGG  
AGGAAGATGACGGAAGTGGTGGAGTTTGTGCGCGAGTTGCCCCCGCGGCGCGTGCAGTGCGCGGGCGGAAAGTGAAAC  
CGGTGCTGCGGCCCGGCACACGGTGGTCTTACGCGCGCGAGCGTTCCGGCTCCGCTCCAAGCGTCTCTACGACGAGGT  
GTACGGGGACGAGGACATCCTCGAGCAGGCGGTGCGAGCGTCTGGGCGAGTTTGCCTACGGCAAGCGCAGCCGCCCCGCGCC  
CTTGAAAGAGGAGGCGGTGTCCATCCCGCTGGACCACGGCAACCCACGCCGAGCCTGAAGCCGGTGACCCTGCAGCAGGTG  
CTACCGAGCGCGGCGCGCGCCGGGGCTTCAAGCGCGAGGGCGGCGAGGATCTGTACCCGACCATGCAGCTGATGGTGCCC  
AAGCGCCAGAAGCTGGAGGACGTGCTGGAGCACATGAAGGTGACCCCGAGGTGCAGCCGAGGTCAAGGTGCGGCCCATC  
AAGCAGGTGGCCCCGGGCTGGGCGTGACACCGTGGACATCAAGATCCCCACGAGCCCATGGAACGCAGACCGAGCCC  
GTGAAGCCAGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCCAGCACCAGCTTCCACCAGCACTGCGCGAAGAC  
GCAAGTACGGCGCGGCCAGCCTGCTGATGCCAACTACGCGCTGCATCCTTCCATCATCCCCACGCGGGGCTACCGCGGCACG  
CGTTCTACCGCGGCTACACCAGCAGCCGCCCGCAAGACCACCCCGCGCGTCTGTCGAGCCGCCGAGCAGACCCGC  
GACTTCCGCTTGGTGCGGAGAGTGTATCGCAGCGGGCGCGAGCCTCTGACCCTGCCGCGCGCGCTACACCCGAGCATC  
GCCATTTAACTACCGCCTCTACTTGAGATATGGCCCTCACATGCCGCTCCGCGTCCCCATTACGGGTACCGAGGAAGAAA  
GCCGCGCGTAGAAGGCTGACGGGGAACGGGCTGCGTCCCATCACCACCGCGCGGCGCGCCATCAGCAAGCGGTTGGG  
GGGAGGCTTCTGCCCGCGCTGATCCCCATCATCGCCGCGCGATCGGGGCGATCCCCGGCATAGCTTCCGTGGCGGTGCAG  
GCCTCTCAGCGCCACTGAGACACAAAAAGCATGGATTGTAAATAAAAAAAATGGACTGACGCTCCTGGTCTGTGATGT  
GTGTTTTAGATGGAAGACATCAATTTTTCTGCTCCCTGGCACCCGACACGGCACGCGGCCGTTTATGGGCACTGGAGCGACA  
TCGGCAACAGCCAAGTGAACGGGGGCGCCTTCAATTGGAGCAGTCTCTGGAGCGGGCTTAAGAATTCGGGTCCACGCTCAA  
AACCTATGGCAACAAGGCTGGAACAGCAGCACAGGGCAGGCGCTGAGGGAAAAGCTGAAAGAACAGAACTTCCAGCAGAA  
GGTGGTTGATGGCCTGGCCTCAGGCATCAACGGGGTGGTTGACCTGGCCAACCAGGCCGTGCAGAAACAGATCAACAGCCGC  
CTGGACGCGGTCCCGCCGCGGGTCCGTGGAGATGCCCCAGGTGGAGGAGGAGCTGCCTCCCCTGGACAAGCGCGGCGAC  
AAGCGACCGGTCCCGACGCGGAGGAGACGCTGCTGACGCACACGACGAGCGCCCCCGTACGAGGAGGCGGTGAAACTG  
GGCCTGCCACACGCGGCCCGTGGCGCCTCTGGCCACCGGAGTGTGAAACCCAGCAGCAGCCAGCCCGCGACCCCTGGACT  
TGCTCCGCTCGCCCCCTCCACAGTGGCTAAGCCCTGCCCGGTGGCCGTGCGCTGCGCGCCCCCGAGGCCGCCCCAG  
GCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGGGAGTGACAGTGTGAAGCGCCGCGCTGCTATTTAAAGACAC  
TGAGCGCTTAACTTGCTGTGTGTATGTATGTCCGCCGACCAGAAGGAGGAGTGTGAAGAGGCGCGTCCCGAGTT  
GCAAGATGGCAACCCATCGATGCTGCCCCAGTGGGCGTACATGCACATCGCCGGACAGGACGCTTCGGAGTACCTGAGTCC  
GGGTCTGGTGCAGTTCGCCCCGCGCCACAGACACCTACTCAGTCTGGGGAACAAGTTTAGGAACCCACGGTGGCGCCACGC  
ACGATGTGACCACCGACCGCAGCCAGCGGTGACGCTGCGCTTCGTGCCCGTGACCGCGAGGACAACACCTACTCGTACAA  
AGTGCGCTACACGCTGGCCGTGGGCGACAACCGGTGCTGGACATGGCCAGCACCTACTTTGACATCCGCGGCGTGTGGAC  
CGGGGCCCTAGCTTCAAACCTACTCTGGCACCGCTACAACAGCCTAGCTCCCAAGGGAGCTCCCAATTCAGCCAGTGGGA  
GCAAGCAAAAACAGGCAATGGGGAACTATGGAACACACACATATGGTGTGGCCCAATGGGCGGAGAGAATATTACAAA  
AGATGGTCTTCAAATTGGAAGTACGTTACAGCGAATCAGAATAAACCAATTTATGCCGACAAAACATTTCAACCAGAACCGC  
AAGTAGGAGAAGAAAATTGGCAAGAACTGAAAATTTTATGGCGGTAGAGCTCTTAAAAAGACACAAACATGAAACCTTG  
CTATGGCTCTATGCTAGACCACCAATGAAAAAGGAGGTCAAGCTAACTTAAAGTTGGAGATGATGGAGTTCAACCAAAAG  
AATTCGACATAGACCTGGCTTTCTTGATACTCCCGGTGGCACCGTGAACGGTCAAGACGAGTATAAAGCAGACATTGTATGT  
ATACCGAAAAACAGTATTTGGAACCTCCAGACACGCATGTGGTATACAAACAGGCAAGGATGATGCAAGTTCTGAAATTAAC  
CTGGTTCAGCAGTCTATGCCAACAGACCCAACTACATTGGGTTACGGGACAACTTTATCGGTCTTATGTACTACAACAGCACT  
GGCAATATGGGTGTGCTTGTGTCAGGCTCCAGCTGAATGCTGTGGTTGATTGCAAGACAGAAACACCGAGCTGTCCTA  
CCAGCTCTTGCTTACTCTTTGGGTGACAGAACCCGGTATTCAGTATGTGGAACAGGCGGTGGACAGTTATGACCCCGATG  
TGCGCATCATCGAAAACCATGGTGTGGAGGATGAATTGCCAACTATTGCTTCCCCTGGACGGCTCTGGCACTAACGCCGCA  
TACCAAGGTGTGAAGTAAAGATGGTCAAGATGGTGATGTTGAGAGTGAATGGGAAAATGACGATACTGTTGCAGCTCGAA



Fig. 25F

ATCAATTATGTAAAGGTAACATTTTCGCCATGGAGATTAATCTCCAGGCTAACCTGTGGAGAAGTTTCTCTACTCGAACGTGG  
CCCTGTACCTGCCCCGACTCCTACAAGTACACGCCGACCAACGTACGCTGCCGACCAACACCAACACCTACGATTACATGAATG  
GCAGAGTGACACCTCCCTCGCTGGTAGACGCCTACCTAACATCGGGGCGCGCTGGTCGCTGGACCCCATGGACAACGTCAAC  
CCCTTCAACCACCACCGCAACGCGGGCCTGCGCTACCGCTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAG  
GTGCCCCAAAAGTTTTTCGCCATCAAGAGCCTCTGCTCCTGCCGGGTCTACACCTACGAGTGGAACCTCCGCAAGGACGTC  
AACATGATCCTGCAGAGCTCCCTAGGCAACGACCTGCGCAGGACGGGGCCTCCATCGCCTTACCAGCATCAACCTCTACGC  
CACCTTCTCCCATGGCGCACAACACCGCCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCTTCAACGA  
CTACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCATCTCCATCCCCTCGCGCAACTGGGC  
CGCCTTCCGCGGATGGTCCTTACGCGCCTGAAGACCCGCGAGACGCCCTCGCTCGGCTCCGGGTTGACCCCTACTTCGTCTA  
CTCGGGCTCCATCCCCTACCTAGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTC  
AGCTGGCCCCGCAACGACCGCCTCTGACGCCAACGAGTTCGAAATCAAGCGCACCGTCGACGGAGAGGGATACAACGTGG  
CCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCACTACAACATCGGCTACCAGGGCTTCTACGTGCC  
GAGGGCTACAAGGACCGCATGTACTCCTTCTCCGCAACTCCAGCCCATGAGCCGCCAGGTCTGGACGAGGTCAACTACAA  
GGACTACCAGGCCGTACCCCTGGCCTACCAGCACAACAACTCGGGCTTCGTGCGCTACCTCGCGCCACCATGCGCCAGGGCC  
AGCCCTACCCCGCCAACTACCCCTACCCGCTCATCGGAAGAGCGCCGTGCGCAGCGTCACCCAGAAAAAGTTCCTCTGCGACC  
GGGTCTGTGGCGCATCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTACCGACCTCGGCCAGAACATGCTCTACGCCA  
ACTCCGCCACGCGCTAGACATGAATTCGAAGTCGACCCCATGGATGAGTCCACCCTTCTCTATGTTGTCTTGAAGTCTTGA  
CGTCGTCCGAGTGACCAAGCCCCACCGCGGCGTCATCGAAGCGTCTACCTGCGCAGCCCTTCTCGGCCGGCAACGCCACCA  
CCTAAGCCGCTCTTGCTTCTGCAAGATGACGGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATCTCCGCGACCTGGGCTGC  
GGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCCCTGGATTATGCCCCGCACAAGCTGGCCTGCGCCATCGTGAACAC  
GGCCGGCCGCGAGACCGGGGCGAGCACTGGCTGGCCTTCGCTGGAACCCGCGCTCCACACATGCTACCTCTTGACCCCT  
TCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACAGTTCGAGTACGAGGGCTGCTGCGTCGACGCGCCTGGCCACCGA  
GGACCGCTGCGTCACCCTGGAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCTGCGGGCTTCTGCTGCATGT  
TCCTGCACGCTTCTGTCAGTGGCCCGACCGCCCATGGACAAGAACCCACCATGAACCTACTGACGGGGTGCCCAACGGC  
ATGCTCCAGTCGCCCCAGGTGGAACCCACCTGCGCCGCAACCAGGAAGCGCTTACCGCTTCTCAATGCCCACTCCGCTAC  
TTTCGCTCCACCGCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCAAGACATGTAAAAAACCGGTGTGTGTAT  
GTGAATGCTTTATTATATAAAGACACATGTTATGCCACCTTCTCTGAGGCTCTGACTTTATTAGAAATCGAAGGGTCT  
GCCGCTCTCGGCATGCCCCGCGGCGAGGATACGTTGCGGAAGTGGTACTTGGGCAGCACTTGAACCTCGGGGATCAGCAG  
CTTGGGCACGGGAGGTGCGGGAACGAGTCGCTCCACAGCTTGCCTGTAGTTGCAGGGCGCCAGCAGGTGCGGCGCGGA  
GATCTTGAATCGCAGTTGGGACCGCGTCTGCGCGGAGAGTTGCGGTACACGGGTTGCAGCACTGGAACACCATCAGG  
GCCGGGTGCTTACGCTTGCCAGCACCGTGCCTGCGGTGATGCCCTCCAGTCCAGATCCTCGGCGTTGGCCATCCGAAGGG  
GGTCATCTTGACAGTCTGCCGCCCATGCTGGGCACGACCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATC  
ATCTGGGCTGCTCGGAGCTCATGCCCGGTACATGGCCTTCATGAAAGCCTCCAGCTGGCGGAAGGCTGCTGCGCCTTGC  
GCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGAGAACTGGTGGTGGCGCAGCCGGCGTCTGTCACGCAGCAGCGCGC  
GTCGTTGTTGGCAGCTGCACACGCTGCGCCCCAGCGTCTGGGTGATCTTGGCCGTTGGGGTCTCCTTCAGCGCGC  
GCTGCCGTTCTCGCTCGCCACATCCATCTCGATAGTGTCTCCTTGGATCATCACGGTCCCGTGCAGGCACCGCAGCTTGC  
CCTCGGCTTCGGTGCAGCCGTGCAGCCACAGCGCGCAGCCGTGCACTCCAGTCTTGTGGGCGATCTGGGAGTGCGAGTG  
CACGAAGCCCTGCAGGAAGCGGCCCATCATCGCGGTGAGGTCTTGTGCTGGTGAAGGTGAGCGGGATGCCGCGGTGCTCC  
TCGTTACATACAGGTGGCAGATGCGGCGGTACACCTCGCCTGCTCGGGCATCAGCTGGAAGGCGGACTTCAGGTGCTCTC  
CACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCCATGCCCTTCTCCAGGCCGAAACGATCGGCAGGCTCAGGGGGTCT  
TCACCGCCATTGTCATCTTAGTCGCCGCCCGGAGGTGAGGGGTGCTTCTCGTCCAGGGTCTCAAACTCGCTTCCGCTCCT  
TCTCGATGATGCGCACGGGGGAAAGCTGAAGCCACGCGCCAGCTCCTCCTCGGCTGCCTTTCGTCCTCGCTGCTCTGG  
CTGATGTCTTGAAGGCACATGCTTGGTCTTGGCGGGTTCTTTTGGGCGGAGAGGCGGCGGCGATGTGCTGGGAGAGC  
GCGAGTCTCGTTACACGACTATTTCTTCTTGGCGCTGTCGAGACACGCGGCGGTAGGCATGCTCTTCTGGGGCA  
GAGGCGGAGGCGAGGGCTCTCGCGTTCGGCGGGCGGCTGGCAGAGCCCTTCCGCGTTCCGGGGTGCCTCTGGCGGC  
GCTGCTGACTGACTTCTCCGCGGCCGCGCATTTGTGTTCTCTAGGGAGCAACAACAAGCATGGAGACTCAGCCATCGTCG  
CCAACATCGCCATCTGCCCCGCGCCACCGCCGACGAGAACCAGCAGCAGAATGAAAGCTTAACCGCCCCGCGCCAGCCC  
CACCTCCGACGCGCGGCCCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGACCTGGGCTACGTGACGCGCGGAG  
CACGAGGAGGAGCTGGCAGCGCGCTTTTACGCCCGGAAGAGAACCACCAAGAGCAGCCAGAGCAGGAAGCAGAGAACGA  
GCAGAACCAGGCTGGGCAGGAGCATGGCGACTACCTGAGCGGGGAGAGGACGTGCTCATCAAGCATCTGGCCCGCAATG  
CATCATCGTCAAGGACGCGCTGCTCGACCGCGCGGAGGTGCCCTCAGCGTGGCGGAGCTCAGCCGCGCTACGAGCGCAAC

Fig. 25G

CTCTTCTCGCCGCGCGTGCCCCCAAGCGCCAGCCCAACGGCACCTGTGAGCCCAACCCGCGCCTCAACTTCTACCCGGTCTTC  
GCGGTGCCCCGAGGGCCTGGCCACCTACCACCTCTTTTTCAAGAACCAAAGGATCCCCGTCTCTGCGCGCCAACCGCACCCGC  
GCCGACGCCCTGCTCAACCTGGGCCCGCGCGCCGCCTACCTGATATCACCTCCTTGGAAGAGGTTCCCAAGATCTTCGAGGG  
TCTGGGCAGCGACGAGACTCGGGCCGCGAACGCTCTGCAAGGAAGCGGAGAGGAGCATGAGCACCAAGCGCCCTGGTGGA  
GTTGGAAGGCGACAACGCGCGCCTGGCGGTCTCAAGCGCACGGTCGAGCTGACCCACTTCGCCTACCCGGCGCTCAACCTGC  
CCCCAAGGTCATGAGCGCCGTCTGACCCAGGTGCTCATCAAGCGCGCCTCGCCCTCTCGGAGGAGGAGATGCAGGACCC  
CGAGAGTTCGGACGAGGGCAAGCCGTGGTCAGCGACGAGCAGCTGGCGCGCTGGCTGGGAGCGAGTAGCACCCCCAGAG  
CCTGGAAGAGCGGCGCAAGCTCATGATGGCCGTGGTCTGGTGACCGTGAGCTGGAGTGTCTGCGCCGCTTCTTTGCCGAC  
GCGGAGACCCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGGCACGGGTTCTGTCGCCAGGCCTGCAAGATCTCCA  
ACGTGGAGCTGACCAACCTGGTCTCTACATGGGCATCTGCACGAGAACCCTGGGGCAAAACGTGCTGCACACCACCTG  
CGCGGGGAGGCCCGCGCGACTACATCCGCGACTGCGTCTACCTGTACCTTGCCACACCTGGCAGACGGGCATGGGCGTGT  
GGCAGCAGTGCCTGGAGGAGCAGAACCTGAAAGAGCTTGCAAGCTCTGCAGAAAGAACCTCAAGGCCCTGTGGACCGGGTT  
ACTTTATGAGCCAAAGCATGTTGCAAAACTTTGCTCTTTTCATCTCGAACGCTCCGGGATCTGCCCCGACCTGCTCCGCGCT  
GCCCTCGGACTTCGTGCGCTGACCTTCCGCGAGTGCCCCCGCGCTCTGGAGCCACTGCTACTTGCTGCGCTGGCCAACTA  
CCTGGCCTACCACTCGGACGTGATCGAGGACGTGAGCGGCGAGGGTCTGCTGGAGTGCCACTGCCCTGCAACCTCTGCACG  
CCGACCCGCTCCCTGGCCTGCAACCCCGAGCTGTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGCCCCGCGCA  
CGGCGAGGGCAAGGGGGGTCTGAAACTCACCCGGGGTGTGGACCTCGGCCTACTTGCGCAAGTTCGTGCCCGAGGACTAC  
CATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCAGCCGCCCAAGGCCGAGCTGTGGCCTGCGTCATCACCCAGGGGGC  
CATCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTCTGCTGAAAAAGGGCCACGGGGTCTACTTGGAACCCC  
AGACCGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCGAGGAAGCAGCAAGAAGCTGAAAGTGAGCTGCCGCCG  
CCGGAGGATTTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGGAGGAGGAGATGGAAGACTGGGACAGCACTCAGGCAG  
AGGAGGACAGCCTGCAAGACAGTCTGGAGGAGGAAGACGAGGTGGAGGAGGCAGAGGAAGAAGCAGCCGCCGCGCAGACC  
GTCGTCTCGGCGGAGAAAGCAAGCAGCACGGATACCATCTCGCTCCGGGTCCGGGTCGCGGCGGCCGGGCCACAGTAG  
GTGGGACGAGACCGGGCGCTTCCCGAACCCACCACCCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCTGGCGGGG  
GCACAAAAACGCCATCGTCTCTGCTTGAAGCCTGCGGGGGCAACATCTCTTCACCCGCGCTACCTGCTCTTCCACCGCGG  
GGTGAACCTCCCCGCAACATCTTGCACTTACTACCGTCACTCCACAGCCCTACTACTGTTTCAAGAAGAGGCAGAAACCCA  
GCAGCAGCAGAAAACAGCGGCAGCAGCAGCTAGAAAATCCACAGCGGCGGCAGGTGGACTGAGGATCGCGGCGAACGAG  
CCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTTTCCACCCTCTATGCCATCTTCAGCAGAGTCGGGGGCGAGGAGCAGG  
AACTGAAAGTCAAGAACCCTTCTGCGCTCGCTACCCGCGATTGTCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTC  
TCGAGGACGCGGAGGCTCTCTTCAACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCCGCGCCCGCCACACACGGAAG  
GCGGGAATTACGTACCACTGCGCCCTTCGCCGACCATCATGAGCAAAGAGATTCCACGCTTACATGTGGAGCTACCAG  
CCCCAGATGGGCTGGCCGCGCGCGCCGAGGACTACTCCACCCGATGAAGTGGCTCAGTGCCGGGCGCGGATGATCTC  
ACGGGTGAATGACATCCGCGCCACCGAAACAGATACTCTAGAACAGTCAGCGATCACCGCCACGCCCCGCCATCACCTTA  
ATCCGCGTAATTGGCCCGCGCCCTGGTGTACCAGGAAATTTCCAGCCACGACCGTACTACTTCCGCGAGACGCCAGGGC  
GAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCCGGCGCGCGCCCTGTGTGTCACCGCCCCGCTCAGGGTATAAAGCG  
GCTGGTGATCCGAGGAGAGGCACACAGCTCAACGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTC  
CAACTCGCCGATCGGGGAGATCTTCTTCACGCCTCGTCAGGCCGTCTGACTTTGGAGAGTTCGTCTCGACGCCCGCTCG  
GGCGGCATCGGCACTCTCAGTTCTGGAGGAGTTCCTCCCTCGGTCTACTTCAACCCCTTCTCCGGTCCCCCGGCCACTAC  
CCGGACGAGTTCATCCGAACCTTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAATGTCCCATGGTGGCGCAGCTG  
ACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCCGCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGC  
TGCCCCGAGGAGCACCTCAGGGCCAGCCACGGAGTGCGGATCATCGTGAAGGGGGCCTCGACTCCACCTGCTTCGGAT  
CTTCAGCCAGCGACCGATCCTGGTCGAGCGCGAACAAGGACAGACCCTTCTACTTTGTACTGCATCTGCAACACCCCGGCCT  
GCATGAAAGTCTTTGTTGTCTGCTGTGTAAGTATAAAGCTGAGATCAGCGACTACTCCGACTCGATTGTGGTGTTC  
CTGCTATCAACCGGTCCCTGTTCTTACCAGGGAACGAGACCGAGCTCCAGCTCCAGTGTAAAGCCCCACAAGAAGTACCTACCT  
GGCTGTTCCAGGGTCCCCGATCGCGGTTGTCAACCACTGCGACAACGACGGAGTCCTGCTGAGCGGCCCTGCCAACCTTACTT  
TTTCCACCCGAGAAAGCAAGCTCCAGCTCTTCAACCTTCTCCCGGGACCTATCAGTGCCTCTCAGGACCCTGCCATCACAC  
CTTCCACCTGATCCGAATACCACAGCGCCGCTCCCCGCTACTAACAACCAAACTACCCACCAACGCCACCGTCGCGACCTTTCC  
TCTGAATCTAATAACCACTACCGGAGGTGGCTTCTGCTGTTAGTGCTCCCCGTCCGTCGACCCCCGGTCCCCCACTCAGTCCCC  
CGAGGAGGTTTCGCAAATGCAAAATCCAAGAACCTGGAATTCCTCAAATGCTACCGCCAAAAATCAGACATGCATCCAGCT  
GGATCATGATCATTGGGATCGTGAACATTCTGGCCTGCACCTCATCTCCTTTGTGATTACCCCTGCTTTGACTTTGGTTGGAA  
CTCGCCAGAGGCGCTATCTCCGCTGAACCTGACACACCACACAGCAGCAACCTCAGGCACACGCACTACCAACACCACA  
GCCTAGGCCACAATACATGCCATATTAGACTATGAGGCGGAGCCACAGCGACCCATGCTCCCCGCTATTAGTTACTTCAATCT  
AACCGGCGGAGATGACTGACCACTGGCCAATAACAACGTCAACGACCTTCTCCTGGACATGGACGGCCGCGCCTCGGAGCA  
GCGACTCGCCCAACTTCGATTCTGTCAGCAGCAGGAGAGAGCCGTCAAGGAGCTGCAGGACGGCATAGCCATCCACAGTGC  
AAGAGAGGCATCTTCTGCCTGGTGAACAGGCCAAGATCTCTACGAGGTACCCAGACCGACCATCGCCTCTCTACGAGCT  
CCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTGGAGTCAACCCATCGTCATACCCAGCAGTCGGGCGATACCAAGGGGT

Fig. 25H

GCATCCAAGTCTCTGCGACTCCCCGACTGCGTCCACACTCTGATCAAGACCCCTCTGCGGCCTCCGCGACCTCCTCCCATGAA  
CTAATCACCCCTTATCCAGTGAAATAAAGATCATATTGATGATGATTTAAATAAAAAAATAATCATTTGATTTGAAATAAAGA  
TACAATCATATTGATGATTTGAGTTTAAACAAAAATAAGAATCACTTACTTGAAATCTGATACCAGGTCTCTGTCCATGTTTTCT  
GCCAACACCACCTCACTCCCTCTTCCAGCTCTGGTACTGACGGCCCCGGCGGGCTGCAAATCTCTCCACACGCTGAAGGGG  
ATGTCAAATCTCTGCTCCCTCAATCTTATTTTATCTTCTATCAGATGTCCAAAAAGCGCGTCCGGGTGGATGATGACTTCGA  
CCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCCTCATCAACCCCCCTTCGTCTCTCAGATGGATTCCAAGAG  
AAGCCCTGGGGGTGTTGTCCTGCGACTGGCTGACCCCGTCAACCAAGAACGGGGAAATCACCTCAAGCTGGGAGAGG  
GGGTGGACCTCGACTCGTGGGAAAACTCATCTCAACACGGCCACCAAGGCCGCCGCCCTCTCAGTATTTCAAACAACACC  
ATTTCCCTTAAACTGCTGCCCTTTCTACAACAACATGGAATTTAAGCCTCAATGTCTCCACACCATTAGCAGTATTTCCAC  
ATTTAACACTTTAGGCATAAGTCTTGAAACGGTCTCAGACTTCAAATAAGTTGTTGACTGTACAATAACTCATCTCTTACA  
TTCAGCTCAAATAGCATCACAGTAAAAACAGACAAAGGGCTATATATTAAGTCCAGTGGAACAGAGGACTTGAGGGTAATAT  
AAGCCTAAAAAGAGGACTAGTTTTTGACGGTAATGCTATTGCAACATATATTGAAATGGCTTAGACTATGGATCTTATGATAG  
TGATGGAAAAACAAGACCGTAATTACCAAAATTGGAGCAGGATTAATTTTGATGCTAACAAAGCAATAGCTGTCAAAGTAG  
GCACAGGTTAAGTTTTGACTCCGCTGGTGCCTTGACAGCTGGAAACAAACAGGATGACAAGCTAACACTTTGGACTACCCCT  
GACCCAAGCCCTAATTGTCAATTACTTTAGACAGAGATGCCAAATTTACTCTCTGTCTTACAAAATGCGGTAGTCAAATACTAG  
GCACTGTGGCAGTGGCGGTGTTACTGTAGGATCAGCACTAAATCCAATTAATGACACAGTCAAAAGCGCCATAGTTTTCTTA  
GATTTGATTCGATGGTGTACTCATGTCAAATCATCAATGGTAGGTGATTACTGGAACCTTAGGGAGGGACAGACCACTCAA  
AGTGATAGCCTATACAAATGCTGTGGGATTCATGCCAAATATAGGTGCATATCCAAAACCCAAAGTAAACACCTAAAAATAG  
CATAGTCAGTCAGGTATATTTAACTGGAGAACTACTATGCCAATGACACTAACCTAATTTCAATGGCACTGATGAAAAAGA  
CACAACCCAGTTAGCACCTACTCTATGACTTTTACATGGCAGTGGACTGGAGACTATAAGGACAAAAATATTACCTTTGTCTAC  
CAACTCATTTCTTTTTCTACATCGCCAGGAATAATCCACCCAGCAAGCCAAACCCCTTTTCCACACCTTTTGTCTATATGGA  
AACTCTGAAACAGAAAAATAAGTTCAAGTGTTTTATTGAATCAACAGTTTTTACAGGACTCGAGCAGTTATTTTCTCCACCT  
CCCAGGACATGGAATACACCACCTCTCCCCCGCACAGCCTTGAACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCT  
CCACGTTCCACACAGTTTCAGAGCGAGCCAGTCTCGGATCGGTGAGGAGATGAAACCTCCGGGCACTCCCGCATCTGCACC  
TCACAGCTCAACAGCTGAGGATTGCTCGGTGGTGGGATCACGGTTATCTGGAAGAAGCAGAAGAGCGGCGGTGGGAATC  
ATAGTCCGCGAACGGGATCGGCCGGTGGTGTGCATCAGGCCCGCAGCAGTCGCTGCCGCCGCCGCTCCGTCAAGCTGCTG  
CTCAGGGGGTTCGGGTCCAGGGACTCCCTCAGCATGATGCCACGGCCCTCAGCATCAGTCGTCTGGTGCGGCGGGCGCAGC  
AGCGCATGCGAATCTCGCTCAGGTCACTGCAGTACGTGCAACACAGGACCACAGGTTGTTCAACAGTCCATAGTTCAACACG  
CTCCAGCCGAAACTCATCGCGGAAGGATGCTACCCACGTGGCCGTCGTACCAGATCCTCAGGTAAATCAAGTGGCGCTCCCT  
CCAGAAGACGCTGCCATGTACATGATCTCCTGGGCATGTGGCGGTTACCACTCCCGGTACCACATCACCTCTGGTTGAA  
CATGCAGCCCCGGATGATCCTGCGGAACACAGGGCCAGCACCGCCCCGCCCATGCAGCGAAGAGACCCCGGATCCCGG  
CAATGACAATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATAT  
GCTCATGCATCTCTCAGCACTCTCAGCTCCTCGGGGTCAAACCATATCCAGGGCACGGGGAATCTTGACAGGACAGCGA  
ACCCCGCAGAACAGGGGAATCCTCGCACATAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCC  
TCCACCAGAGAAGCGCGGGTCTCGGTCTCTCACAGCGTGGAAGGGGGCCGGCCGATACGGGTGATGGCGGGACCGGGCT  
GATCGTGTCTCGACCGTGTCTGATGATGAGTGTCTTTCGGACATTTTCTGACTTGCTGTAGCAGAACCTGGTCCGGGCGCTGCA  
CACCGATCGCCGGCGGGCTCTCGGCGCTTGAACGCTCGGTGTTAAAGTTGTAAGAACAGCCACTCTCTCAGACCGTGCAGCA  
GATCTAGGGCTCAGGAGTGATGAAGATCCCATCATGCCTGATAGCTCTGATCACATCGACCACCGTGGAATGGGCCAGGGCC  
AGCCAGATGATGCAATTTTGTGGGTTTCGGTGACGGCGGGGAGGGAAGAAGCAAGGAACCATGATTAACCTTTAATCCA  
AACGGTCTCGGAGCACTTCAAAATGAAGTACGGAGATGGCACCTCTCGCCCCGCTGTGTTGGTGGAAAAACAGCCAG  
GTCAAAGGTGATACGGTCTCGAGATGTTCCACGGTGGCTTCCAGCAAAGCCTCCACGCGACATCCAGAAACAAGACAATAG  
CGAAAGCGGGAGGGTCTCTAATCTCAACCATCATGTTACACTCCTGCACCATCCCAAGATAATTTTCATTTTCCAGCCTTG  
AATGATTGAACTAGTTCCTGAGGTAAATCCAAGCCAGCCATGATAAAAAAGCTCGCGCAGAGCACCTCCACCGGCATTCTTA  
GCACACCTCATAATCCAAGATATTCTGCTCCTGGTTCACCTGAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGA  
TCCCTGAGCTCCTCCCTCAGCAATAACTGTAAGTACTCTTTCATATCGTCTCCGAAATTTTAGCCATAGGACCCCAAGGAATAA  
GAGAAGGGCAAGCCACATTACAGATAAACCGAAGTCCCCCAGTGAGCATTGCCAATGTAAGATTGAAATAAGCATGCTG  
GCTAGACCCGGTGATATCTTCCAGATAACTGGACAGAAAAATCGGGTAAGCAATTTTAAAGAAATCAACAAAAGAAAAATCTT  
CCAGGTGCACGTTTAGGGCTCGGGAACAACGATGGAGTAAGTGCAAGGGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTG  
TAAAAAACAACAAATAAAACATTAAACCATGCTAGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCCAGCACCAAGGAGGCC  
ACGGGGTCTCCGGCGCGACCTCGTAAAAATGTGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGT  
GAATGATTGAGAAGAAGCATACCCCCGGAACATTGGAGTCCGTGAGTGAAAAAAGCGGCCGAGGAAGCAATGAGGCA  
CTACAACGCTCACTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATTTTCAAGTGCCTAAAAATGTAATTA  
CTCCCTCTGTCACAGGCAGCGAAGCTCCGATCCCTCCAGATACACATACAAAGCCTCAGCGTCCATAGCTTACCGAGCGGCA  
GCAGCAGCGGCACACAACAGGCGCAAGAGTCAGAGAAAAGACTGAGCTTAACCTGTCCGCCGCTCTCTGCTCAATATATAG  
CCCCAGATCTCACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAGCACACGCCAGAAACC  
GGTGACACACTCAGAAAAATACGCGCACTTCTCAAACGGCCAAACTGCCGTATTTCCGGGTTCACACGCTACGTATCAAAA  
CACGACTTTCAAATTCGTCGACCGTTAAAAACATCACCCGCCCGCCCTAACGGTCCGCGCTCCCGCAGCCAATCACCTTCT  
CCCTCCCCAAATTCAAACAGCTCATTTGATATTAACGCGCACCAAAAGTTGAGGTATATTATTGATGATG

Fig. 25I

**AdC6 020-DU422gp160(E1621) Amino acids – SEQ ID NO: 14****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVI GCGSGDR\*GRGG\*RFDDVAMRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFL  
GGCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDRLRGGFDYRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RLRS  
PDPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMKNLLRVRRFALLRDVRARYTR\*H\*LLTSMPTPIDVN  
DGKWPAWHYAQYMTLWDFPTWQYIYVLVIAITMVMRWFQYINGRG\*RFDSRGFPSLHPIDVNGSLFWHQNRDQDFPKCRNNSA  
PLTQMGGRRVRWEVYISRARLVNRQITRSFI VVYHS\*IANAVSASDITVSNLRLEFDATMRVRGIPRNWPQWWIWGILGFWMI  
CRVVGNDLWVTVYVGVVWKEAKTTLFCASDAKAYDKEVHNWATHACVPTDNPQEI VLENTENFNMWKNDMVDQMHE  
DIISLWDQSLKPCVKLTPLCVTLNCKNVNISANANATATLNSSMNGEIKNCSFNTTTEL RDKKQKVYALFYKPDVVP LNGGEHNETGE  
YILINCNSSTITQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCNNVSTVQCTHGIKPVVSTQ LLLNGSLAEEEEI VRSENLTNNIK  
TIIVHLNKSVEIKTRPNNNTRKSVRIGPGQTFYATGEIIGDIREAHCNISRETWNSTLIQVKEKLREHYNKTIFEPSSGGDLEVTTSHF  
NCRGEFFYCDTTKLFNETKLFNESEYVDNKTIILPCRIKQIINMWQEVGRAMYAPPIEGNITCKSNITGLLLTWDGGENSTEGVFRPG  
GGNMKDNWRSELYKYKVVEIKPLGVAPTSKRKVVGREKRAVGLGAVLLGFLGAAGSTMGAASITLVQARQLLSGIVQQSNLLR  
AIEAQHLLQLTVWGKQLQTRVLAIERYLKDDQLLGLWGCSGLICATAVPWNSSWSNKS LGDIWDNMTWMQWDREISNYTN  
TIFRLLED SQNQKEKEDLLALDSWKNLWNWFDITNWLWYIKIFIMIVGGLIGRLIIFGVLAIVKRV RQGYSPLSFQTLIPNPRGPDR  
LGRIEEEGGEQDKDRSIRLVSGFLALAWDDLRLSLCFSYHQLRDFILTAARAAELLGRSSLRGLRQGW EVLKYLGNLVQYWGLELKRS  
AINLFDTIAIAVAEGTDRIIEVIQRICRAIRYIPTRIRQGF EAALL\*GTSRVDPGGQTADQPRCLLVASHLLFAPPPCLP\*PWKVPLPLSF  
PNKMRKLHRIV\*VGVLFWGVGWGRTARGRIGKTIAGMLGMRWALWLLRRKEPADLQI\*IHLCRVRRKR\*\*NGIMGIMGLH\*\*IG  
QISTYAGHRACGLAPPQDMARVRAQRHDPLQCAPGLPRRHVHALPVQHAICEGAAGARCHVQSEPDGGV\*HECGAVENSEI\*\*I  
QDQVPGLRMRRQARQASARVCGGDDGGPATRSFGVVLQRDGVRLQRGRI\*LE\*VVFAGCEPA\*GAE\*LKSVVFCVLQQHERKRL  
L\*GRGIQLSDGASPLLGSSASECDGIHGGRPARAARELFNPDLRDPPELLVRGRSCRRSCCFRRQRRARNGPGRRLQLSGGQLEFH  
Q\*SRQPERGEAAAADGPARGDPAPGRADPAGGSAAGGDAGRGCHGENQIKNESINKRRRLILTQSLES LDFDSRAVGPGPPVSII  
EHPVDLFDQDPVEVGLDVEVHGHEPVPVGEVAPLQGLVLGDGVNHPVIAGA QGVVLHDVLEEETDGHGQPLGVGVDEPELVGG  
MHAGGDEMHLGLDLEIGDVPQAIPPGVHVVDHQHGVSGALGEFVMQLGREGVKEFGDALVTAQVFHALIHDDGDGPVGGGL  
GKDVSGVGHIVVVVLGELVIGHFNEFGAEGARLGDEGALDPGGVALADLHLPGLLELGGGDHVLRGDEKNGFRGGGDELGRKQ  
VPEQLGLAATGGAVDDPDRQLQVVVEGETAAVLAEEGGHLVHHLAHMHVLAHEFRQEALAPQREELLQRGEVFQRLESVGHGHF  
GEGLLQEFTVPELGDVL\*GISIQQTSSFRGLRLRE\*GTRRWASSEARVRSFQGRRVRSVSVSVTKGCAPGWALARVFRRLIRLV  
ENRSRSAPCASAR\*QLSMSS\*LSASAAWPLARSLPLEVCPQTGQRRDLRA\*SLGARKTDSGA\*ASAPQLAQTVSHSTSQVRSRGLGS  
KTRFPFCLMRFLPLVSMSSCPRWVTKRLSVSP\*TDFMGRSSSGVPRSSS\*RNPAHSETKARVQASTKEATWEG\* RSLSTSGSTFSR  
VCKHMSPTSSTRKVIGL\*V\*AT\*PGVPAGGV\*KGAGPCSSLSGSLRSASCWGRYLSKAGMTSALRLSVSRNEEDLILTVPLETF  
MSPSSIWSEKTIFLLSSLVAKEP\*RALESSLAMERMVWFFLSARSLAAMLSCYTSRATHFHSGKTVVSSSGTILTRQPRLCRVMRSTL  
VATSPRRGSLVQQRPLREKQGGSGSSMSSSGGSASTVKMPGRSSGSK\*LMQVPRLSAACSRTASARS\*GLRGVPQGMGCV  
SAEAYMPQMS\*T\*RGSSRTPM\*VG\*QRPPRMLART\*SYSSCEGARSPVPRLERCGFSAR\*TIWRKMAWELEEMVGLWKMLKWA  
WGRPTESLMKWA\*ESCLATSSAVTRTSRAQ\*SRVSWMMSYLSWPFCHSSRLRRNSSRSFQYSSRGNPS\*SAR\*EPTM\*NWLTA  
L\*AQQPFSTGRA\*ACAALREEVWVRKVSRMTLRNWCLKSRSSQPPCSQSWSKSVRFL\*AGLGKAKVTS LKRIPLARGMKLRVMR  
KGWGTSARLLMTWAARTISSKPLMLCPTM\*SSTNRGRPLTWGSFLSSS\*VSSAGSLSPCCSRAQSATWGLALRKEVQRSTARAVCK  
RSRY\*RNCWPTAIFSGVTQ\*KVRGSPCQRSHLSWRARSWASSTSGSPESFMTSMKGTSCLPKDPIQV\*VSTS\*VRKSLSVRGCEP  
MGKNWISCHQLEEWLLM\*WK\*KCRRRAEHSCLCLYKRPQCSQRCTGCTCCTCTWVPLARNFSGQWSAGGCISCCTTSWPSAW  
PSSASMVVMLTSPRGRQVQTSARTGRRARTRARRPELSRLRRCGVRSVSGSGGARLTCSRFSRARGRSRWYLISTAPLVATSTACRV  
PCPWGATTVPFFLGAASMSVRS GGEDARRAAGAARGPEAGAAGARRRRARAGSGTAPGEDWRERRRDG\*RPGSDASG\*RP  
DP\*V\*T\*KRVRQNNQSYR\*RRPAAGSLARRPSCPGRRSRS\*TARSPPEGLRGRARRRWRPGRWRGCP\* AARRRSCRPRSRRGCR  
PRLRRGRARA\*PPGRG\*ARRGA\*RPRSCRGAGRG\*AWWRCAR\*RRST\*SSGGAASR\*RRPGLPSVPWPRRSPRRS\*KTGSCAPR  
RSTPPPEDG\*ARRWWRAPRRARRPRGAPLPSPLPPPLTSLLLPPQEAVAGEPCVAGGARADGR\*SARWSPRAGDAWSR\*RRAR  
PRGAAA\*RRRASPGGRRGGLRWAGRGR\*RCILSIDP\*GLRART\*ASRDPRDPKTAERRLRASRSRKVG\*ARFLVLRVFGREAGGRC  
CW\*S\*SRRS\*DGGWWRGAPGPWARLAGCADGRPCRRGPDTRWGPCSSPA\*AAPRAPPPRPRGRACA\*ARTRAAAGRAPGR  
RRRAR\*GWPAAGSG\*GWSGSRSSRRSGRLRC\*WCRSSWP\*RTS\*RSGRVARARGT\*GASRRACRRCRRCRRARGTGIRRGSA  
AAGGRAAIARWRGRRARGPRA\*GGGSRRCTWTSR\*CRRRWWRRAGTRGRGRSCAAAGSSWWPRSGP\*GARSRGCSRHTG  
KNESGQRLDSVAWRLSERVGLRVYPGSNLESGWSRS\*RG TGTPVSTQAC\*RNLDQTEAGRFLALVAGHEKLVS AESGRPRWLA  
VVRKNRQGCVA VCPGSSLSARRRPDS AANVGVAAPSFRPLSQPTSPVTERAPLFFSCVFARCI PYCGRCAPT LHHNRPYRSSNSR  
RFCPRPSSSQPLPRRP\*AEPAFSMTWPWK RARGWRGWGRRRRSGTRACR\*KGTLARPTCPSRTCSETGAARS PRRCAPPASTRG

Fig. 25J

GSCGAAWTESGC\*GTRISRRS\*RGSA PRARTWPRPTWSRRTSRP\*RRRATSKNPSTTTTCAR\*SRARR\*PWA\*CTCGTCWRPSCR  
 TPRASR\*RRSCFWWCSTVGTTRRSGRRC\*ISPSRAAGSWTW\*TFCRASWCRSAGCRCPRSWRPSTSRC\*VWASTTLGRSTRPRT  
 CP\*TRR\*RSTGFTCA\*P\*KC\*P\*ATIWGCTATTGCTAR\*APAAGAS\*ATRS\*CTACSGP\*PGPGPRGRATLTWARTCAGSPAAGPW  
 KLPAPVPTWRRWTMRRRRASTWKTDGATVFLDDAATAAAS\*SRDAGGAAEPAVRH\*LLGRLDPGHATHHGADDPQSRSL\*TA  
 ASGQPALGHPGGRGALALEPHAREGAGHRERAGGEQGHPR\*RGRAGVQRAAGARGPLQQHQRADDEPGPHGDRRARGGVAAR  
 AVPPRVEPGLHGGAERLPEHAARQRAPGPGGLHQLHQRADGGRGAPERGVPGAGLLPDQSPGLADREPEPGFQELAGTVG  
 RAGPGRGPRDGVEPADAEAPAAAAGGALHGQRQREPLVPLPA\*PVPRGHRTGARGRADLPGDHPREPRAGPGGPGQPGG  
 HPELPADQPVAEDPAPVRAEHRGGAHPALRAAERGAVPDAGGGHAQRGARHDRAQHGAAQHVPRQPPVHQ\*ADGLLASGGRH  
 ELGLLYQRHLEPALAPAARVLHGRVHRARPQRRVPVGRRGQQRVLAASRNQCRVEERGRGPAAVLGAVRSRGCCRGGARGRQPL  
 PEPALFAEQRAQQRAGSADATAPAGRGGVPERLLVEARAREELPQ\*RDREPGGQDEPLEDVRARAQGRAPS\*QRRHP\*TPAARQ  
 AAGTVGVR\*GFRRRQQRVGLGWEWW\*PVRSPAPPYRAPDVRI\*KNKRRYSRPPWRPACVLLCCL\*\*YDEARVPGSSSLVRERD  
 AAGGGGGDAAPAGGALRAPAVPGAYGGAEQHSLLGAGTLVRYHPVVPVGGQVGRHRLAELPERPQQLPDHRGAEQRFHPHGG  
 QHPDHQL\*RALAVGRPAENHHAHQHAQREVRHVQQVQAGDGLAQDPQRRG\*\*L\*W\*SGRADLRVGGV\*AARGQLLDH  
 DHRSDEQRHHRQLLGGGAAERGAGERHRRREVRAQLPAGLGRPRDRAGDAGRVHQRGLPPRHRPAARLRRGLHREPPQQAGH  
 PQAAALPGGLPDVVRGPGGGQHPRALGCRSLREKQGG\*HRRGDRSRGHRLYRGAGR\*FC\*RCGSGRGG\*NRK\*DSHPAGGEGQ  
 QGQELQARARGQEKHRLPQLVPLQLRRPREGRALLDAAHHLGRHLRRGASLLVAARHDARPGHLPLHASS\*QLPGGGRRAPARLL  
 QELLQRAGRLLAAAARLHLAARLQPLPREPDRPPARAHHYHRQ\*KRSCSHRSRDPAAAQYQPGSPARDRH\*RQTPLPLRLQG  
 PGRSRAARPLEPHLLKNVHSHLAQ\*\*HRLGPARAQDVRRRSPTLHATPRARARALPRSLGRPQGRALAHRRRRDRPGGGRRRA  
 QLHARRRRARLHRGRRRHQRGRRAPVRPHQEPAAAHRPAAPEHPRHARGASLAAQQAHTQGHAGGGQTRGLRQQRRQD  
 PQTRGHGGGGGHRQHVPAAARQVRVGARRRRHRCARARAHPPPSHLKMLT SRC\*CVPAARRMSKRKYKEMLQVIAPEIYGAAA  
 VKEERKPRKLKRVKDKKEEEDDGLVEFVREFAPRRRVQWRGRKVKVLRPGTTVVFTGERSGSASKRSYDEVYGEDILEQAVR  
 LGEFAYGKRSRAPLKEEAVSIPLDHGNPTSLKPVTLQQLVPSAAPRRGFKREGGEDLYPTMQLMVPKRQKLEDVLEHMKVDPEV  
 QPEVKVRPIKQVAPGLGVQTVDIKIPTMETQTEPVKPSTSTMEVQTDWPMPAPASTSTRRRRKYGAASLLMPNYALHPSIITPG  
 YRGTFRYRGYTSSRRRKTTRRRRRSRRSSTATSALVRRVYRSGREPLTLPRARYHPSIAI\*LPPPTCRYGPHMPPPRPHYGLPRKKAAP  
 \*KADGERAASPPAAARHQAVGGRLPARADPHHRRGDRGDRHSFRGGAGLSAPLRHKKAWICNKKKNGLTLLVL\*CVFLDGR  
 HQFFVPGTATRAHAAYVGHLEHRHQPTERGLQLEQSLERA\*EFRVHAQNLWQQGVEQQHRAAGAEGAERTELPAEGG\*WPGL  
 RHQRRG\*PGQPGRAETDQPPGRGPARGVRGDAPGGGGAASPGQARRQATASRRGGDAADAHGRAAPVRGGGETGPAHHA  
 ARGASGHRSAETQQQPARDPGLASASPLHSG\*APAAGGRRVARPPRPPGELAHESEQHRGSGSAECEAPLLLKDTVALNLLVCV  
 YMYVRRPEGGV\*RGASPSCKMATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDRSQR  
 TLRFPVDREDNTYSYKVRYTLAVGDNRVLDMASTYFDIRGVLDRGPSFKPYSGTAYNSLAPKGAPNSSQWEQAKTGNGGTMETH  
 TYGVAPMGENITKDLQIGTDVTANQNKPIYADKTFQPEPQVGEENWQETENFYGGRAKKDTNMKPCYGSYARPTNEKGGQ  
 AKLKVGDDGVPTKEFDIDLAFFDTPGGTVNGQDEYKADIVMYTENTYLETPDTHVYKPGKDDASSEINLVQSQMPNRPNYIGFRD  
 NFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLDSLDRTRYFSMWNQAVDSYDPDVRIIENHGVEDELPNYCFP  
 LDGSGTNAAYQGVKVDGQDGDVESEWENDDTVAARNQLCKGNIFAMEINLQANLWRSFLYSNVALYLPDSYKYPTPTNVTLPN  
 TNYDYMNVRTPPSLVDAVNLIGARWSDPMDNVNPNFHHNRNAGLRYSMLLNGRYVPFHIQVPQKFFAIKSLLLPGSYTYE  
 WNFRKDVNMILQSSLGNDLRTDGASIAFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSFNDYLSAANMLYPIPANATNPISIPS  
 RNWAAFRGWSFTRLKTRETPSLGSGFDYFVYSGSIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVA  
 QCNMTKDWFLVQMLAHYNIGYQGIFYVPEGYKDRMYSFFRNFPMSRQVDEVNYKDYQAVTLAYQHNSGFGVGLAPTMRQ  
 GQPYPANYPYPLIGKSAVASVTQKFLCDRVMWRIPFSSNFMSMGALDGLQNMLYANSAHALDMNFEVDPMDDESTLLVVFV  
 FDVVRVHQPHRGVIEAVYLRTPFSAAGNATT\*AALASCKMTAGSGEQELRAILRDLGCGPCFLGTDFDKRFPFGMAPHLACAIVNTA  
 GRETGGEHWLAFAWNPRSHTCYLDFPFGFSDERLKQIYQFEYEGLLRRSALATEDRCTLKSTQTVQGPRSAACGLFCCMFLHAFV  
 HWPDRPMDKNPTMNLTLGVPNGMLQSPQVEPTLRRNQEALYRFLNAHSAYFRSHRARIKATAFDRMNQDM\*KTGVCM\*MLY  
 S\*\*TAHVYATFEALTFRNRRGSAGSRHGPRAGIRC GTGTWAAAT\*TRGSAAWARGGRGTSRSTACA\*VAGRPAAGRARS\*NRS  
 WDPRSARESCGTRGCTGTPSGPGASRLPAPSRR\*CPRPDPRRWPSRRGSSCRSAAPCWARSACGCNRSAGGSASSGPARRSSC  
 PGTWPS\*KPPAGGRPAAPCRPR\*RRPRRTC\*RTGWWSRRRARSSARRCWPAAPRCAPSGSG\*SWPGWGSPSARAARSRPH  
 SR\*CAPSGSSRSRAGTAACPRLRCSAATARSCTPSSCGRSGSASARSAPSGSPSSRSGSCW\*RSAGCRGAPRSHTGGRCGGTP  
 RPARASAGRRTSGRSPRGTPSAASSLPCSPRPRKRSAGSGGSSPLSS\*SPPRS GGSRPGSQTLCRPSR\*CARGES\*SPRPPAPP  
 RPAFRPRCPG\*CLAKAHAWSCGVSWFAAEAAAAMCWESASSRPRFLLLGRRPRPRGRHASSGAEAEATGSRGSAGGWQSPFR  
 VRGCAPGGAALTDFLRGRPLCSPREQQQAWRLSHRRQHRHLPPPPPTRTSSRMKA\*PPRRPAPPPTPRPQTCKRWRNPSRLTW  
 AT\*RPRSTRRSWQRAFPQRKRTTKSSQSRKQRTSRTRLGTSMAIT\*AGQRTCSSIWPANASSSRTRCSTAPRCPASAWRSSAPTS  
 ATSSRRACPPSASPTAPVSPTRASTSTRSSRCPRWPPTTSFRTKGSPPAAPTAPAPTCTSWAPAPAYLISPWKFRPSSRVWA

Fig. 25K

ATRLGPRTLCKEAERSMSTTAPWWSWKATTRAWRSSARSS\*PTSPTRRSTCPPRS\*APSWTRCSSAPRPSRRRRRCRTPRVRTRA  
SPWSATSSWRAGWERVAPPRAWKSGASS\*WPWSW\*PWSWSVCAASLPTRRPCARSRTCTTSSGTGSCARPASPTWS\*PTW  
SPTWASCTRTAWGKTCTPPCAGRPAATTSATASTCTSATPGRRWACGSSAWRSRT\*KSSASSCRRTSRPCGPGSTSVPPRTW  
PTSSSPSACG\*RCATGCPTL\*AKACCKTFALSSSNAPGSCPPAPRCPRTSR\*PSASAPRRSGATATCCAWPTTWPTTRT\*SRTSAA  
RVCWSATAAATSARRTAPWPATPSC\*ARPRSSAPSSCKAPATARARGV\*NSPRGCGPRPTCASSCPRTTIPSRSGSTRTNPSRPRPS  
CRPASSPRGSPWPNCCKPSRNPKNFC\*KRATGSTWTPRPERSTPASPRMPRGSSKKLKVLPPEDEEDWESSQAEEMEDW  
DSTQAEEDSLQDSLEEEDEVEEAEEEEAAARPSSSAEKASSTDISAPGRGRGGRAHSRWDETGRFPNPTTQTGKKERQGYKSWRG  
HKNAIVSCLQACGGNISFTRRYLLFHRGVNFPNRLHYRHLHSPYCFQEEAETQQQKTSGSSS\*KIHSGGRWTEDRGERAGADP  
GAEPDLSHPLCHLPAESGAGAGTESQEPFSALAHPLQSVSQERRPTSASHSRGRGSLQQVLRAHS\*RVARARPHTEKGGNYVTTC  
ALRPTIMSKEIPTPYMWSYQPMGLAAGAAQDYSTRMNWLSAGPAMISRVNDIRAHNRQILLEQSATATPRHHLNPRNWPAAL  
VYQEIPQPTTVLLPRDAQAEVQLTNSGVQLAGGAALCRHRAQGIKRLVIRGRGTQLNDEVVSSSLGLRPDGVFLAGSGRSSFTPR  
QAVLTLESSSSQPRSGGIGTLQFVEEFTPSVYFNPFSGSPGHYPDEFIPNFDaisesVDGYD\*MSHGGAADLARLRHLDHCRFRCF  
RDLAEFAYFELPEEHPOGPAHGVRIIEGGLDSHLLRIFSQRPLVEREQGQTLTLYCICNHPGLHESLCCLLCTEYNKS\*DQRLRLTRL  
WCSCYQVPVPLHRRERDRAPAPV\*APQEVPHLAVPGLPDRRCQPLRQRSPAERPCQPYFFHPQKQAPALPTLPPRDLVRLRLPS  
HLPPDPEYHSAAPRY\*QPNYPPTPPSRPFL\*I\*YHYRRWLLLLVLRPVDPRSPTQSPPEVRKCKFQEPWFKLCYRQKSDMHPSWI  
MIIGIVNILACTLISFVIYPCDFGWNSEALYLPPEPDTPPQQQQAHALPPQPRPQYMPILDYEAEPQRMPLPAISYFNLTGGDD  
\*PTGQ\*QRQRPSPGHGRPRLGAATRPTSHSSAAGESRQGAAGRSHPPVQERHLLPGETGQDLLRGHPDRPSPLRAPAAAEVH  
LPGRSQPHRHHPAVGRYQGVHPLLLRLRLRPHSDQDPLRPPRPPHELITPLSSEIKIILMMI\*IKKIII\*FEIKIQSY\*\*FEFNKNKESLT  
\*NLIPGLCPCFLPTPPHSPLSSGTAGPGLQTSSTR\*RGCIQPPVQSSFYLLSDVQKARPGG\*\*LRPRLPLRCRQRTDRALHQPLR  
LFRWIPREAPGGVVPATG\*PRHHQERGNHPQAGRGGGPRLVGKTHLQHGHHQRRPSQYFKQHFFP\*NCCPFLQQQWNFKPQC  
LHTISSISHI\*HFRHKS WKRSSDFK\*VVDCTTNSSSYQLK\*HHSKNRQRAIY\*LQWKQRT\*G\*YKPKKRTSF\*R\*CYCNIYWKWLRL  
WIL\*\*\*WKNKTRNYQNWRIKF\*C\*QSNQCQTRHRKF\*LRWCLDSWKQTG\*QANTLDYP\*PKP\*LSITFRQRCQIYSLYKMR\*S  
NTRHCGSGGCYCRISTKSN\*\*HSQKRHSFP\*I\*FRWCTHVKLINGR\*LLEL\*GGTDHSCSLYKCCGIHAKYRCISKPNK\*NT\*K\*HSQ  
SGIFNWRNYYANDTNHNFQWH\*\*KRHNPS\*HLLYDFYMAVDWRL\*GQKYLYCYQLILFFLHRPGIIPPSKPTFPPTTFVYMETLKQK  
NKVQVYF\*INSFTGLEQLFFLHPPRTWNTPPSPPAQ\*P\*TSECHW\*WTCFWSRSTQFQSEPVS DRSGR\*NPPGTPASAPHSSTAED  
CPRWGSRLSGRSRAAVGIIVRERDRPVVSHQAPQQSLPPPLRQAAAQGVVRVQGLPQHDAHGPHQSSGAAGAAHANLAQV  
TAVRATQDHQVQVQSSIVQHAPAETHRGKDATHVAVVPDPQVNVQVALPPEDAHHVHDLGHVAVHHLVPVPHPLVEHAAPDDP  
AEPQGGHRAHRAAKRPRIPAMTMEDPPLVPVDHLGAEQVYVGTAAQAYAHASLQHSQLLGGQNHIPGHGELLQDSEPRRTGQSS  
HITYIVHGGQIAIRQHRVILHQRSAGLGLLTAW\*GGRPIRVMAGRG\*SCSRPCHDAVAFGHFRTCCSRTWSGRCTPIAGGGGLGAW  
NARC\*SCKTATLSDRAADLGPQE\*\*RSHHA\*\*L\*SHRPPWNGPGPAR\*CNFVGFR\*RRGREEQEPP\*LTFNPNGLGALQNEGHGD  
GTSRPRCVGGK\*QPGQR\*YGRDVPRLWPAKPPRAHPETRQ\*RKREGSLIPQPCYTPAPSPDNFHFSSLE\*FELVPEVNPSQP\*\*K  
ARAEHPPPAFLSTPS\*FQDILLVHLQQIDKRNIKISAAIPELLPQQ\*L\*VLFHIVSEIFSHRTPRNKRASHITDKPKSPVSIKCKIEIS  
MLARPGDIFQITGQKIG\*AIFKKINKRKIFQVHV\*GLGNNDGVSARGAFQHG\*LADL\*KNKK\*NIKPC\*PGEQVGKSFSPAPGRPRG  
LRRDPRKNCRYD\*KPSQRDVPGGRR\*FEKKHTPPEHWS\*VKKSGRGSNEALQSLSSPAKRCHADEAQNFQVRKKCNYSPPAQ  
AAKLPIPPDHTKQRP\*LTRQQQRHTTGARVREKTEL\*PVRPLSAQYIAPDLH\*RKQSLKIPAK\*SHTPSTRPETGDTLRKIRALP  
QTAKLPSFPGSHATSSKHDFQIPSTVKNITRPAPNGRRSRSQSPSSLPKFKQLICILTRTKSLRYIID

Fig. 26A

**AdC7 010-DU172gp160(E1622) Nucleic Acids – SEQ ID NO: 7**

CATCATCAATAATATACCTCAAACCTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCCGAGAGACGGGCGACCGTTAGGGGCGGGCGGGTGACGTTTTGATGACGTGGCCGTGAGGCGGAGCCGGTTTGCAA  
GTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTCCCGCGCTCTCTGACAGGAAAT  
GAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGGCCATTTTCGCGCGAAAACCTGAATGAGGAAGTAAAAATCTGAGTAATTT  
CGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTT  
CACCTAAATTTCCCGGTACGGTGTCAAAGTCCGGTGTTTTACGTACGATATCATTTCCCGAAAGTGCCACCTGACCGTAACTA  
TAACGGTCCTAAGGTAGCGAAAGCTCAGATCTCCCGATCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGT  
TAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTAAGCTACAACAAGGCAAGGC  
TTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTG  
ACATTGATTATTGACTAGTATGCCAAGTACGCCCCATTGACGTCAATGACGGTAAATGGCCCCGCTGGCATTATGCCCAGTA  
CATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGTAC  
ATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCA  
CCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAATGGGCGGTAGGCGTGTACGGTGGGAG  
GTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAAC  
GCAGTCAGTGCTTCTGACACAACAGTCTGAACTTAAGGCTAGAGTACTTAATACGACTCACTATAGGCTAGTTAAGGCTAGA  
GTTGACGCCACCATGCGCGTGTATGGGCATCCTGCGCTCTACCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATGC  
TGATGATCTGCAACGTGTGGGGCAACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCT  
GTTCTGCGCCTCCGACGCCAAGGCCCAAGGAGGAGGTGCACAACATCTGGGCCACCCACGCTGCGTGCCACCCGACCCCA  
ACCCCGAGGAGATCGTGCTGAAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACAGATGCACGAGG  
ACATCATCTCCCTGTGGGACCACTCCCTGAAGCCCTGCGTGAAGCTGACCCCTGTGCGTGACCTGAACTGCTCCGACGTGA  
AGATCAAGGGCACCAACGCCACCTACAACAACGCCACCTACAACAACAACACCATCTCCGACATGAAGAACTGCTCCTTCA  
ACACCACCACCGAGATCACCGACAAGAAGAAGAGGAGTACGCCCTGTTCTACAAGCTGGACGTGGTGGCCCTGGACGGCAA  
GGAGACCAACTCCACCAACTCCTCCGAGTACCGCCTGATCAACTGCAACACCTCCGCCGTGACCCAGGCGTGGCCCAAGGTGTC  
CTTCGACCCCATCCCATCCACTACTGCGCCCCCGCCGGTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGG  
CCCCTGCAACAACGTGTCCACCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGTCCACCCAGCTGCTGTGAACGGCTCCCT  
GGCCGAGGAGGAGGTGGTGTATCCGCTTCGAGAACCTGACCAACAACGCCAAGATCATCATCGTGACCTGAACGAGTCCGTG  
GAGATCAACTGCACCCGCCCCTCCAACAACACCCGCAAGTCCGTGCGCATCGGCCCGGCCAGACCTTCTTCGCCACCGGCCA  
CATCATCGGCGACATCCGCCAGGCCACTGCAACATCTCCGCAAGAAGTGGAACACCACCTGCAGCGCGTGAAGGAGAAG  
CTGAAGGAGAAGTTCCCCAACAAGACCATCCAGTTCGCCCCCTCCTCCGGCGGCGACCTGGAGATCACCAACCACTCCTTCAAC  
TGCCGCGGCGAGTTCTTCTACTGCTACACCTCCGACCTGTTCAACTCCACCTACATGTCCAACAACACCGGCGGCGCCAACATC  
ACCCTGCAGTGCCGCATCAAGCAGATCATCCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCGCCGCA  
ACATCACCTGCAAGTCCAACATCACCGCCTGCTGCTGACCCGCGACGGCGGCAAGGAGAAGAACGACACCGAGACCTTCCG  
CCCCGGCGGCGGCGACATGCGCGACAACCTGGCGCTCCGAGCTGTACAAGTACAAGGTGGTGGAGATCAAGCCCTGGGCATC  
GCCCCGACAAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGGCATCGGCGCCGTGTTCTGGGCTTCTCTG  
GGCGCCCGGCGCAGCACCATGGGCGCCGCCAGCATGACCCTGACCGTGCAAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAAGC  
AGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCACATGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGAC  
CCGCGTGCTGGCCATCGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACC  
ACCGCCGTGCCCTGGAACGCCAGCTGGAGCAACAAGAGCTACGAGGAGATCTGGGGCAACATGACCTGGATGCAGTGGGAC  
CGCGAGATCAACAACCTACCAACACCATCTACAGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGAAGGAC  
CTGCTGGCCCTGGACAGCTGGGAGAGCCTGTGGAGCTGGTTCAACATCAACAACTGGCTGTGGTACATCCGCATCTTCATCAT  
CATCGTGGGCGGCTGATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCC  
TGAGCTTCCAGACCTGACCCCCAGCCCCGCGAGCCCGACCGCCTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACC  
GCGCCCGCAGCGTGCGCCTGGTGAACGGCTTCTGGCCCTGGCCTGGGAGGACCTGCGCAGCCTGTGCTGTTTACGCTACCAC  
CGCTGCGCGACCTGATCCTGATCGCCGCCGCGCCGCCCTGCTGGGCCGAGCAGCCTGTGGGGCTGCAGAAGGGCT  
GGGAGGCCCTGAAGTACCTGGGACGCTGGTGCAGTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCTGTTTCGACG  
CCATCGCCATCACCGTGGCCGAGGGCACCGACCGCATCATCAACATCGTGACGCGCATCAGCCGCGCCTTCTACAACATCCCCC  
GCCGCATCCGCCAGGGCTTCGAGGGCACCTGCAAGTAAGGTACCTTAGAGTCGACCCGGGCGGCCAAACCGCTGATCAGCCT  
CGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCGTGCTTCTTGACCTGGAAGGTGCCACTCCCACTGT  
CCTTCTCAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGTGGGGTGGGGCAGGACA

Fig. 26B

GCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACC  
AGCAGATCTGCAGATCTGAATTCATCTATGTCGGGTGCGGAGAAAGAGGTAATGAAATGGCATTATGGGTATTATGGGTCTGC  
ATTAATGAATCGGCCAGATATCGATATGCTGGCCACCGTGATGTGACCTCGACCCCCGCAAGACATGGCCCGAGTTTCGAGC  
ACAACGTCATGACCCGATGCAATGTGCACCTGGGGTCCCGCCGAGGCATGTTTCATGCCCTACCAAGTGAACATGCAATTTGTG  
AAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCCTGACGGGGGTGTTTGACATGAATGTGGAGCTGTGGAAAATTC  
TGAGATATGATGAATCCAAGACCAGGTGCCGGGCTGCGAATGCGGAGGCAAGCACGCCAGGCTTCAGCCCGTGTGTGTGGA  
GGTGACGGAGGACCTGCGACCCGATCATTGGTGTGTCTGCAACGGGACGGAGTTCGGCTCCAGCGGGGAAGAATCTGAC  
TAGAGTGAGTAGTGTTTGGGGGAGGTGGAGGGCTGTATGAGGGGCAGAATGACTAAAATCTGTGTTTTCTGTGTGTGCA  
GCAGCATGAGCGGAAGCGCCTCCTTGAGGGAGGGGTATTAGCCCTATCTGACGGGGCGTCTCCCTCCTGGGCGGGAGT  
GCGTCAGAATGTGATGGGATCCACGTGGACGGCCGGCCGTGACGCCCGGAACTCTCAACCCTGACCTACGCGACCCTG  
AGCTCCTCGTCCGTGGACGCGAGCTGCCGCCGAGCTGCTGCTCCGCCGCCAGCGCCGTGCGCGGAATGGCCCTGGGCGCCG  
GCTACTACAGCTCTCTGGTGGCCAACTCGACTTCCACCAATAATCCCGCCAGCCTGAACGAGGAGAAGCTGCTGCTGCTGATG  
GCCAGCTCGAGGCCCTGACCCAGCGCTGGGCGAGCTGACCCAGCAGGTGGCTCAGCTGCAGGCGGAGACGCGGGCCGCG  
GTTGCCACGGTGAAAACCAATAAAAAATGAATCAATAAATAACGGAGACGGTTGTTGATTTTAACACAGAGTCTTGAATCT  
TTATTTGATTTTCGCGCGCGGTAGGCCCTGGACCACCGGTCTCGATCATTGAGCACCCGGTGGATTTTTCAGGACCCGGTA  
GAGGTGGGCTTGATGTTGAGGTACATGGGCATGAGCCCGTCCCGGGGGTGGAGGTAGCTCCATTGCAGGGCCTCGTGCTC  
GGGGGTGGTGTGTAAATCACCCAGTCATAGCAGGGGCGCAGGGCGTGGTGCTGCACGATGTCCTTGAGGAGGAGACTGAT  
GGCCACGGGCGAGCCCTTGGTGTAGGTGTTGACGAACCTGTTGAGCTGGGAGGGATGCATGCGGGGGGAGATGAGATGCAT  
CTTGGCCTGGATCTTGAGATTGGCGATGTTCCGCCAGATCCGCCGGGGTTCATGTTGTGCAGGACCACCAGCACGGTGT  
ATCCGGCGCACTTGGGAATTTGTCATGCAACTTGAAGGGAAGGCGTGAAAGAATTTGGAGACGCCCTGTGACCGCCAG  
GTTTTCCATGCACTCATCCATGATGATGGCGATGGGCCGTGGGCGGCGGCTGGGCAAAGACGTTTCGGGGGTGCGACACA  
TCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAATGAATTTGGGGCGGAGGGTGCCGACTGGGGGACGAAGG  
TGCCCTCGATCCCGGGGGCGTAGTTGCCCTCGCAGATCTGCATCTCCAGGCCCTGAGCTCGGAGGGGGGGATCATGTCCACC  
TGCGGGGCGATGAAAAAACGGTTTCCGGGGCGGGGGAGATGAGCTGGGCCGAAAGCAGGTTCCGGAGCAGCTGGGACTT  
GCCGACGCCGTGGGGCCGTAGATGACCCCGATGACCGGCTGCAGGTGGTAGTTGAGGGAGAGACAGCTGCCGTCTCGCG  
GAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCATGTCATGTTCTCGCGCAGAGTTCGCCAGGAGGCGCTCGCCCCCA  
GCGAGAGGAGCTTTGCAGCGAGGCGAAGTTTTTCAGCGGCTTGAGYCCGTGCGCCATGGGCATTTTGGAGAGGGTCTGTTG  
CAAGAGTTCCAGACGGTCCCAGAGCTCGGTGATGTGCTCTAGGGCATCTCGATCCAGCAGACCTCTGTTTCGCGGGTGGG  
GCGACTGCGGGAGTAGGGACACCAGGCGATGGGCGTCCAGCGAGGCCAGGGTCCGGTCTTCCAGGGTGCAGGGTCCGCGT  
CAGCGTGGTCTCCGTACGGTGAAGGGGTGCGCGCCGGGCTGGGCGCTTGCGAGGGTGCGCTTACGGCTCATCCGGCTGGTC  
GAGAACCGCTCCCGGTGCGCGCCCTGCGCGTCCGCCAGGTAGCAATTGAGCATGAGTTCGTAGTTGAGCGCCTCGGCCGCGT  
GGCCCTTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGCAGACGGGACAGAGGAGGGACTTGAGGGCGTAGAGCTTGGGGG  
CGAGGAAGACGGACTCGGGGGCGTAGGCGTCCGCGCCGAGCTGGCGCAGACGGTCTCGCACTCCACGAGCCAGGTGAGGT  
CGGGCCGGTTGGGGTCAAAAACGAGGTTTCTCCGTGCTTTTGATGCGTTTCTTACCTCTGGTCTCCATGAGCTCGTGCCCC  
GCTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACTTATGGGCCGGTCTCGAGCGGGGTGCGCGGTCTCTCGTC  
GTAGAGGAACCCCGCCACTCCGAGACGAAGGCCCGGTCCAGGCCAGCACGAAGGAGGCCACGTGGGAGGGGTAGCGGT  
CGTTGTCCACGAGCGGTCCACCTTCTCCAGGGTATGCAAGCACATGTCCCCCTCGTCCACATCCAGGAAGGTGATTGGCTTGT  
AAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGGTATAAAGGGGGCGGGCCCTGCTCGTCTCACTGTCTTCCG  
GATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATCCCTCTCGAAGGCTGGCATAACCTCGGCACTCAGGTTGTAGTT  
TCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTTGGAGACGCTTTCATGAGCCCTCGTCCATCTGGTCAGAAAAGAC  
GATCTTTTGTGTCGAGCTTGGTGGCGAAGGAGCCGTAGAGGGCGTTGGAGAGGAGCTTGGCGATGGAGCGCATGGTCTG  
GTTCTTTTCTTGTGCGCGCGCTCCTTGGCGGCGATGTTGAGCTGCACGTA CTGCGCGCCACGCACTTCCATTCCGGGGAAGAC  
GGTGGTGAGCTCGTCGGGCACGATTCTGACCCGCCAGCCGCGGTTGTGACAGGTGATGAGGTCCACGCTGGTGGCCACCTCG  
CCGCGCAGGGGCTCGTTGGTCCAGCAGAGGCGCCCGCCCTTGC GCGAGCAGAAGGGGGGACGCGGTCCAGCATGAGCTCG  
TCGGGGGGGTGCGCGTCCACGGTGAAGATGCCGGGCGAAGCTCGGGGTGCAAGTAGCTGATGCAGGTGTCCAGATCGTCC  
AGCGCCGCTTGCCAGTCGCGCACGGCCAGCGCGCTCGTAGGGGCTGAGGGGCGTGCCCGAGGGCATGGGGTGCGTGAGC  
GCGGAGGCGTACATGCCGAGATGTCGTAGACGTAGAGGGGCTCTCGAGGACGCCGATGTAGGTGGGGTAGCAGCGCCCC  
CCGCGGATGCTGGCGCGACGTAGTCGTACAGCTCGTGCGAGGGGCGGAGGAGCCCGTGCCGAGGTTGGAGCGTTGCGGC  
TTTTCGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAGTTGGAGGAGATGGTGGGCTCTGGAAGATGTTGAAGTGG  
GCGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTAGGAGTCTGCAGCTTGGCGACGAGCTCGGCGGTGACGAGG  
ACGTCCAGGGCGCAGTAGTCGAGGGTCTCTGGATGATGTCTACTT GAGCTGGCCCTTCTGCTTCCACAGCTCGCGGTTGAG



Fig. 26C

AAGGAACTCTTCGCGGTCTTCCAGTACTCTTCGAGGGGGAACCCGTCCTGATCGGCACGGTAAGAGCCCACCATGTAGAACT  
GGTTGACGGCCTTGATAGGCGCAGCAGCCCTTCTCCACGGGGAGGGCGTAAGCTTGTGCGGCCTTGCGCAGGGAGGTGTGGG  
TGAGGGCGAAGGTGTGCGGCACCATGACCTTGAGGAACTGGTGCTTGAAGTCGAGGTGTCGCGAGCCGCCCTGCTCCAGAG  
CTGGAAGTCCGTGCGCTTCTTGTAGGCGGGGTGGGCAAAGCGAAAGTAACATCGTTGAAGAGGATCTTGCCCGCGCGGGG  
ATGAAGTTGCGAGTGATGCGGAAAGGCTGGGGCACCTCGGCCCGGTTGTTGATGACCTGGGCGGCGAGGACGATCTCGTCG  
AAGCCGTTGATGTTGTGCCCCACGATGTAGAGTTCCACGAATCGCGGGCGGCCCTTAACGTGGGGCAGCTTCTTGAGCTCGTC  
GTAGGTGAGCTCGGCGGGGTGCTGAGCCCGTGTCTGCTGAGGGGCCAGTCGGCGACGTGGGGGTTGGCGCTGAGGAAGG  
AAGTCCAGAGATCCACGGCCAGGGCGGTCTGCAAGCGGTCCCGGTACTGACGGAAGTCTGGCCACGGCCATTTTTTCGGG  
GGTGACGCGAGTAGAAGGTGCGGGGTGCGCGTGCCAGCGGTCCCACTTGAGCTGGAGGGCGAGGTCTGGGCGAGCTCGAC  
GAGCGGCGGGTCCCCGAGAGTTTCATGACCAGCATGAAGGGGACGAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTT  
TCCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAGCCGATGGGGAAGAACTGGATCTCTGCCACCACTTGG  
AGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGCGCCGAGCACTCGTGCTTGTGTTTATACAAGCGTCCGCA  
GTGCTCGCAACGCTGCACGGGATGCACGTGTGCACGAGCTGTACCTGGGTTCTTTGACGAGGAATTCAGTGGGCAGTGG  
AGCGCTGGCGGCTGCATCTGGTGCTGTACTACGTCTGGCCATCGGCGTGGCCATCGTCTGCCTCGATGGTGGTCATGCTGAC  
GAGCCCGCGCGGGAGGCAGGTCCAGACTTCGGCTCGGACGGGTGCGAGAGCGAGGACGAGGGCGCGCAGGCCGAGCTGT  
CCAGGGTCTGAGACGCTGCGGAGTCAGGTCACTGGGTCAGTGGGACGCGGCGCGCGGTTGACTTGACAGGAGCTTTCCAGGGCGC  
GCGGGAGGTCCAGATGGTACTTGATCTCCACGGCGCCGTTGGTGGCGACGTCCACGGCTTGAGGGTCCCGTGGCCCTGGGG  
CGCCACCACCGTGGCCGTTTCTTCTGGGCGCTGCTTCCATGCCGTCAGAAGCGGCGGCGAGGACGCGCGCGGGGCGGCA  
GGGGCGGCTCGGACCCGAGGACGGGGCGGCGAGGGGCACGTGCGCGCGCGCGCGGGCAGGTTCTGGTACTGCGCCCG  
AGAAGACTGGCGTGAGCGACGACGCGACGTTGACGTCTGGATCTGACGCCTTGGGTGAAGGCCACGGGACCCGTGAGT  
TTGAACCTGAAAGAGAGTTGACAGAAATCAATCTCGGTATCGTTGACGGCGGCCTGCCGAGGATCTCTGACGTCGCCCCGA  
GTTGTCTGGTAGGCGATCTCGGTGATGAAGTCTCGATCTCTCTCTCTGAAGGTCTCGCGGGCGGCGCGCTCGACGGTGG  
CCGCGAGGTCTGGAGATGCGGCCCATGAGCTGCGAGAAGGCGTTTATGCCGCGCTCGTTCCAGACGCGGCTGTAGACCAC  
GGCTCCGTGCGGGTGCAGCGCGCGCATGACCACCTGGGCGAGGTTGAGCTCGACGTGGCGGTGAAGACCGCGTAGTTGCA  
GAGGCGCTGGTAGAGGTAGTTGAGCGTGGTGGCGATGTGCTCGGTGACGAAGAAGTACATGATCCAGCGCGGAGCGGCAT  
CTCGCTGACGTGCGCCAGGGCTTCAAGCGCTCCATGGCCTCGTAGAAGTCCACGGCGAAGTTGAAAACTGGGAGTTGCGC  
GCCGAGACGGTCAACTCTCTCCAGAAGACGGATGAGCTCAGCGATGGTGGCGCGCACCTCGCGCTCGAAGGCCCCGGGG  
GCTCTCTTCTTCCATCTTCTCTCTCCACTAACATCTTCTACTTCTCTCAGGAGGCGGCGGCGGGGAGGGGCCCTGCG  
TCGCCGCGGCGCACGGGACAGCGGTGATGAAGCGCTCGATGGTCTCCCCGCGCGGCGACGCATGGTCTCGGTGACGGC  
GCGCCGCTCTCGCGGGGCGCAGCGTGAAGACGCGCGCGCATCTCCAGGTGGCCGCGGGGGGGTCTCCGTTGGGCGAG  
GGAGAGGGCGCTGACGATGCATCTTATCAATTGGCCGTAGGGACTCCGCGCAAGGACCTGAGCGTCTCGAGATCCACGGGA  
TCCGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGAGTCGCAAGGTAGGCTGAGCCCGTTTCTGTTCTTCGGGGATTTC  
GGGAGGCGGGCGGGCGATGCTGCTGGTATGAAGTTGAAGTAGGCGGTCTGAGACGGCGGATGGTGGCGAGGAGCACCA  
GGTCTTGGGCCGGCTTGTGATGCGCAGACGGTGGCCATGCCCCAGGCGTGGTCTGACACCTGGCGAGGTCTTGTGA  
GTAGTCTGATGAGCCGCTCCACGGGACCTCTCTCTCGCCGCGCGGCGCGTGCATGCGCGTGAGCCGAACCCGCGCTGGG  
GCTGGACGAGCGCCAGGTGCGCGACGACGCGCTCGGCGAGGATGGCTGCTGTATCTGGGTGAGGGTGGTCTGGAAGTCGT  
CGAAGTCGACGAAGCGGTGGTAGGCTCCGGTGTGATGGTATAGGAGCAGTTGGCCATGACGGACCACTGACGGTCTGGT  
GGCCGGTGCACGAGCTCGTGGTACTTGAGGCGGAGTAGGCGCGCGTGTGCAAGATGTAGTCGTTGACGGTGCACGA  
GGTACTGGTATCCGACGAGGAAGTGCGGCGGCGGCTGGCGGTAGAGCGGCCATCGCTCGGTGGCGGGGCGCGCGGCGCG  
AGGTCTCGAGCATGAGGCGGTGGTAGCCGTAGATGTACCTGGACATCCAGGTGATGCCGCGGCGGTGGTGGAGGCGCGC  
GGGAACCTCGCGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGTAGTTTATGGTGGCCGCGGTCTGGCCCGTAGGGCGC  
GCGCAGTCGTGGATGCTCTAGACATACGGGCAAAAACGAAAGCGGTGACGGCTCGACTCCGTGGCCTGGAGGCTAAGCGA  
ACGGGTTGGGCTGCGCGTGTACCCCGGTTCAATCTCAATCAGGCTGGAGCCGAGCTAACGTGGTACTGGCACTCCCGTCT  
CGACCAAGCCTGTAACGAAACCTCCAGGATACGGAGGCGGGTCTTTTTTGGCCTTGGTCTGCTGGTATGAAAACTAGTA  
AGCGCGGAAAGCGACCGCCCGCATGGCTCGCTGCCGTAGTCTGGAGAAAGAATCGCCAGGGTTCGTTGCGGTGTGCCCCG  
GTTGAGCCTCAGCGCTCGGCGCGGCGGATTCCGCGGCTAACGTGGGCGTGGTCTGCCCCGCTGTTTCAAGACCCCTTAGC  
CAGCCGACTTCTCAGTTACGGAGCGAGCCCTCTTTTTCTGTGTTTTTGCAGATGCATCCCGTACTGCGGCAGATGCGCCCC  
CACCCTCCACCTCAACCGCCCTACCGCCGACGAGCAGCAACAGCCGGCGCTTCTGCCCCGCCCCAGCAGCAGCCAGCCACT  
ACCGCGGCGGCGCGCGTGGAGCGGAGCCGCGGCTTCAATGACCTGGCCTTGAAGAGGGCGAGGGGCTGGCGCGGCTGGG  
GGCGTCTGCGCGGAGCGGCACCCGCGCGTGCAGATGAAAAGGACGCTCGCGAGGCCTACGTGCCAAGCAGAACCTGTT  
CAGAGACAGGAGCGGCGAGGAGCCCGAGGAGATGCGCGCCTCCCGCTTCCACGCGGGCGGGAGCTGCGGCGCGGCTGG

Fig. 26D

ACCGAAAGCGGGTGCTGAGGGACGAGGATTCGAGGCGGACGAGCTGACGGGGATCAGCCCCGCGCGCGCACGTGGCC  
 GCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGAGCAACTTCCAAAAATCCTTCAACAACCACGTGCGCA  
 CGCTGATCGCGCGGAGGAGGTGACCCTGGGCCTGATGCACCTGTGGGACCTGCTGGAGGCCATCGTGCAAGACCCACGAG  
 CAAGCCGCTGACGGCGCAGCTGTTTCTGGTGGTGACGACAGTCGGGACAACGAGACGTTAGGGAGGCGCTGCTGAATATC  
 ACCGAGCCCCGAGGGCCGCTGGCTCCTGGACCTGGTGAACATTCTGCAGAGCATCGTGGTGCAGGAGCGCGGGCTGCCGCTGT  
 CCGAGAAGCTGGCGGCTATCAACTTCTCGGTGCTGAGCCTGGGCAAGTACTACGCTAGGAAGATCTACAAGACCCCGTACGTG  
 CCCATAGACAAGGAGGTGAAGATCGACGGGTTTACATGCGCATGACCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGG  
 TGTACCGCAACGACAGGATGCACCGCGCGGTGAGCGCCAGCCGCGCGGCGAGCTGAGCGACGAGGAGCTGATGCACAGCC  
 TGCAGCGGGCCCTGACCGGGGCGGGACCGAGGGGGAGAGCTACTTTGACATGGGCGCGGACCTGCGCTGGCAGCCAGCC  
 GCCGGGCTTGAAGCTGCCGGCGGTTCCCCCTACGTGGAGGAGGTGGACGATGAGGAGGAGGAGGGCGAGTACCTGGAA  
 GACTGATGGCGCGACCGTATTTTTGCTAGATGCAGCAACAGCCACCGCCTCCTGATCCCGGATGCGGGCGGCGCTGCAGAGC  
 CAGCCGTCCGGCATTAACTCCTCGGACGATTGGACCCAGGCCATGCAACGCATCATGGCGCTGACGACCCGCAATCCCGAAGC  
 CTTTAGACAGCAGCCTCAGGCCAACCGGCTCTCGGCCATCCTGGAGGCCGTGGTGCCCTCGCGCTCGAACCCACGCACGAGA  
 AGGTGCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCATCCGCGGCGACGAGGCCGGGCTGGTGTACAACGCGCTGC  
 TGGAGCGCGTGGCCCGCTACAACAGCACCAACGTGCAGACGAACCTGGACCGCATGGTGACCGACGTGCGCGAGGCGGTGT  
 CGCAGCGGAGCGGTTCCACCGCGAGTCGAACCTGGGCTCCATGGTGGCGCTGAACGCCTTCTGAGCACGCAGCCCGCAA  
 CGTGCCCCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCGCTGCGGCTGATGGTGGCCGAGGTGCCCCAGAGCGAGGT  
 GTACCAGTCGGGGCCGGACTIONTTCTCCAGACCAGTCGCCAGGGCTTGACAGACCGTGAACCTGAGCCAGGCTTTCAAGAACT  
 TGCAGGGACTGTGGGGCGTGCAGGCCCGGTGGGGACCGCGCGACGGTGTGAGCCTGCTGACGCCGAACCTGCGCCTGC  
 TGCTGCTGCTGGTGGCGCCCTTACGGACAGCGGCAGCGTGAGCCGCGACTCGTACCTGGGCTACCTGCTTAACCTGTACCGC  
 GAGGCCATCGGGCAGGCGCACGTGGACGAGCAGACCTACCAGGAGATCACCCACGTGAGCCGCGCGCTGGGCCAGGAGGAC  
 CCGGGCAACCTGGAGGCCACCTGAACCTTCTGCTGACCAACCGGTGCGAGAAGATCCCGCCCCAGTACGCGCTGAGCACCGA  
 GGAGGAGCGCATCCTGCGCTACGTGCAGCAGAGCGTGGGGTGTTCTGATGCAGGAGGGGGCCACGCCACGCGCCGCGCT  
 CGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCTCGCAACCGCCGTTTCATCAATAAGCTGATGGACTACTTGCATC  
 GGGCGGCCGCCATGAACCTCGGACTACTTTACCAACGCCATCTTGAACCCGCACTGGCTCCCGCCCGCGGGTCTACACGGGC  
 GAGTACGACATGCCGACCCCAACGACGGGTTCTGTGGGACGACGTGGACAGCAGCGTGTCTCGCCGCGCCCCGCCACCA  
 CCGTGTGGAAGAAAGAGGGCGGGGACCGGCGGCCGTCTCGGCGCTGTCCGGTTCGCGCGGGTGCTGCCGCGCGGTGCTG  
 AGGCCGCCAGCCCCCTCCGAGCCTGCCCTTTTCGCTGAACAGCGTGCGCAGCAGCGAGCTGGGTGCGCTGACGCGGCCGCG  
 CCTGCTGGGCGAGGAGGAGTACCTGAACGACTCCTTGTGAGGCCCGAGCGCGAGAAGAACTTCCCAATAACGGGATAGAG  
 AGCCTGGTGGACAAGATGAGCCGTGGAAGACGTACGCGCACGAGCACAGGGACGAGCCCCGAGCTAGCAGCAGCGCAGGC  
 ACCCGTAGACGCCAGCGACACGACAGGCAGCGGGTCTGGTGTGGGACGATGAGGATCCGCGGACGACAGCAGCGTGTG  
 GACTTGGGTGGGAGTGGTGGTGGTAACCCGTTCTGCTCACTTGCGCCCGTATCGGGCGCTGATGTAAGAATCTGAAAAAT  
 AAAAAACGGTACTACCAAGGCCATGGCGACCAGCGTGCGTTCTTCTGTTGTTTGTAGTAGTATGATGAGGCGCGTGTACC  
 CGGAGGGTCTCTCCCTCGTACGAGAGCGTGATGCAGCAGGCGGTGGCGGCGGCGATGCAGCCCCGCTGGAGGCGCCTTA  
 CGTGCCCCGCGGTACCTGGCGCTACGGAGGGGCGGAACAGCATTGTTACTCGGAGCTGGCACCTTGTACGATACACCC  
 GGTGTACTCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGAACTACCAGAACGACCACAGCAACTTCTGACCACCGTG  
 GTGCAGAAACAGATTTCACCCCCACGGAGGCCAGCACCCAGACCATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCCAGC  
 TGAAAACCATCATGCACACCAACATGCCAACGTGAACGAGTTCATGTACAGCAACAAGTTCAAGGCGCGGGTGATGGTCTCG  
 CGCAAGACCCCCAATGGGGTCGCGGTGGATGAGAATTATGATGGTAGTCAGGACGAGCTGACTTACGAGTGGGTGGAGTTG  
 AGCTGCCCCGAGGGCAACTTCTCGGTGACCATGACCATCGATCTGATGAACAACGCCATCATCGACAACCTTGGCGGTGGGG  
 CGTCAGAACGGGGTGCTGGAGAGCGACATCGGCGTGAAGTTCGACACGCGCAACTTCCGGCTGGGGTGGGACCCCGTGACC  
 GAGCTGGTGATGCCGGGCGTGTACACCAACGAGGCCTTCCACCCGACATCGTCTGCTGCCGGCTGCGGCGTGGACTTCAC  
 CGAGAGCCGCTCAGCAACTGCTGGGCATCCGCAAGCGGCAGCCCTTCCAGGAGGGCTTCCAGATCCTGTACGAGGACCTG  
 GAGGGGGGCAACATCCCCGCGCTCTGGATGTGCAAGCCTATGAGAAAAGCAAGGAGGAGGCCGCGCAGCGCGACCGCA  
 GCCGTGGCCACCGCTTACCGAGGTGCGGGGCGATAATTTTGTAGCGCCGCGGCGAGTGCCGAGGCGGCTGAAACCGAAA  
 GTAAGATAGTCATCCAGCCGGTGGAGAAGGACAGCAAGGACAGGAGCTACAACGTGCTGCGGACAAGAAAAACACCGCCT  
 ACCGCAGCTGGTACCTGGCTACAACCTACGGCGACCCGAGAAGGGCGTGCGCTCCTGGACGCTGCTACCACTCGGACGTC  
 ACCTGCGGCGTGGAGCAAGTCTACTGGTCTGCCCCGACATGATGCAAGACCCGGTCACCTTCCGCTCCACGCGTCAAGTTAG  
 CAACTACCCGGTGGTGGGCGCCGAGCTCCTGCCGCTACTCCAAGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGC  
 TGGCGCCTTCACTCGCTCACGCAGCTTCAACCGCTTCCCCGAGAACCAGATCCTCGTCCGCCCGCCGCGCCACCATTAC  
 CACCGTCAGTGAACCGTTCTGCTCTACAGATCACGGGACCTGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGCGTGA

Fig. 26E

CCGTACTGACGCCAGACGCCGACCTGCCCCTACGTCTACAAGGCCCTGGGCGTAGTCGCGCCGCGCGTCTCTCGAGCCGC  
ACTTCTAAAAAATGTCCATTCTCATCTCGCCAGTAATAACACCGGTTGGGGCCTGCGCGCGCCAGCAAGATGTACGGAGG  
CGCTCGCAACGCTCCACGCAACACCCCGTGC GCGTGC GCGGGCACTTCCGCGCTCCCTGGGGCGCCCTCAAGGGCCGCGTGC  
GCTCGCGCACCACGTCGACGACGTGATCGACCAGGTGGTGGCCGACGCGCGCAACTACACGCCCGCCGCGCGCCCGCCTC  
CACCGTGACGCCGTATCGACAGCGTGGTGGCCGATGCGCGCCGGTACGCCCGCGCCAAGAGCCGCGCGCGGCGCATCGC  
CCGGCGGCACCGGAGCACCCCGCCATGCGCGCGGCGCGAGCCTTGCTGCGCAGGGCCAGGCGCACGGGACGCAGGGCCAT  
GCTCAGGGCGGCCAGACGCGCGGCTCCGGCAGCAGCAGCGCCGGCAGGACCCGACAGCGCGGCCACGGCGGCGGCGG  
CGGCCATCGCCAGCATGTCCCGCCCGCGCGCGCAACGTGTACTGGGTGCGCGACGCCGCCACCGGTGTGCGCGTGCCTGT  
GCGCACCCGCCCCCTCGCACTTGAAGATGCTGACTTCGCGATGTTGATGTGTCCAGCGCGGAGGAGGATGTCCAAGCGCAA  
ATACAAGGAAGAGATGCTCCAGGTCATCGCGCTGAGATCTACGGCCCCGCGGTGAAGGAGGAAAAGAAAGCCCGCAA  
GAAGCGGGTCAAAAAGGACAAAAGGAGGAGGAAGATGTGGACGGACTGGTGGAGTTTGTGCGGAGTTCCGCCCCCGG  
GGCGCGTGCACTGGCGCGGGCGGAAAGTGAAACCGGTGCTGCGGCCCGCACACGGTGGTCTTACGCCCGCGAGCGTT  
CCGGCTCCGCTCAAGCGCTCTACGACGAGGTGTACGGGGACGAGGACATCCTCGAGCAGGCGGTGAGCGTCTGGGCGA  
GTTTGCTTACGGCAAGCGCAGCCGCCCCGCGCCCTTGAAAGAGGAGGCGGTGTCCATCCCGCTGGACCACGGCAACCCACG  
CCGAGCCTGAAGCCGTGACCTGCAGCAGGTGCTGCCGAGCGCGCGCCGCGCGCGGGGCTTCAAGCGCGAGGGCGGCGAG  
GATCTGTACCCGACCATGCAGCTGATGGTGCCCAAGCGCCAGAAGCTGGAGGACGTGCTGGAGCACATGAAGGTGGACCCG  
AGGTGCAGCCCGAGGTCAAGGTGCGGCCCATCAAGCAGGTGGCCCCGGGCTGGGCGTGACAGCCGTGGACATCAAGATCC  
CCACGGAGCCCATGGAACGCAGACCGAGCCCGTGAAGCCAGCACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCC  
GGCGCCGGCTTCCACCACTCGCGAAGACGCAAGTACGGCGCGGCCAGCCTGCTGATGCCAACTACGCGTGCATCCTTCCA  
TCATCCCCACGCCGGGCTACCGCGGCACGCGCTTACCGCGGTACACCAGCAGCCGCCGCAAGACCACCCCGCGCGC  
CGTCGTCGACCCGCCGAGCAGCACCAGCGACTTCCGCCCGCGCCCTGGTGCGGAGAGTGATCCGCGAGCGGGCGGAGCCTC  
TGACCCTGCGCGCGCGCGCTACCACCGAGCATCGCCATTAACTCTGCCGTGCGCTCCTACTTGAGATATGGCCCTACAT  
GCCGCTCCGCGTCCCCATTACGGGCTACCGAGGAAGAAAGCCGCGCCGTAGAAGGCTGACGGGGAACGGGCTGCGTCGCC  
ATCACACCGCGCGGCGCGGCCATCAGCAAGCGGTTGGGGGAGGCTTCTGCCCGCGCTGATCCCCATCATCGCCGCGGC  
GATCGGGGCGATCCCCGGCATAGCTTCCGTGGCGGTGCAGGCCTCTCAGCGCCACTGAGACACAGCTTGAAAAATTTGTAATA  
AAAAAATGGAAGTACGCTCCTGGTCTGTGATGTGTGTTTTAGATGGAAGACATCAATTTTCGTCCCTGGCACCAGCGACAG  
GCACGCGGCCGTTTATGGGACCTGGAGCGACATCGGCAACAGCCAACTGAACGGGGGCGCCTCAATTGGAGCAGTCTCTG  
GAGCGGGCTTAAGAATTCGGGTCCACGCTCAAAACCTATGGCAACAAGGCGTGGAACAGCAGCAGGGCAGGCGCTGAG  
GGAAGGCTGAAAGAGCAGAACTTCCAGCAGAAGGTGGTGCATGGCCTGGCCTCGGGCATCAACGGGGTGGTGGACCTGGC  
CAACCAGGCCGTGCAGAAACAGATCAACAGCCGCTGGACGCGGTCCCGCCCGCGGGGTCCGTGGAGATGCCCCAGGTGGA  
GGAGGAGTGCCTCCCCTGGACAAGCGCGGCGACAAGCGACCGGTCCCGACGCGGAGGAGACGCTGCTGACGACACGGA  
CGAGCCGCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCACCACGCGGCCGCTGGCGCCTCTGGCCACCGGGGTGCTG  
AAACCAGCAGCAGCAGCCAGCCGCGACCTGGACTTGCCTCCGCTGCTTCCGCCCCCTCCACAGTGCTAAGCCCTGCCG  
CCGGTGGCGTGCCTGCGCGCGCCCCCGAGGCCGCCCGAGGCGAACTGGCAGAGCACTCTGAACAGCATCGTGGGTCTGG  
GAGTGACAGAGTGTAAGCGCGCGCTGCTATTAAGACACTGTAGCGCTTAACTTGCTTGTCTGTGTATATGTATGTCC  
GCCGACCAGAAGGAGGAAGAGGCGCGTGCAGGAGTTGCAAGATGGCCACCCATCGATGCTGCCCACTGGGCGTACATGC  
ACATCGCCGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGTGAGTTCGCCCGCGCCACAGACACCTACTTCACTGTG  
GGGAACAAGTTTAGGAACCCACGGTGGCGCCACGCACGATGTGACCACCGACCGCAGCCAGCGGCTGACGCTGCGTTCG  
TGCCCGTGGACCGGAGGACAACACCTACTCGTACAAAGTGCCTACACGCTGGCCGTGGGCGACAACCGCGTGTGGACAT  
GGCCAGCACCTACTTTGACATCCGCGGCGTGTGGATCGGGGGCCAGCTTCAAACCTACTCCGGCACCGCCTACAACAGCC  
TGGCTCCAAGGGAGCGCCAAACACTTGGCAGTGACATATAAGCTGGTGATACTGATACAGAAAAACCTATACATATGGA  
AATGCACCTGTGCAAGGCATTAGCATTACAAAGGATGGTATTCAACTTGGAAGTACAGCGATGGTCAGGCAATCTATGCAGA  
CGAAACTTATCAACCAGAGCCTCAAGTGGGTGATGCTGAATGGCATGACATCACTGGTACTGATGAAAAATATGGAGGCAGA  
GCTCTTAAGCCTGACACCAAAATGAAGCCTTGCTATGGTTCTTTGCAAGCCTACCAATAAAGAAGGAGGCCAGGCAAATGT  
GAAAACCGAAACAGGCGGTACCAAGAATATGACATTGACATGGCATTCTTCGATAATCGAAGTGCAGCTGCCGCCGCGCTA  
GCCCCAGAAATTGTTTGTATACTGAGAATGTGGATCTGGAACTCCAGATACCCATATTGTATACAAGGCAGGTACAGATGA  
CAGTAGCTCTTCTATCAATTTGGGTGAGCAGTCCATGCCAACAGACCAACTACATTGGCTTCAGAGACAACCTTATCGGTCT  
GATGTACTACAACAGCACTGGCAATATGGGTGTAAGTGGTGGACAGGCTCCAGCTGAATGCTGTGGTGGACTTGACAGGAC  
AGAAACACCGAACTGTCTACCAGCTCTTGTGACTCTCTGGGTGACAGAACCAGGTATTTAGTATGTGGAATCAGGCGGT  
GGACAGTTATGACCCCGATGTGCGCATTATTGAAAATCACGGTGTGGAGGATGAACTTCTAACTATTGCTTCCCCCTGGATGC  
TGTGGGTAGAAGTATACTTACCAGGGAATTAAGGCCAATGGTGATAATCAAACCACTGGACCAAGATGATACTGTTAATG

Fig. 26F

ATGCTAATGAATTGGGCAAGGGCAATCCTTCGCCATGGAGATCAACATCCAGGCCAACCTGTGGCGAACTTCTCTACGCG  
AACGTGGCGCTGTACTGCCCCGACTCCTACAAGTACACGCCGGCCAACATCACGCTGCCACCAACACCAACACCTACGATTAC  
ATGAACGGCCGCTGGTGGCGCCCTCGCTGGTGGACGCCTACATCAACATCGGGGCGCGCTGGTCTGGACCCCATGGACA  
ACGTCAACCCCTTCAACCACACCGCAACGCGGGCCTGCGATACCGTCCATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCC  
ACATCCAGGTGCCCCAAAAGTTTTTCGCCATCAAGAGCCTCCTGCTCCTGCCGGGTCTACACCTACGAGTGGAACCTTCGCA  
AGGACGTCAACATGATCCTGCAGAGCTCCCTCGGCAACGACCTGCGCACGGACGGGGCCTCCATCGCCTTCACCAGCATCAAC  
CTCTACGCCACCTTCTCCCCATGGCGCACAACACCGCCTCCACGCTCGAGGCCATGCTGCGCAACGACACCAACGACCAGTCC  
TTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCAACGCCACCAACGTGCCATCTCCATCCCCTCGCGCA  
ACTGGGCGCGCTTCCGCGGCTGGTCTTCACGCGCCTCAAGACCCGCGAGACGCCCTCGCTCGGCTCCGGGTTTCGACCCCTACT  
TCGTCTACTCGGGCTCCATCCCCTACCTCGACGGCACCTTCTACCTCAACCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCC  
TCCGTCAGCTGGCCCGGCAACGACCGCCTCCTGACGCCAACGAGTTCGAAATCAAGCGCACCGTCGACGGAGAGGGGTACA  
ACGTGGCCCAAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATGCTGGCCCACTACAACATCGGCTACCAGGGCTTCTAC  
GTGCCCGAGGGCTACAAGGACCGCATGTACTCCTTCTCCGCAACTTCAGCCCATGAGCCGCCAGGTCTGGACGAGGTCAA  
CTACAAGGACTACCAGGCCGTACCCCTGGCCTACCAGCACAACAACCTCGGGCTTCGTCCGCTACCTCGCGCCCAACATGCGCC  
AGGGCCAGCCCTACCCCGCCAACCTACCCCTACCCGCTCATCGGCAAGAGCGCGTTCGCCAGCGTCAACCAGAAAAAGTTCTC  
TGCGACCGGGTCATGTGGCGCATCCCCTTCTCCAGCAACTTCATGTCCATGGGCGCGCTCACCGACCTCGGCCAGAACATGCTC  
TACGCCAACTCCGCCCACGCGCTAGACATGAATTCGAAGTCGACCCCATGGATGAGTCCACCTTCTCTATGTTGCTTCGAA  
GTCTTCGACGTCTCGAGTGCACAGCCCCACCGCGGCTCATCGAGGCCGTCTACCTGCGCACGCCCTTCTCGGCCGGCAA  
CGCCACCACCTAAGCCTCTTGCTTCTTGCAAGATGACGGCCTGCGCGGGCTCCGGCGAGCAGGAGCTCAGGGCCATCCTCCGC  
GACCTGGGCTGCGGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCCGGGATTTCATGGCCCCGACAAGCTGGCCTGCGC  
CATCGTCAACACGGCCGGCGCGAGACCGGGGGCGAGCACTGGCTGGCCTTCGCTGGAACCCGCGCTCCACACCTGCTAC  
CTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACCAGTTCGAGTACGAGGGCCTGCTGCGTCGACGCGC  
CCTGGCCACCGAGGACCGTGCCTGACCTGAAAAAGTCCACCCAGACCGTGCAGGGTCCGCGCTCGGCCGCTGCGGGCTC  
TTCTGCTGCATGTTCTGACGCCTTCGTGCACTGGCCGACCGCCCCATGGACAAGAACCCACCATGAACCTGCTGACGGGG  
GTGCCAACGGCATGCTCCAGTCGCCCCAGGTGGAACCCACCCTGCGCCGCAACCAGGAGGCGCTCTACCGCTTCTCAACGC  
CCTACTCCGCTACTTTCGCTCCACCGCGCGCATCGAGAAGGCCACCGCCTTCGACCGCATGAATCAAGACATGTAATCCGG  
TGTGTGTATGTGAATGCTTTATTCATATAATAAACAGCACATGTTTATGCCACCTTCTCTGAGGCTCTGACTTTATTTAGAAATC  
GAAGGGGTCTGCGGCTCTCGGCATGGCCCGCGGGCAGGGATACGTTGCGGAACCTGGTACTTGGGCAGCCACTTGAACCTG  
GGGATCAGCAGCTTCGGCACGGGGAGGTTCGGGGAACGAGTCGCTCCACAGCTTGCAGGTGAGTTGCAGGGCGCCAGCAGG  
TCGGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCGCGCGCGAGAGTTACGGTACACGGGGTTGCAGCACTGGA  
ACACCATCAGGGCCGGGTGCTTCAGCTCGCCAGCACCGTCGCGTCGGTGATGCCCTCCAGTCCAGATCCTCGCGTTGGCC  
ATCCCGAAGGGGGTTCATCTGCAGGTCTGCCGCCCATGCTGGGCACGCAGCCGGGCTTGTTGTTGCAATCGCAGTGCAGGG  
GGATCAGCATCATCTGGGCTGCTCGGAGCTCATGCCGGGTACATGGCCTTCATGAAAGCCTCCAGCTGGCGGAAGGCCTGC  
TGCCTTTCGCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGAGAAGTGGTTGGTGGCGCAGCCAGCGTCTGTCACGC  
AGCAGCGCGCTGCTTGTGGCCAGCTGCACACGCTGCGCCCCAGCGGTTCTGGGTGATCTTGGCCCGGTTCGGGGTTCTCC  
TTCAGCGCGCTGCCGTTCTCGCTCGCCACATCCATCTCGATCGTGTGCTCCTTCTGGATCATCACGTCCTCGTGCAGGCACC  
GCAGTTGCCCTCGGCTCGGTGCACCCGTGCAGCCACAGCGCGCAGCCGGTGCTCTCCAGTTCTTGTTGGGCGATCTGGGAG  
TGCGAGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATCGTGGTCAGGGTCTTGTGCTGGTGAAGGTACGCGGAATGCCGC  
GGTGTCTCTCGTTCACATACAGGTGGCAGATACGGCGGTACACCTCGCCCTGCTCGGGCATCAGCTGGAAGGCGGACTTCAG  
GTCGCTCTCCACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCCATGCCCTTCTCCAGGCCGAAACGATCGGCAGGCTCAG  
GGGGTTCTTACCGTTGTCTTAGTCGCCGCCGCCGAAGTCAGGGGGTCTGTTCTCGTCCAGGGTCTCAAACACTCGCTTGC  
GTCTTCTCGGTGATGCGCACGGGGGAAAGCTGAAGCCACGGCCGCGAGCTCCTCCTCGGCTGCCCTTTCGTCTCGCTGT  
CCTGGCTGATGTCTGCAAGGCACATGCTTGGTCTTTCGGGGTTTCTTTTGGGCGCGAGAGGCGGCGGGCGGAGACGTGCT  
GGGCGAGCGGAGTTCTCGCTACACGACTATTTCTTCTCTTGGCCGTCTGCGAGACCACGCGGGGTAGGCATGCCTCTT  
CTGGGGCAGAGGCGGAGGCGACGGGCTCTCGCGTTTCGGCGGGCGGCTGGCAGAGCCCTTCCGCGTTTCGGGGGTGCGCTC  
CTGGCGGCGCTGCTGACTGACTTCTCCGCGGCCGGCCATTGTGTTCTCTAGGGAGCAAGCATGGAGACTCAGCCATCGT  
CGCCAACATCGCCATCTGCCCCCGCGCGCGGACGAGAACCAGCAGCAGCAGAATGAAAGCTTAACCGCCCCGCGGCCAGC  
CCCACCTCCGACGCCGAGCCCCAGACATGCAAGAGATGGAGGAATCCATCGAGATTGACCTGGGCTACGTGACGCCCGCGG  
AGCACGAGGAGGAGCTGGCAGCGCGCTTTTCAGCCCCGAAGAGAACCACCAAGAGCAGCCAGAGCAGGAAGCAGAGAGC  
GAGCAGAACCAGGCTGGGCTCGAGCATGGCGACTACCTGAGCGGGCAGAGGACGTGCTCATCAAGCATCTGGCCGCCAA  
TGATCATCGTCAAGGACGCGCTGCTGACCGCGCCGAGGTGCCCTCAGCGTGGCGGAGCTCAGCCGCGCTACGAGCGCA

Fig. 26G

ACCTCTTCTCGCCGCGCTGCCCCCAAGCGCCAGCCCAACGGCACCTGCGAGCCCAACCCGCGCTCAACTTCTACCCGGTCT  
TCGCGGTGCCCCAGGCCCTGGCCACCTACCACCTTTTTCAAGAACCAAGGATCCCCGTCTCTGCCGCGCCAACCGCACCC  
GCGCCGACGCCCTGCTCAACCTGGGCCCCGGCGCCCGCTACCTGATATCGCCTCCTTGGAAGAGGTTCCCAAGATCTTCGAG  
GGTCTGGGACGACGAGACTCGGGCCGCAACGCTCTGCAAGGAAGCGGAGAGGAGCATGAGCACCACAGCGCCCTGGTG  
GAGTTGGAAGGCGACAACGCGCGCTGGCGGTCTCAAGCGCACGGTCGAGCTGACCCACTTCGCCTACCCGGCGCTCAACC  
TGCCCCCAAGGTCATGAGCGCCGTATGGACCAGGTGCTCATCAAGCGCGCCTCGCCCCTCTCGGAGGAGGAGATGCAGGA  
CCCCGAGAGCTCGGACGAGGGCAAGCCCGTGGTCAGCGACGAGCAGCTGGCGCGCTGGCTGGGAGCGAGTAGCACCCCCCA  
GAGCTGGAAGAGCGGCGCAAGCTCATGATGGCCGTGGTCTGGTGACCGTGGAGCTGGAGTGTCTGCGCCGCTTCTTCGCC  
GACGCGGAGACCTGCGCAAGGTCGAGGAGAACCTGCACTACCTCTTCAGACACGGGTTCTGCGCCAGGCTGCAAGATCT  
CCAACGTGGAGCTGACCAACCTGGTCTCTACATGGGCATCTGCACGAGAACCGCTGGGGCAGAAGTGTGACACACCAC  
CTGCGCGGGGAGGCCCGCCGCGACTACATCCGCGACTGCGTCTACCTGTACCTCTGCCACACCTGGCAGACGGGCATGGGCG  
TGTGGCAGCAGTGCCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAAGCTCCTGCAGAAGAACCTCAAGGCCCTGTGGACCGG  
GTTGACGAGCGCACCAACCGCCGCGGACCTGGCCGACCTCATCTTCCCCGAGCGCCTGCGGTGACGCTGCGCAACGGGCTGC  
CCGACTTTATGAGCCAAAGCATGTTGCAAACTTTGCTCTTTTCATCTCGAACGCTCCGGGATCCTGCCCGCCACCTGCTCCGC  
GCTGCCCTCGGACTTCGTGCCGTGACCTCCGCGAGTGCCCCCGCGCTCTGGAGCCACTGCTACCTGCTGCGCTGGCCAA  
CTACCTGGCCTACCACTCGGACGTGATCGAGGACGTACGCGCGAGGGCTGCTCGAGTGCCACTGCCGTGCAACCTTGCA  
CGCCGACCGCTCCCTGGCTGCAACCCCCAGCTGCTGAGCGAGACCCAGATCATCGGCACCTTCGAGTTGCAAGGCCCCGGC  
GAGGGCAAGGGGGTCTGAAACTACCCCGGGGCTGTGGACCTCGGCCTACTTGCGCAAGTTCGTGCCGAGGACTACCATC  
CCTTCGAGATCAGTTCTACGAGGACCAATCCAGCCGCCAAGGCCGAGCTGTCGGCTGCGTCATACCCAGGGGGCCATC  
CTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTTCTGCTGAAAAAGGGCCACGGGGTCTACTTGACCCCCAGAC  
CGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCGAGGAAGCAGCAAGAAGCTGAAAGTGGAGTGCCGCGCGCGC  
CGGAGGATTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGGAGGAGGAGATGGAAGACTGGGACAGCACTCAGGCAGA  
GGAGGACAGCTGCAAGACAGTCTGGAGGAGGAAGACGAGGTGGAGGAGGCAGAGGAAGAAGCAGCCGCCAGACCG  
TCGTCTCGGCGGAGGAGGAGAAAGCAAGCAGCACGGATACCATCTCCGCTCCGGGTGCGGGTTCGCGCGCGCCGGCCAC  
AGTAGATGGGACGAGACCGGGCGCTTCCGAACCCACCACCAGACCGGTAAGAAGGAGCGGCAGGGATACAAGTCTGG  
CGGGGGCAGAAAAACGCCATCGTCTCTGCTTGAAGCCTGCGGGGGCAACATCTCCTTACCCGGCGCTACCTGCTCTTCAC  
CGCGGGTGAACTTCCCCGCAACATTTGCACTTACTACCGTCACCTCCACAGCCCCTACTACTGTTTCAAGAAGAGGCAGAA  
ACCCAGCAGCAGCAGCAGCAGCAAAAAACAGCGGCAGCAGCTAGAAAAATCCACAGCGGCGGCAGGTGGACTGAGGATCGC  
GGCGAACGAGCCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTTTCCACCTCTATGCCATCTTCCAGCAGAGTCGGGGG  
CAAGAGCAGGAAGTCAAAGTCAAGAACCCTTCTGCGCTCGCTCACCCGAGTTGTCTGTATCACAAGAGCGAAGACCAACT  
TCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGCGCGCTCACTCTTAAAGAGTAGCCCGCGCCCGCCACA  
CACGGAAGGCGGGAATTACGTACCACTGCGCCCTTCGCGGACCATCATCATGAGCAAAGAGATTCCACGCCTTACA  
TGTGGAGCTACCAGCCCCAGATGGGCTGGCCGCGCGCGCCAGGACTACTCCACCCGATGAACTGGCTCAGTGCCGG  
GCCCGCATGATCTCACGGGTGAATGACATCCGCGCCACCGAAACAGATACTCCTAGAACAGTCAGCGATACCGCCACGC  
CCCCCATACCTTAATCCGCGTAATTGGCCCGCGCCCTGGTGTACCAGGAAATCCCCAGCCACGACCGTACTACTTCCGC  
GAGACGCCAGGCCGAAGTCCAGCTGACTAACTCAGGTGTCCAGCTGGCCGCGCGCGCCGCTGTGTGCTACCGCCCCGCT  
CAGGGTATAAAGCGGCTGGTGATCCGAGGCAGAGGCACACAGCTCAACGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGA  
CCTGACGGAGTCTTCAAACCTGCGCGGATCGGGGAGATCTTCTTACGCCTCGTCAGGCCGTCTGACTTTGGAGAGTTCGTCC  
TCGAGCCCCGCTCGGGTGGCATCGGCACTCTCAGTTCGTGGAGGAGTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGC  
TCCCCCGGCACTACCCGACGAGTTCATCCGAACCTCGACGCCATCAGCGAGTCGGTGGACGGCTACGATTGAATGTCCA  
TGGTGGCGCGGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCCGCGCTTCCGCTGCTTCGCTCGGGATCTCGCCGAGT  
TTGCTACTTTGAGCTGCCGAGGAGCACCTCAGGGCCCGGCCACGGAGTGCGGATCGTCGTGAAGGGGTCTCGACTC  
CCACCTGCTTCGGATCTTACGCCAGCGTCCGATCCTGGCCGAGCGCGAGCAAGGACAGACCTTCTGACCTGTACTGCATCTG  
CAACCACCCCGGCTGCATGAAAGTCTTTGTTGTCTGCTGTGACTGAGTATAATAAAGCTGAGATCAGCGACTACTCCGGAC  
TTCCGTGTGTTCTGCTATCAACCAGTCCCTGTTCTTACCGGGAACGAGACCGAGCTCCAGTCCAGTGAAGCCCCACAAGA  
AGTACCTCACCTGGCTGTTCCAGGGCTCTCCGATCGCGTTGTCAACCACTGCGACAACGACGGAGTCTGCTGAGCGGCCCT  
GCCAACCTTACTTTTTCAACCCGAGAAGCAAGCTCCAGCTTCCAACCTTCTCCCCGGGACCTATCAGTGCGTCTCGGGAC  
CCTGCCATCACACCTTCCACCTGATCCGAATACCACAGCGTCGCTCCCCGCTACTAACAACCAAACTACCCACCAACGCCACCG  
TCGCGACCGCGGACATGTACAGAGCTCGAGAAGTACTAGGCCACAATACATGCCATATTAGACTATGAGGCCGAGCCACAG  
CGACCCATGCTCCCCGCTATTAGTTACTTAATCTAACCGGCGGAGATGACTGACCCACTGGCCAACAACAACGTCAACGACCT  
TCTCTGGACATGGACGGCCGCGCTCGGAGCAGCGACTCGCCAACTTCGCATTCGCCAGCAGCAGGAGAGAGCCGTCAAG

Fig. 26H

GAGCTGCAGGACGGCATAGCCATCCACCAGTGCAAGAAAGGCATCTTCTGCCTGGTGAAACAGGCCAAGATCTCTACGAGG  
TCACCCCGACCGACCATCGCTCTCTACGAGCTCCTGCAGCAGCGCCAGAAGTTCACCTGCCTGGTCGGAGTCAACCCCATCG  
TCATCACCCAGCAGTCGGGCGATACCAAGGGGTGCATCCACTGCTCCTGCGACTCCCCGACTGCGTCCACACTCTGATCAAGA  
CCCTCTGCGGCCTCCGCGACCTCCTCCCCATGAACTAATCACCCCTTATCCAGTGAAATAAATATCATATTGATGATGATTTAA  
ATAAAAAATAATCATTTGATTGAAATAAAGATACAATCATATTGATGATTTGAGTTTTAAAAATAAAGAATCACTTACTTGAA  
ATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACCTCACTCCCCTCTCCAGCTCTGGTACTGCAGACCCCGGG  
GCTGCAAACTTCTCCACACGCTGAAGGGGATGTCAAATTCCTCTGTCCCTCAATCTTCATTTTATCTTCTATCAGATGTCCAAA  
AAGCGCTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGATGCAGACAACGCACCGACCGTGCCCTTCATCAACCC  
CCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCTGGGGGTGCTGCCCTGCGACTGGCTGACCCCGTCACCCACCAAGAA  
CGGGGAAATCACCTCAAGCTGGGAGAGGGGTGGACCTCGACTCCTCGGGAAGTCACTCTCCAACACGGCCACCAAGGCC  
GCCGCCCTCTCAGTTTTTCCAACAACACCATTTCCCTTAACATGGATAACCCCTCTTTATACCAAGATGGAAAATTATCTTACA  
AGTTTCTCCACCGTTAAACATATTAATAAACAACCATTTCTGAACACATTAGCTGTAGCTTATGGATCAGGTTTAGGACTGAGTGG  
TGGCACTGCTCTTGCAGTACAGTTGGCCTCTCCACTCACTTTTGATGAAAAAGGAAATATTAATAAATTAACCTAGCCAGTGGTCC  
ATTAACAGTTGATGCAAGTCGACTTAGTATCAACTGCAAAAGAGGGGTCACTGTCACTACCTCAGGAGATGCAATTGAAAGCA  
ACATAAGCTGGCCTAAAGGTATAAGATTTGAAGGTAATGGCATAGCTGCAACATTGGCAGAGGATTGGAATTTGGAACCAC  
TAGTACAGAGACTGATGTACAGATGCATACCCAATTCAAGTTAAATTGGGTACTGGCCTTACCTTTGACAGTACAGGCGCCAT  
TGTTGCTTGGAACAAAAGAGGATGATAAATTACATTATGGACCACAGCCGACCCCTCGCCAAATTGCAAAATATACTTGAAAA  
AGATGCCAACTCACACTTTGCTTGACAAAGTGTGGAAGTCAAATTTCTGGGTACTGTGACTGTATTGGCAGTGAATAATGGAA  
GTCTCAACCCCAATCAAAACAGTAAGCACTGCACTCGTCTCCCTCAAGTTTGATGCAAGTGGAGTTTTGCTAAGCAGCTCCA  
CATTAGACAAAGAATATTGGAACCTCAGAAAGGGAGATGTTACACCTGCTGAGCCCTATACTAATGCTATAGGTTTTATGCCTA  
ACATAAAGGCCTATCTAAAAACACATCTGCAGCTTCAAAAAGCCATATTGTCACTCAAGTTTATCTCAATGGGGATGAGGCCA  
AACCCTGATGCTGATTATTACTTTTAAAGAACTGAGGATGCAACTTGACCTACAGTATCACTTTTCAATGGAAATGGGATA  
GTACTAAGTACACAGGTGAAACACTTGCTACCAGCTCCTTACCTTCTCTACATCGCCCAAGAATGAACACTGTATCCCACCT  
GCATGCCAACCCCTCCACCCCACTCTGTCTATGGAAAAAAGTCTGAAGCACAAAATAAAATAAAGTTCAAGTGTTTTATTGATT  
CAACAGTTTTACAGGATTCGAGCAGTTATTTTTCTCCACCTCCAGGACATGGAATACACCACCTCTCCCCCGCACAGCCT  
TGAACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTCCACACAGTTTCAGAGCGAGCCAGTCTCGGGTCCG  
TCAGGGAGATGAAACCTCCGGGCACTCCCGCATCTGCACCTCACAGCTCAACAGCTGAGGATTGTCTCGGTGGTCCGGGATC  
ACGTTATCTGGAAGAAGCAGAAGAGCGGGCGGTGGGAATCATAGTCCGCGAACGGGATCGGCCGGTGGTGTGCATCAGGC  
CCCGCAGCAGTCGCTCGCCGCGCTCCGTCAAGTGCTGCTCAGGGGTCCGGGTCCAGGACTCCCTCAGCATGATGCC  
ACGGCCCTCAGCATAGTCGTCTGGTGCGGGCGGCGCAGCGCATGCGGATCTCGCTCAGGTCGTGCTGACGTACGTGCAAC  
ACAGGACCACAGGTTGTTCAACAGTCCATAGTTCAACACGCTCCAGCCGAAACTCATCGCGGAAGGATGCTACCCACGTGG  
CCGTCTGATCAGATCCTCAGGTAATCAAGTGGCGTCCCTCCAGAACGCTGCCACGTACATGATCTCCTTGGGCATGTGG  
CGGTTACACCTCCCGGTACCACATACCCCTCTGGTTGAACATGCAGCCCCGATGATCCTGCGGAACCACAGGGCCAGCAC  
CGCCCCGCCCGCATGCAGCGAAGAGACCCCGGTCCCGGCAATGGCAATGGAGGACCCACCGCTCGTACCCGTGGATCATC  
TGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATGCATCTTTCAGCACTCTCAGTCTCTCGGGGTCAA  
AACATATCCAGGGCACGGGGAATCTTGACAGGACAGCGAACCCCGCAGAACAGGGCAATCCTCGCACATAACTTACATTGT  
GCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCAGAGAAGCGCGGGTCTCGGTCTCTCACAGCGTGG  
TAAGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGTGATCGTGTTCGCGACCGTGTGATGATGCAAGTGTCTTTCGGAC  
ATTTTCTACTTGCTGTAGCAGAACCTGGTCCGGGCGTGCACACCGATCGCGGCGGCGGTCCCGCGCTTGGAAACGCTCGG  
TGTTGAAATTGTAACACGCACTCTCAGACCGTGACAGCTTAGGGCTCAGGAGTGATGAAGATCCCATGCTGCTG  
ATAGCTCTGATCACATCGACCACCGTGAATGGGCCAGACCCAGCCAGATGATGCAATTTTGTGGGTTTCGGTGACGGCGGG  
GGAGGGAAGAACAGGAAGAACCATGATTAACCTTTAATCAAACGGTCTCGGAGCACTTCAAAATGAAGGTGCGGGAGATGG  
CACCTCTCGCCCCGCTGTGTTGGTGGAAAATAACAGCCAGGTCAAAGGTGATACGGTCTCGAGATGTTCCACGGTGGCTTC  
CAGCAAAGCCTCCACGCGCATCCAGAAACAAGACAATAGCGAAAGCGGAGGGTTCTTAATTCCTCAATCATCATGTTAC  
ACTCCTGCACCATCCCCAGATAATTTTCAATTTTCCAGCCTGAATGATTGAACTAGTTCTGAGGTAAATCCAAGCCAGCCAT  
GATAAAGAGCTCGCGCAGAGCGCCTCCACCGGCACTTCTAAGCACACCCCTCATAATCCAAGATATTCTGCTCCTGGTTCACC  
TGACAGCAGATTGACAAGCGGAATATCAAATCTCTGCCGCGATCCCTAAGTCTCCTCCTCAGCAATAACTGTAAGTACTCTTTC  
ATATCCTCTCCGAAATTTTAGCCATAGGACCACAGGAATAAGATTAGGGCAAGCCACAGTACAGATAAACCGAAGTCTCTCC  
CAGTGAGCATTGCCAAATGCAAGACTGCTATAAGCATGTGCTGCTAGACCCGGTGATATCTCCAGATAACTGGACAGAAAATC  
ACCCAGCAATTTTTAAGAAAAATCAACAAAAGAAAAATCTCTCAGGTGACCGTTTAGAGCCTCGGGAACAACGATGAAGTAAA  
TGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAATAAACAATAAATAAATTAACCATGCTAGCCTGGCGA  
ACAGGTGGGTAAATCGTTCTCTCCAGCACAGGACAGGCCACGGGTCTCCGGCGCGACCTCGTAAAAATTGTGCTATGATT  
GAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTGACAAGATGAATACACCCCGGAACATTGGCGTCC  
GCGAGTGAAAAAAGCGCCGAGGAAGCAATAAGGCACTACAATGCTCAGTCTCAAGTCCAGCAAAGCGATGCCATGCGGAT  
GAAGCACAAAATCCTCAGGTGCGTACAAAATGTAATTACTCCCTCTGCACAGGCAGCGAAGCCCCGATCCCTCAGATACA  
CATACAAAGCCTCAGCGTCCATAGCTTACCGAGCAGCAGCACACAACAGGCGCAAGAGTCAGAGAAAGGCTGAGCTTAACC  
TGTCACCCGCTCTCTGCTCAATATATAGCCAGATCTACACTGACGTAAAGGCCAAAGTCTAAAAATACCCGCCAAATAATCA  
CACACGCCCAGCACACGCCCAGAAACCGGTGACACACTCAAAAAATACGCGCACTTCTCAAACGCCCAAATGCCGTCAATT  
CCGGGTTCCACGTACGTATCGGAATTCGACTTTCAAATTCGTGACCGTTAAAAACGTACCCCGCCCCGCCCTAACGGT  
CGCCGCTCTCTCGGCAATCACCTTCTCCCTCCCAAATTCAAACAGCTCATTTGCATATTAACGCGCACCAAAAGTTGAGGT  
ATATTATTGATGATG

Fig. 26I

**AdC7 010-DU172gp160(E1622) Amino acids – SEQ ID NO: 15****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVGIGRETGDR\*GRGG\*RFDDVAVRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFLG  
 GCK\*KRAIFARKLNEEVKI\*VISRLWQGGVFAEGRVDFDLRGGFDIRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RKLRS  
 DPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMNLLRVRRFALLRDVRARYTR\*H\*LLTSMPTSPIDVND  
 GKWPAWHYAQYMTLWDFPTWQYIYVLVIAITMVMRFWQYINGRG\*RFDSRGFSPSLHPIDVNGSLFWHQNRDQFPCRNNSAP  
 LTQMGGRRVRWEVVISRARLVNRQITRSFIADVYHS\*IANAVSASDTSVSNLRLEYLRLTIG\*LRLEFDATMRVMGILRSYQQWWI  
 WGILGFWMMLMNCNVWGNLWVTVYGVVWKEAKTTLFCASDAKAHKEEVHNIWATHACVPTDPNPQEIVLKNVTENFNMWK  
 NDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLNCSVDVKIKGTATYNNATYNNNNNTISDMKNCSFNNTTEITDKKKKEYALFYKLDV  
 VALDGKETNSTNSSEYRLINCNTSAVTQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCNNVSTVQCTHGKIPVSTQLLNG  
 SLAEVEVIRFENLTNNAKIIVHLNESVEINCTRPSNTRKSVRIGPGQTFATGDIIGDIRQAHCNISRKKWNTTLQRVKEKLEKFPN  
 KTIQFAPSSGGDLEITTHSFNCRGEFFCYTDLFNSTYMSNNTGGANITLQCRIKQIIRMWQGVQAMYPPIAGNITCKSNITGLL  
 LTRDGGKEKNDTETFRPGGDMRDNRSELYKYKVVEIKPLGIAPDAKARRVVEREKRAVGIGAVFLGFLGAAGSTMGAASMTLT  
 VQARQLLSGIVQQSNLLRAIEAQQHMLQLTVWGIKQLQTRVLAIERLYKDDQLLGIWGCSCGLICTTAVPNASWSNKSYYEIIW  
 GNMTWMQWDREINNYNTIYSLLEESQNQKEKNEKDLLALDSWESLWSWFNITNWLWYIRIFIIIVGGGLIGLRIIFAVLSIVNRVRQ  
 GYSPLSFQTLTPSPREPDLRGRIEEEGGEQDRARSVRLVNGFLALAWEDLRSCLFSYHRLRDLILIAARAAALLGRSSLWGLQKGWE  
 ALKYLGLSLVQYWGLELKKSAISLFDIAITVAEGTDRIINIVQRISAFYNIPRRIRQGFEATLQ\*GTSRVDPPGGQTADQPRCLLVASHL  
 LFAPPPCLP\*PWKVPLPSFPNKMRLHRIV\*VGVILFWGVGWGRTARGRIGKTIAGMLGMRWALWLLRRKEPADLQI\*IHLCRVR  
 RKR\*\*NGIMGIMGLH\*\*IGQISICWPPCM\*PRTPARHGPSSSTTS\*PDAMCTWGPAEACSCPTSATCNL\*RCCWSPMPCPE\*A\*R  
 GCLT\*MWSCGKF\*DMMNPRPGAGPANAEASTPGFSPCVWR\*RTCDPIIWCCPATGRSSAPAGKNLTRVSSVWGRWRACMRG  
 RMTKICVFLCVA\*\*\*AEAPPLREGYSALI\*RGVSPPGRECVRM\*WDPRWTAGPCSPRTLQP\*PTRP\*APRPWTQLPPQLLLPPPAP  
 CAEWPWAPATTALWWPTRLPIIPA\*TRRSCC\*WPSRP\*PSAWAS\*PSRWLSCRRRRGPRLPR\*KPNKK\*INK\*TETVDFNT  
 ES\*IFI\*FFARGRPWTTGLDH\*APGGFFPGPRGGLGC\*GTWA\*ARPGGGSSAGPRARGWCKSPSHSRGAGRGAARCP\*GG  
 D\*WPRAAPWCRC\*RTC\*AGRDACGR\*DAWPGS\*DWRCRPDPAGGSCCAGPPARCIRRTWGICHATWKGRRERIWRPCD  
 RPFPGCTHP\*\*WRWARRPGQRFFGGRTHRSCGP\*ARHRPF\*\*IWGGGCTGGRCPRSRGRSCPRRSASPR\*ARRGGSC  
 PAGR\*KKRFPGRGR\*AGPKAGSGAAGTCRSRWGR\*PR\*PAAGGS\*GRDSCRPGGGGPPRSSRAHACSRARVPPGGARPPAR  
 GALAARRSFSA\*XRPPWAFWRGVARVPDGPARR\*CALGHLDPADLLSVRGATAGVGHQAMGVQRGQGPVLPGSQGPQR  
 GLRHGEGVRAGLGACEGALQAHAGREPLVPGALRVGQVAIEHEFVVERLGRVALGAELTFGSVSADGTEEGLEGVELGGEEDGLG  
 GVGVRAAAGADGLALHEPGEVGPVGKNEVSSVLFDAFLTSLGLHELVSPLDKEAVRVPVDRLYGPVLERGA AVLVEEPRPLRDE  
 GPGPGQHEGGHVGGVAVVVHQRVHLLQGMQAHVPLVHIQEGDWLVSVGHVTGGPGRGGIKGGGPLLVTVFRIAVQERQLLG\*  
 VFPLEGWHLNLTQVVSF\*KRGDFDIDGAVGDAFHEPLVHLVRKDDLFFVELGGEGAVEGVGEELGDGAHGLVLFLVGALLGGDVE  
 LHVLRHALPFGEDGGELVGHDSPPAAVVQGDDEVHAGGHAAQGLVGPAEAPALARAEGGQRVQHELVGGVGVHGEDAGQK  
 LGVEVADAGVQIVQRRLPVAGHQRALVGAEGRAPGHGVRERGGVHAADVVDVEGLLEDADVGGVAAPPADAGAHVVVQLVRG  
 REEPRAEVGALRLFGAVDDLAEDGVGVGGDGGPLEDVEVGVGQADRVDPDEVGVLQLGDELGGDEDVQGA VVEGLDDVLE  
 LALLPQLAVEKELFAVLPVLFEGEPVLIGTVRAHHVELVDGLVGAAALLHGEVSLCGLAQGGVGEGEVGAHHDLEELVEVEVVA  
 AALLPELEVRALLVGGVGQSESNIVEEDLARAGHEVASDAERLGHLPVDDLGGEDDLVEAVDVVPDDVEFHESRAALNVGQLE  
 LVVGELGGVAEPVLEGPVGDVGVAEEGSPHIGQGGLQAVPVLTELAHGHFFGGDAVEGAGVAVPAVPLEGEVVGELDER  
 RVPGEFHDQHEGDELLAEGPHPGVGFHIVGEEEPFGARMRADGEELDLLPVGGMADVMEVEMPTARRALVLFIQASAVLATL  
 HGMHVLHELVLGSFDEEFQWAVERWRLHLVLYVLAIGVAIVCLDGGHADEPAREAGPDFGSDGSESEDEGAQAGAVQGPETLRS  
 QVSGQRRRAVDLQELFQGAREVQMVLDLHGA VGGDVHGLQGPVPLGRHHRAPFLGRCFHAGQKRRRGRAPGGRGSGPGGR  
 GGRGTSAPRAGRFWYCARRRLA\*ATTRRLTSWI\*RLVWKATGPVSNLKESSTESISVSLTAACRRISCTSPESLW\*AISVMNCSISS  
 \*RSPRPARSTVAARSLEMRPMSCEKAFMPASFQTRL\*TTAPSGSRARMITTWARLSSTWRVKTA\*LQRRW\*R\*LSVAMCSVTKKY  
 MIQRRSGISLTSRASKRSMAS\*KSTAKLKNWELRAETVNSSRRRMSSAMVARTSRSKAPGGSSSSSSSTNISSTSSSGGGGGGG  
 ALRRRRRTGRRSMKRMVSPRRRMVSVTARPSSRGRSVKTPPRISRWPPEGSPPLGRERALTMLHINWPVGTTPRKDLSVSRSTGSE  
 NR\*TKASSQSQSGRLSPVSCSSGISGGGRAMLLVMKLK\*AVLRRRMVARSTRSLGPACWMRRRSAMPQAWS\*HLARSL\*\*SCM  
 SRSTGTSSSPARPCMRVSPNPRWGWSARSATTRSARMACCIWVRVWVWKSSTKRW\*APVLMV\*EQLAMTDQLTVWWPGRT  
 SSWYLRE\*ARVSKM\*SLQVRTRYWYPTKCGGGWR\*SGHRSVAGAPGARSSSMRRW\*P\*MYLDIQVMPAAVVEARGNSRTRF  
 QMLRSGRK\*FMVAAVWPVRRASQSWML\*TYGQKRKRSAARLRGLEAKRTGWAARVPRFESRI RLEPQLTWYWHSLRDPSSLTKPP  
 GYGGGSFFGLGRWS\*KTSKRGKRPPAMARCSLEKESPLRCGVPRFEPQRSAPAGFRG\*RGRGCPVVS KTP\*PADFSSYGASPSF  
 SCVFARCIPIYCGRCAPTLHLNRPYRRSSNSRRFCPRPSSQPLPRPP\*AEPAFSMTWPWKRARGWRGWGRRRRSGTRACR\*KG



Fig. 26J

TLARPTCPSRTCSETGAARSPRRCAPPASTRGGSCGAAWTESGC\*GTRISRRTS\*RGSA PRARTWPRPTWSRRTSRP\*RRRATSKNP  
STTTCAR\*SRARR\*PWA\*CTCGTCWRPSCRTPRASR\*RRSCFWWCSTVGTTRRSGRRC\*ISPSRAAGSWTW\*TFCRASWCRSAG  
CRCPRSWRLSTSRC\*AWASTTLGRSTRPRTCP\*TRR\*RSTGFTCA\*P\*KC\*P\*ATIWGCTATTGCTAR\*APAAGAS\*ATRS\*CTACS  
GP\*PGPGPRGRATLTWARTCAGSPAAGPWKLPAVPPTWRRWTMRRRRASTWKTDGATVFLDAAATATAS\*SRDAGGAAEPAV  
RH\*LLGRLDPGHATHHGAADDPQSRL\*TAASGQPALGHPGGRGALALEPHAREGAGHRERAGGEQGHPRRRGRAGVQRAAGAR  
GPLQQHQRADEPGPHGDRRARGGVAARAVPPRVEPLHGGAERLPEHAARQRAPGPGGLHQLHQRAAADGGRGAPERGVV  
GAGLLPDQSPGLADREPEPGFQELAGTVGRAGPGRGPRDGPVADAEAPAAAAGGALHGQRQREPRLVPLPA\*PVPRGHRA  
GARGRADLPGDHPREPRAGPGGPGQPGGHELPADQPAEDPAPVRAEHRGGAHPALRAAERGAVPDAGGGHAQRRARHDR  
AQHGAQHVRSPVPHQ\*ADGLLASGGRHELGLLYQRHLEPALAPAARVLHGRVRHARPQRRVPVGRRGQQRVLAAPRHHRVEE  
RGRGPAAVLGAVRSRGCCRGGA\*GRQPLPEPALFAEQRAQQRAGSADAAAPAGRGGVPERLLVEARAREELPQ\*RDREPGQDE  
PLEDVRARAQGRAPS\*QQRHRP\*TPATRQAAGSGVGR\*GFRRRQQRVGLGWEEWW\*PVRSLAPPYRAPDVRI\*KNKKRYSRPR  
WRPACVLLCCL\*\*YDEARVPGSSSLVRERDAAGGGGGDAAPAGGALRAPAVPGAYGGAEQHSLLGAGTLVRYHPVVPGGQQV  
GGHRLAELPERPQQLPDHRGAEQRFHPHGGQHPDHQL\*RALAVGRPAENHHAHQHAQREVRHVQQVQAGDGLAQDPQW  
GRGG\*EL\*W\*SGRADLRVGGV\*AARGQLLDHHRSDQRHHRQLLGGGASERGAGERHREVRHAQLPAGLGPRDRAGDAG  
RVHQRLPPRHRPAARLRRGLHREPPQQPAGHPQAAALPGGLPDPVRGPGGGQHPRALGCRSL\*EKQGGRRSGDRSRGHRLY  
RGAGR\*FC\*RRSGRGG\*NRK\*DSHPAGGEGQQQQLQRRARGQEKHRLPQLVPLQLRRPREGRALLDAAHHLGRHLRRGASLL  
VAARHDARPGHPLHASS\*QLPGGGRRAPARLLQELLQRRAGRLAAAAARLHLAARLQPLPREPDPRPPARAHYHRQ\*KRSCSHR  
SRDPAQAQQYPGSPARDRH\*RQTPHLRLQGPGRSRAARPLEPHLLKNVHSHLAQ\*\*HRLGPARAQQDVRRRSPTLHATPRARA  
RALPRSLGRPGPRALAHRRRRDRPGGGRRALHARRRARLHRGRHRQRGGRCAPVRPRQEPAAAHRAPEHPRHARGAS  
LAAQQAHTGTQHAQGGQTRGLRQQRRQDPQTRGHGGGGGHRQHVPAAARQVRLGARRRHRCARARAHPPSHLKMITS  
RC\*CVPAARRMSKRKYKEMLQVIAPEIYGPVKEERKPRKLKRVKKDKKEEEDVDGLVEFVREFAPRRRVQWRGRKVKPVLPGT  
TVVFTPGERSGSASKRSYDEVYGEDILEQAVERLGEFAYGKRSRPAPLKEEAVSIPLDHGNPTSLKPVTLQQLVPSAAPRRGFKREG  
GEDLYPTMQLMVPKRQKLEDVLEHMKVDPEVQPEVKVRPIKQVAPGLGVQTVDIKIPTMETQTEPVKPTSTMEVQTDPMWP  
APASTRRRRKYGAASLLMPNYALHPSIPTPGYRGTFRYGYTSSRRKTTTTRRRRRRTRRSSTATSAAALVRRVYRSGREPLTLPRARY  
HPSIAI\*LCRRLLADMALTCRLRPITGYRGRKPRRRRLTGNGLRHHHRRRRRAISKRLGGGLPALIPIIAAIGAIPGIASVAVQASQ  
RH\*DTAWKICNKKMD\*RSWSCDVC\*MEDINFSSLA PRHGTRPFMGTSWSDIGNSQLNGGAFNWSSLWSGLKNFGSTLKTYGNK  
AWNSTGQALREKLKEQNFQKQVVDGLASGINGVVDLANQAVQKQINSRLDAVPPAGSVEMPQVEELPLDKRGDKRPRDAE  
ETLLHTDEPPPYEEAVKLGLPTTRPVAPLATGVLPKSSSSQPATLDLPPASRPSTVAKPLPPVAVASRAPRGRPQANWQSTLNSIV  
GLGVQSVKRRRCY\*KTL\*RLTCLSVICMSADQKEEEARRRVARWPPHRCPSGRCTCTSPDRTLST\*VRVWCSSPAPQTPTS VWG  
TSLGTPRWRPRTM\*PPTAAS\*RCASCPTARTTPTRTKCATRWPWATTACWTWPAPTLSAACWIGGPASNPPTAPPTAWL  
PRERPTLASGHIKLVILIKKPIHMEMHLCKALALQRMVFNLELTAMVRQSMQTKLINQSLKWVMLNGMTSLVLMKNMEAEALLSL  
TPK\*SLAMVLLPSLPIKKEARQM\*KPKQAVPKNMTLTHSSIEVQLPPA\*PQKLCILRMWIIWKLQIPILYTRQVQMTVALLSIWVS  
SPCPTDPTTLASETTLSV\*CTTTALAIWVYWLDRPPS\*MLWWTCTETPNCPTSSCLTLWVTEPGISVCGIRRWTVMTPMCALKIT  
VWRMNFILTASPWMLWVELILTRELPMVIKPPGPKMILLMMLNWARAILSPWRSTSRPTCGGTSSTRTWRCTCPTPTSTRRP  
TSRCPPTPTTIT\*TAAWWRPRWWTPTSTSGRAGRWTPTTSTPTTTATRACDTAPCSWATGATCPTSRCPKSFSPSRASCSCP  
GPTPTSGTSARTST\*SCRAPSATTCARTGPPSPSPASTSTPPSSPWRTTTPPSPRPPCATTPTTSTSTTSRPTCSTPSRPTPTCPSPS  
PRATGPPSAAGPSRASRPARRPRAPGSTPTSSTRAPSPTSTAPSTSTTPSRSPSPSTPPSAGPATTAS\*RPTSSKSAPSTERGTTWP  
SAT\*PRTGWSRCWPPTTSATRASTCPRATRTACTPSSATSP\*AARSWTRSTTRTRPSPWPTSTTRASSATSRPPCARASPTPPT  
TPTRSSARAPSPASPRKSSATGSCGASPSATSCPWARSPSARTCSTPTPPT\*ISKSTPWSMPPFMSLSSKSSSTSECTSPTAAS  
SRPSTCARPSRPATPPPKPLASCKMTACAGSGEQELRAILRDLGCGPCFLGTDFDKRFGFMAPHLKACAIVNTAGRETGGHEWLFAFA  
WNPRSHTCYLDFPGFSDERLKQIYQFEYEGLLRRSALATEDRCVTLEKSTQTVQGPRSAACGLFCCMFLHAFVHWPDRPMDKNPT  
MNLLTGVPNGMLQSPQVEPTLRRNQEALYRFLNAHSAYFRSHRARIKATAFDRMNQDM\*SGVCM\*MLYSS\*\*TAHVYATFSEA  
LTLFRNRRGSAGSRHGPRAGIRCGTGTWAAT\*TRGSAASARGGRGTSRSTACA\*VAGRPAGRARRS\*NRSWDPRSARESYGTRGC  
STGTPSGPGASRSPASRR\*CPRPDPRRWPSRRGSSCRSAAPCWARSACGCNRSAGGSASSGPARRSCPGTWPS\*KPPAGGRP  
AAPCRPR\*RRPRTC\*RTGWWSRQRRARSSARRCWPAAPRCAPSGSG\*SWPGRGSPSARAARSRSPHPSRSCAPSGSSRSRAGT  
AACPRPRCTRAATARSRCPSSCGRSGSASARSPAGSGPSSWSGSCW\*RSAECRGAPRSHTGGRYGGTTPRPARASAGRRTSGRSP  
RGTGPSAASSLPCSPRPKRSAGSGGSSPLSS\*SPPKSGGRSRPGSQTACRPSR\*CARGES\*SPRPPAPRPAFRPRCPG\*CLAKAH  
AWSCGVSWFAEAAAETCWAASSRSPRLFLLGRRPRPRGGRHASSGAEEATGSRGSAGGWQSPFRVRGCAPGGAALTDFLR  
GRPLCSPREQAWRLSHRRQHRHLPPPPPTRTSSSRMKA\*PPRRPAPPPTPQPQTCKRWRNPSRLTWAT\*RPRSTRRSWQRAFQP  
RKRTTKSSQSRKQASRTRLGSSMATT\*AGQRTCCSSIWPANASSRTRCSTAPRCPSAWRSSAAPTSTSSRRACPPSASPTAPASP  
TRASTSTRSSRCRPPWPTTFSRTKGSPPAAPTAPAPTPCSTWAPAPAYLISPPWKFRPSSRVWAATRLGPRTLCKEAERSMSTT



Fig. 26K

APWWSWKATTRAWRSSARSS\*PTSPTRRSTCPPRS\*APSWTRCSSAPRPSRRRCRTPRARTRASPWSATSSWRAGWERVAP  
 PRAWKSGASS\*WPWSW\*PWSWSVCAASSPTRRPCARSRRCTTSSDTGSCARPARSPTWS\*PTWSPTWASCTRATWGRCTCTP  
 PCAGRPAATTSATASTCTSATPGRRRAWACGSSAWRSRT\*KSSASSCRTRSRCGPGSTSAPPRTWPTSSSPSACG\*RCATGCPTL\*  
 AKACCKTFALSSSNAPGSCPPAPRCPTSCR\*PSASAPRRSGATATCCAWPTTWPTTRT\*SRTSAARACSSATAAATSARRTAPWP  
 ATPSC\*ARPRSSAPSSCKAPARARGV\*NSPRGCGPRPTCASSCPRTTIPSRSGSTRNPSRPRPSCRPPASSPRGPSWPNCPSRNP  
 AK\*KRATGSTWTPRPERSTPASPRMPRGSSKKLKVLPPEDELEEDWESSQAEEEEMEDWDSTQAEEDSLQDSLEEEDEVEEA  
 EEEEEARPSSAAEEKASSTDTISAPGRGRGGRASRWDETRFPNPTTQTGKKERQGYKSWRGHKNAIVSCLQACGGNISFTRR  
 YLLFHRGVNFPNRILHYRHLHSPYCFQEEAETQQQQQQKTSGSS\*KIHSGGRWTEDRGERAGADPGAEPDLSHPLCHLPAES  
 GARAGTESQEPFSALAHPLQSVSQERRPTSASRGRGSLQQLVLAHS\*RVARARPHTEKGGNYVTTCALRPTIIMSKEIPTPYMWS  
 YQPQMGLAAGAAQDYSTRMNWLSAGPAMISRVNDIRAHNRNQLLEQSAITATPRHHLNPRNWPAAALVYQEIQQPTTVLLPRDAQ  
 AEVQLTNSGVQLAGGAALCRHRPAQGIKRLVIRGRGTQLNDEVSSSLGLRPDGVFQLAGSGRSSFTPRQAVLTLESSSQPRSGGI  
 GTLQFVEEFTPSVYFNPFSGSPGHYPDEFIPNFDaisesVDGYD\*MSHGGAADLARLRHLDHCRFRFCFARDLAEFAYFELPEEHPQG  
 PAHGVRIVVEGGLDShLLRIFSQRPIAEREQGTLLTYLCINHPGLHESLCCLCTEYNKS\*DQRLLRTSVCSYQPVPLHRRERDRA  
 PAPV\*APQEVPHLAVPGLSDRRRCQPLRQRSPAERPQYFFHPQKQAPALPTLPPRDLSVRLGTLPSHLPPDPEYHSVAPRY\*QPN  
 YPPTPPSRPRTCTELEKY\*ATIHAIHRL\*GRATATHAPRY\*LLQSNRRR\*LTHWPTTTSTTFSWTWTAAPRSSDSPNFAFASSRREPSR  
 SCRTA\*PSTSARKASSAW\*NRPRSPTSRPTIASPTSSCSSARSSPAWSESTPSSSPSSRAIPRGASTAPATPPTASTL\*SRPSAASATS  
 SP\*TNHPLIQ\*NKYHIDDLNKK\*SFDLK\*RYNHIDDLSEKK\*RITYLKS DTRSLSMFSANTTSLPSSQLWYCRPRAANFLHTLKGMS  
 NSSCPSIFILSSIRCPKSASGWMMTSTPSTPTMQTTHRPCSPSTPPSSQLQMDSKRSPWGCCPCDWLTSPSPRTGKSPSSWERGWT  
 TPRESSPTPRPPPLSVFPTTFFPLTWIPLFIPKMENYPYKFLHR\*TY\*NQPF\*TH\*L\*LMDQV\*D\*VVALLLQYSWPLSHLLMKKE  
 ILKLT\*PVVH\*QLMQVDLVSTAKEGSLSLPQEMQLKAT\*AGLKV\*DLKVMA\*LQTLAEDWNLEPLVQLRMSQMHTQFKLNWVLA  
 LPLTVQAPLLLGTKRMINLHYGPQPTPRQIAKYTLKMPNSHFA\*QSVEVKFWVL\*LYWQ\*IMEVSTQSQTQ\*ALHSSPSSLMQVE  
 FC\*AAPH\*TKNIGTSEREMLHLLSPILML\*VLCLT\*RPILKTHLQLKAILSVKFISMGMMPNH\*C\*LLLLMKLRMLQAPTVSLFNNG  
 IVLSTQVKHLLPAPSPSPSPKNEHCIPPCMPTLPTPLCLWKKL\*STK\*NKVQVY\*FNSFTGFEQLFFLHPRTWNTPPSPPAQ\*TS  
 ECHW\*WTCFWSRSTQFQSEPVSGRSGR\*NPPGTPASAPHSSTAEDCPRWSGSRSLSGRSRAAVGIIVRERDRPVVSHQAPQQSL  
 PPPLRQAAAQGVVRVQGLPQHDAHGPHQSSGAAGAAAHADLAQVA AVRATQDHQVVQQSIVQHAPAETHRGKDATHVAVVP  
 DPQVNQVALPPEAAHVHDLGHVAVHHLVPVPHPLVEHAAPDDPAEPQGQHRPARHAAKRPRVPAMAMEDPPLVPVDHLGA  
 EQVYVGTAQAYAHASLQHSQLLGGQNHIPGHGELLQDSEPRRTGQSSHITYIVHGQGIQIRQHRVILHQRSAGLGLLTAW\*GGPIR  
 VMAGRG\*SCSRPCHDAVAFGHFRTCCSRTWSGRCTPIAGGGPGAWNARC\*NCKTATLS DRAADLGPQE\*\*RSHHA\*\*L\*SHRPP  
 WNGPDPAR\*CNFVGFR\*RRGREEQEEP\*LTFNPNGLGALQNEGRGDGTSRPRCVGGK\*QPGQR\*YGRDVPRLWPAKPPRAHP  
 ETRQ\*RKREGSLIPQSSCYTPAPSPDNFHFSSLE\*FELVPEVNPSPQ\*\*RARAERPPAFLSTPS\*FQDILLVHLQQIDKRNKISAAIPK  
 LLPQQ\*L\*VLFHILSEIFSHRTTRNKIRASHSTDKPKSSPVSIKCKTAISMLARP GDIFQITGQKITQAIFKKINKRKILQVHV\*SLGNND  
 EVNASGAFQHG\*LADL\*KTKNKTNLHASLANRWVNRSLQHQAAGHVSGATLVKIVAMIENHHRETFVAGVNDSTR\*IHPRNIGV  
 RE\*KKAPEEAI RHYNASQVQSQSDAMRMKHKILRCVQNVITPLLHRQSRPSRLQIHQSLSVHSLPSSSTQQAQSEK\*ALTCPPAL  
 CSIYSPDLH\*RKQGSLKIPAK\*SHTPSTRPETGDTLKKIRALPQTPKLPSPFGSHATSSEDFQIPSTVKNVTRPAPNGRPSLGQSPSSLP  
 KFKQLICILTRTKSLRYIID

Fig. 27A

**AdC7 010-DU422gp160(E1623) Nucleic Acids – SEQ ID NO: 8**

CATCATCAATAATATACCTCAAACCTTTTGGTGCGGTTAATATGCAAATGAGCTGTTTGAATTTGGGGAGGGAGGAAGGTGAT  
TGGCCGAGAGACGGGCGACCGTTAGGGGCGGGGCGGGTGACGTTTTGATGACGTGGCCGTGAGGCGGAGCCGGTTTGCAA  
GTTCTCGTGGGAAAAGTGACGTCAAACGAGGTGTGGTTTGAACACGGAAATACTCAATTTTCCCGCGCTCTCTGACAGGAAAT  
GAGGTGTTTCTGGGCGGATGCAAGTGAAAACGGGCCATTTTCGCGCGAAAACTGAATGAGGAAAGTAAAAATCTGAGTAATTT  
CGCGTTTATGGCAGGGAGGAGTATTTGCCGAGGGCCGAGTAGACTTTGACCGATTACGTGGGGGTTTCGATTACCGTATTTTT  
CACCTAAATTTCCCGGTACGGTGTCAAAGTCCGGTGTTTTACGTACGATATCATTTCCCCGAAAGTGCCACCTGACCGTAACTA  
TAACGGTCCTAAGGTAGCGAAAGCTCAGATCTCCCGATCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGT  
TAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTGCTGAGTAGTGCGCGAGCAAAATTAAGCTACAACAAGGCAAGGC  
TTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTG  
ACATTGATTATTGACTAGTATGCCAAGTACGCCCCATTGACGTCAATGACGGTAAATGGCCCCGCTGGCATTATGCCCAGTA  
CATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGTAC  
ATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCA  
CCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCATTGACGCAATGGGCGGTAGGCGTGTACGGTGGGAG  
GTCTATATAAGCAGAGCTCGTTTGTGTAACCGTCAGATCACTAGAAGCTTTATTGCGGTAGTTTATCACAGTTAAATTGCTAAC  
GCAGTCAGTGCTTCTGACACAACAGTCTCGAACTTAAGGCTAGAGTTCGACGCCACCATGCGCGTGCGCGGCATCCCCCGCAA  
CTGGCCCCAGTGGTGGATCTGGGGCATCTGGGCTTCTGGATGATCATCATCTGCCGCGTGGTGGGCAACCTGGACCTGTGG  
GTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCTGTTCTGCGCCTCCGACGCCAAGGCCTACGACA  
AGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAACCCCAAGGAGATCGTGCTGGAGAACGTGAC  
CGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACGAGGACATCATCTCCCTGTGGGACCACTCCCTGAAG  
CCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCTGAACTGCAAGAACGTGAACATCTCCGCCAACGCCAACGCCACCGCCAC  
CCTGAACTCTCCATGAACGGCGAGATCAAGAACTGCTCCTTCAACACCACCACCGAGCTGCGCGACAAGAAGCAGAAGGTGT  
ACGCCCTGTTCTACAAGCCCCGACGTGGTGCCCTGAACGGCGCGGAGCACAACGAGACCGGCGAGTACATCTGATCAACTG  
CAACTCTCCACCATCACCCAGGCCTGCCCAAGGTGTCTTCGACCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTACGCC  
ATCCTGAAGTGCAACAACAAGACCTTCAACGGCACCGGCCCTGCAACAACGTGTCCACCGTGACGTGCACCCACGGCATCAA  
GCCCGTGGTGTCCACCCAGCTGCTGCTGAACGGCTCCCTGGCCGAGGAGGAGATCATCGTGCGCTCCGAGAACCTGACCAAC  
AACATCAAGACCATCATCGTGACCTGAACAAGTCCGTGGAGATCAAGTGACCCGCCCAACAACAACACCCGCAAGTCCGT  
GCGCATCGGCCCGGCCAGACCTTCTACGCCACCGCGAGATCATCGGCGACATCCGCGAGGCCCACTGCAACATCTCCGCG  
AGACCTGGAACCTCACCTGATCCAGGTGAAGGAGAAGCTGCGCGAGCACTACAACAAGACCATCAAGTTCGAGCCCTCCTCC  
GGCGGCGACCTGGAGGTGACCACCACTCCTTCAACTGCCGCGGCGAGTTCTTCTACTGCGACACCACCAAGCTGTTCAACGA  
GACCAAGCTGTTCAACGAGTCCGAGTACGTGGACAACAAGACCATCATCTGCCCTGCCGATCAAGCAGATCATCAACATGT  
GGCAGGAGGTGGGCCGCGCCATGTACGCCCCCCCATCGAGGGCAACATCACCTGCAAGTCCAACATCACCGGCCTGCTGCT  
GACCTGGGACGGCGGCGAGAACTCACCGAGGGCGTGTTCGCCCGGCGGCGGCAACATGAAGGACAAGTGGCGCTCCGA  
GCTGTACAAGTACAAGGTGGTGGAGATCAAGCCCTGGGCGTGGCCCCACCAAGAGCAAGCGCAAGGTGGTGGGCCGCGA  
GAAGCGCGCGTGGGCGTGGGCGCGTGTGCTGCTGGGCTTCTGGGCGCGCGGCGAGCACCATGGGCGCGCGCCAGCATCACC  
CTGACCGTGACGGCCCGCCAGCTGCTGAGCGGCATCGTGACGAGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGC  
ACCTGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGACCCCGTGTGGCCATCGAGCGCTACCTGAAGGACCAGCA  
GCTGCTGGGCGTGTGGGGCTGCAGCGGCAAGCTGATCTGCGCCACCGCGTGCCTGGAACAGCAGCTGGAGCAACAAGAG  
CCTGGGCGACATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAGATCAGCAACTACCAACACCATCTTCCGCTGC  
TGGAGGACAGCCAGAACCAGCAGGAGAAGAAGCAGAGGACCTGCTGGCCCTGGACAGCTGGAAGAACCTGTGGAACCTGGT  
TCGACATACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCATCTTCGGCG  
TGCTGGCCATCGTGAAGCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCCAGACCCTGATCCCCAACCCCGCGGCCCGGAC  
CGCCTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACAAGGACCGCAGCATCCGCTGGTGAGCGGCTTCTGGCCCTG  
GCCTGGGACGACCTGCGCAGCCTGTGCCTGTTACGTACACACAGCTGCGCGACTTCATCCTGACCGCCGCGCGCGCGCCGA  
GCTGCTGGGCCGAGCAGCCTGCGCGGCTGCAGCGCGCTGGGAGGTGCTGAAGTACCTGGGCAACCTGGTGCAGTACTG  
GGGCTGGAGCTGAAGCGCAGCGCCATCAACCTGTTGACACCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATC  
GAGGTGATCCAGCGCATCTGCCGCGCCATCCGCTACATCCCCACCGCATCCGCCAGGGCTTCGAGGCCGCGCTGCTGTAAGG  
TACCTCTAGAGTCGACCCGGGCGGCCAAACCGCTGATCAGCTCGACTGTGCTTCTAGTTGCCAGCCATCTGTTGTTGCCCC  
TCCCCCGTGCCTTCTTACCCTGGAAGGTGCCACTCCACTGTCTTCTCTAATAAAATGAGGAAATTGCATCGCATTTGTCTGA  
GTAGGTGTCAATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCT

Fig. 27B

GGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCAGATCTGCAGATCTGAATTCATCTATGTCGGGTGCGG  
AGAAAGAGGTAATGAAATGGCATTATGGGTATTATGGGTCTGCATTAATGAATCGGCCAGATATCGATATGCTGGCCACCGTG  
CATGTGACCTCGCACCCCGCAAGACATGGCCCGAGTTCGAGCACAACGTCATGACCCGATGCAATGTGCACCTGGGGTCCCG  
CCGAGGCATGTTATGCCCTACCACTGCAACATGCAATTTGTGAAGGTGCTGCTGGAGCCCGATGCCATGTCCAGAGTGAGCC  
TGACGGGGGTGTTTGACATGAATGTGGAGCTGTGGAAAATTCTGAGATATGATGAATCCAAGACCAGGTGCCGGGCTGCGA  
ATGCGGAGGCAAGCACGCCAGGCTTCAGCCCGTGTGTGTGGAGGTGACGGAGGACCTGCGACCCGATCATTTGGTGTGTCC  
TGCAACGGGACGGAGTTCGGCTCCAGCGGGGAAGAATCTGACTAGAGTGAGTAGTGTGGGGGAGGTGGAGGGCTTGAT  
GAGGGGCGAATGACTAAAATCTGTGTTTTCTGTGTGTCAGCAGCATGAGCGGAAGCGCTCCTTTGAGGGAGGGGTAT  
TCAGCCCTTATCTGACGGGGCGTCTCCCTCTGGGCGGGAGTGCGTCAGAATGTGATGGGATCCACGGTGGACGGCCGGCC  
CGTGACGCCCGCAACTCTCAACCCTGACCTACGCGACCCTGAGCTCCTCGTCCGTGGACGAGCTGCCCGCCGAGCTGCTG  
CTTCGCCCGCCAGCGCGTGCGCGGAATGGCCCTGGGCGCCGGCTACTACAGCTCTCTGGTGGCCAACTCGACTTCCACCAAT  
AATCCCGCCAGCCTGAACGAGGAGAAGCTGCTGCTGCTGATGGCCAGCTCGAGGCCCTGACCCAGCGCCTGGGCGAGCTGA  
CCCAGCAGGTGGCTCAGCTGCAGGCGGAGACGCGGGCCGCGTTGCCACGGTGAAAACCAATAAAAAATGAATCAATAAAT  
AAACGGAGACGGTGTGATTAAACAGAGTCTGAATCTTATTTGATTTTCGCGCGCGGTAGGCCCTGGACCACCGGTC  
TCGATCATTGAGCACCCGGTGATTTTTCCAGGACCCGGTAGAGGTGGGCTTGATGTTGAGGTACATGGGCATGAGCCCGT  
CCCGGGGGTGAGGTAGCTCATTGACGGGCTCGTGCTCGGGGGTGGTGTGTAAATCACCAGTCATAGCAGGGGCGCA  
GGGCGTGGTGCTGCACGATGTCCTTGAGGAGGAGACTGATGGCCACGGGCGAGCCCTTGGTGTAGGTGTTGACGAACCTGTT  
GAGCTGGGAGGGATGCATGCGGGGGGAGATGAGATGCATCTTGGCCTGGATCTTGAGATTGGCGATGTTCCCGCCAGATCC  
CGCCGGGGGTTTATGTTGTGACGAGACCACGACGCGGTGATCCGCGCACTTGGGGAATTTGTCATGCAACTTGAAGGGA  
AGGCGTGAAAGAATTTGGAGACGCCCTTGACCGCCAGGTTTTCCATGCACTCATCCATGATGATGGCGATGGGCGCGTGG  
GCGGCGGCTGGGCAAGACGTTTCGGGGGTCGACACATCGTAGTTGTGGTCTGGGTGAGCTCGTCATAGGCCATTTAA  
TGAATTTGGGGCGGAGGGTGCCGACTGGGGGACGAAGGTGCCCTCGATCCCGGGGCGTAGTTGCCCTCGCAGATCTGCAT  
CTCCCAGGCCTTGAGCTCGGAGGGGGGATCATGTCCACCTGCGGGGCGATGAAAAAACGGTTTCCGGGGCGGGGAGAT  
GAGCTGGGCGGAAAGCAGGTTCCGGAGCAGCTGGGACTTGCCGCGAGCCGGTGGGGCCGTAGATGACCCGATGACCGGCTG  
CAGGTGGTAGTTGAGGGAGAGACAGTGCCTGCTCGCGAGGAGGGGGGCCACCTCGTTCATCATCTCGCGCACATGCATG  
TTCTCGCGCACGAGTTCGCCAGGAGGCGCTCGCCCCCAGCGAGAGGAGCTCTTGACGCGAGGCGAAGTTTTTCAGCGGCTT  
GAGYCCGTCGGCATGGGCATTTGGAGAGGGTCTGTTGCAAGAGTTCCAGACGGTCCAGAGCTCGGTGATGTGCTTAGG  
GCATCTCGATCCAGCAGACCTCTCGTTTCGCGGGTTGGGGCGACTGCGGGAGTAGGGCACCAGGCGATGGGCGTCCAGCGA  
GGCCAGGGTCCGGTCTTCCAGGGTCGAGGGTCCGCGTCAGCGTGGTCTCCGTACGGTGAAGGGGTGCGCGCCGGGCTG  
GGCGCTTGCGAGGGTGCGCTTCAGGCTCATCCGGCTGGTCGAGAACCCTCCCGTCCGCGCCCTGCGCGTCGGCCAGGTAG  
CAATTGAGCATGAGTTCGTAGTTGAGCGCTCGGCCGCTGGCCCTTGGCGCGGAGCTTACCTTTGGAAGTGTGTCCGAGAC  
GGGACAGAGGAGGACTTGAGGGCGTAGAGCTTGGGGGCGAGGAAGACGGAAGTCCGGGGCGTAGGCGTCCGCGCCGAG  
CTGGCGCAGACGGTCTCGCACTCCAGAGCCAGGTGAGGTGGGGCGGTTGGGGTCAAAAACGAGGTTTCTCCGTGCTTTTT  
GATGCGTTTCTTACCTCTGGTCTCCATGAGCTCGTGTCCTCGTGGGTGACAAAGAGGCTGTCCGTGTCCCGTAGACCGACTT  
TATGGGCCGGTCTCGAGCGGGGTGCCGCGTCTCGTCTAGAGGAACCCCGCCACTCCGAGACGAAGGCCCGGGTCCAG  
GCCAGCACGAAGGAGGCCACGTGGGAGGGGTAGCGTCTGTGTCACACGCGGGTCCACCTTCTCCAGGGTATGCAAGCACA  
TGTCCTCTCGTCCACATCCAGGAAGGTGATTGGCTTGAAGTGTAGGCCACGTGACCGGGGGTCCCGGCCGGGGGGTATA  
AAAGGGGGCGGGCCCTGCTCGTCTCACTGTCTTCCGGATCGCTGTCCAGGAGCGCCAGCTGTTGGGGTAGGTATTCCTCT  
CGAAGGCTGGCATAACCTCGGCACTCAGGTTGTGAGTTCTAGAAACGAGGAGGATTTGATATTGACGGTGCCGTTGGAGAC  
GCCTTTCATGAGCCCTCGTCCATCTGGTCAGAAAAGACGATCTTTTTGTTGTCGAGCTTGGTGGCGAAGGAGCCGTAGAGGG  
CGTTGGAGAGGAGCTTGGCGATGGAGCGCATGGTCTGTTCTTTTCTTGTGCGCGCGCTCCTTGGCGGCGATGTTGAGCTGC  
ACGTACTCGCGCGCCACGCACTTCCATTCCGGGAAGACGGTGGTGAGCTCGTGGGCGACGATTCTGACCCGCCAGCCGCGGTT  
GTGACGGGTGATGAGGTCCACGCTGGTGCCACCTCGCCGCGCAGGGGCTGTTGGTCCAGCAGAGCGCCCGCCCTTGGCG  
GAGCAGAAGGGGGGCGAGCGGTCCAGCATGAGCTCGTGGGGGGGTGCGGCTCCACGGTGAAGATGCCGGGCGAAGCTC  
GGGGTCAAGTAGCTGATGAGGTGTCCAGATCGTCCAGCGCGCTTGCCAGTCGCGCACGGCCAGCGCGCGCTCGTAGGGG  
CTGAGGGGCGTGCCCGAGGGCATGGGGTGCGTGAGCGCGGAGGCGTACATGCCGAGATGTCGTAGACGTAGAGGGGCTCC  
TCGAGGACGCCGATGTAGGTGGGGTAGCAGCGCCCCCGCGGATGCTGGCGCGCACGTAGTCGTACAGCTCGTGCGAGGGC  
GCGAGGAGCCCGTGCCGAGGTTGGAGCGTTGCGGCTTTTGGCGCGGTAGACGATCTGGCGGAAGATGGCGTGGGAGTTG  
GAGGAGATGGTGGGCTCTGGAAGATGTTGAAGTGGGCGTGGGGCAGGCCGACCGAGTCCCTGATGAAGTGGGCGTAGGA  
GTCCTGCAGCTTGGCGACGAGCTCGGCGGTGACGAGGACGTCCAGGGCGCAGTAGTCGAGGGTCTTTGGATGATGTCGTAC  
TTGAGCTGGCCCTTCTGCTCCACAGCTCGCGGTTGAGAAGGAACCTTCGCGGTCTTCCAGTACTCTTCGAGGGGGAACCCG

Fig. 27C

TCCTGATCGGCACGGTAAGAGCCCACCATGTAGAACTGGTTGACGGCCTTGTAGGCGCAGCAGCCCTTCTCCACGGGGAGGG  
CGTAAGCTTGTGCGGCCTTGCAGAGGGAGGTGTGGGTGAGGGCGAAGGTGTGCGCACCATTGACCTTGAGGAACTGGTGCT  
TGAAGTCGAGGTCTGTCGAGCCGCCCTGCTCCAGAGCTGGAAGTCCGTGCGCTTCTGTAGGCGGGGTGGGCAAAGCGAA  
AGTAACATCGTTGAAGAGGATCTTGCCCGCGCGGGGCATGAAGTTGCGAGTGATGCGGAAAGGCTGGGGCACCTCGGCCCG  
GTTGTTGATGACCTGGGCGGCGAGGACGATCTCGTGAAGCCGTTGATGTTGTGCCCAGCATGTAGAGTTCCACGAATCGC  
GGGCGGCCCTTAACGTGGGGCAGCTTCTTGAGCTCGTCGTAGGTGAGCTCGGCGGGGTCTGCTAGCCCGTGTCTGCTGAGGG  
CCCAGTCGGCGACGTGGGGGTGGCGCTGAGGAAGGAAGTCCAGAGATCCACGGCCAGGGCGGTCTGCAAGCGGTCCCGGT  
ACTGACGGAAGTGTGCCCCACGGCCATTTTTTCGGGGGTGACGCAGTAGAAGGTGCGGGGTGCGCGTGCCAGCGGTCCCA  
CTTGAGCTGGAGGGCGAGGTCTGGGCGAGCTCGACGAGCGGCGGTCCCCGAGAGTTTCATGACCAGCATGAAGGGGAC  
GAGCTGCTTGCCGAAGGACCCCATCCAGGTGTAGGTTTCCACATCGTAGGTGAGGAAGAGCCTTTCGGTGCGAGGATGCGAG  
CCGATGGGGAAGAACTGGATCTCTGCCACCAGTTGGAGGAATGGCTGTTGATGTGATGGAAGTAGAAATGCCGACGGCGC  
GCCGAGCACTCGTGCTTGTGTTTATACAAGCGTCCGAGTGCTCGCAACGCTGCACGGGATGCACGTGCTGCACGAGCTGTAC  
CTGGGTTCTTTGACGAGGAATTCAGTGGGCAGTGGAGCGCTGGCGGCTGCATCTGGTGCTGTACTACGTCTGGCCATCGG  
CGTGCCATCGTCTGCCTCGATGGTGGTCATGCTGACGAGCCGCGCGGGAGGCAGGTCCAGACTTCGGCTCGGACGGGTGCG  
GAGAGCGAGGACGAGGGCGCGCAGGCCGAGCTGTCCAGGGTCTGAGACGCTGCGGAGTCAGGTCAGTGGGCAGCGGCG  
GCGCGCGTTGACTTGACGAGGCTTTCCAGGGCGCGCGGGAGGTCCAGATGGTACTTGATCTCCACGGCGCGGTTGGTGGC  
GACGTCCACGGCTTGACGGGTCCCCTGCCCCGGGGCGCCACCACCGTGCCCCGTTTCTTCTGGGCGCTGCTTCATGCCGGT  
CAGAAAGCGCGCGGAGGACGCGCGCCGGGCGGCAGGGGCGGCTCGGGACCCGAGGCAGGGGCGGCAGGGGCACGTGCG  
CGCCGCGCGCGGGCAGGTTCTGGTACTGCGCCGAGAAAGACTGGCGTGAGCGACGACGCGACGCGGTTGACGTCTGGATCT  
GACGCTCTGGGTGAAGGCCACGGACCCGTGAGTTTGAACCTGAAAGAGAGTTCGACAGAATCAATCTCGGTATCGTTGAC  
GGCGGCTGCGCAGGATCTCTGCACGTGCCCCAGTTGTCTGGTAGGCGATCTCGGTATGAAGTGTGATCTCTCTCTC  
CTGAAGGTCTCCGCGGCGCGCGCTCGACGGTGGCCGCGAGGTGCTTGGAGATGCGGCCCATGAGTGTGAGAAGGCGTT  
CATGCCGGCCTCGTTCCAGACGCGGCTGTAGACCAGGCTCCGTGCGGGTTCGCGCGCGCATGACCACCTGGGCGAGGTTG  
AGCTCGACGTGGCGCGTGAAGACCGCGTAGTTGCAGAGCGCTGGTAGAGGTAGTTGAGCGTGGTGCGATGTGCTCGGTG  
ACGAAGAAGTACATGATCCAGCGGCGGAGCGGCATCTCGTGACGTGCGCCAGGGCTTCAAGCGCTCCATGGCCTCGTAGA  
AGTCCACGGCGAAGTTGAAAACTGGGAGTTGCGCGCGGAGACGGTCAACTCTCTCCAGAAGACGGATGAGCTCAGCGAT  
GGTGGCGCGCACCTCGCGCTCGAAGGCCCGGGGGGCTCCTTCTTCCATCTCTCTCTCCACTAACATCTCTTACTTCC  
TCCTCAGGAGGCGGCGGGGGAGGGGCCCTGCGTGC CGGCGCGCACGGGCGAGCGGTGATGAAGCGCTCGATGGT  
CTCCCCGCGCGGCGACGCATGGTCTCGGTGACGGCGCGCCGTCTCGCGGGGCGCAGCGTGAAGACGCCGCGCGCATC  
TCCAGGTGGCCGCGGGGGGCTCCGTTGGGCAGGAGAGGGCGCTGACGATGCATCTTATCAATTGGCCGTAGGGACTC  
CGCGCAAGGACCTGAGCGTCTCGAGATCCACGGATCCGAAAACCGCTGAACGAAGGCTTCGAGCCAGTCGAGTCGAAGG  
TAGGCTGAGCCCGTTTCTTGTCTTGGGGATTTCGGGAGGCGGGCGGGCGATGCTGCTGGTGATGAAGTTGAAGTAGGCG  
GTCCTGAGACGCGGATGGTGGCGAGGAGCACAGGTCTTGGGCCGGCTGCTGGATGCGCAGACGGTCGGCCATGCC  
CAGGCGTGGTCTGACACCTGGCGAGGTCTTGTAGTAGTCTGATGAGCCGCTCCACGGGCACCTCTCTCGCCGCGCG  
GCCGTGCATGCGCGTGAGCCGAACCCGCGTGGGGCTGGACGAGCGCCAGGTGCGCGACGACGCGCTCGGCGAGGATGGC  
CTGCTGTATCTGGGTGAGGGTGGTCTGGAAGTCGTGAAGTCGACGAAGCGGTGGTAGGCTCCGTTGTTGATGGTATAGGA  
GCAGTTGGCATGACGGACAGTTGACGGTCTGGTGCCGGGTGCGACGAGCTCGTGGTACTTGAGGCGGAGTAGGCGCG  
CGTGTCGAAGATGTAGTCGTTGCAGGTGCGCACGAGGTAAGTATCCGACGAGGAAGTGC GGCGCGGCTGGCGGTAGAG  
CGGCCATCGTCTGGTGGCGGGGCGCCGGGCGGAGGTCTCGAGCATGAGGCGGTGGTAGCCGTAGATGTACCTGGACAT  
CCAGGTGATGCCGGCGCGGTGGTGGAGGCGCGCGGAACTCGCGGACGCGGTTCCAGATGTTGCGCAGCGGCAGGAAGT  
AGTTCATGGTGGCGCGGTCTGGCCGTGAGGCGCGCGCAGTCGTGGATGCTCTAGACATACGGGCAAAAACGAAAGCGGTC  
AGCGGCTCGACTCCGTGGCTGGAGGCTAAGCGAACGGGTTGGGCTGCGCGTGTACCCCGTTTCAATCTCGAATCAGGCTG  
GAGCCGAGCTAACGTGGTACTGGCACTCCGTTCTCGACCAAGCCTGTAACGAAACCTCAGGATACGGAGGCGGGTGGT  
TTTTGGCCTTGGTGTGTCATGAAAACTAGTAAGCGCGGAAAGCGACCGCCGCGATGGCTGCTGCGTAGTCTGGAG  
AAAGAATCGCCAGGGTTGCGTTGCGGTGTGCCCCGTTTCAGCCTCAGCGCTCGGCGCGGCGGATTCCGCGGCTAACGTG  
GGCGTGGTGTGCCCCGTGTTTCAAGACCCCTTAGCCAGCCGACTTCTCCAGTTACGGAGCGAGCCCTCTTTTCTGTGTTTT  
TGCCAGATGCATCCCGTACTGCGGCAGATGCGCCCCACCCTCCACCTCAACCGCCCTACCGCCGAGCAGCAGCAACAGCC  
GGCGTCTGCCCCCGCCAGCAGCAGCCAGCCACTACCGCGGCGGCGCGGTGAGCGGAGCCGGCGTTCAGTATGACCTG  
GCCTTGAAGAGGGCGAGGGGCTGGCGCGGCTGGGGCGTCTGCGCGGAGCGGCACCCGCGCGTGACATGAAAAGGGA  
CGCTCGGAGGCTACGTGCCCAAGCAGAACCTGTTAGAGACAGGAGCGGCGAGGAGCCGAGGAGATGCGCGCCTCCCG  
CTTCCACGCGGGGCGGGAGCTGCGGCGCGGCTGGACCGAAAGCGGGTGTGAGGGACGAGGATTCGAGGCGGACGAGC

Fig. 27D

TGACGGGGATCAGCCCCGCGCGCGCACGTGGCCGCGGCCAACCTGGTCACGGCGTACGAGCAGACCGTGAAGGAGGAGA  
GCAACTTCCAAAAATCCTTCAACAACACGTGCGCACGCTGATCGCGCGCAGGAGGTGACCCTGGGCTGATGCACCTGTGG  
GACCTGCTGGAGGCCATCGTGCAAGACCCACGAGCAAGCCGCTGACGGCGCAGCTGTTTCTGGTGGTGCAGCACAGTCGGG  
ACAACGAGACGTTACGGGAGGCGCTGCTGAATATCACCGAGCCGAGGGCCGCTGGCTCCTGGACCTGGTGAACATTCTGCA  
GAGCATCGTGGTGCAGGAGCGCGGGTGTCCGAGAAAGCTGGCGGCTATCAACTTCTCGGTGCTGAGCCTGGGCAAG  
TACTACGCTAGGAAGATCTACAAGACCCGTACGTGCCATAGACAAGGAGGTGAAGATCGACGGGTTTTACATGCGCATGA  
CCCTGAAAGTGCTGACCCTGAGCGACGATCTGGGGGTGTACCGAACGACAGGATGCACCGCGCGGTGAGCGCCAGCCGCC  
GGCGCGAGCTGAGCGACCAGGAGCTGATGCACAGCCTGCAGCGGGCCCTGACCGGGCCGGGACCGAGGGGGAGAGCTAC  
TTTGACATGGGCGCGGACCTGCGCTGGCAGCCAGCCGCCGGCCCTTGAAGCTGCCGGCGGTTCCCCCTACGTGGAGGAGG  
TGGACGATGAGGAGGAGGAGGGCGAGTACCTGGAAGACTGATGGCGCGACCGTATTTTTGCTAGATGCAGCAACAGCCACC  
GCCTCCTGATCCCGCATGCGGGCGGCGCTGCAGAGCCAGCCGTCCGGCATTAACTCCTCGACGATTGGACCCAGGCCATGC  
AACGCATCATGGCGCTGACGACCCGCAATCCCGAAGCCTTTAGACAGCAGCCTCAGGCCAACGGCTCTCGGCCATCCTGGAG  
GCCGTGGTGCCTCGCGCTCGAACCCACGCACGAGAAGGTGCTGGCCATCGTGAACGCGCTGGTGGAGAACAAGGCCATCC  
GCGGCGACGAGGCCGGGCTGGTGTACAACGCGCTGCTGGAGCGCTGGCCCGCTACAACAGCACCAACGTGCAGACGAACC  
TGGACCGCATGGTGACCGACGTGCGCGAGGCGGTGTCGACGCGCAGCGGTTCCACCGCAGTGAACCTGGGCTCCATGGT  
GGCGCTGAACGCCTTCTGAGCACGCAGCCGCCAACGTGCCCGGGGCCAGGAGGACTACACCAACTTCATCAGCGCGCTG  
CGGCTGATGGTGGCCGAGGTGCCCCAGAGCGAGGTGTACCAGTCGGGGCCGGACTACTTCTCCAGACCAAGTCGCCAGGGCT  
TGCAGACCGTGAACCTGAGCCAGGCTTTCAAGAACTTGACAGGACTGTGGGGCGTGCAGGCCCGGCTCGGGGACCGCGCGA  
CGGTGTCGAGCCTGCTGACGCCGAACTCGCGCTGCTGCTGCTGCTGGTGGCGCCCTTACGGACAGCGGCAGCGTGAGCCG  
CGACTCGTACCTGGGTACCTGCTTAACCTGTACCGCGAGGCCATCGGGCAGGCGCACGTGGACGAGCAGACCTACCAGGAG  
ATCACCCACGTGAGCCGCGCTGGGCCAGGAGGACCCGGGCAACCTGGAGGCCACCCTGAACCTCCTGCTGACCAACCGGT  
CGCAGAAGATCCCGCCCCAGTACGCGCTGAGCACCGAGGAGGAGCGCATCCTGCGCTACGTGCAGCAGAGCGTGGGGCTGTT  
CCTGATGCAGGAGGGGGCCACGCCAGCGCCGCGCTCGACATGACCGCGCGCAACATGGAGCCCAGCATGTACGCTCGCAAC  
CGCCCGTTCATCAATAAGCTGATGGACTACTTGATCGGGCGGCCCATGAACCTCGGACTACTTTACCAACGCCATCTTGAAC  
CCGCACTGGCTCCCGCCGCGGGTCTACACGGGCGAGTACGACATGCCCGACCCCAACGACGGGTTCTGTGGGACGACG  
TGGACAGCAGCGTGTCTCGCCGCGCCCGCCACCACCGTGTGGAAGAAAGAGGGCGGGGACCGCGGCCGTCTCGGCGC  
TGTCGGTTCGCGCGGGTGTGCGCGCGCGGTGCTGAGGCCGCCAGCCCTTCCCGAGCCTGCCCTTTCTGCTGAACAGCGTG  
CGCAGCAGCGAGCTGGGTGGGTGACGCGGCCGCGCTGCTGGGCGAGGAGGAGTACCTGAACGACTCCTGTTGAGGCC  
GAGCGCGAGAAGAACTTCCCAATAACGGGATAGAGAGCCTGGTGGACAAGATGAGCCGCTGGAAGACGTACGCGCACGAG  
CACAGGGACGAGCCCCGAGCTAGCAGCAGCGCAGGCACCCGTAGACGCCAGCGACACGACAGGCAGCGGGGTCTGGTGTGG  
GACGATGAGGATTCGCCGACGACAGCAGCGTGTGGACTTGGGTGGGAGTGGTGGTGGTAACCCGTTCTGCTACTTGCGCC  
CCCGTATCGGGCGCTGATGTAAGAATCTGAAAAAATAAAAAACGGTACTACCAAGGCCATGGCGACCAGCGTGCGTTCTTC  
TCTGTTGTTGTAGTAGTATGATGAGGCGCGTGTACCCGAGGGTCTCTCTCCTCGTACGAGAGCGTGATGCAGCAGGCGGT  
GGCGGGCGCATGCAGCCCCGCTGGAGGCGCCTTACGTGCCCCGCGGTACCTGGCGCTACGGAGGGGCGGAACAGCAT  
TCGTTACTCGGAGCTGGCACCTTGTACGATACCACCCGTTGTACCTGGTGGACAACAAGTCGGCGGACATCGCCTCGCTGA  
ACTACCAGAACGACCACAGCAACTTCTGACCACCGTGGTGCAGAACAACGATTTACCCCCACGAGGCCAGCACCCAGACC  
ATCAACTTTGACGAGCGCTCGCGGTGGGGCGGCCAGCTGAAAACCATCATGCACACCAACATGCCAACGTGAACGAGTTCAT  
GTACAGCAACAAGTTCAAGGCGCGGTGATGGTCTCGCGCAAGACCCCAATGGGGTTCGCGGTGGATGAGAATTATGATGGT  
AGTCAGGACGAGCTGACTTACGAGTGGGTGGAGTTTGAAGCTGCCGAGGGCAACTTCTCGGTGACCATGACCATCGATCTGA  
TGAACAACGCCATCATCGACAATACTTGGCGGTGGGGCGTCAGAACGGGGTGTGGAGAGCGACATCGGCGTGAAGTTCTG  
ACACGCGCAACTTCCGGCTGGGCTGGGACCCGTGACCGAGCTGGTGTGCGGGCGTGTACACCAACGAGGCCTTCCACCC  
CGACATCGTCTGCTGCCCGGTGCGGCGTGGACTTACCGAGAGCCGCTCAGCAACCTGCTGGGCATCCGCAAGCGGCAG  
CCCTTCCAGGAGGGCTTCCAGATCCTGTACGAGGACCTGGAGGGGGGCAACATCCCCGCGCTCTTGGATGTGGAAGCCTATGA  
GAAAAGCAAGGAGGAGGCCGCGCAGCGGCGACCGCAGCGGTGGCCACCGCCTTACCGAGGTGCGGGGCGATAATTTTGC  
TAGCGCCGCGCAGTGGCCGAGGCGGTGAAACCGAAAGTAAGATAGTCATCCAGCCGGTGGAGAAGGACAGCAAGGACA  
GGAGCTACAACGTGCTCGCGGACAAGAAAAACACCGCCTACCGCAGCTGGTACCTGGCCTACAACTACGGCGACCCGAGAA  
GGGCGTGCCTCTGGACGTGCTCACCACTCGGACGTACCTGCGGCGTGGAGCAAGTCTACTGGTCTGCTGCCGACATGA  
TGCAAGACCCGGTACCTTCCGCTCCACGCGTCAAGTTAGCAACTACCCGGTGGTGGGCGCGAGTCTGCCCCGTCTACTCCA  
AGAGCTTCTTCAACGAGCAGGCCGTCTACTCGCAGCAGCTGCGCGCCTTCACTCGCTCACGCACGTCTTCAACCGCTTCCCCG  
AGAACCAGATCCTCGTCCGCCCGCCGCGCCACCATACCACCGTCAGTGAACAGTTCTGCTCTCACAGATCACGGGACCC  
TGCCGCTGCGCAGCAGTATCCGGGGAGTCCAGCGCGTGACCGTCACTGACGCCAGACGCCGCACTGCCCTACGTCTACAAG

Fig. 27E

GCCCTGGGCGTAGTCGCGCCGCGCGTCTCTCGAGCCGCACCTTCTAAAAAATGTCCATTCTCATCTCGCCAGTAATAACACC  
GGTTGGGGCCTGCGCGCGCCAGCAAGATGTACGGAGGCGCTCGCCAACGCTCCACGCAACACCCCGTGC GCGTGCGCGGGC  
ACTTCGCGCTCCCTGGGGCGCCCTCAAGGGCCGCGTGCGCTCGCGCACCACCGTCGACGACGTGATCGACCAGGTGGTGGC  
CGACGCGCGCAACTACACGCCCCGCGCGCGCCGCTCCACCGTGACGCGCTCATCGACAGCGTGGTGGCCGATGCGCGC  
CGGTACGCCCCGCGCCAAGAGCCGCGCGCGGCGCATCGCCCGCGGCGACCGGAGCACCCCGCCATGCGCGCGGCGCGAGCC  
TTGCTGCGCAGGGCCAGGCGCACGGGACGACGGGCCATGCTCAGGGCGGCGACGCGCGGCTCCGGCAGCAGCAGCGCC  
GGCAGGACCCGAGACGCGCGGCCACGGCGCGGCGCGGCCATCGCCAGCATGTCCCGCCCGCGGCGCGGCAACGTGTAC  
TGGGTGCGCGACGCGGCCACCGGTGTGCGCGTGCCCGTGCGCACCCGCCCCCTCGCACTTGAAGATGCTGACTTCGCGATGT  
TGATGTGTCCAGCGGCGAGGAGGATGTCAAGCGCAAATAACAAGGAAGAGATGCTCCAGGTCATCGCGCTGAGATCTACG  
GCCCCGCGGTGAAGGAGGAAAGAAAGCCCCGAAACTGAAGCGGGTCAAAAAGGACAAAAAGGAGGAGGAAGATGTGGAC  
GGACTGGTGGAGTTTGTGCGCGAGTTCGCCCCCGGCGGCGCGTGAGTGGCGCGGGCGGAAAGTGAAACCGGTGCTGCGG  
CCCGGCACACGGTGGTCTTCACGCCCCGCGAGCGTTCGGGCTCCGCTCCAAGCGCTCTACGACGAGGTGTACGGGGACG  
AGGACATCCTCGAGCAGGCGGTGAGCGTCTGGGCGAGTTTGCTTACGGCAAGCGCAGCCGCCCGCGCCCTTGAAAGAGGA  
GGCGGTGTCCATCCCGCTGGACCACGGCAACCCACGCCGAGCTGAAGCCGGTGACCTGCAGCAGGTGCTGCCGAGCGCG  
GCGCCGCGCGGGGCTTCAAGCGCGAGGGCGGCGAGGATCTGTACCCGACCATGCAGCTGATGGTGCCAAGCGCCAGAAG  
CTGGAGGACGTGCTGGAGCACATGAAGGTGGACCCCGAGGTGCAGCCCGAGGTCAAGGTGCGGCCCATCAAGCAGGTGGCC  
CCGGGCTGGGCGTGACACCGTGGACATCAAGATCCCCACGGAGCCCATGGAAACGCAGACCGAGCCCGTGAAGCCAGC  
ACCAGCACCATGGAGGTGCAGACGGATCCCTGGATGCCGGCGCGGCTTCCACCACTCGCCGAAGACGCAAGTACGGCGCGG  
CCAGCCTGCTGATGCCAACTACGCGCTGCATCTTCCATCATCCCCACGCCGGGTACCGCGGCACGCGCTTCTACCGCGGCT  
ACACCAGCAGCCGCCGAAGACCACCCGCGCGCGCTGCTGCGACCCGCGCAGCAGCACCGCGACTTCCGCCCGCGCC  
CTGGTGCGGAGAGTGTACCGCAGCGGGCGGAGCCTCTGACCTGCCGCGCGCGCTACCAACCGAGCATGCCATTTAACT  
CTGCCGTGCGCTCTACTTGCAGATATGGCCCTCACATGCCGCTCCGCTCCCCATTACGGGCTACCGAGGAAGAAAGCCGC  
GCCGTAGAAGGCTGACGGGGAACGGGTGCGTCCCATCACACCGCGCGGCGCGCCATCAGCAAGCGGTTGGGGGGA  
GGTTCTCGCCGCGCTGATCCCCATCATCGCCGCGGCGATCGGGGCGATCCCCGGCATAGTTCCGTGGCGGTGCAGGCCTC  
TCAGCGCCACTGAGACACAGCTTGAAAAATTTGTAATAAAAAAATGGACTGACGCTCTGGTCTGTGATGTGTGTTTTAGAT  
GGAAGACATCAATTTTCTCCCTGGCACC GCGACACGGCAGCGCGCGCTTATGGGCACCTGGAGCGACATCGGCAACAGCC  
AACTGAACGGGGGCGCCTCAATTGGAGCAGTCTTGAGCGGGCTTAAGAATTTGGGTCCACGCTCAAAACCTATGGCAAC  
AAGGCGTGGAACAGCAGCACAGGGCAGGCGCTGAGGGAAAAGCTGAAAGAGCAGAACTTCCAGCAGAAAGGTGGTCGATGG  
CCTGGCCTCGGGCATCAACGGGGTGGTGGACCTGGCCAACAGGCGCTGCAGAAAACAGATCAACAGCCGCTGGACGCGGTC  
CCGCCCCGCGGGTCCGTGGAGATGCCCCAGGTGGAGGAGGAGTGCTCCCTGGACAAGCGCGGCGACAAGCGACCGCGT  
CCCGACGCGGAGGAGACGCTGCTGACGCACACGGACGAGCCGCCCCGTACGAGGAGGCGGTGAAACTGGGTCTGCCACC  
ACGCGGCCGCTGGCGCTCTGGCCACCGGGTGTGAAACCCAGCAGCAGCAGCCAGCCCGGACCCCTGGACTTGCCTCCGC  
CTGCTTCCGCCCCCTCCACAGTGCTAAGCCCTGCCGCGGTGGCGTGCCTGCGCGCGCCCCCGAGGCCGCCCCCAGGCG  
AACTGGCAGAGCACTCTGAACAGCATCGTGGTCTGGGAGTGACAGTGTGAAGCGCGCGCTGCTATTAAGACACTGT  
AGCGCTTAACCTGCTGTGTGTATGTATGTCCGCCGACCAGAAGGAGGAAGAGGCGCTGCGCGAGTTGCAAGATG  
GCCACCCCATCGATGCTGCCCACTGGGCGTACATGCACATCGCCGACAGGACGCTTCGGAGTACCTGAGTCCGGGTCTGGT  
GCAGTTCGCCCCGCCACAGACACTTCACTGCTGGGGAACAAGTTAGGAACCCACGGTGGCGCCACGCACGATGTGA  
CCACCGACCGCAGCCAGCGGCTGACGCTGCGCTTCTGCCCCGTGGACCGCGAGGACAACACCTACTCGTACAAAGTGCGCTAC  
ACGCTGGCCGTGGGCGACAACCGCGTGTGGACATGGCCAGCACCTACTTTGACATCCGCGCGCTGCTGGATCGGGGGCCCA  
GCTTCAAACCTACTCCGGCACCGCCTACAACAGCCTGGCTCCCAAGGGAGCGCCCAACACTTGCCAGTGGACATATAAGCT  
GGTGATACTGATACAGAAAAAACCATAACATATGGAATGCACCTGTGCAAGGCATTAGCATTACAAAGGATGGTATTCAACT  
TGAAACTGACAGCGATGGTCAGGCAATCTATGCAGACGAACTTATCAACCAGAGCCTCAAGTGGGTGATGCTGAATGGCAT  
GACATCACTGGTACTGATGAAAAATATGGAGGCAGAGCTCTTAAGCCTGACACCAAATGAAGCCTTGCTATGGTCTTTTTGCC  
AAGCTACCAATAAAGAAAGGAGGCCAGGCAAATGTGAAAACCGAAACAGGCGGTACCAAAGAATATGACATTGACATGGCAT  
TCTTCGATAATCGAAGTGACGCTGCCGCCGCTAGCCCCAGAAATTGTTTGTATACTGAGAATGTGGATCTGGAACTCCAG  
ATACCCATATTGTATACAAGGCAGGTACAGATGACAGTAGCTCTTCTATCAATTTGGGTGAGCAGTCCATGCCAACAGACCCA  
ACTACATTGGCTTCAGAGACAACCTTATCGGTCTGATGTACTACAACAGCACTGGCAATATGGGTGTAAGTGGTGGACAGGCC  
TCCAGCTGAATGCTGTGGTGGACTTGACAGACAGAAACACCGAACTGTCTACCAGCTCTGCTTGACTCTCTGGGTGACAG  
AACCAGGTATTTCACTATGTGGAATCAGGCGGTGGACAGTTATGACCCGATGTGCGCATTATTGAAAATCACGGTGTGGAG  
GATGAACTTCTAACTATTGCTTCCCCCTGGATGCTGTGGGTAGAACTGATACTTACCAGGGAATTAAGGCCAATGGTGATAAT  
CAAACCACTGGACCAAAGATGATACTGTTAATGATGCTAATGAATTGGGCAAGGGCAATCCTTTCGCCATGGAGATCAACAT

Fig. 27F

CCAGGCCAACCTGTGGCGGAACTTCCTCTACGCGAACGTGGCGCTGTACCTGCCCCACTCCTACAAGTACACGCCGGCCAACA  
TCACGCTGCCACCAACACCAACACCTACGATTACATGAACGGCCGCGTGGTGGCGCCCTCGCTGGTGGACGCCTACATCAAC  
ATCGGGGGCGCGCTGGTCGCTGGACCCCATGGACAACGTCAACCCCTTCAACCACCACCGCAACGCGGGCCTGCGATACCGCTC  
CATGCTCCTGGGCAACGGGCGCTACGTGCCCTTCCACATCCAGGTGCCCCAAAAGTTTTTCGCCATCAAGAGCCTCCTGCTCCT  
GCCCGGGTCTACACCTACGAGTGGAACTTCCGCAAGGACGTCAACATGATCTGCAGAGCTCCCTCGGCAACGACCTGCGCA  
CGGACGGGGCCTCCATCGCCTTACCAGCATCAACCTCTACGCCACCTTCTCCCCATGGCGCACAACACCGCCTCCACGCTCG  
AGGCCATGCTGCGCAACGACACCAACGACCAGTCTTCAACGACTACCTCTCGGCGGCCAACATGCTCTACCCCATCCCGGCCA  
ACGCCACCAACGTGCCATCTCCATCCCCTCGCGCAACTGGGCGCGCTTCCGCGGTGGTCTTACGCGCCTCAAGACCCGCG  
AGACGCCCTCGCTCGGCTCCGGTTGACCCCTACTTCGTCTACTCGGGTCCATCCCCTACCTCGACGGCACCTTCTACCTCAA  
CCACACCTTCAAGAAGGTCTCCATCACCTTCGACTCCTCCGTAGCTGGCCCGGCAACGACCGCCTCCTGACGCCAACGAGTT  
CGAAATCAAGCGCACCGTCGACGGAGAGGGGTACAACGTGGCCAGTGCAACATGACCAAGGACTGGTTCCTGGTCCAGATG  
CTGGCCCACTACAACATCGGCTACCAAGGCTTCTACGTGCCGAGGGTACAAGGACCGCATGTACTCCTTCTCCGCAACTTC  
CAGCCCATGAGCCGCCAGGTCTGGACGAGGTCAACTACAAGGACTACCAGGCCGTACCCCTGGCCTACCAGCACAACAACTC  
GGGCTTCGTGCGCTACCTCGCGCCACCATGCGCCAGGGCCAGCCCTACCCCGCCAACTACCCCTACCCGCTCATCGGCAAGA  
GCGCCGTGCGCAGCGTCAACCAGAAAAAGTTCCTCTGCGACCGGGTCTGTGGCGCATCCCCTTCTCCAGCAACTTCATGTCCA  
TGGGCGCGCTACCGACCTCGGCCAGAACATGCTCTACGCCAACTCCGCCACGCGCTAGACATGAATTTGAAAGTCGACCCC  
ATGGATGAGTCCACCTTCTCTATGTTGTCTTGAAGTCTTCGACGTCTCGAGTGCACAGCCCCACCGCGCGTCTATCGAG  
GCCGTCTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACCACCTAAGCCTCTTGCTTCTTGAAGATGACGGCCTGCGCGGG  
CTCCGGCGAGCAGGAGCTCAGGGCCATCCTCGCGACCTGGGCTGCGGGCCCTGCTTCTGGGCACCTTCGACAAGCGCTTCC  
CGGGATTCTAGGCCCCGACAAGCTGGCTGCGCCATCGTCAACACGGCCGGCCGAGACCGGGGGCGAGCACTGGCTGG  
CCTTCGCTGGAACCCGCGCTCCACACCTGTACTCTTCGACCCCTTCGGGTTCTCGGACGAGCGCCTCAAGCAGATCTACC  
AGTTGAGTACGAGGGCCTGCTGCGTCGACGCGCCTGGCCACCGAGGACCGCTGCGTCACCCTGAAAAGTCCACCCAGAC  
CGTGACGGGTCCGCGCTCGGCCGCTGCGGGTCTTCTGCTGCATGTTCTGACGCCTTCGTGCACTGGCCCCACCGCCCCAT  
GGACAAGAACCCACCATGAACTTGCTGACGGGGGTGCCAACGGCATGCTCCAGTGCAGCCAGGTGGAACCCACCCTGCGC  
CGCAACCAGGAGGCGCTCTACCGCTTCTCAACGCCCACTCCGCTACTTTCGCTCCACCGCGCGCATCGAGAAGGCCACC  
GCCTTCGACCGCATGAATCAAGACATGTAATCCGGTGTGTGTATGTGAATGCTTTATTCATCATAATAAACAGCACATGTTTAT  
GCCACCTTCTCTGAGGCTCTGACTTTATTTAGAAATCGAAGGGTTCTGCGGGCTCTCGGCATGGCCCGCGGGCAGGGATACG  
TTGCGGAACTGGTACTTGGGCAGCCACTTGAACCTCGGGGATCAGCAGCTTCGGCACGGGGAGGTGCGGGGAACGAGTCGCTCC  
ACAGCTTGCAGTGAAGTTCAGGGGCGCCAGCAGGTGCGGCGCGGAGATCTTGAAATCGCAGTTGGGACCCGCGTTCTGCGC  
GCGAGAGTTACGGTACACGGGGTTGACGCACTGGAACACCATCAGGGCCGGGTGCTTACGCTCGCCAGCACCGTCGCGTCG  
GTGATGCCCTCCACGTCCAGATCCTCGGCGTTGGCCATCCGAAGGGGGTCTGCTTGCAGGTCTGCCGCCCATGCTGGGCAC  
GCAGCCGGGCTTGTGGTTGCAATCGCAGTGCAGGGGGATCAGCATCATCTGGGCTGCTCGGAGCTCATGCCGGGTACATG  
GCCTTCATGAAAGCTCCAGTGGCGGAAGGCTGCTGCGCTTGGCGCCCTCGGTGAAGAAGACCCCGCAGGACTTGCTAGA  
GAACTGGTTGGTGGCGCAGCCAGCGTCTGCACGACGAGCGCGCTGTTGTTGGCAGCTGCACCAGCTGCGCCCCCAG  
CGGTTCTGGGTGATCTTGGCCCGGTGCGGGTCTCCTTCAGCGCGCGTCCCCGTTCTCGCTCGCCACATCCATCTCGATCGTG  
TGCTCCTTCTGGATCATCACGGTCCCGTGCAGGACCCGAGCTTGCCTCGGCCTCGGTGCACCCGTGCAGCCACAGCGCGCA  
GCCGGTGTCTCCAGTCTTGTGGGCGATCTGGGAGTGCAGTGCACGAAGCCCTGCAGGAAGCGGCCCATCATCGTGGTC  
AGGGTCTTGTGCTGGTGAAGGTACGCGGAATGCCGCGTCTCCTCGTTACATACAGGTGGCAGATACGGCGGTACACCTC  
GCCCTGCTCGGGCATCAGCTGGAAGGCGGACTTCAGGTGCTCTCCACGCGGTACCGGTCCATCAGCAGCGTCATCACTTCCA  
TGCCCTTCTCCAGGCCGAAACGATCGGCAGGCTCAGGGGGTCTTACCGTTGTCTATCTAGTCGCCGCCGCCGGAAGTCAGG  
GGGTGTTCTGCTCAGGGTCTCAAACTCGCTTGCCGTCTTCTCGGTGATGCGCACGGGGGGAAAGCTGAAGCCACGGC  
CGCAGCTCCTCCTCGGCCTGCCTTTCGTCTCGCTGTCTGGCTGATGTCTTGAAAGGCACATGCTTGGTCTTGGGGGTTTC  
TTTTTGGGCGGCGAGAGGCGGCGGCGGAGACGTGCTGGGCGAGCGGAGTTCTCGCTCACCAGACTATTTCTTCTCTTGGCC  
GTCGTCCGAGACCACGCGCGGTAGGCATGCCTTCTGGGGCAGAGGCGGAGGCGACGGGCTCTCGCGGTTGGCGGGCG  
GCTGGCAGAGCCCCCTCCGCGTTCGGGGTGCCTCTGGCGCGCTGCTCTGACTGACTTCTCCGCGGCGCGCCATTGTGT  
TCTCTAGGGAGCAAGCATGGAGACTCAGCCATCGTCGCAACATCGCCATCTGCCCCCGCGCGCGGACGAGAACCAGCAG  
CAGCAGAATGAAAGCTTAACCGCCCCGCCGCCAGCCCCACCTCCGACGCCGAGCCCCAGACATGCAAGAGATGGAGGAAT  
CCATCGAGATTGACCTGGGCTACGTGACGCCCGCGGAGCAGGAGGAGGTGGCAGCGCGCTTTTCAGCCCCGGAAGAGA  
ACCACCAAGAGCAGCCAGAGCAGGAAGCAGAGAGCGAGCAGAACCAGGCTGGGCTCGAGCATGGCGACTACCTGAGCGGG  
GCAGAGGACGTGCTCATCAAGCATCTGGCCCGCAATGCATCATCGTCAAGGACGCGCTGCTGACCGCGCGGAGGTGCCCT  
CAGCGTGCGGAGCTCAGCCGCGCTACGAGCGCAACCTTCTCGCGCGCGTGCCCCCAAGCGCCAGCCCAACGGCACCT

Fig. 27G

GCGAGCCCAACCCGCGCCTCAACTTCTACCCGGTCTTCGCGGTGCCCGAGGCCCTGGCCACCTACCACCTCTTTTTCAAGAACC  
AAAGGATCCCCGTCTCTGCGCGCCAACCGCACCCGCGCGGACGCCCTGCTCAACCTGGGCCCCGGCGCCCGCTACCTGAT  
ATCGCCTCCTTGAAGAGGTTCCCAAGATCTTCGAGGGTCTGGGACGCGACGAGACTCGGGCCGCAACGCTCTGCAAGGAA  
GCGGAGAGGAGCATGAGCACCACAGCGCCTGGTGGAGTTGGAAGGCGACAACGCGCGCTGGCGGTCTCAAGCGCACGG  
TCGAGCTGACCCACTTCGCTACCCGGCGCTCAACCTGCCCCCAAGGTCTGAGCGCGTCTGAGGACAGGTGCTCATCAAG  
CGCGCTCGCCCTCTCGGAGGAGGAGATGCAGGACCCCGAGAGCTCGGACGAGGGCAAGCCCGTGGTCAGCGACGAGCAG  
CTGGCGCGCTGGCTGGGAGCGAGTAGCACCCCCAGAGCCTGGAAGAGCGGCGCAAGCTCATGATGGCCGTGGTCTGGTG  
ACCGTGGAGCTGGAGTGTCTGCGCCGCTTCTTCGCGACGCGGAGACCCCTGCGCAAGGTGAGGAGAACCTGCACTACCTCT  
CAGACACGGGTTCTGTCGCCAGGCCTGCAAGATCTCCAACGTGGAGCTGACCAACCTGGTCTCTACATGGGCATCTGCACG  
AGAACCGCCTGGGGCAGAACGTGTGACACCACCTGCGCGGGGAGGCCCGCGGCGACTACATCCGCGACTGCGTCTACCT  
GTACCTCTGCCACACCTGGCAGACGGGCATGGGCGTGTGGCAGCAGTGCTGGAGGAGCAGAACCTGAAAGAGCTCTGCAA  
GCTCTGCAGAAGAACCTCAAGGCCCTGTGGACCGGGTTCGACGAGCGCACACCAGCCGCGGACCTGGCCGACCTCATCTTCC  
CCGAGCGCCTGCGGCTGACGCTGCGCAACGGGTGCCCGACTTATGAGCCAAAGCATGTTGCAAACTTTGCTCTTTTCATCC  
TCGAACGCTCCGGGATCTGCCCCGACCTGCTCCGCGCTGCCCTCGGACTTCGTGCGGCTGACCTTCGCGAGTGCCCCCGC  
CGCTCTGGAGCCACTGCTACCTGCTGCGCCTGGCCAACTACCTGGCTACCACTCGGACGTGATCGAGGACGTGACGCGGCGAG  
GGCCTGCTCGAGTGCCACTGCCGCTGCAACCTCTGCACGCCGACCGCTCCCTGGCCTGCAACCCCCAGCTGCTGAGCGAGAC  
CCAGATCATCGGCACCTTCGAGTTGCAAGGCCCGGCGAGGGCAAGGGGGGTCTGAAACTACCCCGGGGTGTGGACCTCG  
GCCTACTTGCGCAAGTTCTGTGCCGAGGACTACCATCCCTTCGAGATCAGGTTCTACGAGGACCAATCCAGCCGCCCCAAGGC  
CGAGTGTGCGCCTGCGTCATCACCCAGGGGGCCATCCTGGCCCAATTGCAAGCCATCCAGAAATCCCGCCAAGAATTTCTGC  
TGAAAAAGGGCCACGGGGTCTACTTGACCCCCAGACCGGAGAGGAGCTCAACCCAGCTTCCCCAGGATGCCCGAGGAA  
GCAGCAAGAAGCTGAAAGTGGAGTGCCGCCGCCGCGGAGGATTGGAGGAAGACTGGGAGAGCAGTCAGGCAGAGGAG  
GAGGAGATGGAAGACTGGGACAGCACTCAGGCAGAGGAGGACAGCCTGCAAGACAGTCTGGAGGAGGAAGACGAGGTGG  
AGGAGGCAGAGGAAGAAGCAGCCGCCGACCGTCTGCTCTCGGCGGAGGAGGAGAAAGCAAGCAGCACGGATACCATC  
TCCGCTCCGGGTGCGGGTTCGCGCGCGGCCGGCCACAGTAGATGGGACGAGACCGGGCGCTTCCGAACCCACCACCCAGA  
CCGGTAAGAAGGAGCGGCAGGGATACAAGTCTGGCGGGGGCACAAAAACGCCATCGTCTCTGCTTGAAGCCTGCGGGG  
GCAACATCTCCTTACCCGGCGCTACCTGCTCTTCCACCGCGGGGTGAATTTCCCCGCAACATCTTGCACTTACTACCGTCACT  
CCACAGCCCCCTACTACTGTTTCAAGAAGAGGAGCAGAAACCCAGCAGCAGCAGCAGCAGCAAAAACAGCGGCAGCAGCTAG  
AAAATCCACAGCGGCGGCAGGTGGACTGAGGATCGCGGCGAACGAGCCGGCGCAGACCCGGGAGCTGAGGAACCGGATCTT  
TCCACCCCTCTATGCCATCTTCCAGCAGAGTTCGGGGGCAAGAGCAGGAAGTCAAGAACCCTTCTCTGCGCTCGCTCA  
CCCGCAGTTGTCTGTATCACAAGAGCGAAGACCAACTTCAGCGCACTCTCGAGGACGCCGAGGCTCTCTTCAACAAGTACTGC  
GCGCTCACTCTTAAAGAGTAGCCCGCGCCCGCCACACACGGAAAAAGGCGGGAATTACGTACCACCTGCGCCCTTCGCCCCG  
ACCATCATATGAGCAAGAGATTCCACGCCTTACATGTGGAGCTACCAGCCCCAGATGGGCTGGCCGCCGCGCGCCGCCA  
GGACTACTCCACCCGATGAAGTGGCTCAGTGCCGGGCCCGCATGATCTCACGGGTGAATGACATCCGCGCCACCCGAAACC  
AGATACTCTAGAACAGTCAGCGATCACCGCCACGCCCGCCATCACCTTAATCCGCGTAATTGGCCCGCCGCCCTGGTGTACC  
AGGAAATTTCCAGCCACGACCGTACTACTTCCGCGAGACGCCAGGCCGAAAGTCCAGCTGACTAACTCAGGTGTCCAGCTG  
GCCGGCGGCGCCGCCCTGTGTCTGTCACCGCCCCGCTCAGGGTATAAAGCGGCTGGTGTATCCGAGGCAGAGGCACACAGCTCA  
ACGACGAGGTGGTGAGCTCTTCGCTGGGTCTGCGACCTGACGGAGTCTTCCAACCTCGCCGATCGGGGAGATCTTCTTCACG  
CCTCGTCAGGCCGTCTGACTTTGGAGAGTTCGTCTCGCAGCCCCGCTCGGGTGGCATCGGCACTTCCAGTTCTGTGGAGGA  
GTTCACTCCCTCGGTCTACTTCAACCCCTTCTCCGGCTCCCCGGCCACTACCCGGACGAGTTCATCCCGAACTTCGACGCCATC  
AGCGAGTCGGTGGACGGCTACGATTGAATGTCCCATGGTGGCGCGGCTGACCTAGCTCGGCTTCGACACCTGGACCACTGCC  
GCCGCTTCGCTGCTTCGCTCGGGATCTCGCCGAGTTTGCCTACTTTGAGCTGCCCCGAGGAGCACCTCAGGGCCCCGGCCAC  
GGAGTGGGATCGTCTGCAAGGGGGTCTCGACTCCACCTGCTTCGGATCTTCAGCCAGCGTCCGATCCTGGCCGAGCGCG  
AGCAAGGACAGACCTTCTGACCCTGTACTGCATCTGCAACACCCCGCCTGCATGAAAGTCTTTGTTGTCTGCTGTGTACTG  
AGTATAATAAAAGTGAGATCAGCGACTACTCCGACTTCGTGTGTTCTGCTATCAACCAGTCCCTGTTCTTACCAGGGAAC  
GAGACCGAGCTCCAGTCCAGTGTAAAGCCCCACAAGAAGTACCTCACCTGGCTGTTCCAGGGCTCTCGATCGCCGTTGTCAA  
CCACTGCGACAACGACGGAGTCTGCTGAGCGGCCCTGCCAACCTTACTTTTTCCACCCGAGAAGCAAGTCCAGCTCTTCCA  
ACCCTTCTCCCCGGGACCTATCAGTGCGTCTCGGGACCTGCCATCACACCTTCCACCTGATCCGAATACACAGCGTCGCTC  
CCCCTACTAAACAACTACCCACCAACGCCACCGTTCGCGACCGCGGACATGTACAGAGCTCGAGAAGTACTAGGCCACA  
ATACATGCCCATATTAGACTATGAGGCCGAGCCACAGCGACCATGCTCCCCGCTATTAGTTACTTCAATCTAACCGGCGGAGA  
TGACTGACCCACTGGCCAACAACAACGTCAACGACCTTCTCCTGGACATGGACGGCCGCGCCTCGGAGCAGCGACTCGCCAA  
CTTCGATTCGCCAGCAGCAGGAGAGAGCCGTCAAGGAGCTGCAGGACGGCATAGCCATCCACCAAGTGAAGAAAGGCATCT



Fig. 27H

TCTGCCTGGTGAAACAGGCCAAGATCTCTACGAGGTACCCCGACCGACCATCGCCTCTCTACGAGCTCCTGCAGCAGCGCC  
AGAAGTTCACCTGCCTGGTCGGAGTCAACCCCATCGTCATACCCAGCAGTCGGGCGATACCAAGGGGTGCATCCACTGCTCC  
TGCGACTCCCCGACTGCGTCCACACTCTGATCAAGACCCTCTGCGGCCCTCCGCGACCTCCTCCCATGAACTAATCACCCCTT  
ATCCAGTGAAATAAATATCATATTGATGATGATTTAAATAAAAAATAATCATTTGATTTGAAATAAAGATACAATCATATTGATG  
ATTTGAGTTTTAAAAAATAAAGAATCACTTACTTGAAATCTGATACCAGGTCTCTGTCCATGTTTTCTGCCAACACCACCTCACTC  
CCCTCTTCCAGCTCTGGTACTGCAGACCCCGCGGGCTGCAAACTTCTCCACACGCTGAAGGGGATGTCAAATTCCTCCTGT  
CCCTCAATCTTCATTTTATCTTCTATCAGATGTCCAAAAAGCGCTCCGGGTGGATGATGACTTCGACCCCGTCTACCCCTACGA  
TGAGACAACGCACCGACCGTGCCCTTCATCAACCCCCCTTCGTCTCTTCAGATGGATTCCAAGAGAAGCCCCCTGGGGGTGCT  
GTCCTGCGACTGGCTGACCCCGTCACCAACAAGACGGGGAAATCACCTCAAGCTGGGAGAGGGGGTGGACCTCGACTCC  
TCGGGAAAACTCATCTCCAACACGGCCACCAAGGCCGCCGCCCTCTCAGTTTTTCCAACAACACCATTTCCCTAACATGGATA  
CCCCTCTTTATACCAAAGATGGAAAATTATCCTTACAAGTTTCTCCACCGTTAAACATATTAATAACACCATTTCTGAACACATTA  
GCTGTAGCTTATGGATCAGGTTTAGGACTGAGTGGTGGCACTGCTCTTGCAGTACAGTTGGCCTCTCCACTCACTTTTGATGAA  
AAAGGAAATATTAATAAATTAACCTAGCCAGTGGTCCATTAAACAGTTGATGCAAGTCGACTTAGTATCAACTGCAAAAGAGGGGT  
CACTGTCACTACCTCAGGAGATGCAATTGAAAGCAACATAAGCTGGCCTAAAGGTATAAGATTGAAGGTAATGGCATAGCTG  
CAAACATTGGCAGAGGATTGGAATTTGGAACCACTAGTACAGAGACTGATGTCACAGATGCATACCAATTCAAGTTAAATTG  
GGTACTGGCCTTACCTTTGACAGTACAGGCGCCATTGTTGCTTGAACAAAGAGGATGATAAACTTACATTATGGACCACAGC  
CGACCCCTCGCCAAATTGCAAAATATACTTGAAAAAGATGCCAACTCACACTTTGCTTGACAAAGTGGAAGTCAAATTC  
GGGTACTGTGACTGTATTGGCAGTGAATAATGGAAGTCTCAACCAATCACAAACACAGTAAGCACTGCACTCGTCTCCCTCAA  
GTTTGATGCAAGTGGAGTTTGTCTAAGCAGCTCCACATTAGACAAAGAATATTGGAACCTCAGAAAGGGAGATGTTACACCTG  
CTGAGCCCTATACTAATGCTATAGGTTTTATGCTAACATAAAGGCCTATCTAAAAACACATCTGCAGCTTCAAAAGCCATAT  
TGTCAGTCAAGTTTATCTCAATGGGGATGAGGCCAAACCACTGATGCTGATTATTACTTTTAAATGAAACTGAGGATGCAACTTG  
CACCTACAGTATCACTTTCAATGGAATGGGATAGTACTAAGTACACAGGTGAAACACTTGCTACCAAGCTCCTTCACCTTCTCC  
TACATCGCCCAAGAATGAACACTGTATCCACCTGCATGCCAACCTTCCACCCCACTCTGTCTATGGAAAAACTCTGAAGC  
ACAAAATAAAATAAAGTTCAAGTGTATTATTGATTCAACAGTTTACAGGATTGAGCAGTTATTTTTCTCCACCTCCCAGGA  
CATGGAATACACCACCTCTCCCCCGCACAGCCTTGAACATCTGAATGCCATTGGTGATGGACATGCTTTTGGTCTCCACGTTT  
CACACAGTTTCAGAGCGAGCCAGTCTCGGGTGGTCCAGGAGATGAAACCTCCGGGCACTCCCGCATCTGCACCTCACAGCT  
CAACAGCTGAGGATTGCTCGGTGGTCCGGATCAGCGTTATCTGGAAGAAGCAGAAGAGCGGGTGGGAATCATAGTCC  
GCGAACGGGATCGGCCGGTGGTGTGCGATCAGGCCCGCACAGCATCGCTGCCCGCGCGCTCCGTCAAGCTGCTGTCTGAGG  
GGTCCGGGTCCAGGACTCCCTCAGCATGATGCCACGGCCCTCAGCATCAGTCTGCTGGTGCGGCGGGCGCAGCAGCGCAT  
GCGGATCTCGTCAAGTCTGCTGAGTACGTGCAACACAGGACCACAGGTTGTCAACAGTCCATAGTTCAACACGCTCCAGC  
CGAAACTCATCGCGGGAAGGATGCTACCCACGTGGCGTCTGACCAGATCCTCAGGTAAATCAAGTGGCGCTCCCTCCAGAAC  
ACGCTGCCACGTACATGATCTCCTTGGGCATGTGGCGTTTACCACCTCCCGGTACCACATCACCTCTGGTTGAACATGCAG  
CCCCGGATGATCTGCGGAACACAGGGCCAGACCGCCCCGCCCGCCATGCAGCGAAGAGACCCCGGTCCCGGCAATGGC  
AATGGAGGACCCACCGCTCGTACCCGTGGATCATCTGGGAGCTGAACAAGTCTATGTTGGCACAGCACAGGCATATGCTCATG  
CATCTCTTCAGCACTCTCAGCTCCTCGGGGTCAAACCATATCCAGGGCACGGGAACTCTTGCAAGGACAGCGAACCCCGC  
AGAACAGGGCAATCCTCGCACATAACTTACATTGTGCATGGACAGGGTATCGCAATCAGGCAGCACCGGGTGATCCTCCACCA  
GAGAAGCGCGGTCTCGGTCTCCTCACAGCGTGGAAGGGGGCCGGCCGATACGGGTGATGGCGGGACGCGGTGATCGTG  
TTCGCGACCGTGTGATGATGCAGTTGCTTTCGGACATTTTCGTACTTGCTGTAGCAGAACCTGGTCCGGGCGCTGCACACCGAT  
CGCCGGCGGCGGTCCCGCGCTTGAACGCTCGGTGTTGAAATTGAAAAACAGCCACTCTCTCAGACCGTGCAGCAGATCTAG  
GGCCTCAGGAGTGAAGATCCCATCATGCCTGATAGCTCTGATCAGTACGACACCGTGGAAATGGGCCAGACCCAGCCAGA  
TGATGCAATTTTGTGGTTTGGTGACGGCGGGGAGGAAGAACAGGAAGAACCATGATTAAATTTTAAATCCAAACGGTC  
TCGGCACTTTCAAATTAAGGTGCGGAGATGGCACTCTCGCCCCGCTGTGTTGGTGGAAATAACAGCCAGTCAAG  
GTGATACGGTTCTCGAGATGTTCCACGGTGGCTTCCAGCAAAGCCTCCACGCGCATCCAGAAACAAGACAATAGCGAAAGC  
GGGAGGGTTCTCAATTCCTCAATCATGTTACACTCTGCACCATCCCCAGATAATTTTCATTTTCCAGCCTTGAATGATTC  
GAACTAGTTCCTGAGGTAAATCCAAGCCAGCCATGATAAAGAGCTCGCGCAGAGCGCCCTCCACCGGCATTCTTAAGCACACC  
CTCATAATTCCAAGATATTCTGCTCTGGTTACCTGCAGCAGATTGACAAGCGGAATATCAAAATCTCTGCCGCGATCCCTAA  
GCTCCTCCCTCAGCAATAACTGTAAGTACTCTTCATATCTCTCGAAATTTTATGCCATAGGACCACAGGAATAAGATTAGG  
GCAAGCCACAGTACAGATAAACCGAAGTCTCCCCAGTGAGCATTGCCAAATGCAAGACTGCTATAAGCATGCTGGCTAGACC  
CGGTGATATCTTCAGATAACTGGACAGAAAATCACCCAGGCAATTTTAAAGAAAATCAACAAAAGAAAAATCCTCCAGGTGC  
ACGTTTAGAGCCTCGGGAACAACGATGAAGTAAATGCAAGCGGTGCGTTCCAGCATGGTTAGTTAGCTGATCTGTAAAAACA  
AAAAATAAAACATTAACCATGCTAGCCTGGCGAACAGGTGGGTAAATCGTTCTCTCCAGCACACAGGCAGGCCACGGGGTCTC  
CGGCGCGACCTCGTAAAAATTGTCGCTATGATTGAAAACCATCACAGAGAGACGTTCCCGGTGGCCGGCGTGAATGATTCTGA  
CAAGATGAATACACCCCGGAACATTGGCGTCCGCGAGTGAAAAAAGCGCCGAGGAAGCAATAAGGCACTACAATGCTCA  
GTCTCAAGTCCAGCAAAGCGATGCCATGCGGATGAAGCACAAAATCCTCAGGTGCGTACAAAATGTAATTACTCCCTCTGC  
ACAGGCAGCGAAGCCCCCGATCCCTCCAGATACACATACAAAAGCCTCAGCTCCATAGCTTACCGAGCAGCAGCACACAACAG  
CGCAAGAGTCAGAGAAAGGCTGAGCTCTAACCTGTCCACCCGCTCTGCTCAATATATAGCCAGATCTACACTGACGTAA  
AGGCCAAAGTCTAAAAATACCCGCCAAATAATCACACACGCCCAGCACACGCCCAGAAACCGGTGACACACTCAAAAAATAC  
GCGCACTTCTCAAACGCCCAAACCTGCCGTATTTCCGGGTTCCACGCTACGTCATCGGAATTCGACTTTCAAATTCGTCGAC  
CGTAAAAACGTACCCGCCCGGCCCTAACGGTGCCTCTCGGCCAATCACCTTCTCCTCCCAAATTCAAACAGCTC  
ATTTGCATATTAACGCGCACCAAAAGTTTGAGGTATATTATTGATGATG

Fig. 27I

**AdC7 010-DU422gp160(E1623) Amino acids – SEQ ID NO: 16****The symbol “ \* ” refers herein to stop codons in the non coding regions**

HHQ\*YTSNFWCALICK\*AV\*IWGGRKVIGRETGDR\*GRGG\*RFDDVAVRRSRFASSRGKSDVKRGVV\*TRKYSIFPRSLTGNEVFLG  
 GCK\*KRAIFARKLNNEEVKI\*VISRLWQGGVFAEGRVDFDLRGGFDIRIFHLNFRVRCQSPVFLRTISFPRKCHLTVTITVLR\*RKLRS  
 DPLWCTLSTICSDAA\*LSQYLLPACVLEVAE\*CASKI\*ATTRQGLTDNCMKNLLRVRRFALLRDVARYTR\*H\*LLTSMPTSTPIDVND  
 GKWPAWHYAQYMTLWDFPTWQYIYVLVIAITMVMRFWQYINGRG\*RFDSRGFSLHPIDVNGSLFWHQNRDFPKCRNNSAP  
 LTQMGGRRVRWEVYISRARLVNRQITRSFIADVHS\*IANAVSASDTSVSNLRFEDATMRVRGIPRNWPQWWIWGILGFWMIIC  
 RVVGNLDLWVTVYGVVWKEAKTTLFCASDAKAYDKEVHNWATHACVPTDNPQEIENVNTENFMWKNDMVDQMHE  
 IISLWDQSLKPCVKLTPLCVTLNCKNVNISANANATATLNSSMNGEIKNCSENTTTELDRDKKQKVYALFYKPDVPLNGGEHNETGEY  
 ILINCNSSTITQACPKVSFDPPIPIHYCAPAGYAILKCNKTFNGTGPCNNVSTVQCTHGIKPVVSTQLLNGSLAEEEEIIVRSENLTNNIKT  
 IIVHLNKSVEIKCTRPNNNTRKSVRIGPGQTFYATGEIIGDIREAHCNISRETWNSTLIQVKEKLEHYNKTIKFEPSSGGDLEVTTHSFN  
 CRGEFFYCDTTKLFNETKLFNESEYVDNKTIILPCRIKQIINMWQEVGRAMYAPPIEGNITCKSNITGLLLTWDGGENSTEGVFRPGG  
 GNMKDNWRSELYKYKVEIKPLGVAPTCKSRKVVGREKRAVGLGAVLLGLGAAGSTMGAASITLVQARQLLSGIVQQSNLLRA  
 IEAQQLHLLQTLVWGIKQLQTRVLAIERYLKQQLLGLWGCSGLICATAVPWNSSWSNKSGLDIWDNMTWMQWDREISNYNTNTI  
 FRLLDSQNNQKEKNEKDLLALDSWKNLWNWFDITNWLWYIKIFIMIVGGIIGLRIIFGVLAIVKRVRGYSPLSFQTLIPNPRGPDRL  
 GRIEEEGGEQDKDRSIRLVSGFLALAWDDLRLSLCLFSYHQLRDFILTAARAAELLGRSSLRGLQRGWEVLKYLGNLVQYWGLELKRS  
 AILFDITIAIAVAEGTDRIIEVIQRICRAIRYIPTRIRQGFEAALL\*GTSRVDPGGQTADQPRCLLVASHLLFAPPPCLP\*PWKVPLPLSFPN  
 KMRKLHRIV\*VGILFWGVGWGRTARGRIGKTIAGMLGMRWALWLLRRKEPADLQI\*IHLCRVRRKR\*\*NGIMGIMGLH\*\*IGQI  
 SICWPPCM\*PRTPARHGPSSTTS\*PDAMCTWGPAEACSCPTSATCNL\*RCCWSPMPCPE\*A\*RGCLT\*MWSCGKF\*DMMNPR  
 PGAGPANAEASTPGFSPCVWR\*RTCDPIIWCCPATGRSSAPAGKNLTRVSSVWGRWRACMRGRMTKICVFLCVA\*\*\*AEAPPL  
 REGYSALI\*RGVSPPGRECVRM\*WDPRTWAGPCSPRTLQP\*PTRP\*APRPWTQLPPQLLLPPAPCAEWPWAPATTALWWPTRL  
 PPIPPA\*TRRSSCC\*WPSSRP\*PSAWAS\*PSRWLSCRRRRRGPRLPR\*KPNKK\*INK\*TETVDFNTES\*IFI\*FFARGRPWTTGLDH\*  
 APGGFFPGPGRGGLGC\*GTWA\*ARPGGGGSSIAGPRARGWCCKSPSHSRGAGRGAARCP\*GGD\*WPRAAPWCRC\*RTC\*AGR  
 DACGR\*DASWPGS\*DWRCRDPAGGSCCAGPPARCIRRTWGICHATWKGRRIEWRPCDRPGFPCTHP\*\*WRWARGRRP  
 GQRRFGGRTHRSCGPG\*ARHRPF\*\*IWGGGCPTGGRRCPRSRGRSCPRRSASPRP\*ARRGGSCPPAGR\*KKRFPGRGR\*AGPKAG  
 SGAAGTCRSRWGR\*PR\*PAAGGS\*GRDSCRPGGGGPPRSSRAHACSARVPPGGARPPARGALAARRSFSA\*\*XRRPWAF  
 WRGSVARVPDGPARR\*CALGHLDPADLLSVRGATAGVGHQAMGVQRGQGPVLPQSQGPQRGLRHGEGVRAGLGACEGAL  
 QAHPAGREPLPVGALRVGQVAIEHEFVVERLGRVALGAELTFGSVSADGTEEGLEGVELGGEEDGLGGVGVRAAAGADGLALHEP  
 GEVGPVGVKNEVSSVLFDAFLTSLGHELVSLPGDKEAVRVPVDRLYGPVLERGA AVLVEEPRPLRDEGPGPGQHEGGHVGGVAV  
 VVHQRVHLLQGMQAHVPLVHIQEGDWLVSVGHVTGGPGRGGIKGGGPLLVTVFRIAVQERQLLG\*VFPLEGWHNLGTQVVSF\*  
 KRGGFDIDGAVGDAFHEPLVHLVRKDDLFFVELGGEGAVEGVGEELGDGAHGLVFLVVGALLGGDELHVLAHALPFGEDGGELV  
 GHSDPPAAVVQGDEVHAGGHAAQGLVGPAEAPALARAEGGQRVQHELVGGVGVHGEDAGQKLGVEVADAGVQIVQRRPLV  
 AHGQRALVGAEGRAPGHGVRERGGVHAADVVDVEGLLEDADVGGVAAPPADAGAHVVVQLVRGREEPRAEVGALRLFGAVDD  
 LAEDGVGVGGDGGPLEDEVGVGQADRVPEDEVGVVLQGLDELGGDEDVQGA VVEGLLDDVLELALLLPQLAVEKELFAVLVPL  
 FEGEPVLIGTVRAHHVELVDGLVGAAALLHGEVSLCGLAQGGVGEGEVVAHHDLEELVLEEVVAAALLPELEVRALLVGGVGQS  
 ESNIVEEDLARAGHEVASDAERLGHLPVDDDLGGEDDLVEAVDVVPDDVEFHESRAALNVGQLELVVGGELGGAEPVLLGEPVG  
 DVGVAEEGSPEIHGQGLQAVPVLTLLAHGHFFGGDAVEGAGVAVPAVPLEGEVVGELDERRVPGEFHDQHEGDELLAEGP  
 HPGVGFHIVGEEEPFGARMRADGEELDLPVVGGMADVMEVEMPTARRALVLFIQASAVLATLHGMHVLHLYLGSFDEEFQ  
 WAVERWRLHLVLYVLAIGVAIVCLDGGHADEPAREAGPDFGSDGSESEDEGAQAGAVQGPETLSQVSGQRRRAVDLQELFQG  
 AREVQMVLDLHGA VGGDVHGLQGPVPLGRHHRAPFLGRCFHAGQKRRRGRAPGGRRGSGPGRGGRGTSAPRAGRFWYCAR  
 RRLA\*ATTRRLTSWI\*RLWVKATGPVSLNLKESSTESISVSLTAACRRISCTSPELSW\*AISVMNCSSISS\*RSRPARSTVAARSLEMR  
 PMSCEKAFMPASFQTRL\*TTAPSGSRARMTTWARLSSTWRVKTA\*LQRRW\*R\*LSVVAMCSVTKKYMIQRRSGISLTSRASKRS  
 MAS\*KSTAKLKNWELRAETVNSSRRRMSSAMVARTSRKAPGGSSSSISSTNISSTSSSGGGGGGALRRRRRTGRRSMKRSM  
 VSPRRRRMVSVTARPSRGRSVKTPPRISRWPGGSP LGRERALT MHLINWPVGT PRKDL SVSRSTGSENR\*TKASSQSQSQGRLS  
 PVSCSSGISGGGRAMLLVMKLK\*AVLRRRMVARSTRSLGPACWMRRRSAMPQAWS\*HLARSL\*\*SCMSRSTGTSSSPARPCMRV  
 SPNPRWGWTARSATTSARMACCIWVRVWVKSSKSTKRW\*APVLMV\*EQLAMTDQLTVWWPGRTSSWYLRE\*ARVSKM\*  
 SLQVRTRYWYPTKCGGGWR\*SGHRSVAGAPGARSSSMRRW\*P\*MYLDIQVMPAAVVEARGNSRTRFQMLRSGRK\*FMVA  
 AVWPVRAQSWML\*TYGQKRKRSARLRGLEAKRTGWAARVPRFESRIRLEPQLTWYWSRLDPSLLTKPPGYGGGSSFFGLGRWS\*  
 KTSKRGRPPAMARCRLSEKESPLRCGVPRFEPQRSAPAGFRG\*RGRGCPVVS KTP\*PADFSSYGASPSFCVFARCIPIYCGRCAPT  
 LHLNRPYRRSSSNSRRFCPRPSSSQPLRRPP\*AEPAFSMTWPWKARGWRGWGRRRRSGTRACR\*KGTLARPTCPSRTCSETGA

Fig. 27J

ARSPRRCAPASTRGGSCGAAWTESGC\*GTRISRRTS\*RGSA PRARTWPRPTWSRRTSRP\*RRRATSKNPSTTTTCAR\*SRARR\*PW  
 A\*CTCGTCWRPSCRTPRASR\*RRSCFWWCSTVGTTTSSRRRC\*ISPSRAAGSWTW\*TFCRASWCRSAGCRCPRSWRLSTSRC\*A  
 WASTTLGRSTRPRTCP\*TRR\*RSTGFTCA\*P\*KC\*P\*ATIWGCTATTGCTAR\*APAAGAS\*ATRS\*CTACSGP\*PGPGPRGRATLTW  
 ARTCAGSPAAGPWKLPAVPPTWRRWTMRRRRASTWKTDGATVFLDDAATAS\*SRDAGGAAEPAVRH\*LLGRDPGHATHHG  
 ADDPQSRSL\*TAASGPALGHPGGRGALALEPHAREGAGHRERAGGEQGHPRRRRGRAGVQRAAGARGPLQQHQRADEPGPHG  
 DRRARGGVAARAVPPRVEPLHGGAERLPEHAARQRAPGPGGLHQLHQRAAADGGRGAPERGVVPGAGLLLPDQSPGLADREP  
 EPGFQELAGTVGRAGPGRGPRDGVPEADAELAPAAAAGGALHGQRQREPRVPLPA\*PVPRGHRAGARGRADLPGDHPREPR  
 AGPGGPGQPGGHPPELADQPAEDPAPVRAEHRGGAHPALRAAERGAVPDAGGGHAQRRARHDAQHGAQHVSQPPVHQ\*  
 ADGLLASGGRHELGLLYQRHLEPALAPAARVLHGRVRHARPQRRVPVGRRGQQRVLAAPRHHRVEERGRGPAAVLGAVRSRGCC  
 RGG\*GRQPLPEPALFAEQRAQQRAGSADAAAPAGRGVPERLLVEARARELPQ\*RDREPGGQDEPLEDVRARAQGRAPS\*QQ  
 RRHP\*TPATRQAAGSGVGR\*GFRRRQQRVGLGWEWW\*PVRSLAPPYRAPDVRI\*KNKKRYSRPRWPACVLLCCL\*\*YDEARV  
 PGGSSSLVRERDAAGGGGGDAAPAGGALRAPAVPGAYGGAEQHSLLGAGTLVRYHPVVPGGQQVGGHRLAELPERPQQLPDHR  
 GAEQRFHPHGGQHPDHQL\*RALAVGRPAENHHAHQHAQRERVHVQQVQAGDGLAQDPQWGRGG\*EL\*W\*SGRADLRV  
 GGV\*AARGQLLDHHRSDERHHRQLLGGGASERGAGERHRRERVHAQLPAGLGRDRAGDAGRVRHQRGLPPRHRPAARLR  
 RGLHREPPQQPAGHPQAAALPGGLPDPVRGPGGGQHPRALGCRSL\*EKQGGRRSGDRSRGHRLYRGAGR\*FC\*RRGSGRGG\*  
 NRK\*DSHPAGGEGQQQELQARAGQEKHRLPQLVPLQLRRPREGRALLDAAHHLGRHLRRGASLLVAARHDARPGHLLPHASS  
 \*QLPGGGRRAPARLLQELLQARAGLLAAARLHLAHLARLQPLPREDPDPPPARAHYHRQ\*KRSCSHRSRDPAAAQQYQGPSPARD  
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 EYVGDEDILEQAVERLGEFAYGKRSRPAPLKEEAVSIPLDHGNPTSLKPVTLQQLPSAAPRRGFKREGGEDLYPTMQLMVPKRQK  
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Fig. 27K

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368530-7006W01\_SequenceListing\_ST25.txt  
SEQUENCE LISTING

<110> The Wistar Institute of Anatomy and Biology  
ERTL, Hildegund C.J.  
ZHOU, Xiang Yang

<120> Compositions and Methods of Replication Deficient Adenoviral  
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<130> 368530-7006W01(00039)

<150> US 62/369,288  
<151> 2016-08-01

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## 368530-7006W01\_SequenceListing\_ST25.txt

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| aggctagagt  | tcgacgccac | catgcgcgtg  | cgcggcatcc  | cccgcaactg | gccccagtgg  | 1260 |
| tggatctggg  | gcatcctggg | cttctggatg  | atcatcatct  | gccgcgtggt | gggcaacctg  | 1320 |
| gacctgtggg  | tgaccgtgta | ctacggcgtg  | cccgtgtgga  | aggaggccaa | gaccaccctg  | 1380 |
| ttctgcgcct  | ccgacgccaa | ggcctacgac  | aaggaggtgc  | acaacgtgtg | ggccaccac   | 1440 |
| gcctgcgtgc  | ccaccgaccc | caacccccag  | gagatcgtgc  | tggagaacgt | gaccgagaac  | 1500 |
| ttcaacatgt  | ggaagaacga | catggtggac  | cagatgcacg  | aggacatcat | ctccctgtgg  | 1560 |
| gaccagtccc  | tgaagccctg | cgtgaagctg  | acccccctgt  | gcgtgaccct | gaactgcaag  | 1620 |
| aacgtgaaca  | tctccgccaa | cgccaacgcc  | accgccaccc  | tgaactcctc | catgaacggc  | 1680 |
| gagatcaaga  | actgctcctt | caacaccacc  | accgagctgc  | gcgacaagaa | gcagaaggtg  | 1740 |
| tacgccctgt  | tctacaagcc | cgacgtggtg  | ccccgaacg   | gcggcgagca | caacgagacc  | 1800 |
| ggcgagtaca  | tcctgatcaa | ctgcaactcc  | tccaccatca  | cccaggcctg | ccccaaagg   | 1860 |
| tccttcgacc  | ccatcccat  | ccactactgc  | gccccgcgcg  | gctacgccat | cctgaagtgc  | 1920 |
| aacaacaaga  | ccttcaacgg | caccggcccc  | tgcaacaacg  | tgtccaccgt | gcagtgcacc  | 1980 |
| cacggcatca  | agcccgtggt | gtccaccacg  | ctgctgctga  | acggctccct | ggccgaggag  | 2040 |
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| atcggccccg  | gccagacctt | ctacgccacc  | ggcgagatca  | tcggcgacat | ccgcgaggcc  | 2220 |
| cactgcaaca  | tctcccgcga | gacctggaac  | tccaccctga  | tccaggtgaa | ggagaagctg  | 2280 |
| cgcgagcact  | acaacaagac | catcaagttc  | gagccctcct  | ccggcggcga | cctggagggtg | 2340 |
| accaccact   | ccttcaactg | ccgcggcgag  | ttcttctact  | gcgacaccac | caagctgttc  | 2400 |
| aacgagacca  | agctgttcaa | cgagtccgag  | tacgtggaca  | acaagaccat | catcctgccc  | 2460 |
| tgccgcatca  | agcagatcat | caacatgtgg  | caggaggtgg  | gccgcgccat | gtacgcccc   | 2520 |
| cccatcgagg  | gcaacatcac | ctgcaagtcc  | aacatcaccg  | gcctgctgct | gacctgggac  | 2580 |
| ggcggcgaga  | actccaccga | gggcgtgttc  | cgccccggcg  | gcggcaacat | gaaggacaac  | 2640 |
| tggcgctccg  | agctgtacaa | gtacaagggtg | gtggagatca  | agcccctggg | cgtggcccc   | 2700 |
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| atcaagcagc  | tgcagacccg | cgtgctggcc  | atcgagcgct  | acctgaagga | ccagcagctg  | 2880 |
| ctgggcctgt  | ggggctgctc | cggcaagctg  | atctgcgcca  | ccgccgtgcc | ctggaactcc  | 2940 |
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## 368530-7006W01\_SequenceListing\_ST25.txt

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| caggagaaga | acgagaagga  | cctgctggcc | ctggactcct  | ggaagaacct  | gtggaactgg | 3120 |
| ttcgacatca | ccaactggct  | gtggttaagg | acctctagag  | tcgacccggg  | cggccaaacc | 3180 |
| gctgatcagc | ctcgactgtg  | ccttctagtt | gccagccatc  | tgttgtttgc  | ccctcccccg | 3240 |
| tgccttcctt | gaccctggaa  | ggtgccactc | ccactgtcct  | ttcctaataa  | aatgaggaaa | 3300 |
| ttgcatcgca | ttgtctgagt  | aggtgtcatt | ctattctggg  | gggtgggggtg | gggcaggaca | 3360 |
| gcaaggggga | ggattgggaa  | gacaatagca | ggcatgctgg  | ggatgcggtg  | ggctctatgg | 3420 |
| cttctgaggc | ggaaagaacc  | agcagatctg | cagatctgaa  | ttcatctatg  | tcgggtgcgg | 3480 |
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| cgtgcagccc | gcgaactctt  | caaccctgac | ctacgcgacc  | ctgagctcct  | cgtccgtgga | 4200 |
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| cccgtgggcg  | gcggcctggg  | caaagacgtt  | tcgggggtcg | gacacatcgt  | agttgtggtc | 5100 |
| ctgggtgagc  | tcgtcatagg  | ccattttaat  | gaatttgggg | cggaggggtgc | ccgactgggg | 5160 |
| gacgaagggtg | ccctcgatcc  | cgggggcgta  | gttgcctcg  | cagatctgca  | tctcccaggc | 5220 |
| cttgagctcg  | gaggggggga  | tcatgtccac  | ctgcggggcg | atgaaaaaaaa | cggtttccgg | 5280 |
| ggcgggggag  | atgagctggg  | ccgaaagcag  | gttccggagc | agctgggact  | tgccgcaacc | 5340 |
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| gcgcacgagt  | tccgccagga  | ggcgctcgcc  | ccccagcgag | aggagctctt  | gcagcgaggc | 5520 |
| gaagtttttc  | agcggcttga  | gtccgtcggc  | catgggcatt | ttggagaggg  | tctgttgcaa | 5580 |
| gagttccaga  | cgggtcccaga | gctcgggtgat | gtgctctagg | gcatctcgat  | ccagcagacc | 5640 |
| tcctcgtttc  | gcgggttggg  | gcgactgcgg  | gagtagggca | ccaggcgatg  | ggcgtccagc | 5700 |
| gagggccagg  | tccggtcctt  | ccagggccgc  | agggtcgcg  | tcagcgtggt  | ctccgtcacg | 5760 |
| gtgaaggggt  | gcgcgccggg  | ctgggcgctt  | gcgaggggtc | gcttcaggct  | catccggctg | 5820 |
| gtcgagaacc  | gctcccggtc  | ggcgccctgc  | gcgtcggcca | ggtagcaatt  | gagcatgagt | 5880 |
| tcgtagttga  | gcgcctcggc  | cgcgtggccc  | ttggcgcgga | gcttaccttt  | ggaagtgtgt | 5940 |
| ccgcagacgg  | gacagaggag  | ggacttgagg  | gcgtagagct | tgggggagag  | gaagacggac | 6000 |
| tcgggggagc  | aggcgtccgc  | gccgcagctg  | gcgcagacgg | tctcgcactc  | cacgagccag | 6060 |
| gtgaggtcgg  | ggcgggtggg  | gtcaaaaacg  | aggtttcctc | cgtgcttttt  | gatgcgtttc | 6120 |
| ttacctctgg  | tctccatgag  | ctcgtgtccc  | cgctgggtga | caaagaggct  | gtccgtgtcc | 6180 |
| ccgtagaccg  | actttatggg  | ccggtcctcg  | agcgggggtc | cgcggtcctc  | gtcgtagagg | 6240 |
| aaccccgccc  | actccgagac  | gaaggcccgg  | gtccaggcca | gcacgaagga  | ggccacgtgg | 6300 |
| gaggggtagc  | ggtcgttgtc  | caccagcggg  | tccaccttct | ccagggtatg  | caagcacatg | 6360 |
| tccccctcgt  | ccacatccag  | gaaggtgatt  | ggcttgtaag | tgtaggccac  | gtgaccgggg | 6420 |
| gtcccgggccg | ggggggtata  | aaagggggcg  | ggccccgtct | cgtcctcact  | gtcttccgga | 6480 |
| tcgctgtcca  | ggagcgccag  | ctgttggggg  | aggtattccc | tctcgaaggc  | gggcatgacc | 6540 |
| tcggcactca  | ggttgtcagt  | ttctagaaaac | gaggaggatt | tgatattgac  | ggtgccgttg | 6600 |
| gagacgcctt  | tcatgagccc  | ctcgtccatt  | tggtcagaaa | agacgatctt  | tttgttgtcg | 6660 |
| agcttgggtg  | cgaaggagcc  | gtagagggcg  | ttggagagca | gcttggcgat  | ggagcgcatg | 6720 |
| gtctggttct  | tttccttgtc  | ggcgcgctcc  | ttggcggcga | tgttgagctg  | cacgtactcg | 6780 |



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|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| cgcgccacgc | acttccattc | ggggaagacg  | gtggtgagct | cgtcgggcac  | gattctgacc  | 6840 |
| cgccagccgc | ggttgtgcag | ggtgatgagg  | tccacgctgg | tggccacctc  | gccgcgcagg  | 6900 |
| ggctcgttgg | tccagcagag | gcgcccgcgc  | ttgcgcgagc | agaagggggg  | cagcgggtcc  | 6960 |
| agcatgagct | cgtcgggggg | gtcggcgctc  | acggtgaaga | tgccgggcag  | gagctcgggg  | 7020 |
| tcgaagtagc | tgatgcaggt | gcccagattg  | tccacgcgcc | cttgccagtc  | gcgcacggcc  | 7080 |
| agcgcgcgct | cgtaggggct | gaggggcgtg  | ccccagggca | tggggtgcgt  | gagcgcggag  | 7140 |
| gcgtacatgc | cgcagatgtc | gtagacgtag  | aggggctcct | cgaggacgcc  | gatgtagggtg | 7200 |
| gggtagcagc | gccccccgcg | gatgctggcg  | cgcacgtagt | cgtacagctc  | gtgcgagggc  | 7260 |
| gcgaggagcc | ccgtgccgag | gttgagcgct  | tgcggctttt | cggcgcggta  | gacgatctgg  | 7320 |
| cggaagatgg | cgtgggagtt | ggaggagatg  | gtgggccttt | ggaagatgtt  | gaagtgggcg  | 7380 |
| tggggcaggc | cgaccgagtc | cctgatgaag  | tgggcgtagg | agtcctgcag  | cttggcgacg  | 7440 |
| agctcggcgg | tgacgaggac | gtccagggcg  | cagtagtcga | gggtctcttg  | gatgatgtca  | 7500 |
| tacttgagct | ggcccttctg | cttcacacagc | tcgcggttga | gaaggaaactc | ttcgcggtcc  | 7560 |
| ttccagtact | cttcgagggg | gaacccgtcc  | tgatcggcac | ggtaagagcc  | caccatgtag  | 7620 |
| aactggttga | cggccttgta | ggcgcagcag  | cccttctcca | cggggagggc  | gtaagcttgc  | 7680 |
| gcggccttgc | gcagggaggt | gtgggtgagg  | gcgaagggtg | cgcgcaccat  | gaccttgagg  | 7740 |
| aactggtgct | tgaagtcgag | gtcgtcgcag  | ccgccctgct | cccagagttg  | gaagtcctgt  | 7800 |
| cgcttcttgt | aggcgggggt | aggcaaagcg  | aaagtaacat | cgttgaagag  | gatcttgccc  | 7860 |
| gcgcggggca | tgaagttgcg | agtgatgcgg  | aaaggctggg | gcacctcggc  | ccggttggtg  | 7920 |
| atgacctggg | cggcgaggac | gatctcgtcg  | aagccgttga | tgttggtgccc | gacgatgtag  | 7980 |
| agttccacga | atcgcggggc | gcccttgacg  | tggggcagct | tcttgagctc  | gtcgtagggtg | 8040 |
| agctcggcgg | ggtcgctgag | cccgtgctgc  | tcgagggccc | agtcggcgac  | gtgggggttg  | 8100 |
| gcgctgagga | aggaagtcca | gagatccacg  | gccagggcgg | tctgcaagcg  | gtcccggtag  | 8160 |
| tgacggaact | gttggtccac | ggccattttt  | tcgggggtga | cgcagtagaa  | ggtgcggggg  | 8220 |
| tcgccgtgcc | agcgggtcca | cttgagctgg  | agggcgaggt | cgtgggcgag  | ctcgacgagc  | 8280 |
| ggcgggtccc | cggagagttt | catgaccagc  | atgaagggga | cgagctgctt  | gccgaaggac  | 8340 |
| cccatccagg | tgtaggtttc | cacatcgtag  | gtgaggaaga | gcctttcggt  | gcgaggatgc  | 8400 |
| gagccgatgg | ggaagaactg | gatctcctgc  | caccagttgg | aggaatggct  | gttgatgtga  | 8460 |
| tggaagtaga | aatgccgacg | gcgcgccgag  | cactcgtgct | tgtgtttata  | caagcgtccg  | 8520 |
| cagtgtcgc  | aacgctgcac | gggatgcacg  | tgctgcacga | gctgtacctg  | ggttcctttg  | 8580 |
| gcgaggaatt | tcagtgggca | gtggagcgct  | ggcggctgca | tctcgtgctg  | tactacgtct  | 8640 |

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|             |             |             |             |            |            |       |
|-------------|-------------|-------------|-------------|------------|------------|-------|
| tggccatcgg  | cgtggccatc  | gtctgcctcg  | atggtgggtca | tgctgacgag | cccgcgcggg | 8700  |
| aggcaggtcc  | agacctcggc  | tcggacgggt  | cggagagcga  | ggacgagggc | gcgcaggccg | 8760  |
| gagctgtcca  | gggtcctgag  | acgctgcgga  | gtcaggtcag  | tgggcagcgg | cggcgcgcgg | 8820  |
| ttgacttgca  | ggagcttttc  | cagggcgcgc  | gggaggtcca  | gatggtactt | gatctccacg | 8880  |
| gcgccgttgg  | tggctacgtc  | cacggcttgc  | agggtgccgt  | gcccctgggg | cgccaccacc | 8940  |
| gtgccccgtt  | tcttcttggg  | cgctgcttcc  | atgtcgggtca | gaagcggcgg | cgaggacgcg | 9000  |
| cgccggggcgg | cagggggcggc | tcggggccccg | gaggcagggg  | cggcaggggc | acgtcggcgc | 9060  |
| cgcgcgcggg  | caggttctgg  | tactgcgccc  | ggagaagact  | ggcgtgagcg | acgacgcgac | 9120  |
| ggttgacgtc  | ctggatctga  | cgctcttggg  | tgaaggccac  | gggacccgtg | agtttgaacc | 9180  |
| tgaaagagag  | ttcgacagaa  | tcaatctcgg  | tatcgttgac  | ggcggcctgc | cgcaggatct | 9240  |
| cttgcacgtc  | gcccaggttg  | tcctggtagg  | cgatctcggg  | catgaactgc | tcgatctcct | 9300  |
| cctctgaag   | gtctccgcgg  | ccggcgcgct  | cgacggtggc  | cgcgaggtcg | ttggagatgc | 9360  |
| ggcccatgag  | ctgcgagaag  | gcgttcatgc  | cggcctcgtt  | ccagacgcgg | ctgtagacca | 9420  |
| cggctccgtc  | ggggtcgcgc  | gcgcgcatga  | ccacctgggc  | gaggttgagc | tcgacgtggc | 9480  |
| gcgtgaagac  | cgcgtagttg  | cagaggcgct  | ggtagaggta  | gttgagcgtg | gtggcgatgt | 9540  |
| gctcggtgac  | gaagaagtac  | atgatccagc  | ggcggagcgg  | catctcgtcg | acgtcgccca | 9600  |
| gggcttccaa  | gcgttccatg  | gcctcgtaga  | agtccacggc  | gaagttgaaa | aactgggagt | 9660  |
| tgcgcgccga  | gacgggtcaac | tcctcctcca  | gaagacggat  | gagctcggcg | atggtggcgc | 9720  |
| gcacctcgcg  | ctcgaaggcc  | ccgggggggct | cctcttccat  | ctcctcctct | tcctcctcca | 9780  |
| ctaacatctc  | ttctacttcc  | tcctcaggag  | gcggtggcgg  | gggagggggc | ctgcgtcgcc | 9840  |
| ggcggcgcac  | gggcagacgg  | tcgatgaagc  | gctcgtatgt  | ctccccgcgc | cggcgacgca | 9900  |
| tggctctcgg  | gacggcgcgc  | ccgtcctcgc  | ggggccgcag  | catgaagacg | ccgccgcgca | 9960  |
| tctccagggtg | gccgccgggg  | gggtctccgt  | tgggcaggga  | gagggcgctg | acgatgcatc | 10020 |
| ttatcaattg  | acccgtaggg  | actccgcgca  | aggacctgag  | cgtctcgaga | tccacgggat | 10080 |
| ccgaaaaccg  | ctgaacgaag  | gcttcgagcc  | agtcgcagtc  | gcaaggtagg | ctgagcccgg | 10140 |
| tttcttggtc  | ttcgggtatt  | tggtcgggag  | gcgggcgggc  | gatgctgctg | gtgatgaagt | 10200 |
| tgaagtaggc  | ggtcctgaga  | cggcggtatg  | tggcgaggag  | caccaggtcc | ttgggcccgg | 10260 |
| cttgctggat  | gcgcagacgg  | tcggccatgc  | cccaggcgtg  | gtcctgacac | ctggcgaggt | 10320 |
| ccttgtagta  | gtcctgcatg  | agccgctcca  | cgggcacctc  | ctcctcgccc | gcgcggccgt | 10380 |
| gcatgcgcgt  | gagcccgaac  | ccgcgctgcg  | gctggacgag  | cgccaggtcg | gcgacgacgc | 10440 |
| gctcggtgag  | gatggcctgc  | tggatctggg  | tgaggggtgt  | ctggaagtcg | tcgaagtcga | 10500 |
| cgaagcgggtg | gtaggctccg  | gtgttgatgg  | tgtaggagca  | gttggccatg | acggaccagt | 10560 |

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|             |            |             |             |             |            |       |
|-------------|------------|-------------|-------------|-------------|------------|-------|
| tgacggtctg  | gtggccgggt | cgcacgagct  | cgtggtactt  | gaggcgcgag  | taggcgcgcg | 10620 |
| tgtcgaagat  | gtagtcgttg | caggcgcgca  | cgaggtactg  | gtatccgacg  | aggaagtgcg | 10680 |
| gcggcggctg  | gcggtagagc | ggccatcgct  | cggtggcggg  | ggcgcggggc  | gcgaggtcct | 10740 |
| cgagcatgag  | gcggtggtag | ccgtagatgt  | acctggacat  | ccaggtgatg  | ccggcggcgg | 10800 |
| tggtggaggc  | gcgcgggaac | tcgcggacgc  | ggttccagat  | gttgcgcagc  | ggcaggaagt | 10860 |
| agttcatggt  | ggccgcggtc | tggcccgtga  | ggcgcgcgca  | gtcgtggatg  | ctctagacat | 10920 |
| acgggcaaaa  | acgaaagcgg | tcagcggctc  | gactccgtgg  | cctggaggct  | aagcgaacgg | 10980 |
| gttgggctgc  | gcgtgtaccc | cggttcgaat  | ctcgaatcag  | gctggagccg  | cagctaactg | 11040 |
| ggtactggca  | ctcccgtctc | gacccaagcc  | tgctaacgaa  | acctccagga  | tacggaggcg | 11100 |
| ggtcgttttt  | tggccttggg | cgctggatcat | gaaaaactag  | taagcgcgga  | aagcggccgc | 11160 |
| ccgcgatggc  | tcgctgccgt | agtctggaga  | aagaatcgcc  | agggttgctg  | tgcggtgtgc | 11220 |
| cccggttcga  | gcctcagcgc | tcggcgccgg  | ccggattccg  | cggctaactg  | gggcgtggct | 11280 |
| gccccgtcgt  | ttccaagacc | ccttagccag  | ccgacttctc  | cagttacgga  | gcgagcccct | 11340 |
| cttttttttt  | cttgtgtttt | tgccagatgc  | atcccgtact  | gcggcagatg  | cgccccacc  | 11400 |
| ctccaccaca  | accgccccta | ccgcagcagc  | agcaacagcc  | ggcgcttctg  | ccccgcgcc  | 11460 |
| agcagcagcc  | agccactacc | gcggcggccg  | ccgtgagcgg  | agccggcgtt  | cagtatgacc | 11520 |
| tggccttggg  | agagggcgag | gggctggcgc  | ggctgggggc  | gtcgtcgccg  | gagcggcacc | 11580 |
| cgcgcggtgca | gatgaaaagg | gacgctcgcg  | aggcctacgt  | gccaagcag   | aacctgttca | 11640 |
| gagacaggag  | cggcgaggag | cccgaggaga  | tgcgcgcctc  | ccgcttcac   | gcggggcggg | 11700 |
| agctgcggcg  | cggcctggac | cgaaagcggg  | tgctgaggga  | cgaggatttc  | gaggcggacg | 11760 |
| agctgacggg  | gatcagcccc | gcgcgcgcgc  | acgtggccgc  | ggccaacctg  | gtcacggcgt | 11820 |
| acgagcagac  | cgtgaaggag | gagagcaact  | tcaaaaaatc  | cttcaacaac  | cacgtgcgca | 11880 |
| cgctgatcgc  | gcgcgaggag | gtgaccctgg  | gcctgatgca  | cctgtgggac  | ctgctggagg | 11940 |
| ccatcgtgca  | gaaccccacg | agcaagccgc  | tgacggcgca  | gctgtttctg  | gtggtgcagc | 12000 |
| acagtcggga  | caacgagacg | ttcaggaggag | cgctgctgaa  | tatcaccgag  | cccgagggcc | 12060 |
| gctggctcct  | ggacctggtg | aacattttgc  | agagcatcgt  | ggtgcaggag  | cgcgggctgc | 12120 |
| cgctgtccga  | gaagctggcg | gccatcaact  | tctcggtgct  | gagtctgggc  | aagtactacg | 12180 |
| ctaggaagat  | ctacaagacc | ccgtacgtgc  | ccatagacaa  | ggagggtgaag | atcgacgggt | 12240 |
| tttacatgcg  | catgaccctg | aaagtgtgta  | ccctgagcga  | cgatctgggg  | gtgtaccgca | 12300 |
| acgacaggat  | gcaccgcgcg | gtgagcgcca  | gccgccggcg  | cgagctgagc  | gaccaggagc | 12360 |
| tgatgcacag  | cctgcagcgg | gccctgaccg  | gggccggggac | cgagggggag  | agctactttg | 12420 |

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|          |       |          |       |         |       |          |        |         |        |          |          |       |       |
|----------|-------|----------|-------|---------|-------|----------|--------|---------|--------|----------|----------|-------|-------|
| acatggg  | gcgc  | ggacctg  | gcgc  | tggcagc | cca   | gccgccg  | ggc    | cttggaa | gct    | gccggc   | ggtt     | 12480 |       |
| ccccctac | gt    | ggaggag  | gtg   | gacgatg | agg   | aggagg   | agg    | cgagtac | ctg    | gaagact  | gat      | 12540 |       |
| ggcgcg   | accg  | tat      | ttttt | gct     | agatg | cagca    | acagcc | accg    | ccgccg | cctc     | ctgatccc | gc    | 12600 |
| gatgcg   | ggcg  | gcgctg   | caga  | gccagcc | gtc   | cggcatta | aac    | tcctc   | ggacg  | attgg    | accca    | 12660 |       |
| ggccatg  | caa   | cgcatcat | gg    | cgctgac | gac   | ccgcaat  | ccc    | gaagc   | cttta  | gacagc   | agcc     | 12720 |       |
| tcaggcca | aac   | cggctctc | gg    | ccatcct | gga   | ggccgtg  | ggtg   | ccctc   | gcgct  | cgaacccc | ac       | 12780 |       |
| gcacgaga | aag   | gtgctgg  | cca   | tcgtgaa | cgc   | gctggtg  | ggag   | aacaagg | cca    | tccgcg   | gtga     | 12840 |       |
| cgaggcc  | ggg   | ctggtgt  | taca  | acgcgct | gct   | ggagcgc  | gtg    | gcccgc  | taca   | acagcac  | caa      | 12900 |       |
| cgtgcag  | acg   | aacctgg  | acc   | gcatggt | gac   | cgacgtg  | cgc    | gaggc   | ggtgt  | cgacgc   | gca      | 12960 |       |
| gcggtt   | ccac  | cgcgagt  | cga   | acctggg | ctc   | catggtg  | ggcg   | ctgaac  | gcct   | tcctgag  | cac      | 13020 |       |
| gcagccc  | gcc   | aacgtg   | cccc  | ggggcc  | agga  | ggactac  | acc    | aactt   | catca  | gcgcg    | ctg      | 13080 |       |
| gctgatg  | gtg   | gccgag   | gtc   | cccagag | cga   | ggtgtac  | cag    | tcgggg  | ccgg   | actactt  | cctt     | 13140 |       |
| ccagacc  | agt   | cgccagg  | gct   | tgcagac | cgt   | gaacctg  | agc    | caggctt | tca    | agaactt  | gca      | 13200 |       |
| gggactg  | tgg   | ggcgtg   | cagg  | ccccggt | cgg   | ggaccgc  | gcg    | acggtg  | tcga   | gcctg    | ctg      | 13260 |       |
| gccgaac  | tcg   | cgctg    | ctgc  | tgctg   | ctggt | ggcgcc   | ctt    | acggac  | agcg   | gcagc    | gtg      | 13320 |       |
| ccgcgac  | tcg   | tacctgg  | gct   | acctg   | cttaa | cctgtac  | cgc    | gaggcc  | atcg   | gacagg   | cga      | 13380 |       |
| cgtggac  | gag   | cagacct  | acc   | aggagat | cac   | ccacgtg  | agc    | cgcg    | gcgtg  | gccagg   | agga     | 13440 |       |
| cccggg   | caac  | ctggagg  | cca   | ccctga  | actt  | cctgctg  | acc    | aaccggt | cgc    | agaagat  | ccc      | 13500 |       |
| gccccag  | tac   | gcgctg   | agca  | ccgagg  | agga  | gcgcac   | cctg   | cgctac  | gtgc   | agcagag  | cgt      | 13560 |       |
| ggggctg  | ttc   | ctgatg   | cagg  | aggggg  | ccac  | gcccagc  | gcg    | gcgctc  | gaca   | tgaccg   | cgcg     | 13620 |       |
| caacatg  | gag   | cccagcat | gt    | acgccc  | gcaa  | ccgccc   | gttc   | atcaata | aagc   | tgatgg   | acta     | 13680 |       |
| cttgcac  | cgg   | gcggcc   | gcca  | tgaact  | cgga  | ctacttt  | acc    | aacgcc  | atct   | tgaaccc  | gca      | 13740 |       |
| ctggct   | ccccg | ccgccc   | gggt  | tctacac | ggg   | cgagtac  | gac    | atgccc  | gacc   | ccaacg   | acg      | 13800 |       |
| gttcctg  | tgg   | gacgac   | gtg   | acagcag | cgt   | gttctc   | gccg   | cgtccag | gaa    | ccaatg   | ccgt     | 13860 |       |
| gtggaag  | aaa   | gagggc   | gggg  | accggc  | ggcc  | gtcctc   | ggcg   | ctgtcc  | ggtc   | gcgcgg   | gtgc     | 13920 |       |
| tgccgc   | ggcg  | gtgccc   | gagg  | ccgccag | ccc   | cttccc   | gagc   | ctgcc   | ctttt  | cgctga   | acag     | 13980 |       |
| cgtgcg   | cagc  | agcgag   | ctgg  | gtcggc  | tgac  | gcgacc   | gcg    | ctgctg  | ggcg   | aggagg   | agta     | 14040 |       |
| cctgaac  | gac   | tcctt    | gttga | ggccc   | gagcg | cgagaaga | aac    | ttcccca | aata   | acggg    | ataga    | 14100 |       |
| gagcctg  | ggtg  | gacaaga  | tga   | gccgct  | ggaa  | gacgtac  | gcg    | cacgag  | caca   | gggacg   | agcc     | 14160 |       |
| ccgagc   | tagc  | agcgcag  | gca   | cccgtag | acg   | ccagcgg  | cac    | gacagg  | cagc   | ggggact  | ggt      | 14220 |       |
| gtgggac  | gat   | gaggatt  | ccg   | ccgacg  | acag  | cagcgtg  | ttg    | gactt   | gggtg  | ggagt    | ggtg     | 14280 |       |
| taacccg  | ttc   | gctcac   | cctgc | gcccc   | gtat  | cgggcg   | cctg   | atgta   | aagaat | ctgaaaa  | aaat     | 14340 |       |

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|             |            |            |            |            |            |       |
|-------------|------------|------------|------------|------------|------------|-------|
| aaaagacggt  | actcaccaag | gccatggcga | ccagcgtgcg | ttcttctctg | ttgtttgtag | 14400 |
| tagtatgatg  | aggcgcgtgt | acccggaggg | tcctcctccc | tcgtacgaga | gcgtgatgca | 14460 |
| gcaggcgggtg | gcggcggcga | tgcagccccc | gctggaggcg | ccttacgtgc | ccccgcggta | 14520 |
| cctggcgcct  | acggaggggg | ggaacagcat | tcgttactcg | gagctggcac | ccttgtacga | 14580 |
| taccacccgg  | ttgtacctgg | tggacaacaa | gtcggcagac | atcgccctcg | tgaactacca | 14640 |
| gaacgaccac  | agcaacttcc | tgaccaccgt | ggtgcagaac | aacgatttca | ccccacgga  | 14700 |
| ggccagcacc  | cagaccatca | actttgacga | gcgctcgcgg | tggggcggcc | agctgaaaac | 14760 |
| catcatgcac  | accaacatgc | ccaacgtgaa | cgagttcatg | tacagcaaca | agttcaaggc | 14820 |
| gcgggtgatg  | gtctcgcgca | agacccccaa | cggggtggat | gatgattatg | atggtagtca | 14880 |
| ggacgagctg  | acctacgagt | gggtggagtt | tgagctgcc  | gagggcaact | tctcggtgac | 14940 |
| catgaccatc  | gatctgatga | acaacgccat | catcgacaac | tacttggcgg | tggggcggca | 15000 |
| gaacgggggtg | ctggagagcg | acatcggcgt | gaagttcgac | acgcgcaact | tccggctggg | 15060 |
| ctgggacccc  | gtgaccgagc | tggtgatgcc | gggcgtgtac | accaacgagg | ccttccaccc | 15120 |
| cgacatcgtc  | ctgctgcccc | gctgcggcgt | ggacttcacc | gagagccgcc | tcagcaacct | 15180 |
| gctgggcatc  | cgcaagcggc | agcccttcca | ggagggcttc | cagatcctgt | acgaggacct | 15240 |
| ggagggggggc | aacatccccg | cgctcttggg | tgctgaagcc | tacgagaaaa | gcaaggagga | 15300 |
| tagcaccgcc  | gcggcgaccg | cagccgtggc | caccgcctct | accgaggtgc | ggggcgataa | 15360 |
| ttttgctagc  | gctgcggcag | cggccgaggc | ggctgaaacc | gaaagtaaga | tagtcatcca | 15420 |
| gccggtggag  | aaggacagca | aggacaggag | ctacaacgtg | ctcgcggaca | agaaaaacac | 15480 |
| cgcctaccgc  | agctggtacc | tggcctacaa | ctacggcgac | cccgagaagg | gcgtgcgctc | 15540 |
| ctggacgctg  | ctcaccacct | cggacgtcac | ctgcggcgtg | gagcaagtct | actggtcgct | 15600 |
| gcccgacatg  | atgcaagacc | cggtcacctt | ccgctccacg | cgtcaagtta | gcaactaccc | 15660 |
| ggtggtgggc  | gccgagctcc | tggcgtcta  | ctccaagagc | ttcttcaacg | agcaggccgt | 15720 |
| ctactcgcag  | cagctgcgcg | ccttcacctc | gctcacgcac | gtcttcaacc | gcttccccga | 15780 |
| gaaccagatc  | ctcgtccgcc | cgcccgcgcc | caccattacc | accgtcagtg | aaaacgttcc | 15840 |
| tgctctcaca  | gatcacggga | ccctgccgct | gcgcagcagt | atccggggag | tccagcgcgt | 15900 |
| gaccgtcact  | gacgccagac | gccgcacctg | cccctacgtc | tacaaggccc | tgggcgtagt | 15960 |
| cgcgccgcgc  | gtcctctcga | gccgcacctt | ctaaaaaatg | tccattctca | tctcgcccag | 16020 |
| taataacacc  | ggttgggggc | tgcgcgcgcc | cagcaagatg | tacggaggcg | ctcgccaacg | 16080 |
| ctccacgcaa  | caccccgtgc | gcgtgcgcgg | gcaattccgc | gctccctggg | gcgccctcaa | 16140 |
| gggccgcgtg  | cgctcgcgca | ccaccgtcga | cgacgtgatc | gaccaggtgg | tggccgacgc | 16200 |

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|            |             |            |             |            |             |       |
|------------|-------------|------------|-------------|------------|-------------|-------|
| gcgcaactac | acgcccgcgcg | ccgcgcccgt | ctccaccgtg  | gacgccgtca | tcgacagcgt  | 16260 |
| ggtggccgac | gcgcgcccgt  | acgcccgcac | caagagccgg  | cggcggcgca | tcgcccggcg  | 16320 |
| gcaccggagc | acccccgcca  | tgcgcgcggc | gcgagccttg  | ctgcgcaggg | ccaggcgcac  | 16380 |
| gggacgcagg | gccatgctca  | gggcggccag | acgcgcggcc  | tccggcagca | gcagcgccgg  | 16440 |
| caggacccgc | agacgcgcgg  | ccacggcggc | ggcggcgggc  | atcgccagca | tgtcccggcc  | 16500 |
| gcggcgcggc | aacgtgtact  | gggtgcgcga | cgccgccacc  | ggtgtgcgcg | tgcccgtgcg  | 16560 |
| cacccgcccc | cctcgcactt  | gaagatgctg | acttcgcgat  | gttgatgtgt | cccagcgggc  | 16620 |
| aggaggatgt | ccaagcgcaa  | atacaaggaa | gagatgctcc  | aggtcatcgc | gcctgagatc  | 16680 |
| tacggccccg | cggcggcggt  | gaaggaggaa | agaaagcccc  | gcaaactgaa | gcgggtcaaa  | 16740 |
| aaggacaaaa | aggaggagga  | agatgacgga | ctggtggagt  | ttgtgcgcga | gttcgcccc   | 16800 |
| cggcggcgcg | tgcagtggcg  | cgggcgga   | gtgaaaccgg  | tgtgcggcc  | cggcaccacg  | 16860 |
| gtggtcttca | cgccggcgga  | gcgttcggc  | tccgctcca   | agcgctccta | cgacgaggtg  | 16920 |
| tacggggacg | aggacatcct  | cgagcaggcg | gtcgagcgtc  | tgggcgagtt | tgcgtacggc  | 16980 |
| aagcgcagcc | gccccgcgcc  | cttgaaagag | gaggcgggtg  | ccatcccgt  | ggaccacggc  | 17040 |
| aacccacgc  | cgagcctgaa  | gccggtgacc | ctgcagcagg  | tgctaccgag | cgcggcgcgc  | 17100 |
| cgccggggct | tcaagcgcgga | gggcggcgag | gatctgtacc  | cgaccatgca | gctgatgggtg | 17160 |
| cccaagcgcc | agaagctgga  | ggacgtgctg | gagcacatga  | aggtggaccc | cgaggtgcag  | 17220 |
| cccgaggtca | aggtgcggcc  | catcaagcag | gtggccccgg  | gcctgggct  | gcagaccgtg  | 17280 |
| gacatcaaga | tccccacgga  | gcccattgga | acgcagaccg  | agcccgtgaa | gcccagcacc  | 17340 |
| agcaccatgg | aggtgcagac  | ggatcccctg | atgccagcac  | cagcttcac  | cagcactcgc  | 17400 |
| cgaagacgca | agtacggcgc  | ggccagcctg | ctgatgccca  | actacgcgct | gcaccccttc  | 17460 |
| atcatcccca | cgccgggcta  | ccgcggcacg | cgcttctacc  | gcggctacac | cagcagccgc  | 17520 |
| cgccgcaaga | ccaccacccg  | ccgccgtcgt | cgcagccgcc  | gcagcagcac | cgcgacttcc  | 17580 |
| gccttggtgc | ggagagtgtg  | tcgcagcggg | cgcgagcctc  | tgaccctgcc | gcgcgcgcgc  | 17640 |
| taccacccga | gcacgcgccat | ttaactaccg | cctcctactt  | gcagatatgg | ccctcacatg  | 17700 |
| ccgcctccgc | gtccccatta  | cgggctaccg | aggaagaaaag | ccgcgccgta | gaaggctgac  | 17760 |
| ggggaacggg | ctgcgtcgcc  | atcaccaccg | gcggcggcgc  | gccatcagca | agcggttggg  | 17820 |
| gggaggcttc | ctgcccgcgc  | tgatcccat  | catcgccgcg  | gcgatcgggg | cgatccccgg  | 17880 |
| catagcttcc | gtggcgggtg  | aggcctctca | gcgccactga  | gacacaaaaa | agcatggatt  | 17940 |
| tgtaataaaa | aaaaaaatgg  | actgacgctc | ctggtcctgt  | gatgtgtgtt | tttagatgga  | 18000 |
| agacatcaat | ttttcgtccc  | tggcaccgcg | acacggcacg  | cgcccggtta | tgggcacctg  | 18060 |
| gagcgacatc | ggcaacagcc  | aactgaacgg | gggcgccttc  | aattggagca | gtctctggag  | 18120 |

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|            |            |            |            |             |             |       |
|------------|------------|------------|------------|-------------|-------------|-------|
| cgggcctaag | aatttcgggt | ccacgctcaa | aacctatggc | aacaaggcgt  | ggaacagcag  | 18180 |
| cacagggcag | gcgctgaggg | aaaagctgaa | agaacagaac | ttccagcaga  | aggtggttga  | 18240 |
| tggcctggcc | tcaggcatca | acggggtggt | tgacctggcc | aaccaggccg  | tcagaaaaca  | 18300 |
| gatcaacagc | cgcctggacg | cggtcccgcc | cgcggggtcc | gtggagatgc  | cccaggtgga  | 18360 |
| ggaggagctg | cctcccctgg | acaagcgcg  | cgacaagcga | ccgctcccgc  | acgcggagga  | 18420 |
| gacgtgctg  | acgcacacgg | acgagccgcc | cccgtacgag | gaggcgggtga | aactgggcct  | 18480 |
| gcccaccacg | cggcccgtgg | cgcctctggc | caccggagtg | ctgaaacca   | gcagcagcca  | 18540 |
| gcccgcgacc | ctggacttgc | ctccgcctcg | cccctccaca | gtggctaagc  | ccctgccgcc  | 18600 |
| ggtggccgtc | gcgtcgcgcg | ccccccgagg | ccgccccag  | gcgaactggc  | agagcactct  | 18660 |
| gaacagcatc | gtgggtctgg | gagtgcagag | tgtgaagcgc | cgccgctgct  | attaaaagac  | 18720 |
| actgtagcgc | ttaacttgct | tgtctgtgtg | tatatgtatg | tccgccgacc  | agaaggagga  | 18780 |
| gtgtgaagag | gcgcgtcgcc | gagttgcaag | atggccaccc | catcgatgct  | gccccagtgg  | 18840 |
| gcgtacatgc | acatcgccgg | acaggacgct | tcggagtacc | tgagtccggg  | tctggtgcag  | 18900 |
| ttcgcccgcg | ccacagacac | ctacttcagt | ctggggaaca | agtttaggaa  | ccccacggtg  | 18960 |
| gcgcccacgc | acgatgtgac | caccgaccgc | agccagcggc | tgacgctgcg  | cttcgtgccc  | 19020 |
| gtggaccgcg | aggacaacac | ctactcgtac | aaagtgcgct | acacgctggc  | cgtgggcgac  | 19080 |
| aaccgcgtgc | tggacatggc | cagcacctac | tttgacatcc | gcggcgtgct  | ggaccggggc  | 19140 |
| cctagcttca | aaccctactc | tggcaccgcc | tacaacagcc | tagctcccaa  | gggagctccc  | 19200 |
| aattccagcc | agtgggagca | agcaaaaaca | ggcaatgggg | gaactatgga  | aacacacaca  | 19260 |
| tatggtgtgg | ccccaatggg | cggagagaat | attacaaaag | atggtcttca  | aattggaact  | 19320 |
| gacgttacag | cgaatcagaa | taaaccaatt | tatgccgaca | aaacatttca  | accagaaccg  | 19380 |
| caagtaggag | aagaaaattg | gcaagaaact | gaaaactttt | atggcggtag  | agctcttaaa  | 19440 |
| aaagacacaa | acatgaaacc | ttgctatggc | tcctatgcta | gaccaccaa   | tgaaaaagga  | 19500 |
| ggtcaagcta | aacttaaagt | tggagatgat | ggagttccaa | ccaaagaatt  | cgacatagac  | 19560 |
| ctggctttct | ttgatactcc | cggtggcacc | gtgaacggtc | aagacgagta  | taaagcagac  | 19620 |
| attgtcatgt | ataccgaaaa | cacgtatttg | gaaactccag | acacgcatgt  | ggtatacaaa  | 19680 |
| ccaggcaagg | atgatgcaag | ttctgaaatt | aacctggttc | agcagtctat  | gcccacacaga | 19740 |
| cccaactaca | ttgggttcag | ggacaacttt | atcggtctta | tgtactacaa  | cagcactggc  | 19800 |
| aatatgggtg | tgcttgctgg | tcaggcctcc | cagctgaatg | ctgtggttga  | tttgcaagac  | 19860 |
| agaaacaccg | agctgtccta | ccagctcttg | cttgactctt | tgggtgacag  | aaccgggtat  | 19920 |
| ttcagtatgt | ggaaccaggc | ggtggacagt | tatgaccccg | atgtgcgcat  | catcgaaaac  | 19980 |

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|             |             |             |            |            |            |       |
|-------------|-------------|-------------|------------|------------|------------|-------|
| catggtgtgg  | aggatgaatt  | gccaaaactat | tgcttcccct | tggacggctc | tggcactaac | 20040 |
| gccgcatacc  | aagggtgtgaa | agtaaaagat  | ggtcaagatg | gtgatgttga | gagtgaatgg | 20100 |
| gaaaatgacg  | atactgttgc  | agctcgaaat  | caattatgta | aaggtaacat | tttcgccatg | 20160 |
| gagattaatc  | tccaggctaa  | cctgtggaga  | agtttcctct | actcgaacgt | ggccctgtac | 20220 |
| ctgcccgact  | cctacaagta  | cacgccgacc  | aacgtcacgc | tgccgaccaa | caccaacacc | 20280 |
| tacgattaca  | tgaatggcag  | agtgacacct  | ccctcgctgg | tagacgccta | cctcaacatc | 20340 |
| ggggcgcgct  | ggtcgctgga  | ccccatggac  | aacgtcaacc | ccttcaacca | ccaccgcaac | 20400 |
| gcggggcctgc | gctaccgctc  | catgctcctg  | ggcaacgggc | gctacgtgcc | cttccacatc | 20460 |
| cagggtgcccc | aaaagttttt  | cgccatcaag  | agcctcctgc | tcctgcccgg | gtcctacacc | 20520 |
| tacgagtgga  | acttccgcaa  | ggacgtcaac  | atgatcctgc | agagctccct | aggcaacgac | 20580 |
| ctgcgcacgg  | acggggcctc  | catcgccctt  | accagcatca | acctctacgc | caccttcttc | 20640 |
| cccatggcgc  | acaacaccgc  | ctccacgctc  | gaggccatgc | tgcgcaacga | caccaacgac | 20700 |
| cagtccttca  | acgactacct  | ctcggcgggc  | aacatgctct | accccatccc | ggccaacgcc | 20760 |
| accaacgtgc  | ccatctccat  | cccctcgcg   | aactggggcg | ccttccgcg  | atggtccttc | 20820 |
| acgcgcctga  | agaccgcga   | gacgcccctg  | ctcggctccg | ggttcgaccc | ctacttcgtc | 20880 |
| tactcgggct  | ccatccccta  | cctagacggc  | accttctacc | tcaaccacac | cttcaagaag | 20940 |
| gtctccatca  | ccttcgactc  | ctccgtcagc  | tggcccggca | acgaccgcct | cctgacgccc | 21000 |
| aacgagttcg  | aaatcaagcg  | caccgtcgac  | ggagagggat | acaacgtggc | ccagtgaac  | 21060 |
| atgaccaagg  | actggttcct  | ggtccagatg  | ctggcccact | acaacatcgg | ctaccagggc | 21120 |
| ttctacgtgc  | ccgagggcta  | caaggaccgc  | atgtactcct | tcttccgcaa | cttccagccc | 21180 |
| atgagccgcc  | aggtcgtgga  | cgaggtaaac  | tacaaggact | accaggccgt | caccctggcc | 21240 |
| taccagcaca  | acaactcggg  | cttcgtcggc  | tacctcgcg  | ccaccatgcg | ccagggccag | 21300 |
| ccctaccccc  | ccaactaccc  | ctacccgctc  | atcggaaga  | gcgccgtcgc | cagcgtcacc | 21360 |
| cagaaaaagt  | tcctctgcga  | ccgggtcatg  | tggcgcaccc | ccttctccag | caacttcatg | 21420 |
| tccatgggcg  | cgctcaccga  | cctcggccag  | aacatgctct | acgccaactc | cgccacgcg  | 21480 |
| ctagacatga  | atttcgaagt  | cgaccccatg  | gatgagtcca | cccttctcta | tgttgtcttc | 21540 |
| gaagtcttcg  | acgtcgtccg  | agtgaccag   | ccccaccgcg | gcgtcatcga | agccgtctac | 21600 |
| ctgcgcacgc  | ccttctcggc  | cggcaacgcc  | accacctaag | ccgctcttgc | ttcttgcaag | 21660 |
| atgacggcgg  | gctccggcga  | gcaggagctc  | agggccatcc | tccgcgacct | gggctgcggg | 21720 |
| ccctgcttcc  | tgggcacctt  | cgacaagcgc  | ttccctggat | tcatggcccc | gcacaagctg | 21780 |
| gcctgcgcca  | tcgtgaacac  | ggccggccgc  | gagaccgggg | gcgagcactg | gctggccttc | 21840 |
| gcctggaacc  | cgcgctccca  | cacatgctac  | ctcttcgacc | ccttcgggtt | ctcggacgag | 21900 |



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|             |            |            |             |             |             |       |
|-------------|------------|------------|-------------|-------------|-------------|-------|
| cgctcaagc   | agatctacca | gttcgagtac | gagggcctgc  | tgcgtcgag   | cgccctggcc  | 21960 |
| accgaggacc  | gctgcgtcac | cctggaaaag | tccacccaga  | ccgtgcaggg  | tccgcgctcg  | 22020 |
| gccgcctgcg  | ggctcttctg | ctgcatgttc | ctgcacgcct  | tcgtgcaactg | gcccgaaccgc | 22080 |
| cccatggaca  | agaacccac  | catgaactta | ctgacggggg  | tgcccaacgg  | catgctccag  | 22140 |
| tcgccccagg  | tggaacccac | cctgcgccgc | aaccaggaag  | cgctctaccg  | cttcctcaat  | 22200 |
| gcccactccg  | cctactttcg | ctcccaccgc | gcgcgcatcg  | agaaggccac  | cgcttctgac  | 22260 |
| cgcatgaatc  | aagacatgta | aaaaaccggt | gtgtgtatgt  | gaatgcttta  | ttcataataa  | 22320 |
| acagcacatg  | tttatgccac | cttctctgag | gctctgactt  | tatttagaaa  | tcgaaggggt  | 22380 |
| tctgccggct  | ctcggcatgg | cccgcgggca | gggatacgtt  | gcggaactgg  | tacttgggca  | 22440 |
| gccacttgaa  | ctcggggatc | agcagcttgg | gcacggggag  | gtcggggaac  | gagtcgctcc  | 22500 |
| acagcttgcg  | cgtgagttgc | agggcgccca | gcaggtcggg  | cgcgagatc   | ttgaaatcgc  | 22560 |
| agttgggacc  | cgcttctgc  | gcgcgagagt | tgcggtacac  | ggggttgag   | caactggaaca | 22620 |
| ccatcagggc  | cgggtgcttc | acgcttgcca | gcaccgtcgc  | gtcgggtgatg | ccctccacgt  | 22680 |
| ccagatcctc  | ggcgttgccc | atcccgaagg | gggtcatctt  | gcaggtctgc  | cgcccatgc   | 22740 |
| tgggcacgca  | gccgggcttg | tggttgcaat | cgagtgagc   | ggggatcagc  | atcatctggg  | 22800 |
| cctgctcgga  | gctcatgccc | gggtacatgg | ccttcatgaa  | agcctccagc  | tggcgggaagg | 22860 |
| cctgctgcgc  | cttgccgccc | tcggtgaaga | agaccccgca  | ggacttgcta  | gagaactggt  | 22920 |
| tgggtggcgca | gccggcgctc | tgcacgcagc | agcgcgcgtc  | gttgttgccc  | agctgcacca  | 22980 |
| cgctgcgccc  | ccagcgggtc | tgggtgatct | tggcccgggt  | ggggttctcc  | ttcagcgcgc  | 23040 |
| gctgcccgtt  | ctcgtctgcc | acatccatct | cgatagtgtg  | ctccttctgg  | atcatcacgg  | 23100 |
| tcccgctgag  | gcaccgcagc | ttgccctcgg | cttcggtgca  | gccgtgcagc  | cacagcgcgc  | 23160 |
| agccgggtgca | ctcccagttc | ttgtgggcga | tctgggagtg  | cgagtgcacg  | aagccctgca  | 23220 |
| ggaagcggcc  | catcatcgcg | gtcaggggtc | tgttgcgtgt  | gaaggtcagc  | gggatgccgc  | 23280 |
| ggtgctcctc  | gttcacatac | aggtggcaga | tgcggcggtg  | cacctcgccc  | tgctcgggca  | 23340 |
| tcagctggaa  | ggcggacttc | aggtcgctct | ccacgcggta  | ccggtccatc  | agcagcgtca  | 23400 |
| tcacttccat  | gcccttctcc | caggccgaaa | cgatcggcag  | gctcaggggg  | ttcttcaccg  | 23460 |
| ccattgtcat  | cttagtcgcc | gccgccgagg | tcaggggggtc | gttctcgtcc  | aggggtctcaa | 23520 |
| acactcgctt  | gccgtccttc | tcgatgatgc | gcacgggggg  | aaagctgaag  | cccacggccg  | 23580 |
| ccagctcctc  | ctcggcctgc | ctttcgtcct | cgctgtcctg  | gctgatgtct  | tgcaaaggca  | 23640 |
| catgcttggg  | cttgccgggt | ttcttttttg | gcggcagagg  | cggcgccgat  | gtgctgggag  | 23700 |
| agcgcgagtt  | ctcgttcacc | acgactatct | cttcttcttg  | gccgtcgtcc  | gagaccacgc  | 23760 |

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|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| ggcggtaggc  | atgcctcttc  | tggggcagag  | gcggaggcga | cgggctctcg  | cggttcggcg  | 23820 |
| ggcggctggc  | agagccccctt | ccgcgttcgg  | gggtgcgctc | ctggcggcgc  | tgctctgact  | 23880 |
| gacttcctcc  | gcggccggcc  | attgtgttct  | cctagggagc | aacaacaagc  | atggagactc  | 23940 |
| agccatcgtc  | gccaacatcg  | ccatctgccc  | ccgccgccac | cgccgacgag  | aaccagcagc  | 24000 |
| agaatgaaag  | cttaaccgcc  | ccgccgccc   | gccccacctc | cgacgccgcg  | gccccagaca  | 24060 |
| tgcaagagat  | ggaggaatcc  | atcgagattg  | acctgggcta | cgtgacgccc  | gcggagcacg  | 24120 |
| aggaggagct  | ggcagcgcg   | ttttcagccc  | cggaagagaa | ccaccaagag  | cagccagagc  | 24180 |
| aggaagcaga  | gaacgagcag  | aaccaggctg  | ggcacgagca | tggcgactac  | ctgagcgggg  | 24240 |
| cagaggacgt  | gctcatcaag  | catctggccc  | gccaatgcat | catcgtcaag  | gacgcgctgc  | 24300 |
| tcgaccgcgc  | cgaggtgccc  | ctcagcgtag  | cggagctcag | ccgcgcctac  | gagcgcaacc  | 24360 |
| tcttctcgcc  | gcgcgtgccc  | cccaagcgcc  | agcccaacgg | cacctgtgag  | cccaacccgc  | 24420 |
| gcctcaactt  | ctacccggtc  | ttcgcggtgc  | ccgaggccct | ggccacctac  | cacctctttt  | 24480 |
| tcaagaacca  | aaggatcccc  | gtctcctgcc  | gcgccaaccg | caccgcgcgc  | gacgccctgc  | 24540 |
| tcaacctggg  | ccccggcgcc  | cgcctacctg  | atatcacctc | cttggaagag  | gttcccaaga  | 24600 |
| tcttcgaggg  | tctgggcagc  | gacgagactc  | gggcccgcga | cgctctgcaa  | ggaagcggag  | 24660 |
| aggagcatga  | gcaccacagc  | gccctggtgg  | agttggaagg | cgacaacgcg  | cgcctggcgg  | 24720 |
| tcctcaagcg  | cacggtcgag  | ctgaccctact | tcgcctaccc | ggcgctcaac  | ctgcccccca  | 24780 |
| aggatcatgag | cgccgtcatg  | gaccagggtc  | tcacaaagcg | cgccctcgccc | ctctcggagg  | 24840 |
| aggagatgca  | ggacccccgag | agttcggacg  | agggcaagcc | cgtggtcagc  | gacgagcagc  | 24900 |
| tggcgcgctg  | gctgggagcg  | agtagcacc   | cccagagcct | ggaagagcgg  | cgcaagctca  | 24960 |
| tgatggccgt  | ggctctgggtg | accgtggagc  | tggagtgtct | gcgccgcttc  | tttgccgacg  | 25020 |
| cggagaccct  | gcgcaaggtc  | gaggagaacc  | tgcactacct | cttcaggcac  | gggttcgtgc  | 25080 |
| gccaggcctg  | caagatctcc  | aacgtggagc  | tgaccaacct | ggtctcctac  | atgggcatcc  | 25140 |
| tgcacgagaa  | ccgcctgggg  | caaaacgtgc  | tgcacaccac | cctgcgcggg  | gaggcccgcc  | 25200 |
| gcgactacat  | ccgcgactgc  | gtctacctgt  | acctctgcca | cacctggcag  | acgggcatgg  | 25260 |
| gcgtgtggca  | gcagtgcctg  | gaggagcaga  | acctgaaaga | gctctgcaag  | ctcctgcaga  | 25320 |
| agaacctcaa  | ggccctgtgg  | accgggttcg  | acgagcgtac | caccgcctcg  | gacctggccg  | 25380 |
| acctcatctt  | ccccgagcgc  | ctgcggctga  | cgctgcgcaa | cgggctgccc  | gactttatga  | 25440 |
| gccaaaagcat | gttgcaaaac  | tttcgctctt  | tcacctctga | acgctccggg  | atcctgccccg | 25500 |
| ccacctgctc  | cgcgctgccc  | tcggacttcg  | tgccgctgac | cttccgcgag  | tgccccccgc  | 25560 |
| cgctctggag  | ccactgctac  | ttgctgcgcc  | tggccaacta | cctggcctac  | cactcggacg  | 25620 |
| tgatcgagga  | cgtcagcggc  | gagggctctgc | tggagtgcc  | ctgccgctgc  | aacctctgca  | 25680 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |            |             |             |       |
|------------|------------|------------|------------|-------------|-------------|-------|
| cgccgcaccg | ctccctggcc | tgcaaccccc | agctgctgag | cgagaccag   | atcatcggca  | 25740 |
| ccttcgagtt | gcaaggcccc | ggcgacggcg | agggcaaggg | gggtctgaaa  | ctcaccgccg  | 25800 |
| ggctgtggac | ctcggcctac | ttgcgcaagt | tcgtgcccga | ggactaccat  | cccttcgaga  | 25860 |
| tcaggttcta | cgaggaccaa | tcccagccgc | ccaaggccga | gctgtcggcc  | tgcgtcatca  | 25920 |
| cccagggggc | catcctggcc | caattgcaag | ccatccagaa | atccccgcaa  | gaatttctgc  | 25980 |
| tgaaaaaggg | ccacggggtc | tacttggacc | cccagaccgg | agaggagctc  | aaccccagct  | 26040 |
| tccccagga  | tgccccgagg | aagcagcaag | aagctgaaag | tggagctgcc  | gccgccggag  | 26100 |
| gatttggagg | aagactggga | gagcagtcag | gcagaggagg | aggagatgga  | agactggggac | 26160 |
| agcactcagg | cagaggagga | cagcctgcaa | gacagtctgg | aggaggaaga  | cgaggtggag  | 26220 |
| gaggcagagg | aagaagcagc | cgccgccaga | ccgtcgtcct | cggcggagaa  | agcaagcagc  | 26280 |
| acggatacca | tctccgctcc | gggtcggggg | cgcgccggcc | gggcccacag  | taggtggggac | 26340 |
| gagaccgggc | gcttcccga  | ccccaccacc | cagaccggtg | agaaggagcg  | gcagggatac  | 26400 |
| aagtcctggc | gggggcacaa | aaacgccatc | gtctcctgct | tgcaagcctg  | cgggggcaac  | 26460 |
| atctccttca | cccggcgcta | cctgctcttc | caccgcgggg | tgaacttccc  | ccgcaacatc  | 26520 |
| ttgcattact | accgtcacct | ccacagcccc | tactactggt | tccaagaaga  | ggcagaaaacc | 26580 |
| cagcagcagc | agaaaaccag | cggcagcagc | agctagaaaa | tccacagcgg  | cggcaggtgg  | 26640 |
| actgaggatc | gcggcgaaac | agccggcgca | gaccggggag | ctgaggaacc  | ggatctttcc  | 26700 |
| caccctctat | gccatcttcc | agcagagtcg | ggggcaggag | caggaaactga | aagtcaagaa  | 26760 |
| ccgttctctg | cgctcgctca | cccgcagttg | tctgtatcac | aagagcgaag  | accaacttca  | 26820 |
| gcgcactctc | gaggacgccg | aggctctctt | caacaagtac | tgcgcgctca  | ctcttaaaga  | 26880 |
| gtagcccgcg | cccggccaca | cacggaaaaa | ggcgggaatt | acgtcaccac  | ctgcgccctt  | 26940 |
| cgcccgacca | tcatgagcaa | agagattccc | acgccttaca | tgtggagcta  | ccagccccag  | 27000 |
| atgggcctgg | ccgccggcgc | cgcccaggac | tactccaccc | gcatgaactg  | gctcagtgcc  | 27060 |
| gggcccgcga | tgatctcacg | ggtgaatgac | atccgcgccc | accgaaacca  | gatactccta  | 27120 |
| gaacagtcag | cgatcaccgc | cacgccccgc | catcacctta | atccgcgtaa  | ttggcccgcc  | 27180 |
| gccctggtgt | accaggaaat | tccccagccc | acgaccgtac | tacttccgcg  | agacgcccg   | 27240 |
| gccgaagtcc | agctgactaa | ctcaggtgtc | cagctggccg | gcggcgccgc  | cctgtgtcgt  | 27300 |
| caccgccccg | ctcagggtat | aaagcggctg | gtgatccgag | gcagaggcac  | acagctcaac  | 27360 |
| gacgaggtgg | tgagctcttc | gctgggtctg | cgacctgacg | gagtcttcca  | actcgccgga  | 27420 |
| tcggggagat | cttccttcac | gcctcgtcag | gccgtcctga | ctttggagag  | ttcgtcctcg  | 27480 |
| cagccccgct | cgggcggcat | cggcactctc | cagttcgtgg | aggagtacac  | tccctcggtc  | 27540 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |            |             |            |       |
|------------|------------|------------|------------|-------------|------------|-------|
| tacttcaacc | ccttctccgg | ctcccccggc | cactaccg   | acgagttcat  | cccgaacttc | 27600 |
| gacgccatca | gcgagtcggt | ggacggctac | gattgaatgt | cccatgggtg  | cgagctgac  | 27660 |
| ctagctcggc | ttcgacacct | ggaccactgc | cgccgcttcc | gctgcttcgc  | tcgggatctc | 27720 |
| gccgagtttg | cctactttga | gctgcccag  | gagcaccctc | agggcccagc  | ccacggagtg | 27780 |
| cggatcatcg | tcgaaggggg | cctcgactcc | cacctgcttc | ggatcttcag  | ccagcgaccg | 27840 |
| atcctggtcg | agcggaaca  | aggacagacc | cttcttactt | tgtactgcat  | ctgcaaccac | 27900 |
| cccggcctgc | atgaaagtct | ttgttgctg  | ctgtgtactg | agtataataa  | aagctgagat | 27960 |
| cagcgactac | tccggactcg | attgtgggtg | tcctgctatc | aaccgggtccc | tgttcttcac | 28020 |
| cggaacgag  | accgagctcc | agctccagt  | taagccccac | aagaagtacc  | tcacctggct | 28080 |
| gttccagggc | tccccgatcg | ccgttgctaa | ccactgagac | aacgacggag  | tcctgctgag | 28140 |
| cggccctgcc | aaccttactt | tttccacccg | cagaagcaag | ctccagctct  | tccaaccctt | 28200 |
| cctccccggg | acctatcagt | gcgtctcagg | accctgccat | cacaccttcc  | acctgatccc | 28260 |
| gaataccaca | gcgccgctcc | ccgctactaa | caaccaaact | acccaccaac  | gccaccgtcg | 28320 |
| cgacctttcc | tctgaatcta | ataccactac | cggaggtggc | ttctgctgtt  | agtgtctccc | 28380 |
| cgtcccgctg | acccccggtc | ccccactcag | tccccgagg  | aggttcgcaa  | atgcaaattc | 28440 |
| caagaaccct | ggaaattcct | caaagtctac | cgccaaaaat | cagacatgca  | tcccagctgg | 28500 |
| atcatgatca | ttgggatcgt | gaacattctg | gcctgcaccc | tcattctcctt | tgtgatttac | 28560 |
| ccctgctttg | actttgggtg | gaactcgcca | gaggcgctct | atctcccgcc  | tgaacctgac | 28620 |
| acaccaccac | agcagcaacc | tcaggcacac | gcactaccac | caccacagcc  | taggccacaa | 28680 |
| tacatgcccc | tattagacta | tgaggccgag | ccacagcgac | ccatgctccc  | cgctattagt | 28740 |
| tacttcaatc | taaccggcgg | agatgactga | cccactggcc | aataacaacg  | tcaacgacct | 28800 |
| tctcctggac | atggacggcc | gcgcctcgga | gcagcgactc | gcccacttc   | gcattcgtca | 28860 |
| gcagcaggag | agagccgtca | aggagctgca | ggacggcata | gccatccacc  | agtgaagag  | 28920 |
| aggcatcttc | tgcttggtga | aacaggccaa | gatctcctac | gaggtcacc   | agaccgacca | 28980 |
| tcgcctctcc | tacgagctcc | tgacgagcg  | ccagaagttc | acctgcctgg  | tcggagtcaa | 29040 |
| ccccatcgtc | atcaccacgc | agtcggggcg | taccaagggg | tgcattccact | gctcctgcga | 29100 |
| ctcccccgac | tgctccaca  | ctctgatcaa | gacctctgc  | ggcctccgcg  | acctctccc  | 29160 |
| catgaactaa | tcacccctt  | atccagtga  | ataaagatca | tattgatgat  | gatttaaata | 29220 |
| aaaaaaataa | tcatttgatt | tgaaataaag | atacaatcat | attgatgatt  | tgagtttaac | 29280 |
| aaaaataaag | aatcacttac | ttgaaatctg | ataccaggtc | tctgtccatg  | ttttctgcc  | 29340 |
| acaccacctc | actccctct  | tcccagctct | ggtactgcag | gccccggcgg  | gctgcaaact | 29400 |
| tcctccacac | gctgaagggg | atgtcaaatt | cctcctgtcc | ctcaatcttc  | attttatctt | 29460 |

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|            |            |             |            |             |            |       |
|------------|------------|-------------|------------|-------------|------------|-------|
| ctatcagatg | tccaaaaagc | gcgtccgggt  | ggatgatgac | ttcgacccccg | tctaccacct | 29520 |
| cgatgcagac | aacgcaccga | ccgtgccctt  | catcaacccc | cccttcgtct  | cttcagatgg | 29580 |
| attccaagag | aagccccctg | gggtgttg    | cctgcgactg | gctgacccccg | tcaccaccaa | 29640 |
| gaacggggaa | atcacctca  | agctgggaga  | gggggtggac | ctcgactcgt  | cgggaaaact | 29700 |
| catctccaac | acggccacca | aggccgccgc  | ccctctcagt | atttcaaaca  | acaccatttc | 29760 |
| ccttaaaact | gctgccccct | tctacaacaa  | caatggaact | ttaagcctca  | atgtctccac | 29820 |
| accattagca | gtatttccca | catttaacac  | tttaggcata | agtcttgga   | acggctctca | 29880 |
| gacttcaaat | aagtgttga  | ctgtacaact  | aactcatcct | cttacattca  | gctcaaatag | 29940 |
| catcacagta | aaaacagaca | aagggctata  | tattaactcc | agtggaaaca  | gaggacttga | 30000 |
| ggctaata   | agcctaaaaa | gaggactagt  | ttttgacggt | aatgctattg  | caacatatat | 30060 |
| tggaaatggc | ttagactatg | gatcttatga  | tagtgatgga | aaaacaagac  | ccgtaattac | 30120 |
| caaaattgga | gcaggattaa | attttgatgc  | taacaaagca | atagctgtca  | aactaggcac | 30180 |
| aggtttaagt | tttgactccg | ctgggtgcct  | gacagctgga | aacaaacagg  | atgacaagct | 30240 |
| aacactttgg | actacccctg | acccaagccc  | taattgtcaa | ttactttcag  | acagagatgc | 30300 |
| caaatttact | ctctgtctta | caaaatgcgg  | tagtcaaata | ctaggcactg  | tggcagtggc | 30360 |
| ggctgttact | gtaggatcag | cactaaatcc  | aattaatgac | acagtcaaaa  | gcgccatagt | 30420 |
| tttccttaga | tttgattccg | atgggtgtact | catgtcaaac | tcacatggtg  | taggtgatta | 30480 |
| ctggaacttt | agggagggac | agaccactca  | aagtgtagcc | tatacaaatg  | ctgtgggatt | 30540 |
| catgccaaat | ataggtgcat | atccaaaaac  | ccaaagtaaa | acacctaata  | atagcatagt | 30600 |
| cagtcaggta | tatttaactg | gagaaaactac | tatgccaatg | acactaacca  | taactttcaa | 30660 |
| tggcactgat | gaaaaagaca | caacccccagt | tagcacctac | tctatgactt  | ttacatggca | 30720 |
| gtggactgga | gactataagg | acaaaaatat  | tacctttgct | accaactcat  | tctctttttc | 30780 |
| ctacatcgcc | caggaataat | cccacccagc  | aagccaaccc | cttttcccac  | cacctttgtc | 30840 |
| tatatggaaa | ctctgaaaca | gaaaaataaa  | gttcaagtgt | tttattgaat  | caacagtttt | 30900 |
| acaggactcg | agcagttatt | tttctccac   | cctcccagga | catggaatac  | accaccctct | 30960 |
| ccccccgcac | agccttgaac | atctgaatgc  | cattggtgat | ggacatgctt  | ttggtctcca | 31020 |
| cggtccacac | agtttcagag | cgagccagtc  | tcggatcggt | cagggagatg  | aaaccctccg | 31080 |
| ggcactcccc | catctgcacc | tcacagctca  | acagctgagg | attgtcctcg  | gtggtcggga | 31140 |
| tcacggttat | ctggaagaag | cagaagagcg  | gcggtgggaa | tcatagtccg  | cgaacgggat | 31200 |
| cggccggtgg | tgctgcatca | ggccccgcag  | cagtcgctgc | cgccgccgct  | ccgtcaagct | 31260 |
| gctgctcagg | gggttcgggt | ccagggactc  | cctcagcatg | atgccacg    | ccctcagcat | 31320 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|                        |                        |                        |       |
|------------------------|------------------------|------------------------|-------|
| cagtcgtctg gtgcggcg    | cgagcagcg catgcgaatc   | tcgctcaggt cactgcagta  | 31380 |
| cgtgcaacac aggaccacca  | ggttggttcaa cagtccatag | ttcaaacacgc tccagccgaa | 31440 |
| actcatcgcg ggaaggatgc  | taccacagtg gccgtcgtac  | cagatcctca ggtaaatcaa  | 31500 |
| gtggcgctcc ctccagaaga  | cgctgcccacat gtacatgac | tccttgggca tgtggcggtt  | 31560 |
| caccacctcc cgggtaccaca | tcaccctctg gttgaacatg  | cagccccgga tgatcctgcg  | 31620 |
| gaaccacagg gccagcaccg  | ccccgcccgc catgcagcga  | agagaccccg gatcccgga   | 31680 |
| atgacaatgg aggaccacc   | gctcgtaccc gtggatcatc  | tgggagctga acaagtctat  | 31740 |
| gttggcacag cacaggcata  | tgctcatgca tctcttcagc  | actctcagct cctcgggggt  | 31800 |
| caaaaccata tcccagggca  | cggggaactc ttgcaggaca  | gcgaaccccg cagaacaggg  | 31860 |
| caatcctcgc acataactta  | cattgtgcat ggacagggta  | tcgcaatcag gcagcaccgg  | 31920 |
| gtgatcctcc accagagaag  | cgcggtctc ggtctcctca   | cagcgtggta agggggccgg  | 31980 |
| ccgatacggg tgatggcg    | acgcggtga tcgtgttctc   | gaccgtgtca tgatgcagtt  | 32040 |
| gctttcggac attttcgtac  | ttgctgtagc agaacctggt  | ccgggcgctg cacaccgatc  | 32100 |
| gccggcgggc gtctcggcgc  | ttggaacgct cgggtgttaa  | gttgtaaaac agccactctc  | 32160 |
| tcagaccgtg cagcagatct  | agggcctcag gaggatgaa   | gatcccatca tgcctgatag  | 32220 |
| ctctgatcac atcgaccacc  | gtggaatggg ccaggcccag  | ccagatgatg caattttgtt  | 32280 |
| gggtttcggg gacggcgggg  | gagggaagaa caggaagaac  | catgattaac ttttaatcca  | 32340 |
| aacggtctcg gagcacttca  | aaatgaagggt cacggagatg | gcacctctcg ccccgctgt   | 32400 |
| gttgggtggaa aataacagcc | aggtcaaagg tgatacgggt  | ctcgagatgt tccacggtgg  | 32460 |
| cttcagcaa agcctccacg   | cgcacatcca gaaacaagac  | aatagcgaaa gcgggaggg   | 32520 |
| tctctaattc ctcaaccatc  | atgttacact cctgcaccat  | cccagataa ttttcatttt   | 32580 |
| tccagccttg aatgattcga  | actagttcct gaggtaaatc  | caagccagcc atgataaaaa  | 32640 |
| gctcgcgag agcaccctcc   | accggcattc ttaagcacac  | cctcataatt ccaagatatt  | 32700 |
| ctgctcctgg ttcacctgca  | gcagattgac aagcggaata  | tcaaaatctc tgccgcgac   | 32760 |
| cctgagc                |                        |                        | 32767 |

<210> 2  
 <211> 32767  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificially Synthesized

|                       |                       |                          |
|-----------------------|-----------------------|--------------------------|
| <400> 2               |                       |                          |
| catcatcaat aatatacctc | aaacttttgg tgcgcgtaa  | tatgcaaagt agctgtttga 60 |
| atttgggggag ggaggaagg | gattggctgc gggagcggcg | accgttaggg gcggggcg 120  |

368530-7006W01\_SequenceListing\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgacgttttg atgacgtggc tatgaggcgg agccggtttg caagttctcg tgggaaaagt  | 180  |
| gacgtcaaac gaggtgtggt ttgaacacgg aaataactcaa ttttcccgcg ctctctgaca | 240  |
| ggaaatgagg tgtttctggg cggatgcaag tgaaaacggg ccattttcgc gcgaaaactg  | 300  |
| aatgaggaag tgaaaatctg agtaatttcg cgtttatggc agggaggagt atttgccgag  | 360  |
| ggccgagtag actttgaccg attacgtggg ggtttcgatt accgtatttt tcacctaaat  | 420  |
| ttccgcgtac ggtgtcaaag tccggtgttt ttacgtacga tatcatttcc ccgaaagtgc  | 480  |
| cacctgaccg taactataac ggtcctaagg tagcgaaagc tcagatctcc cgatccccta  | 540  |
| tggtgactc tcagtacaat ctgctctgat gccgcatagt taagccagta tctgctccct   | 600  |
| gcttgtgtgt tggaggtcgc tgagtagtgc gcgagcaaaa ttttaagctac aacaaggcaa | 660  |
| ggcttgaccg acaattgcat gaagaatctg cttaggggta ggcgttttgc gctgcttcgc  | 720  |
| gatgtacggg ccagatatac gcgttgacat tgattattga ctagtattta atagtaatca  | 780  |
| attacggggc cattagttca tagcccatat atggagttcc gcgttacata acttacggta  | 840  |
| aatggcccg cttggctgacc gcccaacgac ccccgcccat tgacgtcaat aatgacgtat  | 900  |
| gttcccatag taacgccaat agggactttc cattgacgtc aatgggtgga gtatttacgg  | 960  |
| taaactgccc acttggcagt acatcaagtg tatcatatgc caagtacgcc ccctattgac  | 1020 |
| gtcaatgacg gtaaattggc cgcttggcat tatgcccagt acatgacctt atgggacttt  | 1080 |
| cctacttggc agtacatcta cgtattagtc atcgctatta ccatggtgat gcggttttgg  | 1140 |
| cagtacatca atgggcgtgg atagcggttt gactcacggg gatttccaag tctccacccc  | 1200 |
| attgacgtca atgggagttt gttttggcac caaaatcaac gggactttcc aaaatgtcgt  | 1260 |
| aacaactccg ccccatgac gcaaatggg cgttaggcgtg tacggtggga ggtctatata   | 1320 |
| agcagagctc gtttagtgaa ccgtcagatc actagaagct ttattgcggt agtttatcac  | 1380 |
| agttaaattg ctaacgcagt cagtgttct gacacaacag tctcgaactt aagctgcaga   | 1440 |
| agttggtcgt gaggcactgg gcaggtaagt atcaagggta caagacaggt ttaaggagac  | 1500 |
| caatagaaac tgggcttgtc gagacagaga agactcttgc gtttctgata ggcacctatt  | 1560 |
| ggtcttactg acatccactt tgcctttctc tccacagggtg tccactccca gttcaattac | 1620 |
| agctcttaag gctagagtac ttaatacgac tcactatagg ctacgcccac catgggcgcc  | 1680 |
| agagccagcg tgctgagcgg gggagagctg gatcgctggg aaaagattag actgaggccc  | 1740 |
| ggagggaaga aaaagtacaa gctgaaacac atcgtgtggg ccagcaggga gctggagcgc  | 1800 |
| ttcgcgtga accccggact gctggagacc tccgaaggct gtcggcagat cctggggcag   | 1860 |
| ctgcagcctt ccctgcagac aggctccgag gagctgcggt ctctgtataa tacagtggcc  | 1920 |
| acactgtact gtgtgcacca gcggattgag gtgaaggata caaaagaggc cctggagaag  | 1980 |

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|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| attgaggagg  | agcagaacaa | gagcaagaag  | aaagcccagc  | aggccgccgc  | cgacaccggc  | 2040 |
| aatagctccc  | aggtgagcca | gaactatcca  | attgtgcaga  | atctgcaggg  | ccagatggtg  | 2100 |
| caccaggcca  | tttccccacg | gacactgaac  | gcctgggtga  | aggtgggtga  | ggagaaggcc  | 2160 |
| ttcagccccg  | aagtgatccc | tatgttttcc  | gccctgtccg  | aaggcgccac  | ccctcaggac  | 2220 |
| ctgaacacca  | tgctgaacac | agtgggggga  | caccaggccg  | ccatgcagat  | gctgaaggaa  | 2280 |
| accatcaacg  | aggaggccgc | cgagtgggat  | cggctgcacc  | ccgtgcacgc  | cgggccaatc  | 2340 |
| gcccctggcc  | agatgaggga | gcccagaggc  | tctgacatcg  | ccggcaccac  | atctaccctg  | 2400 |
| caggaacaga  | tcgggtggat | gaccaataac  | ccaccaatcc  | cagtgggcga  | gatctacaag  | 2460 |
| aggtggatta  | ttctgggact | gaacaaaatt  | gtgcgcatgt  | attcccctac  | atccatcctg  | 2520 |
| gacatcaggc  | agggccctaa | ggaacctttc  | cgcgactacg  | tggatcggtt  | ctacaaaacc  | 2580 |
| ctgcgcgccg  | agcaggccag | ccaggaagtg  | aagaattgga  | tgacagagac  | cctgctggtg  | 2640 |
| cagaacgcca  | atcctgactg | taaaaccatc  | ctgaaggccc  | tgggccctgc  | cgccacactg  | 2700 |
| gaggaaatga  | tgaccgcctg | ccagggcggtg | ggcggccctg  | gccacaaagc  | cagggtgctg  | 2760 |
| gccgaggcca  | tgtctcaggt | gaccaactct  | gccacaatta  | tgatgcagcg  | ggggaacttt  | 2820 |
| cggaaccaga  | ggaagaccgt | gaagtgcctt  | aactgtggca  | aggagggaca  | catcgccaag  | 2880 |
| aattgccgcg  | ccccacggaa | gaaggggtgt  | tggaaatgcg  | ggaaggaggg  | ccaccagatg  | 2940 |
| aaagactgca  | cagagcggca | ggccaacttt  | ctgggcaaga  | tttggcccag  | ccacaagggc  | 3000 |
| cgccccggaa  | actttctgca | gtccaggcct  | gagcctaccg  | ccccccctga  | ggaatccttc  | 3060 |
| cggttcggcg  | aggagacaac | caccccaagc  | cagaagcagg  | aacccatcga  | caaagagctg  | 3120 |
| tacccccctg  | ccagcctgag | atcccctgtt  | gggaatgacc  | ccagctctca  | gtgatgatct  | 3180 |
| agcgtttaaa  | cgggccctct | agagtcgacc  | cgggcggcca  | aaccgctgat  | cagcctcgac  | 3240 |
| tgtgccttct  | agttgccagc | catctgttgt  | ttgcccctcc  | cccgtgcctt  | ccttgaccct  | 3300 |
| ggaagggtgcc | actcccactg | tcctttccta  | ataaaaatgag | gaaattgcat  | cgcatgtgtt  | 3360 |
| gagtaggtgt  | cattctattc | tgggggggtg  | ggtggggcag  | gacagcaagg  | gggaggattg  | 3420 |
| ggaagacaat  | agcaggcatg | ctggggatgc  | ggtgggctct  | atggcttctg  | aggcggaaaag | 3480 |
| aaccagcaga  | tctgcagatc | tgaattcatc  | tatgtcgggt  | gcggagaaaag | aggtaatgaa  | 3540 |
| atggtattat  | gggtattatg | ggtctgcatt  | aatgaatcgg  | tcagatatcg  | acatatgctg  | 3600 |
| gccaccgtgc  | atgtggcctc | gcacccccgc  | aagacatggc  | ccgagttcga  | gcacaacgtc  | 3660 |
| atgacccgct  | gcaatgtgca | cctgggctcc  | cgccgaggca  | tgttcatgcc  | ctaccagtgc  | 3720 |
| aacatgcaat  | ttgtgaaggt | gctgctggag  | cccgatgcca  | tgtccagagt  | gagcctgacg  | 3780 |
| ggggtgtttg  | acatgaatgt | ggagctgtgg  | aaaattctga  | gatatgatga  | atccaagacc  | 3840 |
| aggtgccggg  | cctgcgaatg | cggaggcaag  | cacgccaggc  | ttcagcccgt  | gtgtgtggag  | 3900 |



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|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| gtgacggagg  | acctgcgacc | cgatcatttg | gtgttgcct  | gcaacgggac | ggagttcggc  | 3960 |
| tccagcgggg  | aagaatctga | ctagagtga  | tagtgtttg  | ggctgggtgt | gagcctgcat  | 4020 |
| gaggggcaga  | atgactaaaa | tctgtggttt | tctgtgtgtt | gcagcagcat | gagcggaagc  | 4080 |
| gcctcctttg  | agggaggggt | attcagccct | tatctgacgg | ggcgtctccc | ctcctgggcg  | 4140 |
| ggagtgcgtc  | agaatgtgat | gggatccacg | gtggacggcc | ggcccgtgca | gcccgcgaac  | 4200 |
| tcttcaaccc  | tgacctacgc | gacctgagc  | tcctcgtcg  | tggacgcagc | tgccgccgca  | 4260 |
| gctgctgctt  | ccgccgccag | cgccgtgcgc | ggaatggccc | tgggcgccgg | ctactacagc  | 4320 |
| tctctggtgg  | ccaactcgag | ttccaccaat | aatcccgcga | gcctgaacga | ggagaagctg  | 4380 |
| ctgctgctga  | tggcccagct | cgaggccctg | accagcgcc  | tgggcgagct | gacctagcag  | 4440 |
| gtggctcagc  | tgcaggcgga | gacgcgggcc | gcggttgcca | cggtgaaaac | caaataaaaa  | 4500 |
| atgaatcaat  | aaataaacgg | agacggttgt | tgattttaac | acagagtctt | gaatctttat  | 4560 |
| ttgatttttc  | gcgcgcggtg | ggccctggac | caccggtctc | gatcattgag | cacccggtgg  | 4620 |
| atcttttcca  | ggaccgggta | gagggtgggt | tggatgttga | ggtacatggg | catgagcccg  | 4680 |
| tcccgggggg  | ggaggtagct | ccattgcagg | gcctcgtgct | cggggatggt | gttgtaaatac | 4740 |
| accagtcgat  | agcaggggcg | cagggcggtg | tgctgcacga | tgtccttgag | gaggagactg  | 4800 |
| atggccacgg  | gcagcccctt | ggtgtaggtg | ttgacgaacc | tgttgagctg | ggagggatgc  | 4860 |
| atgcgggggg  | agatgagatg | catcttggcc | tggatcttga | gattggcgat | gttcccgcgc  | 4920 |
| agatcccgcc  | gggggttcat | gttgtgcagg | accaccagca | cgggttatcc | ggtgcacttg  | 4980 |
| gggaatttgt  | catgcaactt | ggaaggggag | gcgtgaaaga | atttgagagc | gcccttgatg  | 5040 |
| ccgccaggt   | tttccatgca | ctcatccatg | atgatggcga | tggggccgtg | ggcgggcgcc  | 5100 |
| tgggcaaaga  | cgtttcgggg | gtcggacaca | tcgtagtgtg | ggtcctgggt | gagctcgtca  | 5160 |
| taggccattt  | taatgaattt | ggggcgagg  | gtgcccagct | gggggacgaa | ggtgccctcg  | 5220 |
| atcccggggg  | cgtagttgcc | ctcgcagatc | tgcattctcc | aggccttgag | ctcggagggg  | 5280 |
| gggatcatgt  | ccacctgcgg | ggcgatgaaa | aaaacggttt | ccggggcggg | ggagatgagc  | 5340 |
| tgggccgaaa  | gcaggttccg | gagcagctgg | gacttgccgc | aaccggtggg | gccgtagatg  | 5400 |
| accccgatga  | ccggctgcag | gtggtagtgt | agggagagac | agctgccgtc | ctcgcggagg  | 5460 |
| agggggggcca | cctcgttcat | catctcgcgc | acatgcatgt | tctcgcgcac | gagttccgcc  | 5520 |
| aggaggcgct  | cgccccccag | cgagaggagc | tcttgacgcg | aggcgaagtt | tttcagcggc  | 5580 |
| ttgagtcggt  | cggccatggg | cattttggag | agggctgtgt | gcaagagttc | cagacgggtcc | 5640 |
| cagagctcgg  | tgatgtgctc | tagggcatct | cgatccagca | gacctcctcg | tttcgcgggt  | 5700 |
| tggggcgact  | gcgggagtag | ggcaccaggc | gatgggcgtc | cagcgaggcc | agggtcgggt  | 5760 |

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|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| ccttccaggg  | ccgcaggggc  | cgcgtcagcg  | tggctctccgt | cacggtgaag  | gggtgcgcgc | 5820 |
| cgggctgggc  | gcttgcgagg  | gtgcgcttca  | ggctcatccg  | gctggtcgag  | aaccgctccc | 5880 |
| ggtcggcgcc  | ctgcgcgtcg  | gccaggtagc  | aattgagcat  | gagttcgtag  | ttgagcgcct | 5940 |
| cggccgcgtg  | gcccttggcg  | cggagcttac  | ctttggaagt  | gtgtccgcag  | acgggacaga | 6000 |
| ggagggactt  | gagggcgtag  | agcttggggg  | cgaggaagac  | ggactcgggg  | gcgtaggcgt | 6060 |
| ccgcgccgca  | gctggcgag   | acggtctcgc  | actccacgag  | ccaggtgagg  | tcggggcggt | 6120 |
| tggggcctaaa | aacgaggttt  | cctccgtgct  | ttttgatgcg  | tttcttacct  | ctggtctcca | 6180 |
| tgagctcgtg  | tccccgctgg  | gtgacaaaga  | ggctgtccgt  | gtccccgtag  | accgacttta | 6240 |
| tgggcccgtc  | ctcgagcggg  | gtgccgcggt  | cctcgtcgta  | gaggaacccc  | gcccactccg | 6300 |
| agacgaaggc  | ccgggtccag  | gccagcacga  | aggaggccac  | gtgggagggg  | tagcggtcgt | 6360 |
| tgtccaccag  | cggttccacc  | ttctccaggg  | tatgcaagca  | catgtccccc  | tcgtccacat | 6420 |
| ccaggaaggt  | gattggcttg  | taagtgtagg  | ccacgtgacc  | gggggtcccc  | gccggggggg | 6480 |
| tataaaaggg  | ggcgggcccc  | tgctcgtcct  | cactgtcttc  | cggatcgcgtg | tccaggagcg | 6540 |
| ccagctgttg  | gggtaggtat  | tccctctcga  | aggcgggcat  | gacctcggca  | ctcaggttgt | 6600 |
| cagtttctag  | aaacgaggag  | gatttgatat  | tgacggtgcc  | gttggagacg  | cctttcatga | 6660 |
| gcccctcgtc  | catttgggtca | gaaaagacga  | tctttttgtt  | gtcgagcttg  | gtggcgaagg | 6720 |
| agccgtagag  | ggcgttggag  | agcagcttgg  | cgatggagcg  | catggtcttg  | ttcttttcct | 6780 |
| tgtcggcgcg  | ctccttggcg  | gcgatgttga  | gctgcacgta  | ctcgcgcgcc  | acgcacttcc | 6840 |
| attcggggaa  | gacggtggtg  | agctcgtcgg  | gcacgattct  | gacccgccag  | ccgcggttgt | 6900 |
| gcagggtgat  | gaggtccacg  | ctggtggcca  | cctcgcgcgc  | caggggctcg  | ttggtccagc | 6960 |
| agaggcgccc  | gcccttgcgc  | gagcagaagg  | ggggcagcgg  | gtccagcatg  | agctcgtcgg | 7020 |
| gggggtcggc  | gtccacggtg  | aagatgccgg  | gcaggagctc  | ggggtcgaag  | tagctgatgc | 7080 |
| aggtgcccag  | attgtccagc  | gccgcttgcc  | agtcgcgcac  | ggccagcgcg  | cgctcgtagg | 7140 |
| ggctgagggg  | cgtgccccag  | ggcatggggg  | gcgtgagcgc  | ggaggcgtag  | atgccgcaga | 7200 |
| tgctgtagac  | gtagaggggc  | tcctcgagga  | cgccgatgta  | ggtggggtag  | cagcgcccc  | 7260 |
| cgcggtatgct | ggcgcgcacg  | tagtcgtaca  | gctcgtgcga  | gggcgcgagg  | agccccgtgc | 7320 |
| cgaggttgga  | gcgttgcggc  | ttttcggcgc  | ggtagacgat  | ctggcggaag  | atggcgtggg | 7380 |
| agttggagga  | gatggtgggc  | ctttggaaga  | tgttgaagtg  | ggcgtggggc  | aggccgaccg | 7440 |
| agtccctgat  | gaagtgggcg  | taggagtcct  | gcagcttggc  | gacgagctcg  | gcggtgacga | 7500 |
| ggacgtccag  | ggcgcagtag  | tcgaggggtct | cttggatgat  | gtcatacttg  | agctggccct | 7560 |
| tctgcttcca  | cagctcgcgg  | ttgagaagga  | actcttcgcg  | gtccttccag  | tactcttcga | 7620 |
| gggggaaccc  | gtcctgatcg  | gcacggtaag  | agcccaccat  | gtagaactgg  | ttgacggcct | 7680 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |            |            |             |             |      |
|------------|-------------|------------|------------|-------------|-------------|------|
| tgtaggcgca | gcagcccttc  | tccacgggga | gggcgtaagc | ttgcgcggcc  | ttgcgcaggg  | 7740 |
| aggtgtgggt | gagggcgaaag | gtgtcgcgca | ccatgacctt | gaggaactgg  | tgcttgaagt  | 7800 |
| cgaggtcgtc | gcagccgccc  | tgctcccaga | gttggaagtc | cgtgcgcttc  | ttgtaggcgg  | 7860 |
| ggtaggcaa  | agcgaaagta  | acatcgttga | agaggatctt | gcccgcgcgg  | ggcatgaagt  | 7920 |
| tgcgagtgat | gcggaaaaggc | tggggcacct | cggcccgggt | gttgatgacc  | tgggcggcga  | 7980 |
| ggacgatctc | gtcgaagccg  | ttgatgttgt | gcccgcagat | gtagagttcc  | acgaatcgcg  | 8040 |
| ggcggccctt | gacgtggggc  | agcttcttga | gctcgtcgta | ggtgagctcg  | gcggggtcgc  | 8100 |
| tgagcccgtg | ctgctcgagg  | gcccagtcgg | cgacgtgggg | gttggcgctg  | aggaaggaag  | 8160 |
| tccagagatc | cacggccagg  | gcggtctgca | agcgggtccc | gtactgacgg  | aactgttggc  | 8220 |
| ccacggccat | tttttcgggg  | gtgacgcagt | agaaggtgcg | ggggtcgccg  | tgccagcggg  | 8280 |
| cccacttgag | ctggagggcg  | aggtcgtggg | cgagctcgac | gagcggcggg  | tccccggaga  | 8340 |
| gtttcatgac | cagcatgaag  | gggacgagct | gcttgccgaa | ggaccccatc  | caggtgtagg  | 8400 |
| tttccacatc | gtaggtgagg  | aagagccttt | cggtcgcagg | atgcgagccg  | atggggaaga  | 8460 |
| actggatctc | ctgccaccag  | ttggaggaat | ggctgttgat | gtgatggaag  | tagaaatgcc  | 8520 |
| gacggcgcg  | cgagcactcg  | tgcttgtgtt | tatacaagcg | tccgcagtgc  | tcgcaacgct  | 8580 |
| gcacgggatg | cacgtgctgc  | acgagctgta | cctgggttcc | tttggcgagg  | aatttcagtg  | 8640 |
| ggcagtgagg | cgctggcggc  | tgcattctgt | gctgtactac | gtcttgggca  | tcggcggtgg  | 8700 |
| catcgtctgc | ctcgatggtg  | gtcatgctga | cgagcccgcg | cgggaggcag  | gtccagacct  | 8760 |
| cggctcggac | gggtcggaga  | gcgaggacga | gggcgcgcag | gccggagctg  | tccagggtcc  | 8820 |
| tgagacgctg | cggagtcagg  | tcagtgggca | gcggcggcgc | gcggttgact  | tgaggagct   | 8880 |
| tttccagggc | gcgcgggagg  | tccagatggt | acttgatctc | cacggcgccg  | ttggtggcta  | 8940 |
| cgtccacggc | ttgcaggggtg | ccgtgcccct | ggggcgccac | caccgtgcc   | cgtttcttct  | 9000 |
| tgggcgctgc | ttccatgtcg  | gtcagaagcg | gcggcgagga | cgcgcgccgg  | gcggcagggg  | 9060 |
| cggctcgggg | cccggaggca  | ggggcggcag | gggcacgtcg | gcgccgcgcg  | cgggcaggtt  | 9120 |
| ctggtactgc | gcccggagaa  | gactggcgtg | agcgacgacg | cgacggttga  | cgtcctggat  | 9180 |
| ctgacgcctc | tgggtgaagg  | ccacgggacc | cgtgagtttg | aacctgaaag  | agagttcgac  | 9240 |
| agaatcaatc | tcggtatcgt  | tgacggcggc | ctgccgcagg | atctcttgca  | cgtcgcccga  | 9300 |
| gttgtcctgg | taggcgatct  | cggtcatgaa | ctgctcgatc | tcctcctcct  | gaaggctctcc | 9360 |
| gcggccggcg | cgctcgacgg  | tggccgcgag | gtcgttgagg | atgcggccca  | tgagctgcga  | 9420 |
| gaaggcggtc | atgccggcct  | cgttccagac | gcggctgtag | accacggctc  | cgtcggggtc  | 9480 |
| gcgcgcgcgc | atgaccacct  | gggcgagggt | gagctcgacg | tggcgcggtga | agaccgcgta  | 9540 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |             |             |             |       |
|-------------|-------------|------------|-------------|-------------|-------------|-------|
| gttgacagagg | cgctggtaga  | ggtagttgag | cgtaggtggcg | atgtgctcgg  | tgacgaagaa  | 9600  |
| gtacatgata  | cagcggcgga  | gcggcatctc | gctgacgtcg  | cccagggctt  | ccaagcggtc  | 9660  |
| catggcctcg  | tagaagtcca  | cggcgaagtt | gaaaaactgg  | gagttgcgcg  | ccgagacggt  | 9720  |
| caactcctcc  | tccagaagac  | ggatgagctc | ggcgatgggtg | gcgcgcacct  | cgcgctcgaa  | 9780  |
| ggccccgggg  | ggctcctctt  | ccatctcctc | ctcttcctcc  | tccactaaca  | tctcttctac  | 9840  |
| ttcctcctca  | ggaggcggtg  | gcgggggagg | ggccctgcgt  | cgccggcggc  | gcacgggcag  | 9900  |
| acggtcgatg  | aagcgctcga  | tggctctccc | gcgccggcga  | cgcatgggtct | cggtgacggc  | 9960  |
| gcgcccgtcc  | tcgcggggcc  | gcagcatgaa | gacgccgccg  | cgcatctcca  | ggtggccgcc  | 10020 |
| gggggggtct  | ccgttgggca  | gggagagggc | gctgacgatg  | catcttatca  | attgaccctg  | 10080 |
| agggactccg  | cgcaaggacc  | tgagcgtctc | gagatccacg  | ggatccgaaa  | accgctgaac  | 10140 |
| gaaggcttcg  | agccagtcgc  | agtcgcaagg | taggctgagc  | ccggtttctt  | gttcttcggg  | 10200 |
| tatttggtcg  | ggaggcgggc  | gggcgatgct | gctgggtgatg | aagttgaagt  | aggcggtcct  | 10260 |
| gagacggcgg  | atggtggcga  | ggagcaccag | gtccttgggc  | ccggcttgct  | ggatgcgcag  | 10320 |
| acggtcggcc  | atgccccagg  | cgtggtcctg | acacctggcg  | aggtccttgt  | agtagtcctg  | 10380 |
| catgagccgc  | tccacgggca  | cctcctcctc | gcccgcgcgg  | ccgtgcatgc  | gcgtgagccc  | 10440 |
| gaaccgcgcg  | tgcggtgga   | cgagcgccag | gtcggcgacg  | acgcgctcgg  | tgaggatggc  | 10500 |
| ctgctggatc  | tgggtgaggg  | tggctctgaa | gtcgtcgaag  | tcgacgaagc  | ggtggtaggc  | 10560 |
| tccggtgttg  | atggtgtagg  | agcagttggc | catgacggac  | cagttgacgg  | tctggtggcc  | 10620 |
| gggtcgcacg  | agctcgtggt  | acttgaggcg | cgagtaggcg  | cgctgtcga   | agatgtagtc  | 10680 |
| gttgacggcg  | cgcacgaggt  | actggtatcc | gacgaggaag  | tgcggcgggc  | gctggcggtg  | 10740 |
| gagcggccat  | cgctcgggtg  | cgggggcgcc | gggcgcgagg  | tcctcgagca  | tgaggcggtg  | 10800 |
| gtagccgtag  | atgtacctgg  | acatccaggt | gatgccggcg  | gcggtgggtg  | aggcgcgcgg  | 10860 |
| gaactcgcgg  | acgcggttcc  | agatgttgcg | cagcggcagg  | aagtagttca  | tgggtggccgc | 10920 |
| ggtctggccc  | gtgaggcgcg  | cgcagtcgtg | gatgctctag  | acatacgggc  | aaaaacgaaa  | 10980 |
| gcggtcagcg  | gctcgactcc  | gtggcctgga | ggctaagcga  | acgggttggg  | ctgcgcgtgt  | 11040 |
| accccggttc  | gaatctcgaa  | tcaggctgga | gccgcagcta  | acgtgggtact | ggcactcccc  | 11100 |
| tctcgaccca  | agcctgctaa  | cgaaacctcc | aggatacggg  | ggcgggtcgt  | tttttggcct  | 11160 |
| tggtcgctgg  | tcatgaaaaa  | ctagtaagcg | cggaaagcgg  | ccgcccgcga  | tggctcgctg  | 11220 |
| ccgtagtctg  | gagaaaagaat | cgccagggtt | gcgttgcggt  | gtgccccggt  | tcgagcctca  | 11280 |
| gcgctcggcg  | ccggccggat  | tccgcggcta | acgtgggcgt  | ggctgccccg  | tcgtttccaa  | 11340 |
| gacccttag   | ccagccgact  | tctccagtta | cggagcgagc  | ccctcttttt  | ttttcttggtg | 11400 |
| tttttgccag  | atgcatcccc  | tactgcggca | gatgcgcccc  | cacctccac   | cacaaccgcc  | 11460 |

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|             |            |             |            |            |             |       |
|-------------|------------|-------------|------------|------------|-------------|-------|
| cctaccgcag  | cagcagcaac | agccggcgct  | tctgcccccg | ccccagcagc | agccagccac  | 11520 |
| taccgcggcg  | gccgccgtga | gcggagccgg  | cgttcagtat | gacctggcct | tggaagaggg  | 11580 |
| cgaggggctg  | gcgcggctgg | gggcgtcgtc  | gccggagcgg | cacccgcgcg | tgcagatgaa  | 11640 |
| aagggacgct  | cgcgaggcct | acgtgcccaa  | gcagaacctg | ttcagagaca | ggagcggcga  | 11700 |
| ggagccccgag | gagatgcgcg | cctccccgctt | ccacgcgggg | cgggagctgc | ggcgcggcct  | 11760 |
| ggaccgaaag  | cgggtgctga | gggacgagga  | tttcgaggcg | gacgagctga | cggggatcag  | 11820 |
| ccccgcgcgc  | gcgcacgtgg | ccgcggccaa  | cctggtcacg | gcgtacgagc | agaccgtgaa  | 11880 |
| ggaggagagc  | aacttccaaa | aatccttcaa  | caaccacgtg | cgcaccttga | tcgcgcgcga  | 11940 |
| ggaggtgacc  | ctgggcctga | tgcacctgtg  | ggacctgctg | gaggccatcg | tgcagaaccc  | 12000 |
| cacgagcaag  | ccgctgacgg | cgcagctgtt  | tctggtggtg | cagcacagtc | gggacaacga  | 12060 |
| gacgttcagg  | gaggcgctgc | tgaatatcac  | cgagcccag  | ggccgctggc | tcctggacct  | 12120 |
| ggtgaacatt  | ttgcagagca | tcgtggtgca  | ggagcgcggg | ctgccgctgt | ccgagaagct  | 12180 |
| ggcggccatc  | aacttctcgg | tgctgagtct  | gggcaagtac | tacgctagga | agatctacaa  | 12240 |
| gaccccgtag  | gtgcccatag | acaaggaggt  | gaagatcgac | gggttttaca | tgcgcatgac  | 12300 |
| cctgaaagtg  | ctgaccctga | gcgacgatct  | gggggtgtac | cgcaacgaca | ggatgcaccg  | 12360 |
| cgcggtgagc  | gccagccgcc | ggcgcgagct  | gagcgaccag | gagctgatgc | acagcctgca  | 12420 |
| gcggggccctg | accggggccg | ggaccgaggg  | ggagagctac | tttgacatgg | gcgcggacct  | 12480 |
| gcgctggcag  | cccagccgcc | gggccttgga  | agctgccggc | ggttccccct | acgtggagga  | 12540 |
| ggtggacgat  | gaggaggagg | agggcgagta  | cctggaagac | tgatggcgcg | accgtatatt  | 12600 |
| tgctagatgc  | agcaacagcc | accgccgccg  | cctcctgac  | ccgcgatgcg | ggcggcgctg  | 12660 |
| cagagccagc  | cgtccggcat | taactcctcg  | gacgattgga | cccaggccat | gcaacgcac   | 12720 |
| atggcgctga  | cgacccgcaa | tcccgaagcc  | tttagacagc | agcctcaggc | caaccggctc  | 12780 |
| tcggccatcc  | tggaggccgt | ggtgccctcg  | cgctcgaacc | ccacgcacga | gaagggtgctg | 12840 |
| gccatcgtga  | acgcgctggt | ggagaacaag  | gccatccgcg | gtgacgaggc | cgggctggtg  | 12900 |
| tacaacgcgc  | tgctggagcg | cgtggcccg   | tacaacagca | ccaacgtgca | gacgaacctg  | 12960 |
| gaccgcatgg  | tgaccgacgt | gcgcgaggcg  | gtgtcgcagc | gcgagcggtt | ccaccgcgag  | 13020 |
| tcgaacctgg  | gctccatggt | ggcgtgaac   | gccttcctga | gcacgcagcc | cgccaacgtg  | 13080 |
| ccccggggcc  | aggaggacta | caccaacttc  | atcagcgcgc | tgcggtgat  | ggtggccgag  | 13140 |
| gtgccccaga  | gcgaggtgta | ccagtcgggg  | ccggactact | tcttccagac | cagtcgccag  | 13200 |
| ggcttgcaga  | ccgtgaacct | gagccaggct  | ttcaagaact | tgcagggact | gtggggcgctg | 13260 |
| caggcccccg  | tcggggaccg | gcgcacggtg  | tcgagcctgc | tgacgccgaa | ctcgcgcctg  | 13320 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |             |             |            |       |
|------------|-------------|-------------|-------------|-------------|------------|-------|
| ctgctgctgc | tgggtggcgcc | cttcacggac  | agcggcagcg  | tgagccgcga  | ctcgtacctg | 13380 |
| ggctacctgc | ttaacctgta  | ccgcgaggcc  | atcggacagg  | cgcacgtgga  | cgagcagacc | 13440 |
| taccaggaga | tcacccacgt  | gagccgcgcg  | ctggggccagg | aggacccggg  | caacctggag | 13500 |
| gccaccctga | acttcctgct  | gaccaaccgg  | tcgcagaaga  | tcccgcccca  | gtacgcgctg | 13560 |
| agcaccgagg | aggagcgcac  | cctgcgctac  | gtgcagcaga  | gcgtggggct  | gttcctgatg | 13620 |
| caggaggggg | ccacgcccag  | cgcggcgctc  | gacatgaccg  | cgcgcaacat  | ggagcccagc | 13680 |
| atgtacgccc | gcaaccgccc  | gttcatcaat  | aagctgatgg  | actacttgca  | tcgggcggcc | 13740 |
| gccatgaact | cggactactt  | taccaacgcc  | atcttgaacc  | cgcaactggc  | cccgccgccc | 13800 |
| gggttctaca | cgggcgagta  | cgacatgccc  | gaccccaacg  | acgggttcct  | gtgggacgac | 13860 |
| gtggacagca | gcgtgttctc  | gccgcgtcca  | ggaaccaatg  | ccgtgtggaa  | gaaagagggc | 13920 |
| ggggaccggc | ggccgtcctc  | ggcgtgttcc  | ggtcgcgcgg  | gtgctgccgc  | ggcggtgccc | 13980 |
| gagggcgcca | gccccctccc  | gagcctgccc  | ttttcgctga  | acagcgtgcg  | cagcagcgag | 14040 |
| ctgggtcggc | tgacgcgacc  | gcgcctgctg  | ggcgaggagg  | agtacctgaa  | cgactccttg | 14100 |
| ttgaggcccc | agcgcgagaa  | gaacttcccc  | aataacggga  | tagagagcct  | ggtggacaag | 14160 |
| atgagccgct | ggaagacgta  | cgcgcacgag  | cacagggacg  | agccccgagc  | tagcagcgca | 14220 |
| ggcacccgta | gacgccagcg  | gcacgacagg  | cagcggggac  | tgggtgtggga | cgatgaggat | 14280 |
| tccgccgacg | acagcagcgt  | gttggaactt  | ggtgggagtg  | gtggtaaccc  | gttcgctcac | 14340 |
| ctgcgcccc  | gtatcgggcg  | cctgatgtaa  | gaatctgaaa  | aaataaaaaga | cggtactcac | 14400 |
| caaggccatg | gcgaccagcg  | tgcgttcttc  | tctgttgttt  | gtagtagtat  | gatgaggcgc | 14460 |
| gtgtaccccg | agggtcctcc  | tccctcgtag  | gagagcgtga  | tgcagcaggc  | ggtggcggcg | 14520 |
| gcgatgcagc | ccccgctgga  | ggcgcccttac | gtgccccgcg  | ggtacctggc  | gcctacggag | 14580 |
| gggcggaaca | gcattcgtta  | ctcggagctg  | gcacccttgt  | acgataccac  | ccggttgtag | 14640 |
| ctggtggaca | acaagtcggc  | agacatcgcc  | tcgctgaact  | accagaacga  | ccacagcaac | 14700 |
| ttcctgacca | ccgtggtgca  | gaacaacgat  | ttcaccccca  | cggaggccag  | caccagacc  | 14760 |
| atcaactttg | acgagcgctc  | gcggtggggc  | ggccagctga  | aaaccatcat  | gcacaccaac | 14820 |
| atgcccaacg | tgaacgagtt  | catgtacagc  | aacaagttca  | aggcgcgggt  | gatggtctcg | 14880 |
| cgcaagaccc | ccaacggggg  | ggatgatgat  | tatgatggta  | gtcaggacga  | gctgacctac | 14940 |
| gagtgggtgg | agtttgagct  | gcccgagggc  | aacttctcgg  | tgaccatgac  | catcgatctg | 15000 |
| atgaacaacg | ccatcatcga  | caactacttg  | gcggtggggc  | ggcagaacgg  | ggtgctggag | 15060 |
| agcgacatcg | gcgtgaagtt  | cgacacgcgc  | aacttccggc  | tgggctggga  | ccccgtgacc | 15120 |
| gagctggtga | tgccgggctg  | gtacaccaac  | gaggccttcc  | accccgacat  | cgtcctgctg | 15180 |
| cccggctgcg | gcgtggactt  | caccgagagc  | cgctcagca   | acctgctggg  | catccgcaag | 15240 |

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|             |             |             |             |            |             |       |
|-------------|-------------|-------------|-------------|------------|-------------|-------|
| cggcagccct  | tccaggaggg  | cttccagatc  | ctgtacgagg  | acctggaggg | gggcaacatc  | 15300 |
| cccgcgctct  | tggatgtcga  | agcctacgag  | aaaagcaagg  | aggatagcac | cgccgcggcg  | 15360 |
| accgcagccg  | tggccaccgc  | ctctaccgag  | gtgcggggcg  | ataattttgc | tagcgctgcg  | 15420 |
| gcagcggccg  | aggcggctga  | aaccgaaagt  | aagatagtca  | tccagccggt | ggagaaggac  | 15480 |
| agcaaggaca  | ggagctacaa  | cgtgctcgcg  | gacaagaaaa  | acaccgccta | ccgcagctgg  | 15540 |
| tacctggcct  | acaactacgg  | cgacccccgag | aagggcgctgc | gctcctggac | gctgctcacc  | 15600 |
| acctcggacg  | tcacctgcgg  | cgtggagcaa  | gtctactggt  | cgctgcccga | catgatgcaa  | 15660 |
| gacccggtca  | ccttccgctc  | cacgcgtcaa  | gttagcaact  | acccggtggt | gggcgccgag  | 15720 |
| ctcctgcccc  | tctactccaa  | gagcttcttc  | aacgagcagg  | ccgtctactc | gcagcagctg  | 15780 |
| cgcgcttca   | cctcgctcac  | gcacgtcttc  | aaccgcttcc  | ccgagaacca | gatcctcgtc  | 15840 |
| cgcccccccg  | cgcccaccat  | taccaccgtc  | agtgaaaacg  | ttcctgctct | cacagatcac  | 15900 |
| gggaccctgc  | cgctgcgcag  | cagtatccgg  | ggagtccagc  | gcgtgaccgt | cactgacgcc  | 15960 |
| agacgccgca  | cctgccccta  | cgtctacaag  | gccctgggcg  | tagtcgcgcc | gcgcgtcctc  | 16020 |
| tcgagccgca  | ccttctaaaa  | aatgtccatt  | ctcatctcgc  | ccagtaataa | caccggttgg  | 16080 |
| ggcctgcgcg  | cgcccagcaa  | gatgtacgga  | ggcgctcgcc  | aacgctccac | gcaacacccc  | 16140 |
| gtgcgcgtgc  | gcgggcactt  | ccgcgctccc  | tggggcgccc  | tcaagggccg | cgtgcgctcg  | 16200 |
| cgcaccaccg  | tcgacgacgt  | gatcgaccag  | gtggtggccg  | acgcgcgcaa | ctacacgccc  | 16260 |
| gccgccgcgc  | ccgtctccac  | cgtggacgcc  | gtcatcgaca  | gcgtggtggc | cgacgcgcgc  | 16320 |
| cggtagcccc  | gcaccaagag  | ccggcggcgg  | cgcacgccc   | ggcggcaccg | gagcaccccc  | 16380 |
| gccatgcgcg  | cggcgcgagc  | cttgtcgcgc  | agggccaggc  | gcacgggacg | cagggccatg  | 16440 |
| ctcagggcgg  | ccagacgcgc  | ggcctccggc  | agcagcagcg  | ccggcaggac | ccgcagacgc  | 16500 |
| gcggccacgg  | cggcggcggc  | ggccatcgcc  | agcatgtccc  | gcccgcggcg | cggcaacgtg  | 16560 |
| tactgggtgc  | gcgacgccgc  | caccggtgtg  | cgcgtgcccc  | tgcgcacccg | ccccctcgc   | 16620 |
| acttgaagat  | gctgacttcg  | cgatgttgat  | gtgtcccagc  | ggcgaggagg | atgtccaagc  | 16680 |
| gcaaatacaa  | ggaagagatg  | ctccagggtca | tcgcgcctga  | gatctacggc | cccgcggcgg  | 16740 |
| cgggtgaagga | ggaaagaaaag | ccccgcaaac  | tgaagcgggt  | caaaaaggac | aaaaaggagg  | 16800 |
| aggaagatga  | cggactggtg  | gagtttgtgc  | gcgagttcgc  | cccccgccgg | cgcgtagcagt | 16860 |
| ggcgcggggcg | gaaagtgaaa  | ccggtgctgc  | ggcccggcac  | cacggtggtc | ttcacgcccg  | 16920 |
| gcgagcgttc  | cggctccgcc  | tccaagcgct  | cctacgacga  | ggtgtacggg | gacgaggaca  | 16980 |
| tcctcgagca  | ggcggtcgag  | cgtctggggcg | agtttgcgta  | cggcaagcgc | agccgccccg  | 17040 |
| cgcccttgaa  | agaggaggcg  | gtgtccatcc  | cgctggacca  | cggcaacccc | acgccgagcc  | 17100 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |            |            |            |       |
|-------------|------------|------------|------------|------------|------------|-------|
| tgaagccggt  | gaccctgcag | caggtgctac | cgagcgccgc | gccgcgccgg | ggcttcaagc | 17160 |
| gcgagggcgg  | cgaggatctg | tacccgacca | tgcagctgat | ggtgcccagg | cgccagaagc | 17220 |
| tggaggacgt  | gctggagcac | atgaagggtg | accccaggt  | gcagcccag  | gtcaagggtc | 17280 |
| ggcccatcaa  | gcaggtggcc | ccgggcctgg | gcgtgcagac | cgtggacatc | aagatcccca | 17340 |
| cggagcccat  | ggaaacgcag | accgagcccg | tgaagcccag | caccagcacc | atggagggtc | 17400 |
| agacggatcc  | ctggatgcc  | gcaccagctt | ccaccagcac | tcgccgaaga | cgcaagtacg | 17460 |
| gcgcggccag  | cctgctgatg | cccaactacg | cgctgcatcc | ttccatcatc | cccacgccgg | 17520 |
| gctaccgcgg  | cacgcgcttc | taccgcggct | acaccagcag | ccgccgccgc | aagaccacca | 17580 |
| cccgcgccgg  | tcgtcgcagc | cgccgcagca | gcaccgcgac | ttccgccttg | gtgcggagag | 17640 |
| tgtatcgcag  | cgggcgcgag | cctctgaccc | tgccgcgcgc | gcgctaccac | ccgagcatcg | 17700 |
| ccatttaact  | accgcctcct | acttgcagat | atggccctca | catgccgcct | ccgcgtcccc | 17760 |
| attacgggct  | accgaggaag | aaagccgcgc | cgtagaaggc | tgacggggaa | cgggctgcgt | 17820 |
| cgccatcacc  | accggcgggc | gcgcgccatc | agcaagcggc | tggggggagg | cttcctgccc | 17880 |
| gcgctgatcc  | ccatcatcgc | cgcggcgatc | ggggcgatcc | ccggcatagc | ttccgtggcg | 17940 |
| gtgcaggcct  | ctcagcgcca | ctgagacaca | aaaaagcatg | gatttcta   | aaaaaaaaaa | 18000 |
| atggactgac  | gctcctggtc | ctgtgatgtg | tgtttttaga | tggaagacat | caatttttcg | 18060 |
| tccctggcac  | cgcgacacgg | cacgcggccg | tttatgggca | cctggagcga | catcggaac  | 18120 |
| agccaactga  | acgggggcgc | cttcaattgg | agcagtctct | ggagcgggct | taagaatttc | 18180 |
| gggtccacgc  | tcaaaacct  | tggcaacaag | gcgtggaaca | gcagcacagg | gcaggcgctg | 18240 |
| agggaaaagc  | tgaagaaca  | gaacttccag | cagaagggtg | ttgatggcct | ggcctcaggc | 18300 |
| atcaacgggg  | tgggtgacct | ggccaaccag | gccgtgcaga | aacagatcaa | cagccgcctg | 18360 |
| gacgcggtcc  | cgcccgcg   | gtccgtggag | atgccccagg | tggaggagga | gctgcctccc | 18420 |
| ctggacaagc  | gcggcgacaa | gcgaccgcgt | cccgcgcgg  | aggagacgct | gctgacgcac | 18480 |
| acggacgagc  | cgccccgta  | cgaggaggcg | gtgaaactgg | gcctgcccac | cacgcggccc | 18540 |
| gtggcgccctc | tggccaccgg | agtgtgaaa  | cccagcagca | gccagccgc  | gaccctggac | 18600 |
| ttgcctccgc  | ctcgccctc  | cacagtggct | aagcccctgc | cgccggtggc | cgtcgcgtcg | 18660 |
| cgcgcccccc  | gaggccgccc | ccaggcgaac | tggcagagca | ctctgaacag | catcgtgggt | 18720 |
| ctgggagtg   | agagtgtgaa | gcgccgccgc | tgtattataa | agacactgta | gcgcttaact | 18780 |
| tgttgtctg   | tgtgtatatg | tatgtccgcc | gaccagaagg | aggagtgtga | agaggcgctg | 18840 |
| cgccgagttg  | caagatggcc | accccatcga | tgtgccccca | gtgggcgtac | atgcacatcg | 18900 |
| ccggacagga  | cgcttcggag | tacctgagtc | cgggtctggt | gcagttcgcc | cgcgccacag | 18960 |
| acacctactt  | cagtctgggg | aacaagttaa | ggaacccccc | ggtggcgccc | acgcacgatg | 19020 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| tgaccaccga  | ccgcagccag  | cggctgacgc  | tgcgcttcgt | gcccgtggac  | cgcgaggaca  | 19080 |
| acacctactc  | gtacaaaagt  | cgctacacgc  | tggccgtggg | cgacaaccgc  | gtgctggaca  | 19140 |
| tggccagcac  | ctactttgac  | atccgcggcg  | tgctggaccg | gggccctagc  | ttcaaaccct  | 19200 |
| actctggcac  | cgcctacaac  | agcctagctc  | ccaagggagc | tccaatttcc  | agccagtggg  | 19260 |
| agcaagcaaa  | aacaggcaat  | gggggaacta  | tggaaacaca | cacatatggt  | gtggccccaa  | 19320 |
| tgggcggaga  | gaatattaca  | aaagatggtc  | ttcaaattgg | aactgacgtt  | acagcgaatc  | 19380 |
| agaataaacc  | aatttatgcc  | gacaaaacat  | ttcaaccaga | accgcaagta  | ggagaagaaa  | 19440 |
| attggcaaga  | aactgaaaac  | ttttatggcg  | gtagagctct | taaaaaagac  | acaaacatga  | 19500 |
| aaccttgcta  | tggctcctat  | gctagaccca  | ccaatgaaaa | aggaggtcaa  | gctaaactta  | 19560 |
| aagttggaga  | tgatggagtt  | ccaaccaaag  | aattcgacat | agacctggct  | ttctttgata  | 19620 |
| ctcccgtggg  | caccgtgaac  | ggtcaagacg  | agtataaagc | agacattgtc  | atgtataccg  | 19680 |
| aaaacacgta  | tttgaaaact  | ccagacacgc  | atgtggtata | caaaccaggc  | aaggatgatg  | 19740 |
| caagtcttga  | aattaacctg  | gttcagcagt  | ctatgcccaa | cagaccaaac  | tacattgggt  | 19800 |
| tcagggacaa  | ctttatcggg  | cttatgtact  | acaacagcac | tggcaatatg  | ggtgtgcttg  | 19860 |
| ctggtcaggc  | ctcccagctg  | aatgctgtgg  | ttgatttgca | agacagaaac  | accgagctgt  | 19920 |
| cctaccagct  | cttgcttgac  | tctttgggtg  | acagaaccgg | gtatttcagt  | atgtggaacc  | 19980 |
| aggcgggtgga | cagttatgac  | cccgatgtgc  | gcatcatcga | aaaccatggt  | gtggaggatg  | 20040 |
| aattgccaaa  | ctattgcttc  | cccttggacg  | gctctggcac | taacgccgca  | taccaagggtg | 20100 |
| tgaaagtaaa  | agatgggtcaa | gatgggtgatg | ttgagagtga | atgggaaaat  | gacgatactg  | 20160 |
| ttgcagctcg  | aaatcaatta  | tgtaaaggta  | acattttcgc | catggagatt  | aatctccagg  | 20220 |
| ctaacctgtg  | gagaagtttc  | ctctactcga  | acgtggccct | gtacctgccc  | gactcctaca  | 20280 |
| agtacacgcc  | gaccaacgtc  | acgctgccga  | ccaacaccaa | cacctacgat  | tacatgaatg  | 20340 |
| gcagagtgc   | acctccctcg  | ctggtagacg  | cctacctcaa | catcgggggc  | cgctggtcgc  | 20400 |
| tggaccccat  | ggacaacgtc  | aacccttca   | accaccaccg | caacgcgggc  | ctgcgctacc  | 20460 |
| gctccatgct  | cctgggcaac  | gggcgctacg  | tgcccttcca | catccagggtg | ccccaaaagt  | 20520 |
| ttttcgccat  | caagagcctc  | ctgctcctgc  | ccgggtccta | cacctacgag  | tggaacttcc  | 20580 |
| gcaaggacgt  | caacatgatc  | ctgcagagct  | ccctaggcaa | cgacctgctc  | acggacgggg  | 20640 |
| cctccatcgc  | cttcaccagc  | atcaacctct  | acgccacctt | cttcccatg   | gcgcacaaca  | 20700 |
| ccgcctccac  | gctcgaggcc  | atgctgcgca  | acgacaccaa | cgaccagtcc  | ttcaacgact  | 20760 |
| acctctcggc  | ggccaacatg  | ctctacccca  | tcccggccaa | cgccaccaac  | gtgcccctct  | 20820 |
| ccatcccctc  | gcgcaactgg  | gccgccttcc  | gcggatggtc | cttcacgcgc  | ctgaagaccc  | 20880 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| gcgagacgcc  | ctcgctcggc  | tccgggttcg  | accctactt  | cgctactcg   | ggctccatcc  | 20940 |
| cctacctaga  | cggcaccttc  | tacctcaacc  | acaccttcaa | gaaggctctcc | atcaccttcg  | 21000 |
| actcctccgt  | cagctggccc  | ggcaacgacc  | gcctcctgac | gccaacgag   | ttcgaaatca  | 21060 |
| agcgcaccgt  | cgacggagag  | ggatacaacg  | tggcccagtg | caacatgacc  | aaggactggg  | 21120 |
| tcctgggtcca | gatgctggcc  | cactacaaca  | tcggctacca | gggcttctac  | gtgcccgagg  | 21180 |
| gctacaagga  | ccgcatgtac  | tccttcttcc  | gcaacttcca | gcccattgagc | cgccaggctcg | 21240 |
| tggacgaggt  | caactacaag  | gactaccagg  | ccgtcaccct | ggcctaccag  | cacaacaact  | 21300 |
| cgggcttcgt  | cggctacctc  | gcgcccacca  | tgcgccaggg | ccagccctac  | cccgccaaact | 21360 |
| accctatccc  | gctcatcggc  | aagagcgccg  | tcgccagcgt | caccagaaaa  | aagttcctct  | 21420 |
| gcgaccgggt  | catgtggcgc  | atcccccttct | ccagcaactt | catgtccatg  | ggcgcgctca  | 21480 |
| ccgacctcgg  | ccagaacatg  | ctctacgcca  | actccgcccc | cgcgctagac  | atgaatttcg  | 21540 |
| aagtcgaccc  | catggatgag  | tccacccttc  | tctatgttgt | cttcgaagtc  | ttcgacgtcg  | 21600 |
| tccgagtgca  | ccagccccac  | cgcggcgctca | tcgaagccgt | ctacctgcgc  | acgcccttct  | 21660 |
| cggccggcaa  | cgccaccacc  | taagccgctc  | ttgcttcttg | caagatgacg  | gcgggctccg  | 21720 |
| gcgagcagga  | gctcagggcc  | atcctccgcg  | acctgggctg | cggggccctgc | ttcctgggca  | 21780 |
| ccttcgacaa  | gcgcttccct  | ggattcatgg  | ccccgcacaa | gctggcctgc  | gccatcgtga  | 21840 |
| acacggccgg  | ccgcgagacc  | gggggcgagc  | actggctggc | cttcgcctgg  | aaccgcgct   | 21900 |
| cccacacatg  | ctacctcttc  | gaccccttcg  | ggttctcgga | cgagcgcttc  | aagcagatct  | 21960 |
| accagttcga  | gtacgagggc  | ctgctgcgtc  | gcagcgccct | ggccaccgag  | gaccgctgcg  | 22020 |
| tcaccctgga  | aaagtccacc  | cagaccgtgc  | agggtcgcgc | ctcggccgcc  | tgcgggctct  | 22080 |
| tctgctgcat  | gttcctgcac  | gccttcgtgc  | actggcccga | ccgccccatg  | gacaagaacc  | 22140 |
| ccaccatgaa  | cttactgacg  | ggggtgcccc  | acggcatgct | ccagtcgccc  | caggtggaac  | 22200 |
| ccaccctgcg  | ccgcaaccag  | gaagcgctct  | accgcttcct | caatgcccac  | tccgcctact  | 22260 |
| ttcgctccca  | ccgcgcgcgc  | atcgagaagg  | ccaccgcctt | cgaccgcatg  | aatcaagaca  | 22320 |
| tgtaaaaaac  | cgggtgtgtg  | atgtgaatgc  | tttattcata | ataaacagca  | catgtttatg  | 22380 |
| ccaccttctc  | tgaggctctg  | actttattta  | gaaatcgaag | gggttctgcc  | ggctctcggc  | 22440 |
| atggcccgcg  | ggcaggggata | cggtgcggaa  | ctggctactg | ggcagccact  | tgaactcggg  | 22500 |
| gatcagcagc  | ttgggcacgg  | ggaggtcggg  | gaacgagtcg | ctccacagct  | tgcgcgtag   | 22560 |
| ttgcagggcg  | cccagcaggt  | cgggcgcgga  | gatcttgaaa | tcgcagttgg  | gacccgcgtt  | 22620 |
| ctgcgcgcga  | gagttgcggt  | acacgggggtt | gcagcactgg | aacaccatca  | gggcccgggtg | 22680 |
| cttcacgctt  | gccagcaccg  | tcgcgtcggg  | gatgccctcc | acgtccagat  | cctcggcggtt | 22740 |
| ggccatcccc  | aaggggggtca | tcttgacagg  | ctgccgcccc | atgctgggca  | cgcagccggg  | 22800 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |            |            |             |       |
|-------------|------------|-------------|------------|------------|-------------|-------|
| cttgtggttg  | caatcgcagt | gcagggggat  | cagcatcatc | tgggcctgct | cggagctcat  | 22860 |
| gcccgggtac  | atggccttca | tgaaagcctc  | cagctggcgg | aaggcctgct | gcgccttgcc  | 22920 |
| gccctcgggtg | aagaagaccc | cgcaggactt  | gctagagaac | tggttggtgg | cgcagccggc  | 22980 |
| gtcgtgcacg  | cagcagcgcg | cgtcgttggt  | ggccagctgc | accacgctgc | gccccagcg   | 23040 |
| gttctgggtg  | atcttggccc | ggttgggggt  | ctccttcagc | gcgcgctgcc | cgttctcgct  | 23100 |
| cgccacatcc  | atctcgatag | tgtgctcctt  | ctggatcatc | acggtcccgt | gcaggcaccg  | 23160 |
| cagcttgccc  | tcggcttcgg | tgcagccgtg  | cagccacagc | gcgcagccgg | tgcactccca  | 23220 |
| gttcttggtg  | gcgatctggg | agtgcgagtg  | cacgaagccc | tgcaggaagc | ggcccatcat  | 23280 |
| cgcggtcagg  | gtcttggtgc | tggatgaagg  | cagcgggatg | ccgcggtgct | cctcgttcac  | 23340 |
| atacaggtgg  | cagatgcggc | ggtacacctc  | gccctgctcg | ggcatcagct | ggaaggcgga  | 23400 |
| cttcaggtcg  | ctctccacgc | ggtaccgggc  | catcagcagc | gtcatcactt | ccatgccctt  | 23460 |
| ctcccaggcc  | gaaacgatcg | gcaggctcag  | ggggttcttc | accgccattg | tcattcttagt | 23520 |
| cgccgccgcc  | gaggtcaggg | ggtcgttctc  | gtccaggggc | tcaaacactc | gcttgccgtc  | 23580 |
| cttctcgatg  | atgcgcacgg | ggggaaaagct | gaagcccacg | gccgccagct | cctcctcggc  | 23640 |
| ctgcctttcg  | tcctcgctgt | cctggctgat  | gtcttgcaaa | ggcacatgct | tggctctgcg  | 23700 |
| gggtttcttt  | ttgggcggca | gaggcggcgg  | cgatgtgctg | ggagagcgcg | agttctcggt  | 23760 |
| caccacgact  | atttcttctt | cttggccgtc  | gtccgagacc | acgcggcggt | aggcatgcct  | 23820 |
| cttctggggc  | agaggcggag | gcgacgggct  | ctcgcggttc | ggcgggcggc | tggcagagcc  | 23880 |
| ccttccgcgt  | tcgggggtgc | gctcctggcg  | gcgctgctct | gactgacttc | ctccgcggcc  | 23940 |
| ggccattgtg  | ttctcctagg | gagcaacaac  | aagcatggag | actcagccat | cgtcgccaac  | 24000 |
| atcgccatct  | gccccgccg  | ccaccgccga  | cgagaaccag | cagcagaatg | aaagcttaac  | 24060 |
| cgccccgccg  | cccagcccca | cctccgacgc  | cgcggcccca | gacatgcaag | agatggagga  | 24120 |
| atccatcgag  | attgacctgg | gctacgtgac  | gcccgcggag | cacgaggagg | agctggcagc  | 24180 |
| gcgcttttca  | gccccggaag | agaaccacca  | agagcagcca | gagcaggaag | cagagaacga  | 24240 |
| gcagaaccag  | gctgggcacg | agcatggcga  | ctacctgagc | ggggcagagg | acgtgctcat  | 24300 |
| caagcatctg  | gcccgccaat | gcatcatcgt  | caaggacgcg | ctgctcgacc | gcgccgaggt  | 24360 |
| gcccctcagc  | gtggcggagc | tcagccgcgc  | ctacgagcgc | aacctcttct | cgccgcgcgt  | 24420 |
| gccccccaag  | cgccagccca | acggcacctg  | tgagcccaac | ccgcgcctca | acttctaccc  | 24480 |
| ggtcttcgcg  | gtgcccaggg | ccctggccac  | ctaccacctc | tttttcaaga | accaaaggat  | 24540 |
| ccccgtctcc  | tgccgcgcca | accgcacccg  | cgccgacgcc | ctgctcaacc | tgggccccgg  | 24600 |
| cgccccgcta  | cctgatatca | cctccttgga  | agaggttccc | aagatcttcg | agggctctggg | 24660 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |             |            |            |       |
|------------|-------------|-------------|-------------|------------|------------|-------|
| cagcgacgag | actcggggccg | cgaacgctct  | gcaaggaagc  | ggagaggagc | atgagcacca | 24720 |
| cagcgccctg | gtggagttgg  | aaggcgacaa  | cgcgcgccctg | gcggtcctca | agcgcacggt | 24780 |
| cgagctgacc | cacttcgcct  | acccggcgct  | caacctgccc  | cccaaggta  | tgagcgccgt | 24840 |
| catggaccag | gtgctcatca  | agcgcgccctc | gcccctctcg  | gaggaggaga | tgcaggaccc | 24900 |
| cgagagtctg | gacgagggca  | agcccgtggt  | cagcgacgag  | cagctggcgc | gctggctggg | 24960 |
| agcgagtagc | acccccaga   | gcctggaaga  | gcggcgcaag  | ctcatgatgg | ccgtggctct | 25020 |
| ggtgaccgtg | gagctggagt  | gtctgcgccg  | cttctttgcc  | gacgcggaga | ccctgcgcaa | 25080 |
| ggtcgaggag | aacctgcact  | acctcttcag  | gcacgggttc  | gtgcgccagg | cctgcaagat | 25140 |
| ctccaacgtg | gagctgacca  | acctggctctc | ctacatgggc  | atcctgcacg | agaaccgcct | 25200 |
| ggggcaaaac | gtgctgcaca  | ccaccctgcg  | cggggaggcc  | cgccgcgact | acatccgcga | 25260 |
| ctgcgtctac | ctgtacctct  | gccacacctg  | gcagacgggc  | atgggcgtgt | ggcagcagt  | 25320 |
| cctggaggag | cagaacctga  | aagagctctg  | caagctcctg  | cagaagaacc | tcaaggccct | 25380 |
| gtggaccggg | ttcgacgagc  | gtaccaccgc  | ctcggacctg  | gccgacctca | tcttccccga | 25440 |
| gcgcctgcgg | ctgacgctgc  | gcaacgggct  | gcccgaactt  | atgagccaaa | gcatgttgca | 25500 |
| aaactttcgc | tctttcatcc  | tcgaacgctc  | cgggatcctg  | cccgccacct | gctccgcgct | 25560 |
| gccctcggac | ttcgtgccgc  | tgaccttccg  | cgagtgcccc  | ccgccgctct | ggagccactg | 25620 |
| ctacttgctg | cgccctggcca | actacctggc  | ctaccactcg  | gacgtgatcg | aggacgtcag | 25680 |
| cggcgagggg | ctgctggagt  | gccactgccg  | ctgcaacctc  | tgcacgccgc | accgctccct | 25740 |
| ggcctgcaac | ccccagctgc  | tgagcgagac  | ccagatcatc  | ggcaccttcg | agttgcaagg | 25800 |
| ccccggcgac | ggcgagggca  | aggggggtct  | gaaactcacc  | ccggggctgt | ggacctcggc | 25860 |
| ctacttgctg | aagttcgtgc  | ccgaggacta  | ccatcccttc  | gagatcaggt | tctacgagga | 25920 |
| ccaatcccag | ccgcccagg   | ccgagctgtc  | ggcctgcgtc  | atcaccag   | gggccatcct | 25980 |
| ggcccaattg | caagccatcc  | agaaaatccc  | ccaagaattt  | ctgctgaaaa | agggccacgg | 26040 |
| ggtctacttg | gacccccaga  | ccggagagga  | gctcaacccc  | agcttcccc  | aggatgcccc | 26100 |
| gaggaagcag | caagaagctg  | aaagtggagc  | tgccgccgcc  | ggaggatttg | gaggaagact | 26160 |
| gggagagcag | tcaggcagag  | gaggaggaga  | tggaagactg  | ggacagcact | caggcagagg | 26220 |
| aggacagcct | gcaagacagt  | ctggaggagg  | aagacgaggt  | ggaggaggca | gaggaagaag | 26280 |
| cagccgccgc | cagaccgtcg  | tcctcggcgg  | agaaagcaag  | cagcacggat | accatctccg | 26340 |
| ctccgggtcg | gggtcgcggc  | ggccggggccc | acagtaggtg  | ggacgagacc | gggcgcttcc | 26400 |
| cgaacccac  | caccagacc   | ggtaagaagg  | agcggcaggg  | atacaagtcc | tggcgggggc | 26460 |
| acaaaaacgc | catcgtctcc  | tgcttgcaag  | cctgcggggg  | caacatctcc | ttcaccggc  | 26520 |
| gctacctgct | cttccaccgc  | ggggtgaact  | tccccgcaa   | catcttgcat | tactaccgtc | 26580 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |             |             |            |       |
|------------|------------|------------|-------------|-------------|------------|-------|
| acctccacag | cccctactac | tgtttccaag | aagaggcaga  | aaccacagcag | cagcagaaaa | 26640 |
| ccagcggcag | cagcagctag | aaaatccaca | gcggcggcag  | gtggactgag  | gatcgcggcg | 26700 |
| aacgagccgg | cgcagacccg | ggagctgagg | aaccggatct  | ttcccaccct  | ctatgccatc | 26760 |
| ttccagcaga | gtcgggggca | ggagcaggaa | ctgaaagtca  | agaaccgttc  | tctgcgctcg | 26820 |
| ctcaccgcga | gttgtctgta | tcacaagagc | gaagaccaac  | ttcagcgcac  | tctcgaggac | 26880 |
| gccgaggctc | tcttcaacaa | gtactgcgcg | ctcactctta  | aagagtagcc  | cgcgcccgcc | 26940 |
| cacacacgga | aaaaggcggg | aattacgtca | ccacctgcgc  | ccttcgcccg  | accatcatga | 27000 |
| gcaaagagat | ttccacgcct | tacatgtgga | gctaccagcc  | ccagatgggc  | ctggccgccg | 27060 |
| gcgcccacca | ggactactcc | acccgcatga | actggctcag  | tgccggggccc | gcgatgatct | 27120 |
| cacgggtgaa | tgacatccgc | gcccaccgaa | accagatact  | cctagaacag  | tcagcgatca | 27180 |
| ccgccacgcc | ccgccatcac | cttaatccgc | gtaattggcc  | cgccgccctg  | gtgtaccagg | 27240 |
| aaattcccca | gcccacgacc | gtactacttc | cgcgagacgc  | ccaggccgaa  | gtccagctga | 27300 |
| ctaactcagg | tgtccagctg | gccggcggcg | ccgccctgtg  | tcgtcaccgc  | cccgtcagg  | 27360 |
| gtataaagcg | gctggtgac  | cgaggcagag | gcacacagct  | caacgacgag  | gtggtgagct | 27420 |
| cttcgctggg | tctgcgacct | gacggagtct | tccaactcgc  | cggatcgggg  | agatcttcct | 27480 |
| tcacgcctcg | tcaggccgtc | ctgactttgg | agagttcgtc  | ctcgcagccc  | cgctcgggcg | 27540 |
| gcacgcggac | tctccagttc | gtggaggagt | tcactccctc  | ggtctacttc  | aaccccttct | 27600 |
| ccggctcccc | cggccactac | ccggacgagt | tcatcccga   | cttcgacgcc  | atcagcgagt | 27660 |
| cggtgagcgg | ctacgattga | atgtcccatg | gtggcgcagc  | tgacctagct  | cggcttcgac | 27720 |
| acctggacca | ctgccgccgc | ttccgctgct | tcgctcggga  | tctcgccgag  | tttgcttact | 27780 |
| ttgagctgcc | cgaggagcac | cctcagggcc | cagcccacgg  | agtgcggatc  | atcgtcgaag | 27840 |
| ggggcctcga | ctcccacctg | cttcggatct | tcagccagcg  | accgatcctg  | gtcgagcgcg | 27900 |
| aacaaggaca | gacccttctt | actttgtact | gcacgtgcaa  | ccaccccggc  | ctgcatgaaa | 27960 |
| gtctttgttg | tctgctgtgt | actgagtata | ataaaaagctg | agatcagcga  | ctactccgga | 28020 |
| ctcgattgtg | gtgttcctgc | tatcaaccgg | tccctgttct  | tcaccgggaa  | cgagaccgag | 28080 |
| ctccagctcc | agtgtgaagc | ccacaagaag | tacctcacct  | ggctgttcca  | gggtcccccg | 28140 |
| atcgccgttg | tcaaccactg | cgacaacgac | ggagtcctgc  | tgagcggccc  | tgccaacctt | 28200 |
| actttttcca | cccgcagaag | caagctccag | ctcttccaac  | ccttcctccc  | cgggacctat | 28260 |
| cagtgcgtct | caggacctg  | ccatcacacc | ttccacctga  | tccgaatac   | cacagcgccg | 28320 |
| ctccccgcta | ctaacaacca | aactaccac  | caacgccacc  | gtcgcgacct  | ttcctctgaa | 28380 |
| tctaatacca | ctaccggagg | tgagctccga | ggtcgaccaa  | cctctgggat  | ttactacggc | 28440 |

368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |             |            |             |       |
|-------------|-------------|------------|-------------|------------|-------------|-------|
| ccctgggagg  | tgggtggggtt | aatagcaaat | aaaaaaaaata | atcatttgat | ttgaaataaaa | 28500 |
| gatacaatca  | tattgatgat  | ttgagtttaa | caaaaaataaa | gaatcactta | cttgaaatct  | 28560 |
| gataccagggt | ctctgtccat  | gttttctgcc | aacaccacct  | cactcccctc | ttcccagctc  | 28620 |
| tgggtactgca | ggccccggcg  | ggctgcaaac | ttcctccaca  | cgctgaagg  | gatgtcaaat  | 28680 |
| tcctcctgtc  | cctcaatctt  | cattttatct | tctatcagat  | gtccaaaaag | cgctgccggg  | 28740 |
| tggatgatga  | cttcgacccc  | gtctaccctt | acgatgcaga  | caacgcaccg | accgtgccct  | 28800 |
| tcatcaaccc  | ccccttcgtc  | tcttcagatg | gattccaaga  | gaagcccctg | ggggtgttgt  | 28860 |
| ccctgcgact  | ggctgacccc  | gtcaccacca | agaacgggga  | aatcaccctc | aagctgggag  | 28920 |
| aggggggtgga | cctcgactcg  | tcgggaaaac | tcatctccaa  | cacggccacc | aaggccgccg  | 28980 |
| cccctctcag  | tatttcaaac  | aacaccattt | cccttaaaac  | tgctgcccct | ttctacaaca  | 29040 |
| acaatggaac  | tttaagcctc  | aatgtctcca | caccattagc  | agtatttccc | acatttaaca  | 29100 |
| ctttaggcat  | aagtcttggg  | aacggtcttc | agacttcaaa  | taagtgtgtg | actgtacaac  | 29160 |
| taactcatcc  | tcttacattc  | agctcaaata | gcatcacagt  | aaaaacagac | aaagggctat  | 29220 |
| atattaactc  | cagtggaaac  | agaggacttg | aggctaatat  | aagcctaaaa | agaggactag  | 29280 |
| tttttgacgg  | taatgctatt  | gcaacatata | ttggaaatgg  | cttagactat | ggatcttatg  | 29340 |
| atagtgatgg  | aaaaacaaga  | cccgtaatga | ccaaaattgg  | agcaggatta | aattttgatg  | 29400 |
| ctaacaaagc  | aatagctgtc  | aaactaggca | caggtttaag  | ttttgactcc | gctggtgcct  | 29460 |
| tgacagctgg  | aaacaaacag  | gatgacaagc | taacactttg  | gactaccctt | gaccaagcc   | 29520 |
| ctaattgtca  | attactttca  | gacagagatg | ccaaattttac | tctctgtctt | acaaaatgcg  | 29580 |
| gtagtcaaat  | actaggcact  | gtggcagtg  | cggtgtttac  | tgtaggatca | gcactaaatc  | 29640 |
| caattaatga  | cacagtcaaa  | agcgccatag | ttttccttag  | atttgattcc | gatggtgtac  | 29700 |
| tcatgtcaaa  | ctcatcaatg  | gtaggtgatt | actggaactt  | tagggaggga | cagaccactc  | 29760 |
| aaagtgtagc  | ctatacaaat  | gctgtgggat | tcatgccaaa  | tataggtgca | tatccaaaaa  | 29820 |
| cccaaagtaa  | aacacctaaa  | aatagcatag | tcagtcaggt  | atatttaact | ggagaaacta  | 29880 |
| ctatgccaat  | gacactaacc  | ataactttca | atggcactga  | tgaaaaagac | acaaccccag  | 29940 |
| ttagcaccta  | ctctatgact  | tttacatggc | agtggactgg  | agactataag | gacaaaaata  | 30000 |
| ttacctttgc  | taccaactca  | ttctcttttt | cctacatcgc  | ccaggaataa | tcccaccag   | 30060 |
| caagccaacc  | ccttttccca  | ccacctttgt | ctatatggaa  | actctgaaac | agaaaaataa  | 30120 |
| agttcaagtg  | ttttattgaa  | tcaacagttt | tacaggactc  | gagcagttat | ttttcctcca  | 30180 |
| ccctcccagg  | acatggaata  | caccaccctc | tcccccgca   | cagccttgaa | catctgaatg  | 30240 |
| ccattgggtga | tggacatgct  | tttggctctc | acgttccaca  | cagtttcaga | gcgagccagt  | 30300 |
| ctcggatcgg  | tcaggggagat | gaaaccctcc | gggcactccc  | gcatctgcac | ctcacagctc  | 30360 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |            |             |       |
|-------------|-------------|-------------|------------|------------|-------------|-------|
| aacagctgag  | gattgtcctc  | ggtggtcggg  | atcacggtta | tctggaagaa | gcagaagagc  | 30420 |
| ggcgggtggga | atcatagtcc  | gcgaacggga  | tcggccggtg | gtgtcgcac  | agggcccgca  | 30480 |
| gcagtcgctg  | ccgccgccgc  | tccgtcaagc  | tgctgctcag | ggggttcggg | tccagggaact | 30540 |
| ccctcagcat  | gatgcccacg  | gccctcagca  | tcagtcgtct | ggtgcggcgg | gcgcagcagc  | 30600 |
| gcattgcgaat | ctcgctcagg  | tcaactgcagt | acgtgcaaca | caggaccacc | aggttggttca | 30660 |
| acagtccata  | gttcaacacg  | ctccagccga  | aactcatcgc | gggaaggatg | ctaccacagt  | 30720 |
| ggccgtcgta  | ccagatcctc  | aggtaaata   | agtggcgctc | cctccagaag | acgctgcca   | 30780 |
| tgtacatgat  | ctccttgggc  | atgtggcggg  | tcaccacctc | ccggtaccac | atcacctct   | 30840 |
| ggttgaacat  | gcagccccgg  | atgatcctgc  | ggaaccacag | ggccagcacc | gccccgccc   | 30900 |
| ccatgcagcg  | aagagacccc  | ggatcccggc  | aatgacaatg | gaggaccac  | cgctcgtacc  | 30960 |
| cgtggatcat  | ctgggagctg  | aacaagtcta  | tgttggcaca | gcacaggcat | atgctcatgc  | 31020 |
| atctcttcag  | cactctcagc  | tcctcggggg  | tcaaaacat  | atcccagggc | acggggaact  | 31080 |
| cttgaggagc  | agcgaacccc  | gcagaacagg  | gcaatcctcg | cacataactt | acattgtgca  | 31140 |
| tggacagggg  | atcgcaatca  | ggcagcaccg  | ggtgatcctc | caccagagaa | gcgcgggtct  | 31200 |
| cgggtctcctc | acagcgtggg  | aagggggccg  | gccgatacgg | gtgatggcgg | gacgcggctg  | 31260 |
| atcgtgttct  | cgaccgtgtc  | atgatgcagt  | tgctttcgga | cattttcgta | cttgctgtag  | 31320 |
| cagaacctgg  | tccgggcgct  | gcacaccgat  | cgccggcggc | ggtctcggcg | cttggaacgc  | 31380 |
| tcgggtgttaa | agttgtaaaa  | cagccactct  | ctcagaccgt | gcagcagatc | tagggcctca  | 31440 |
| ggagtgatga  | agatcccatc  | atgcctgata  | gctctgatca | catcgaccac | cgtggaatgg  | 31500 |
| gccaggccca  | gccagatgat  | gcaattttgt  | tgggtttcgg | tgacggcggg | ggaggggaaga | 31560 |
| acaggaagaa  | ccatgattaa  | cttttaatat  | aaacggtctc | ggagcacttc | aaaatgaagg  | 31620 |
| tcacggagat  | ggcacctctc  | gccccgctg   | tgttgggtga | aaataacagc | cagggtcaaag | 31680 |
| gtgatacggg  | tctcgagatg  | ttccacgggtg | gcttccagca | aagcctccac | gcgcacatcc  | 31740 |
| agaaacaaga  | caatagcgaa  | agcgggaggg  | ttctctaatt | cctcaaccat | catgttacac  | 31800 |
| tcctgcacca  | tccccagata  | attttcattt  | ttccagcctt | gaatgattcg | aactagttcc  | 31860 |
| tgaggtaaat  | ccaagccagc  | catgataaaa  | agctcgcgca | gagcaccctc | caccggcatt  | 31920 |
| cttaagcaca  | ccctcataat  | tccaagatat  | tctgctcctg | gttcacctgc | agcagattga  | 31980 |
| caagcgggaat | atcaaaatct  | ctgccgcgat  | ccctgagctc | ctccctcagc | aataactgta  | 32040 |
| agtactcttt  | catatcgtct  | ccgaaatttt  | tagccatagg | acccccagga | ataagagaag  | 32100 |
| ggcaagccac  | attacagata  | aaccgaagtc  | ccccccagtg | agcattgcca | aatgtaagat  | 32160 |
| tgaaataagc  | atgctgggcta | gacccgggtga | tatcttccag | ataactggac | agaaaatcgg  | 32220 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|                                                                     |       |
|---------------------------------------------------------------------|-------|
| gtaagcaatt ttttaagaaaa tcaacaaaaag aaaaatcttc caggtgcacg tttagggcct | 32280 |
| cgggaacaac gatggagtaa gtgcaagggg tgcgttccag catggtagt tagctgatct    | 32340 |
| gtaaaaaaac aaaaaataaa acattaaacc atgctagcct ggcgaacagg tgggtaaatc   | 32400 |
| gttctctcca gcaccaggca ggccacgggg tctccggcgc gaccctcgta aaaattgtcg   | 32460 |
| ctatgattga aaaccatcac agagagacgt tcccgggtggc cggcgtgaat gattcgagaa  | 32520 |
| gaagcataca cccccggaac attggagtcc gtgagtgaag aaaagcggcc gaggaagcaa   | 32580 |
| tgaggcacta caacgctcac tctcaagtcc agcaaagcga tgccatgcgg atgaagcaca   | 32640 |
| aaattttcag gtgcgtaaaa aatgtaatta ctccccctct gcacaggcag cgaagctccc   | 32700 |
| gatccctcca gatacacata caaagcctca gcgtccatag cttaccgagc ggcagcagca   | 32760 |
| gcggcac                                                             | 32767 |

&lt;210&gt; 3

&lt;211&gt; 32767

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificially Synthesized

&lt;400&gt; 3

|                                                                     |      |
|---------------------------------------------------------------------|------|
| catcatcaat aatatacctc aaacttttgg tgcgcgttaa tatgcaaatg agctgtttga   | 60   |
| atttgggggag ggaggaaggt gattggccga gagacggggcg accgttaggg gcggggcggg | 120  |
| tgacgttttg atgacgtggc cgtgaggcgg agccggtttg caagtctctg tgggaaaagt   | 180  |
| gacgtcaaac gaggtgtggt ttgaacacgg aaataactcaa ttttcccgcg ctctctgaca  | 240  |
| ggaaatgagg tgtttctggg cggatgcaag tgaaaacggg ccattttcgc gcgaaaactg   | 300  |
| aatgaggaag tgaaaatctg agtaatttcg cgtttatggc agggaggagt atttgccgag   | 360  |
| ggccgagtag actttgaccg attacgtggg ggtttcgatt accgtatttt tcacctaaat   | 420  |
| ttccgcgtac ggtgtcaaaag tccggtgttt ttacgtacga tatcatttcc ccgaaaagtgc | 480  |
| cacctgaccg taactataac ggtcctaagg tagcgaaagc tcagatctcc cgatccccta   | 540  |
| tggtgcactc tcagtacaat ctgctctgat gccgcatagt taagccagta tctgctccct   | 600  |
| gcttgtgtgt tggaggtcgc tgagtagtgc gcgagcaaaa ttttaagctac aacaaggcaa  | 660  |
| ggcttgaccg acaattgcat gaagaatctg cttagggtta ggcgttttgc gctgcttcgc   | 720  |
| gatgtacggg ccagatatac gcgttgacat tgattattga ctagtatgcc aagtacgccc   | 780  |
| cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta catgacctta   | 840  |
| tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac catggtgatg   | 900  |
| cggtttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg atttccaagt  | 960  |
| ctccacccca ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg ggactttcca   | 1020 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| aaatgtcgta  | acaactccgc  | cccattgacg | caaattggcg | gtaggcgtgt | acggtgggag  | 1080 |
| gtctatataa  | gcagagctcg  | tttagtgaac | cgtcagatca | ctagaagctt | tattgcggtg  | 1140 |
| gtttatcaca  | gttaaatgac  | taacgcagtc | agtgttctg  | acacaacagt | ctcgaactta  | 1200 |
| aggctagagt  | acttaatacg  | actcactata | ggctagttaa | ggctagagtt | cgacgccacc  | 1260 |
| atgcgcgtga  | tgggcatcct  | gcgctcctac | cagcagtggt | ggatctgggg | catcctgggc  | 1320 |
| ttctggatgc  | tgatgatctg  | caacgtgtgg | ggcaacctgt | gggtgaccgt | gtactacggc  | 1380 |
| gtgcccgtgt  | ggaaggaggc  | caagaccacc | ctgttctgcg | cctccgacgc | caaggcccac  | 1440 |
| aaggaggagg  | tgcacaacat  | ctgggccacc | cacgcctgcg | tggccaccga | ccccaacccc  | 1500 |
| caggagatcg  | tgctgaagaa  | cgtgaccgag | aacttcaaca | tgtggaagaa | cgacatgggtg | 1560 |
| gaccagatgc  | acgaggacat  | catctccctg | tgggaccagt | ccctgaagcc | ctgctgtaag  | 1620 |
| ctgaccccc   | tgtgctgac   | cctgaactgc | tccgacgtga | agatcaaggg | caccaacgcc  | 1680 |
| acctacaaca  | acgccacctg  | caacaacaac | aacaccatct | ccgacatgaa | gaactgctcc  | 1740 |
| ttcaacacca  | ccaccgagat  | caccgacaag | aagaagaagg | agtacgccct | gttctacaag  | 1800 |
| ctggacgtgg  | tggccctgga  | cggcaaggag | accaactcca | ccaactcctc | cgagtaccgc  | 1860 |
| ctgatcaact  | gcaacacctc  | cgccgtgacc | caggcctgcc | ccaagggtgc | cttcgacccc  | 1920 |
| atccccatcc  | actactgcgc  | ccccgccggc | tacgccatcc | tgaagtgcaa | caacaagacc  | 1980 |
| ttcaacggca  | ccggccccctg | caacaacgtg | tccaccgtgc | agtgcaccca | cggcatcaag  | 2040 |
| cccgtgggtgt | ccaccagct   | gctgctgaac | ggctccctgg | ccgaggagga | ggtggtgatc  | 2100 |
| cgcttcgaga  | acctgaccaa  | caacgccaag | atcatcatcg | tgcacctgaa | cgagtccgtg  | 2160 |
| gagatcaact  | gcacccgccc  | ctccaacaac | acccgcaagt | ccgtgcgcac | cggccccggc  | 2220 |
| cagaccttct  | tcgccaccgg  | cgacatcatc | ggcgacatcc | gccaggccca | ctgcaacatc  | 2280 |
| tcccgcaaga  | agtggaacac  | cacctgacg  | cgcgtgaagg | agaagctgaa | ggagaagtgc  | 2340 |
| cccaacaaga  | ccatccagtt  | cgccccctcc | tccggcggcg | acctggagat | caccacccac  | 2400 |
| tccttcaact  | gccgcggcga  | gttcttctac | tgctacacct | ccgacctgtt | caactccacc  | 2460 |
| tacatgtcca  | acaacaccgg  | cggcgccaac | atcacctgc  | agtgccgcat | caagcagatc  | 2520 |
| atccgcatgt  | ggcagggcgt  | gggccaggcc | atgtacgcc  | cccccatcgc | cggcaacatc  | 2580 |
| acctgcaagt  | ccaacatcac  | cggcctgctg | ctgacccgcg | acggcggcaa | ggagaagaac  | 2640 |
| gacaccgaga  | ccttccgccc  | cggcgggcgc | gacatgcgcg | acaactggcg | ctccgagctg  | 2700 |
| tacaagtaca  | aggtggtgga  | gatcaagccc | ctgggcatcg | cccccgacaa | ggccaagctg  | 2760 |
| accgtgcagg  | cccgccagct  | gctgtccggc | atcgtgcagc | agcagtccaa | cctgctgcgc  | 2820 |
| gccatcgagg  | cccagcagca  | catgctgcag | ctgaccgtgt | ggggcatcaa | gcagctgcag  | 2880 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| acccgcgtgc  | tggccatcga  | gcgctacctg  | aaggaccagc  | agctgctggg  | catctggggc | 2940 |
| tgctccggca  | agctgatctg  | caccaccgcc  | gtgccctgga  | acgcctcctg  | gtccaacaag | 3000 |
| tcctacgagg  | agatctgggg  | caacatgacc  | tggatgcagt  | gggaccgcga  | gatcaacaac | 3060 |
| tacaccaaca  | ccatctactc  | cctgctggag  | gagtcccaga  | accagcagga  | gaagaacgag | 3120 |
| aaggacctgc  | tggccctgga  | ctcctgggag  | tccctgtggt  | cctgggtcaa  | catcaccaac | 3180 |
| tggtgtggt   | aaggtaacct  | tagagtcgac  | ccgggcggcc  | aaaccgctga  | tcagcctcga | 3240 |
| ctgtgccttc  | tagttgccag  | ccatctgttg  | tttggccctc  | ccccgtgcct  | tccttgaccc | 3300 |
| tggaagggtc  | cactcccact  | gtcctttcct  | aataaaatga  | ggaaattgca  | tcgcattgtc | 3360 |
| tgagtaggtg  | tcattctatt  | ctgggggggtg | gggtggggca  | ggacagcaag  | ggggaggatt | 3420 |
| gggaagacaa  | tagcaggcat  | gctggggatg  | cggtgggctc  | tatggcttct  | gaggcggaaa | 3480 |
| gaaccagcag  | atctgcagat  | ctgaattcat  | ctatgtcggg  | tgcgagagaaa | gaggtaatga | 3540 |
| aatggcatta  | tgggtattat  | gggtctgcat  | taatgaatcg  | gccagatata  | gatatgctgg | 3600 |
| ccaccgtgca  | tgtgacctcg  | cacccccgca  | agacatggcc  | cgagttcgag  | cacaacgtca | 3660 |
| tgacccgatg  | caatgtgcac  | ctgggggtccc | gccgaggcat  | gttcatgccc  | taccagtgc  | 3720 |
| acatgcaatt  | tgtgaagggtg | ctgctggagc  | ccgatgccat  | gtccagagtg  | agcctgacgg | 3780 |
| gggtgtttga  | catgaatgtg  | gagctgtgga  | aaattctgag  | atatgatgaa  | tccaagacca | 3840 |
| ggtgccgggc  | ctgcgaatgc  | ggaggcaagc  | acgccaggct  | tcagcccgtg  | tgtgtggagg | 3900 |
| tgacggagga  | cctgcgaccc  | gatcatttgg  | tgttgtcctg  | caacgggacg  | gagttcggct | 3960 |
| ccagcgggga  | agaatctgac  | tagagtgagt  | agtgtttggg  | ggagggtggag | ggcttgtatg | 4020 |
| aggggacagaa | tgactaaaaat | ctgtgttttt  | ctgtgtgttg  | cagcagcatg  | agcggaagcg | 4080 |
| cctcctttga  | gggaggggta  | ttcagccctt  | atctgacggg  | gcgtctcccc  | tcctgggcgg | 4140 |
| gagtgcgtca  | gaatgtgatg  | ggatccacgg  | tggacggccg  | gcccgtgcag  | cccgcgaact | 4200 |
| cttcaaccct  | gacctacgcg  | accctgagct  | cctcgtccgt  | ggacgcagct  | gccgccgcag | 4260 |
| ctgctgcttc  | cgccgccagc  | gccgtgcgcg  | gaatggccct  | gggcgccggc  | tactacagct | 4320 |
| ctctggtggc  | caactcgact  | tccaccaata  | atcccgccag  | cctgaacgag  | gagaagctgc | 4380 |
| tgctgctgat  | ggcccagctc  | gaggccctga  | cccagcgccct | gggcgagctg  | acccagcagg | 4440 |
| tggctcagct  | gcaggcggag  | acgcgggccc  | cggttgccac  | ggtgaaaacc  | aaataaaaaa | 4500 |
| tgaatcaata  | aataaacgga  | gacggttgtt  | gattttaaca  | cagagtcttg  | aatctttatt | 4560 |
| tgatttttcg  | cgcgcggtag  | gccctggacc  | accggtctcg  | atcattgagc  | acccggtgga | 4620 |
| ttttttccag  | gacccggtag  | aggtgggctt  | ggatgttgag  | gtacatgggc  | atgagcccgt | 4680 |
| cccggggggtg | gaggtagctc  | cattgcaggg  | cctcgtgctc  | gggggtgggtg | ttgtaaatca | 4740 |
| cccagtcata  | gcagggggcg  | agggcggtgt  | gctgcacgat  | gtccttgagg  | aggagactga | 4800 |

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|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| tggccacggg | cagccccttg | gtgtaggtgt  | tgacgaacct  | gttgagctgg | gagggatgca  | 4860 |
| tgcgggggga | gatgagatgc | atcttggcct  | ggatcttgag  | attggcgatg | ttcccgccca  | 4920 |
| gatcccgccg | ggggttcatg | ttgtgcagga  | ccaccagcac  | ggtgtatccg | gcgcacttgg  | 4980 |
| ggaatttgtc | atgcaacttg | gaagggaagg  | cgtgaaagaa  | tttggagacg | cccttgtgac  | 5040 |
| cgcccagggt | ttccatgcac | tcatccatga  | tgatggcgat  | gggcccgtgg | gcggcggcct  | 5100 |
| gggcaaagac | gtttcggggg | tcggacacat  | cgtagtgtg   | gtcctgggtg | agctcgtcat  | 5160 |
| aggccatttt | aatgaatttg | gggcggaggg  | tgcccgactg  | ggggacgaag | gtgccctcga  | 5220 |
| tcccgggggc | gtagttgccc | tcgcagatct  | gcctctccca  | ggccttgagc | tcggaggggg  | 5280 |
| ggatcatgtc | cacctgcggg | gcgatgaaaa  | aaacggtttc  | cggggcgggg | gagatgagct  | 5340 |
| gggccgaaag | caggttccgg | agcagctggg  | acttgccgca  | gccggtgggg | ccgtagatga  | 5400 |
| ccccgatgac | cggctgcagg | tggtagtga   | gggagagaca  | gctgccgtcc | tcgcggagga  | 5460 |
| ggggggccac | ctcgttcac  | atctcgcgca  | catgcatgtt  | ctcgcgcacg | agttccgccca | 5520 |
| ggaggcgctc | gccccccagc | gagaggagct  | cttgacgca   | ggcgaagttt | ttcagcggct  | 5580 |
| tgagyccgtc | ggccatgggc | attttggaga  | gggtctgttg  | caagagttcc | agacggtccc  | 5640 |
| agagctcggg | gatgtgctct | agggcatctc  | gatccagcag  | acctcctcgt | ttcgcggggt  | 5700 |
| ggggcgactg | cgggagtagg | gcaccaggcg  | atgggcgtcc  | agcgaggcca | gggtccggtc  | 5760 |
| cttccagggt | cgcagggtcc | gcgtcagcgt  | ggtctccgtc  | acggtgaagg | ggtgcgcgcc  | 5820 |
| gggctgggcg | cttgcgaggg | tgcgcttcag  | gctcatccgg  | ctggtcgaga | accgctcccg  | 5880 |
| gtcggcgccc | tgcgcgtcgg | ccaggtagca  | attgagcatg  | agttcgtagt | tgagcgcctc  | 5940 |
| ggccgcgtgg | cccttggcgc | ggagcttacc  | tttggaaagt  | tgtccgcaga | cgggacagag  | 6000 |
| gagggacttg | agggcgtaga | gcttgggggg  | gaggaagacg  | gactcggggg | cgtaggcgtc  | 6060 |
| cgcgccgcag | ctggcgcaga | cggctctcga  | ctccacgagc  | caggtagagt | cgggccgggt  | 6120 |
| ggggtcaaaa | acgaggtttc | ctccgtgctt  | tttgatgcgt  | ttcttacctc | tgggtctccat | 6180 |
| gagctcgtgt | ccccgctggg | tgacaaaagag | gctgtccgtg  | tccccgtaga | ccgactttat  | 6240 |
| gggccgggtc | tcgagcgggg | tgccgcggtc  | ctcgtcgtag  | aggaaccccc | cccactccga  | 6300 |
| gacgaaggcc | cgggtccagg | ccagcacgaa  | ggaggccacg  | tgggaggggt | agcggtcgtt  | 6360 |
| gtccaccagc | gggtccacct | tctccagggt  | atgcaagcac  | atgtccccct | cgtccacatc  | 6420 |
| caggaagggt | attggcttgt | aagtgtaggc  | cacgtgaccg  | ggggtcccgg | ccgggggggt  | 6480 |
| ataaaagggg | gcgggcccct | gctcgtcctc  | actgtcttcc  | ggatcgctgt | ccaggagcgc  | 6540 |
| cagctgttgg | ggtaggattt | ccctctcgaa  | ggctggcata  | acctcggcac | tcaggttgtc  | 6600 |
| agtttctaga | aacgaggagg | atttgatatt  | gacgggtgccg | ttggagacgc | ctttcatgag  | 6660 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cccctcgtcc atctgggtcag aaaagacgat ctttttgttg tcgagcttgg tggcgaagga  | 6720 |
| gccgtagagg gcgttggaga ggagcttggc gatggagcgc atgggtctggt tcttttcctt  | 6780 |
| gtcggcgcg ctccttggcgg cgatgttgag ctgcacgtac tcgcgcgcca cgcacttcca   | 6840 |
| ttcggggaag acggtggtga gctcgtcggg cacgattctg acccgccagc cgcggttgtg   | 6900 |
| cagggtgatg aggtccacgc tgggtggccac ctcgccgcgc aggggctcgt tgggtccagca | 6960 |
| gaggcgcccc cccttgcgcg agcagaaggg gggcagcggg tccagcatga gctcgtcggg   | 7020 |
| ggggtcggcg tccacggtga agatgccggg cagaagctcg gggtcgaagt agctgatgca   | 7080 |
| ggtgtccaga tcgtccagcg ccgcttgcca gtcgcgcacg gccagcgcgc gctcgtaggg   | 7140 |
| gctgagggggc gtgccccagg gcatgggggtg cgtgagcgcg gaggcgtaca tgccgcagat | 7200 |
| gtcgtagacg tagaggggct cctcgaggac gccgatgtag gtggggtagc agcgcccccc   | 7260 |
| gcggatgctg gcgcgcacgt agtcgtacag ctcgtgcgag ggcgcgagga gccccgtgcc   | 7320 |
| gaggttggag cgttgcggct tttcggcgcg gtagacgacg tggcggaaga tggcgtggga   | 7380 |
| gttggaggag atgggtgggccc tctggaagat gttgaagtgg gcgtggggca ggccgaccga | 7440 |
| gtccctgatg aagtgggctg aggagtcctg cagcttggcg acgagctcgg cggtgacgag   | 7500 |
| gacgtccagg gcgcagtagt cgaggggtctc ttggatgatg tcgtacttga gctggccctt  | 7560 |
| ctgcttccac agctcgcggt tgagaaggaa ctcttcgcgg tccttccagt actcttcgag   | 7620 |
| ggggaacccg tcctgatcgg cacggttaaga gcccaccatg tagaactggt tgacggcctt  | 7680 |
| gtaggcgag cagcccttct ccacggggag ggcgtaagct tgtgcggcct tgcgcagga     | 7740 |
| ggtgtgggtg agggcggaagg tgtcgcgcac catgaccttg aggaactggt gcttgaagtc  | 7800 |
| gaggtcgtcg cagccgccct gctcccagag ctggaagtcc gtgcgcttct tgtaggcggg   | 7860 |
| gttgggcaaa gcgaaagtaa catcgttgaa gaggatcttg cccgcgcggg gcatgaagtt   | 7920 |
| gcgagtgatg cggaaaggct ggggcacctc ggcccgggtg ttgatgacct gggcggcgag   | 7980 |
| gacgatctcg tcgaagccgt tgatgttgtg cccgacgatg tagagttcca cgaatcgcgg   | 8040 |
| gcggccctta acgtggggca gcttcttgag ctcgtcgtag gtgagctcgg cggggtcgt    | 8100 |
| gagcccgtgc tgctcgaggg ccagtcggc gacgtggggg ttggcgctga ggaaggaagt    | 8160 |
| ccagagatcc acggccaggg cggtctgcaa gcggtcccgg tactgacgga actgctggcc   | 8220 |
| cacggccatt ttttcggggg tgacgcagta gaagggtcgg gggtcgccgt gccagcggtc   | 8280 |
| ccacttgagc tggagggcga ggtcgtgggc gagctcgacg agcggcgggt ccccgagag    | 8340 |
| tttcatgacc agcatgaagg ggacgagctg cttgccgaag gaccccatcc aggtgtaggt   | 8400 |
| ttccacatcg taggtgagga agagcctttc ggtgcgagga tgcgagccga tggggaagaa   | 8460 |
| ctggatctcc tgccaccagt tggaggaatg gctgttgatg tgatggaagt agaaatgccg   | 8520 |
| acggcgcgcc gagcactcgt gcttgtgttt atacaagcgt ccgcagtgct cgcaacgctg   | 8580 |

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|             |             |            |            |            |             |       |
|-------------|-------------|------------|------------|------------|-------------|-------|
| cacgggatgc  | acgtgctgca  | cgagctgtac | ctgggttcct | ttgacgagga | atttcagtgg  | 8640  |
| gcagtggagc  | gctggcggct  | gcatctggtg | ctgtactacg | tcctggccat | cggcgtggcc  | 8700  |
| atcgtctgcc  | tcgatggtgg  | tcatgctgac | gagcccgcgc | gggaggcagg | tccagacttc  | 8760  |
| ggctcggacg  | ggtcggagag  | cgaggacgag | ggcgcgcagg | ccggagctgt | ccagggtcct  | 8820  |
| gagacgctgc  | ggagtcaggt  | cagtgggcag | cggcggcgcg | cggttgactt | gcaggagctt  | 8880  |
| ttccagggcg  | cgcgggaggt  | ccagatggta | cttgatctcc | acggcgccgt | tggtaggcgac | 8940  |
| gtccacggct  | tgcagggtcc  | cgtgcccctg | gggcgccacc | accgtgcccc | gtttcttctt  | 9000  |
| gggcgctgct  | tccatgccgg  | tcagaagcgg | cggcgaggac | gcgcgccggg | cggcaggggc  | 9060  |
| ggctcgggac  | ccggaggcag  | gggcggcagg | ggcacgtcgg | cgccgcgcgc | gggcaggttc  | 9120  |
| tggtagtcg   | cccggagaag  | actggcgtga | gcgacgacgc | gacggttgac | gtcctggatc  | 9180  |
| tgacgcctct  | gggtgaaggc  | cacgggaccc | gtgagtttga | acctgaaaga | gagttcgaca  | 9240  |
| gaatcaatct  | cggtatcgtt  | gacggcggcc | tgccgcagga | tctcttgcac | gtcgcccag   | 9300  |
| ttgtcctggt  | aggcgatctc  | ggtcataaac | tgctcgatct | cctcctcctg | aaggctctccg | 9360  |
| cggccggcgc  | gctcgacggt  | ggccgcgagg | tcgttggaga | tgcggcccat | gagctgcgag  | 9420  |
| aaggcggttca | tgccggcctc  | gttccagacg | cggctgtaga | ccacggctcc | gtcggggtcg  | 9480  |
| cgcgcgcgca  | tgaccacctg  | ggcgagggtg | agctcgacgt | ggcgcgtgaa | gaccgcgtag  | 9540  |
| ttgcagaggc  | gctggttagag | gtagttgagc | gtggtggcga | tgtgctcggg | gacgaagaag  | 9600  |
| tacatgatcc  | agcggcggag  | cgcatctctg | ctgacgtcgc | ccagggttc  | caagcgctcc  | 9660  |
| atggcctcgt  | agaagtccac  | ggcgaagttg | aaaaactggg | agttgcgcgc | cgagacggtc  | 9720  |
| aactcctcct  | ccagaagacg  | gatgagctca | gcgatggtgg | cgcgcacctc | gcgctcgaag  | 9780  |
| gccccggggg  | gctcctcttc  | ttccatctct | tcctcctcca | ctaactctc  | ttctacttcc  | 9840  |
| tcctcaggag  | gcggcggcgg  | gggagggggc | ctgcgtcgcc | ggcggcgcac | gggcagacgg  | 9900  |
| tcgatgaagc  | gctcgatggt  | ctccccgcgc | cggcgacgca | tggctctcgg | gacggcgcgc  | 9960  |
| ccgtcctcgc  | ggggccgcag  | cgtgaagacg | ccgccgcgca | tctccagggt | gccgccgggg  | 10020 |
| gggtctccgt  | tgggcaggga  | gagggcgctg | acgatgcac  | ttatcaattg | gcccgtaggg  | 10080 |
| actccgcgca  | aggacctgag  | cgtctcgaga | tccacgggat | ccgaaaaccg | ctgaacgaag  | 10140 |
| gcttcgagcc  | agtcgcagtc  | gcaaggtagg | ctgagcccgg | tttcttggtc | ttcggggatt  | 10200 |
| tcgggaggcg  | ggcgggcgat  | gctgctggtg | atgaagttga | agtaggcggg | cctgagacgg  | 10260 |
| cggatggtgg  | cgaggagcac  | caggtccttg | ggcccggctt | gctggatgcg | cagacggtcg  | 10320 |
| gccatgcccc  | aggcgtggtc  | ctgacacctg | gcgaggtcct | tgtagtagtc | ctgcatgagc  | 10380 |
| cgctccacgg  | gcacctcctc  | ctcgcggcgc | cggccgtgca | tgcgcgtgag | cccgaacccg  | 10440 |

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|             |            |             |            |             |             |       |
|-------------|------------|-------------|------------|-------------|-------------|-------|
| cgctggggct  | ggacgagcgc | caggtcggcg  | acgacgcgct | cggcgaggat  | ggcctgctgt  | 10500 |
| atctgggtga  | gggtggtctg | gaagtcgtcg  | aagtcgacga | agcggtggtg  | ggctccggtg  | 10560 |
| ttgatggtat  | aggagcagtt | ggccatgacg  | gaccagttga | cggctctggtg | gccgggtcgc  | 10620 |
| acgagctcgt  | ggtacttgag | gcgcgagtag  | gcgcgcgtgt | cgaagatgta  | gtcgttgacg  | 10680 |
| gtgcgcacga  | ggtactggta | tccgacgagg  | aagtgcggcg | gcggctggcg  | gtagagcggc  | 10740 |
| catcgctcgg  | tggcgggggc | gccgggcgcg  | aggtcctcga | gcatgaggcg  | gtggtagccg  | 10800 |
| tagatgtacc  | tggacatcca | ggtgatgccg  | gcggcggtgg | tggaggcgcg  | cgggaactcg  | 10860 |
| cggacgcggt  | tccagatggt | gcgcagcggc  | aggaagtagt | tcatggtggc  | cgcggtctgg  | 10920 |
| cccgtgaggc  | gcgcgcagtc | gtggatgctc  | tagacatacg | ggcaaaaacg  | aaagcgggtca | 10980 |
| gcggctcgac  | tccgtggcct | ggaggctaag  | cgaacggggt | gggctgcgcg  | tgtaccccg   | 11040 |
| ttcgaatctc  | gaatcaggct | ggagccgcag  | ctaactgtgt | actggcactc  | ccgtctcgac  | 11100 |
| ccaagcctgc  | taacgaaacc | tccaggatac  | ggaggcgggt | cgttttttgg  | ccttggtcgc  | 11160 |
| tggcatgaa   | aaactagtaa | gcgcggaaaag | cgaccgccc  | cgatggctcg  | ctgccgtagt  | 11220 |
| ctggagaaaag | aatcgccagg | gttgcgttgc  | ggtgtgcccc | ggttcgagcc  | tcagcgctcg  | 11280 |
| gcgccggccg  | gattccgcgg | ctaactgtgg  | cgtggctgcc | ccgtcgtttc  | caagaccct   | 11340 |
| tagccagccg  | acttctccag | ttacggagcg  | agcccctctt | tttcttgtgt  | ttttgccaga  | 11400 |
| tgcaccccg   | actgcggcag | atgcgcccc   | accctccacc | tcaaccgccc  | ctaccgccc   | 11460 |
| agcagcagca  | acagccggcg | cttctgcccc  | cgccccagca | gcagccagcc  | actaccgcg   | 11520 |
| cggccgccc   | gagcggagcc | ggcggttcagt | atgacctggc | cttgggaagag | ggcgaggggc  | 11580 |
| tggcgcggct  | gggggcgtcg | tcgccggagc  | ggcaccgcg  | cgtgcagatg  | aaaagggacg  | 11640 |
| ctcgcgaggc  | ctacgtgccc | aagcagaacc  | tggtcagaga | caggagcggc  | gaggagccc   | 11700 |
| aggagatgcg  | cgcctcccgc | ttccacgcgg  | ggcgggagct | gcggcgcggc  | ctggaccgaa  | 11760 |
| agcgggtgct  | gagggacgag | gatttcgagg  | cggacgagct | gacggggatc  | agccccgcgc  | 11820 |
| gcgcgcacgt  | ggccgcggcc | aacctggtca  | cggcgtagca | gcagaccgtg  | aaggaggaga  | 11880 |
| gcaacttcca  | aaaatccttc | aacaaccacg  | tgcgcacgct | gatcgcgcgc  | gaggaggtga  | 11940 |
| ccctgggcct  | gatgcacctg | tgggacctgc  | tggaggccat | cgtgcagaac  | cccacgagca  | 12000 |
| agccgctgac  | ggcgcagctg | tttctggtgg  | tgcagcacag | tcgggacaac  | gagacgttca  | 12060 |
| gggaggcgct  | gctgaatatc | accgagccc   | agggccgctg | gctcctggac  | ctggtgaaca  | 12120 |
| ttctgcagag  | catcggtgtg | caggagcgcg  | ggctgccgct | gtccgagaag  | ctggcggcta  | 12180 |
| tcaacttctc  | ggtgctgagc | ctgggcaagt  | actacgctag | gaagatctac  | aagaccccg   | 12240 |
| acgtgccc    | agacaaggag | gtgaagatcg  | acgggtttta | catgcgcatg  | accctgaaa   | 12300 |
| tgctgaccct  | gagcgacgat | ctgggggtgt  | accgcaacga | caggatgcac  | cgcgcggtga  | 12360 |

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|             |            |             |             |            |            |       |
|-------------|------------|-------------|-------------|------------|------------|-------|
| gcgccagccg  | ccggcgcgag | ctgagcgacc  | aggagctgat  | gcacagcctg | cagcgggccc | 12420 |
| tgaccggggc  | cgggaccgag | ggggagagct  | actttgacat  | gggcgcggac | ctgcgctggc | 12480 |
| agcccagccg  | ccgggccttg | gaagctgccg  | gcggttcccc  | ctacgtggag | gaggtggacg | 12540 |
| atgaggagga  | ggagggcgag | tacctggaag  | actgatggcg  | cgaccgtatt | tttgctagat | 12600 |
| gcagcaacag  | ccaccgcctc | ctgatccccg  | gatgcggggc  | gcgctgcaga | gccagccgtc | 12660 |
| cggcattaac  | tcctcggacg | attggaccca  | ggccatgcaa  | cgcacatgg  | cgctgacgac | 12720 |
| ccgcaatccc  | gaagccttta | gacagcagcc  | tcaggccaac  | cggctctcgg | ccatcctgga | 12780 |
| ggccgtgggtg | ccctcgcgct | cgaacccccac | gcacgagaag  | gtgctggcca | tcgtgaacgc | 12840 |
| gctggtggag  | aacaaggcca | tccgcggcga  | cgaggccggg  | ctggtgtaca | acgcgctgct | 12900 |
| ggagcgcgtg  | gcccgtaca  | acagcaccaa  | cgtgcagacg  | aacctggacc | gcatggtgac | 12960 |
| cgacgtgcg   | gaggcggtgt | cgcagcgca   | gcggttccac  | cgcgagtcga | acctgggctc | 13020 |
| catggtggcg  | ctgaacgcct | tcctgagcac  | gcagcccggc  | aacgtgcccc | ggggccagga | 13080 |
| ggactacacc  | aacttcac   | gcgcgctgcg  | gctgatgggtg | gccgaggtgc | cccagagcga | 13140 |
| ggtgtaccag  | tcggggccgg | actacttctt  | ccagaccagt  | cgccagggt  | tgcagaccgt | 13200 |
| gaacctgagc  | caggctttca | agaacttgca  | gggactgtgg  | ggcgtgcagg | ccccggtcgg | 13260 |
| ggaccgcgcg  | acggtgtcga | gcctgctgac  | gccgaactcg  | cgctgctgc  | tgctgctggt | 13320 |
| ggcgcccttc  | acggacagcg | gcagcgtgag  | ccgcgactcg  | tacctgggct | acctgcttaa | 13380 |
| cctgtaccgc  | gaggccatcg | ggcaggcgca  | cgtggacgag  | cagacctacc | aggagatcac | 13440 |
| ccacgtgagc  | cgcgcgctgg | gccaggagga  | cccgggcaac  | ctggaggcca | ccctgaactt | 13500 |
| cctgctgacc  | aaccggtcgc | agaagatccc  | gccccagtac  | gcgctgagca | ccgaggagga | 13560 |
| gcgcacacctg | cgctacgtgc | agcagagcgt  | ggggctgttc  | ctgatgcagg | agggggccac | 13620 |
| gcccagcgcc  | gcgctcgaca | tgaccgcgcg  | caacatggag  | cccagcatgt | acgctcgcaa | 13680 |
| ccgcccgttc  | atcaataagc | tgatggacta  | cttgcatcgg  | gcggccgcca | tgaactcgga | 13740 |
| ctactttacc  | aacgccatct | tgaacccgca  | ctggctccccg | ccgcccgggt | tctacacggg | 13800 |
| cgagtacgac  | atgcccgacc | ccaacgacgg  | gttcctgtgg  | gacgacgtgg | acagcagcgt | 13860 |
| gttctcgccg  | cgccccgcca | ccaccgtgtg  | gaagaaagag  | ggcggggacc | ggcgccgctc | 13920 |
| ctcggcgctg  | tccggtcgcg | cgggtgctgc  | gcggcggtg   | cctgaggccg | ccagcccctt | 13980 |
| cccagacctg  | cccttttcgc | tgaacagcgt  | gcgcagcagc  | gagctgggtc | ggctgacgcg | 14040 |
| gccgcgcctg  | ctgggcgagg | aggagtacct  | gaacgactcc  | ttgttgaggc | ccgagcgca  | 14100 |
| gaagaacttc  | cccaataacg | ggatagagag  | cctggtggac  | aagatgagcc | gctggaagac | 14160 |
| gtacgcgcac  | gagcacaggg | acgagccccg  | agctagcagc  | agcgcaggca | cccgtagacg | 14220 |

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|             |             |             |             |             |             |       |
|-------------|-------------|-------------|-------------|-------------|-------------|-------|
| ccagcgacac  | gacaggcagc  | ggggtctggt  | gtgggacgat  | gaggattccg  | ccgacgacag  | 14280 |
| cagcgtgttg  | gacttgggtg  | ggagtgggtg  | tggtaacccg  | ttcgctcact  | tgcgcccccg  | 14340 |
| tatcggggcg  | ctgatgtaag  | aatctgaaaa  | aataaaaaaac | ggtactcacc  | aaggccatgg  | 14400 |
| cgaccagcgt  | gcgttcttct  | ctgttgtttg  | tagtagtatg  | atgaggcgcg  | tgtacccgga  | 14460 |
| gggtcctcct  | ccctcgtacg  | agagcgtgat  | gcagcaggcg  | gtggcggcgg  | cgatgcagcc  | 14520 |
| cccgtggag   | gcgccttacg  | tgcccccgcg  | gtacctggcg  | cctacggagg  | ggcggaacag  | 14580 |
| cattcggtac  | tcggagctgg  | cacccttgta  | cgataccacc  | cggttggtacc | tgggtggacaa | 14640 |
| caagtcggcg  | gacatcgccct | cgctgaacta  | ccagaacgac  | cacagcaact  | tcctgaccac  | 14700 |
| cgtggtgacg  | aacaacgatt  | tcacccccac  | ggaggccagc  | accagacca   | tcaactttga  | 14760 |
| cgagcgctcg  | cggtggggcg  | gccagctgaa  | aaccatcatg  | cacaccaaca  | tgcccaacgt  | 14820 |
| gaacgagttc  | atgtacagca  | acaagttcaa  | ggcgcgggtg  | atggtctcgc  | gcaagacccc  | 14880 |
| caatggggtc  | gcggtggatg  | agaattatga  | tggtagtcag  | gacgagctga  | cttacgagtg  | 14940 |
| ggtggagttt  | gagctgcccc  | agggcaactt  | ctcggtgacc  | atgaccatcg  | atctgatgaa  | 15000 |
| caacgccatc  | atcgacaact  | acttggcggg  | ggggcgtcag  | aacgggggtg  | tggagagcga  | 15060 |
| catcggcggtg | aagttcgaca  | cgcgcaactt  | ccggctgggc  | tgggaccccc  | tgaccgagct  | 15120 |
| ggtgatgccg  | ggcgtgtaca  | ccaacgaggc  | cttccacccc  | gacatcgccc  | tgctgccccg  | 15180 |
| ctgcggcggtg | gacttcaccg  | agagccgcct  | cagcaacctg  | ctgggcatcc  | gcaagcggca  | 15240 |
| gcccttccag  | gagggcttcc  | agatcctgta  | cgaggacctg  | gaggggggca  | acatccccgc  | 15300 |
| gctcttggat  | gtcgaagcct  | atgagaaaaag | caaggaggag  | gccgccgcag  | cggcgaccgc  | 15360 |
| agccgtggcc  | accgcctcta  | ccgagggtgcg | gggcgataat  | tttgctagcg  | ccgcggcagt  | 15420 |
| ggccgaggcg  | gctgaaaccg  | aaagtaagat  | agtcatccag  | ccggtggaga  | aggacagcaa  | 15480 |
| ggacaggagc  | tacaacgtgc  | tcgcggacaa  | gaaaaacacc  | gcctaccgca  | gctggtacct  | 15540 |
| ggcctacaac  | tacggcgacc  | ccgagaaggg  | cgtgcgctcc  | tggacgctgc  | tcaccacctc  | 15600 |
| ggacgtcacc  | tgccggcgtg  | agcaagtcta  | ctggtcgtcg  | cccgacatga  | tgcaagaccc  | 15660 |
| ggtcaccttc  | cgctccacgc  | gtcaagttag  | caactaccgc  | gtggtgggcg  | ccgagctcct  | 15720 |
| gcccgtctac  | tccaagagct  | tcttcaacga  | gcaggccgtc  | tactcgcagc  | agctgcgcgc  | 15780 |
| cttcacctcg  | ctcacgcacg  | tcttcaaccg  | cttccccgag  | aaccagatcc  | tcgtccgccc  | 15840 |
| gcccgcgccc  | accattacca  | ccgtcagtga  | aaacgttcct  | gctctcacag  | atcacgggac  | 15900 |
| cctgccgctg  | cgcagcagta  | tccgggggag  | ccagcgcgtg  | accgtcactg  | acgccagacg  | 15960 |
| ccgcacctgc  | ccctacgtct  | acaaggccct  | gggcgtagtc  | gcgccgcgcg  | tcctctcgag  | 16020 |
| ccgcaccttc  | taaaaaatgt  | ccattctcat  | ctcgcccagt  | aataacaccg  | gttggggcct  | 16080 |
| gcgcgcgccc  | agcaagatgt  | acggaggcgc  | tcgccaacgc  | tccacgcaac  | accccggtgcg | 16140 |



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|             |             |             |            |            |            |       |
|-------------|-------------|-------------|------------|------------|------------|-------|
| cgtgcgcggg  | cacttccgcg  | ctccctgggg  | cgccctcaag | ggccgcgtgc | gctcgcgcac | 16200 |
| caccgtcgcg  | gacgtgatcg  | accaggtggg  | ggccgacgcg | cgcaactaca | cgcccggccg | 16260 |
| cgcgcccgcc  | tccaccgtgg  | acgccgtcat  | cgacagcgtg | gtggccgatg | cgcgccggta | 16320 |
| cgcccgcgcc  | aagagccggc  | ggcggcgcat  | cgcccggcgg | caccggagca | cccccgccat | 16380 |
| gcgcgcggcg  | cgagccttgc  | tgcgcagggc  | caggcgcacg | ggacgcaggg | ccatgctcag | 16440 |
| ggcggccaga  | cgcgcgccct  | ccggcagcag  | cagcgccggc | aggacccgca | gacgcgcggc | 16500 |
| cacggcggcg  | gcggcgggca  | tcgccagcat  | gtcccggccg | cggcgcggca | acgtgtactg | 16560 |
| ggtgcgcgac  | gccgccaccg  | gtgtgcgcgt  | gcccgtgcgc | acccgcccc  | ctcgcacttg | 16620 |
| aagatgctga  | cttcgcgatg  | ttgatgtgtc  | ccagcggcga | ggaggatgtc | caagcgcaaa | 16680 |
| tacaaggaag  | agatgctcca  | ggatcatcgc  | cctgagatct | acggccccgc | ggtgaaggag | 16740 |
| gaaagaaagc  | cccgcaaaact | gaagcgggtc  | aaaaaggaca | aaaaggagga | ggaagatgtg | 16800 |
| gacggactgg  | tggagtttgt  | gcgcgagttc  | gcccccgccg | ggcgcgtgca | gtggcgcggg | 16860 |
| cggaaagtga  | aaccggtgct  | gcggccccgc  | accacggtgg | tcttcacgcc | cggcgagcgt | 16920 |
| tccggctccg  | cctccaagcg  | ctcctacgac  | gaggtgtacg | gggacgagga | catcctcgag | 16980 |
| caggcggtcg  | agcgtctggg  | cgagtttgct  | tacggcaagc | gcagccgccc | cgcgcccttg | 17040 |
| aaagaggagg  | cgggtgtccat | cccgtgggac  | cacggcaacc | ccacgccgag | cctgaagccg | 17100 |
| gtgaccttgc  | agcaggtgct  | gccgagcgcg  | gcgccgcgcc | ggggcttcaa | gcgcgagggc | 17160 |
| ggcgaggatc  | tgtacccgac  | catgcagctg  | atggtgcccc | agcgccagaa | gctggaggac | 17220 |
| gtgctggagc  | acatgaaggt  | ggacccccgag | gtgcagcccg | aggtcaaggt | gcggcccatc | 17280 |
| aagcaggtgg  | ccccgggcct  | gggcgtgcag  | accgtggaca | tcaagatccc | cacggagccc | 17340 |
| atggaaaacgc | agaccgagcc  | cgtgaagccc  | agcaccagca | ccatggaggt | gcagacggat | 17400 |
| ccctggatgc  | cggcgccggc  | ttccaccact  | cgccgaagac | gcaagtacgg | cgcgccagc  | 17460 |
| ctgctgatgc  | ccaactacgc  | gctgcacatc  | tccatcatcc | ccacgccggg | ctaccgcggc | 17520 |
| acgcgcttct  | accgcggcta  | caccagcagc  | cgccgcaaga | ccaccacccg | ccgccgccgt | 17580 |
| cgtcgcaccc  | gccgcagcag  | caccgcgact  | tccgccgccg | ccctggtgcy | gagagtgtac | 17640 |
| cgcagcgggc  | gcgagcctct  | gaccttgccg  | cgcgcgcgct | accacccgag | catcgccatt | 17700 |
| taactctgcc  | gtcgcctcct  | acttgagat   | atggccctca | catgccgcct | ccgcgtcccc | 17760 |
| attacgggct  | accgaggaag  | aaagccgcgc  | cgtagaaggc | tgacggggaa | cgggctgcgt | 17820 |
| cgccatcacc  | accggcggcg  | gcgcgccatc  | agcaagcggt | tggggggagg | cttcctgccc | 17880 |
| gcgctgatcc  | ccatcatcgc  | cgcggcgatc  | ggggcgatcc | ccggcatagc | ttccgtggcg | 17940 |
| gtgcaggcct  | ctcagcgcca  | ctgagacaca  | gcttggaata | tttgtaataa | aaaaatggac | 18000 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |            |            |            |       |
|-------------|-------------|------------|------------|------------|------------|-------|
| tgacgctcct  | ggtcctgtga  | tgtgtgtttt | tagatggaag | acatcaattt | ttcgtccctg | 18060 |
| gcaccgcgac  | acggcacgcg  | gccgtttatg | ggcacctgga | gcgacatcgg | caacagccaa | 18120 |
| ctgaacgggg  | gcgccttcaa  | ttggagcagt | ctctggagcg | ggcttaagaa | tttcgggtcc | 18180 |
| acgctcaaaa  | cctatggcaa  | caaggcgtgg | aacagcagca | cagggcaggc | gctgagggaa | 18240 |
| aagctgaaaag | agcagaactt  | ccagcagaag | gtggtcgatg | gcctggcctc | gggcatcaac | 18300 |
| gggggtggtg  | acctggccaa  | ccaggccgtg | cagaaacaga | tcaacagccg | cctggacgcg | 18360 |
| gtcccgcgcc  | cgggggtccgt | ggagatgccc | caggtggagg | aggagctgcc | tcccctggac | 18420 |
| aagcgcggcg  | acaagcgacc  | gcgtcccgac | gcggaggaga | cgctgctgac | gcacacggac | 18480 |
| gagccgcccc  | cgtacgagga  | ggcggtgaaa | ctgggtctgc | ccaccacgcg | gcccgtggcg | 18540 |
| cctctggcca  | ccgggggtgct | gaaacccagc | agcagcagcc | agcccgcgac | cctggacttg | 18600 |
| cctccgcctg  | cttcccgccc  | ctccacagtg | gctaagcccc | tgccgccggt | ggccgtcgcg | 18660 |
| tcgcgcgccc  | cccgaggccg  | cccccaggcg | aactggcaga | gcactctgaa | cagcatcgtg | 18720 |
| ggtctgggag  | tgcagagtgt  | gaagcgccgc | cgctgctatt | aaaagacact | gtagcgctta | 18780 |
| acttgcttgt  | ctgtgtgtat  | atgtatgtcc | gccgaccaga | aggaggaaga | ggcgcgtcgc | 18840 |
| cgagttgcaa  | gatggccacc  | ccatcgatgc | tgccccagtg | ggcgtacatg | cacatcgccg | 18900 |
| gacaggacgc  | ttcggagtac  | ctgagtccgg | gtctggtgca | gttcgccccg | gccacagaca | 18960 |
| cctacttcag  | tctggggaac  | aagtttagga | accccacggt | ggcgcggcac | cacgatgtga | 19020 |
| ccaccgaccg  | cagccagcgg  | ctgacgtgct | gcttcgtgcc | cgtggaccgc | gaggacaaca | 19080 |
| cctactcgta  | caaagtgcgc  | tacacgctgg | ccgtgggcga | caaccgcgtg | ctggacatgg | 19140 |
| ccagcaccta  | ctttgacatc  | cgcggcgtgc | tggatcgggg | gcccagcttc | aaaccctact | 19200 |
| ccggcaccgc  | ctacaacagc  | ctggctccca | agggagcgcc | caacacttgc | cagtggacat | 19260 |
| ataaagctgg  | tgatactgat  | acagaaaaaa | cctatacata | tggaaatgca | cctgtgcaag | 19320 |
| gcattagcat  | tacaaaaggat | ggtattcaac | ttggaactga | cagcgatggg | caggcaatct | 19380 |
| atgcagacga  | aacttatcaa  | ccagagcctc | aagtgggtga | tgctgaatgg | catgacatca | 19440 |
| ctggtactga  | tgaaaaatat  | ggaggcagag | ctcttaagcc | tgacaccaaa | atgaagcctt | 19500 |
| gctatggttc  | ttttgccaaag | cctaccaata | aagaaggagg | ccaggcaaag | gtgaaaaccg | 19560 |
| aaacaggcgg  | taccaaagaa  | tatgacattg | acatggcatt | cttcgataat | cgaagtgcag | 19620 |
| ctgccgccgg  | cctagcccca  | gaaattgttt | tgtatactga | gaatgtggat | ctggaaactc | 19680 |
| cagataccca  | tattgtatac  | aaggcaggta | cagatgacag | tagctcttct | atcaatttgg | 19740 |
| gtcagcagtc  | catgcccac   | agacccaact | acattggctt | cagagacaac | tttatcggtc | 19800 |
| tgatgtacta  | caacagcact  | ggcaatatgg | gtgtactggc | tggacaggcc | tcccagctga | 19860 |
| atgctgtggt  | ggacttgacg  | gacagaaaac | ccgaactgtc | ctaccagctc | ttgcttgact | 19920 |

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|            |            |             |             |             |            |       |
|------------|------------|-------------|-------------|-------------|------------|-------|
| ctctgggtga | cagaaccagg | tatttcagta  | tgtggaatca  | ggcggtaggac | agttatgacc | 19980 |
| ccgatgtgcg | cattattgaa | aatcacgggtg | tggaggatga  | acttcctaac  | tattgcttcc | 20040 |
| ccctggatgc | tgtgggtaga | actgatactt  | accagggaat  | taaggccaat  | ggtgataatc | 20100 |
| aaaccacctg | gaccaaagat | gatactgtta  | atgatgctaa  | tgaattgggc  | aagggcaatc | 20160 |
| ctttcgccat | ggagatcaac | atccaggcca  | acctgtggcg  | gaacttcctc  | tacgcgaacg | 20220 |
| tggcgctgta | cctgcccgc  | tcctacaagt  | acacgccggc  | caacatcacg  | ctgcccacca | 20280 |
| acaccaacac | ctacgattac | atgaacggcc  | gcgtgggtgg  | gccctcgctg  | gtggacgcct | 20340 |
| acatcaacat | cggggcgcg  | tggtcgctgg  | accccatgga  | caacgtcaac  | cccttcaacc | 20400 |
| accaccgcaa | cgcgggcctg | cgataccgct  | ccatgctcct  | gggcaacggg  | cgctacgtgc | 20460 |
| ccttccacat | ccagggtgcc | caaaagtitt  | tcgccatcaa  | gagcctcctg  | ctcctgcccg | 20520 |
| ggctctacac | ctacgagtgg | aacttccgca  | aggacgtcaa  | catgatcctg  | cagagctccc | 20580 |
| tcggcaacga | cctgcgcacg | gacggggcct  | ccatcgccct  | caccagcatc  | aacctctacg | 20640 |
| ccaccttctt | ccccatggcg | cacaacaccg  | cctccacgct  | cgaggccatg  | ctgcgcaacg | 20700 |
| acaccaacga | ccagtccttc | aacgactacc  | tctcggcggc  | caacatgctc  | taccccatcc | 20760 |
| cggccaacgc | caccaacgtg | cccatctcca  | tcccctcgcg  | caactggggc  | gccttccgcg | 20820 |
| gctggtcctt | cacgcgcctc | aagacccgcg  | agacgccctc  | gctcggctcc  | gggttcgacc | 20880 |
| cctacttcgt | ctactcgggc | tccatcccct  | acctcgacgg  | caccttctac  | ctcaaccaca | 20940 |
| ccttcaagaa | ggtctccatc | accttcgact  | cctccgtcag  | ctggcccggc  | aacgaccgcc | 21000 |
| tcctgacgcc | caacgagttc | gaaatcaagc  | gcaccgtcga  | cggagagggg  | tacaacgtgg | 21060 |
| cccagtgcaa | catgaccaag | gactggttcc  | tgggtccagat | gctggcccac  | tacaacatcg | 21120 |
| gctaccaggg | cttctacgtg | cccgagggct  | acaaggaccg  | catgtactcc  | ttcttccgca | 21180 |
| acttccagcc | catgagccgc | caggctcgtg  | acgaggtaa   | ctacaaggac  | taccaggccg | 21240 |
| tcaccctggc | ctaccagcac | aacaactcgg  | gcttcgctcg  | ctacctcgcg  | cccaccatgc | 21300 |
| gccagggcca | gccctacccc | gccaactacc  | cctacccgct  | catcggaag   | agcgccgtcg | 21360 |
| ccagcgtcac | ccagaaaaag | ttcctctgcg  | accgggtcat  | gtggcgcac   | cccttctcca | 21420 |
| gcaacttcat | gtccatgggc | gcgctcaccg  | acctcggcc   | gaacatgctc  | tacgccaact | 21480 |
| ccgcccacgc | gctagacatg | aatttcgaag  | tcgaccccat  | ggatgagtcc  | acccttctct | 21540 |
| atgttgtctt | cgaagtcttc | gacgtcgtcc  | gagtgcacca  | gccccaccgc  | ggcgtcatcg | 21600 |
| aggccgtcta | cctgcgcacg | cccttctcgg  | ccggcaacgc  | caccacctaa  | gcctcttgct | 21660 |
| tcttgcaaga | tgacggcctg | cgcgggctcc  | ggcgagcagg  | agctcagggc  | catcctccgc | 21720 |
| gacctgggct | gcggggcctg | cttcctgggc  | accttcgaca  | agcgcttccc  | gggattcatg | 21780 |

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|             |            |             |             |            |            |       |
|-------------|------------|-------------|-------------|------------|------------|-------|
| gccccgcaca  | agctggcctg | cgccatcgtc  | aacacggccg  | gccgcgagac | cgggggcgag | 21840 |
| cactggctgg  | ccttcgcctg | gaacccgcgc  | tcccacacct  | gctacctctt | cgaccccttc | 21900 |
| gggttctcgg  | acgagcgctt | caagcagatc  | taccagttcg  | agtacgaggg | cctgctgcgt | 21960 |
| cgcagcgccc  | tggccaccga | ggaccgctgc  | gtcaccctgg  | aaaagtccac | ccagaccgtg | 22020 |
| caggggtccgc | gctcggccgc | ctgcgggctc  | ttctgctgca  | tgttcctgca | cgcttctgtg | 22080 |
| cactggcccc  | accgccccat | ggacaagaac  | cccaccatga  | acttgctgac | gggggtgccc | 22140 |
| aacggcatgc  | tccagtcgcc | ccagggtggaa | cccaccctgc  | gccgcaacca | ggaggcgctc | 22200 |
| taccgcttcc  | tcaacgcccc | ctccgcctac  | tttcgctccc  | accgcgcgcg | catcgagaag | 22260 |
| gccaccgcct  | tcgaccgcac | gaatcaagac  | atgtaatccg  | gtgtgtgtat | gtgaatgctt | 22320 |
| tattcatcat  | aataaacagc | acatgtttat  | gccaccttct  | ctgaggctct | gactttattt | 22380 |
| agaaatcgaa  | ggggttctgc | cggtctctcg  | catggcccg   | gggcagggat | acgttgcgga | 22440 |
| actggtactt  | gggcagccac | ttgaactcgg  | ggatcagcag  | cttcggcacg | gggaggtcgg | 22500 |
| ggaacgagtc  | gctccacagc | ttgcgcgtga  | gttgcaaggc  | gcccagcagg | tcgggcgcgg | 22560 |
| agatcttgaa  | atcgcagttg | ggacccgcgt  | tctgcgcgcg  | agagttacgg | tacacggggt | 22620 |
| tgcagcactg  | gaacaccatc | agggccgggt  | gcttcacgct  | cgccagcacc | gtcgcgtcgg | 22680 |
| tgatgccctc  | cacgtccaga | tcctcggcgt  | tggccatccc  | gaagggggtc | atcttgcaag | 22740 |
| tctgccgccc  | catgctgggc | acgcagccgg  | gcttggtggt  | gcaatcgca  | tgcaggggga | 22800 |
| tcagcatcat  | ctgggcctgc | tcggagctca  | tgcccgggta  | catggccttc | atgaaagcct | 22860 |
| ccagctggcg  | gaaggcctgc | tgcgccttgc  | cgccctcggt  | gaagaagacc | ccgcaggact | 22920 |
| tgctagagaa  | ctggttggtg | gcgcagccag  | cgctcgtcac  | gcagcagcgc | gcgtcgttgt | 22980 |
| tggccagctg  | caccacgctg | cgccccagc   | ggttctgggt  | gatcttggcc | cggtcggggt | 23040 |
| tctccttcag  | cgcgcgctgc | ccgttctcgc  | tcgccacatc  | catctcgatc | gtgtgctcct | 23100 |
| tctggatcat  | cacggtcccc | tgcaggcacc  | gcagcttgcc  | ctcggcctcg | gtgcacccgt | 23160 |
| gcagccacag  | cgcgcagccg | gtgctctccc  | agttcttgtg  | ggcgatctgg | gagtgcgagt | 23220 |
| gcacgaagcc  | ctgcaggaag | cggcccatca  | tcgtggtcag  | ggtcttgttg | ctggtgaagg | 23280 |
| tcagcggaat  | gccgcggtgc | tcctcgttca  | catacagggt  | gcagatacgg | cggtagacac | 23340 |
| cgccctgctc  | gggcatcagc | tggaaaggcg  | acttcagggt  | gctctccacg | cggtagccgt | 23400 |
| ccatcagcag  | cgtcatcact | tccatgccct  | tctcccaggc  | cgaaacgac  | ggcaggctca | 23460 |
| gggggttctt  | caccgttgct | atcttagtcg  | ccgccgccga  | agtcaggggg | tcgttctcgt | 23520 |
| ccaggggtctc | aaacactcgc | ttgccgtcct  | tctcgggtgat | gcgcacgggg | ggaaagctga | 23580 |
| agcccacggc  | cgcagctccc | tcctcggcct  | gcctttcgtc  | ctcgtgtccc | tggctgatgt | 23640 |
| cttgcaaagg  | cacatgcttg | gtcttgccgg  | gtttcttttt  | gggcggcaga | ggcggcgccg | 23700 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |            |             |             |       |
|------------|------------|-------------|------------|-------------|-------------|-------|
| gagacgtgct | gggcgagcgc | gagttctcgc  | tcaccacgac | tatttcttct  | ccttggccgt  | 23760 |
| cgtccgagac | cacgcggcgg | taggcatgcc  | tcttctgggg | cagaggcgga  | ggcgacgggc  | 23820 |
| tctcgcggtt | cggcgggagg | ctggcagagc  | cccttccgcg | ttcgggggtg  | cgctcctggc  | 23880 |
| ggcgtgctc  | tgactgactt | cctccgcggc  | cggccattgt | gttctcctag  | ggagcaagca  | 23940 |
| tggagactca | gccatcgctc | ccaacatcgc  | catctgcccc | cgccgccgcc  | gacgagaacc  | 24000 |
| agcagcagca | gaatgaaagc | ttaaccgccc  | cgccgcccag | ccccacctcc  | gacgccgcag  | 24060 |
| ccccagacat | gcaagagatg | gaggaatcca  | tcgagattga | cctgggctac  | gtgacgcccg  | 24120 |
| cggagcacga | ggaggagctg | gcagcgcgct  | tttcagcccc | ggaagagAAC  | caccaagagc  | 24180 |
| agccagagca | ggaagcagag | agcgagcaga  | accaggctgg | gctcgagcat  | ggcgactacc  | 24240 |
| tgagcggggc | agaggacgtg | ctcatcaagc  | atctggcccc | ccaatgcac   | atcgtcaagg  | 24300 |
| acgcgctgct | cgaccgcgcc | gaggtgcccc  | tcagcgtggc | ggagctcagc  | cgcgccctacg | 24360 |
| agcgcaacct | cttctcgcgc | cgcggtgccc  | ccaagcgcca | gccaacggc   | acctgcgagc  | 24420 |
| ccaacccgcg | cctcaacttc | taccgggtct  | tcgcggtgcc | cgaggccctg  | gccacctacc  | 24480 |
| acctcttttt | caagaaccaa | aggatccccg  | tctcctgccg | cgccaaccgc  | acccgcgccg  | 24540 |
| acgccctgct | caacctgggc | cccggcgccc  | gcctacctga | tatcgccctcc | ttggaagagg  | 24600 |
| ttcccaagat | cttcgagggg | ctgggcagcg  | acgagactcg | ggccgcgaac  | gctctgcaag  | 24660 |
| gaagcggaga | ggagcatgag | caccacagcg  | ccctggtgga | gttggaaggc  | gacaacgcgc  | 24720 |
| gcctggcggt | cctcaagcgc | acggtcgagc  | tgacccactt | cgccctaccg  | gcgctcaacc  | 24780 |
| tgccccccaa | ggcatgagc  | gccgtcatgg  | accagggtgt | catcaagcgc  | gcctcgcccc  | 24840 |
| tctcggagga | ggagatgcag | gaccccgaga  | gctcggacga | gggcaagccc  | gtggtcagcg  | 24900 |
| acgagcagct | ggcgcgctgg | ctgggagcga  | gtagcacccc | ccagagcctg  | gaagagcggc  | 24960 |
| gcaagctcat | gatggccgtg | gtcctgggtga | ccgtggagct | ggagtgtctg  | cgccgcttct  | 25020 |
| tcgccgacgc | ggagaccctg | cgcaaggctc  | aggagaacct | gcactacctc  | ttcagacacg  | 25080 |
| ggttcgtgcg | ccaggcctgc | aagatctcca  | acgtggagct | gaccaacctg  | gtctcctaca  | 25140 |
| tgggcatcct | gcacgagaac | cgccctgggg  | agaacgtgct | gcacaccacc  | ctgcgcgggg  | 25200 |
| aggcccgccg | cgactacatc | cgcgactgcg  | tctacctgta | cctctgccac  | acctggcaga  | 25260 |
| cgggcatggg | cgtgtggcag | cagtgcctgg  | aggagcagaa | cctgaaagag  | ctctgcaagc  | 25320 |
| tcctgcagaa | gaacctcaag | gccctgtgga  | ccgggttcga | cgagcgcacc  | accgccgcgg  | 25380 |
| acctggccga | cctcatcttc | cccgagcgcc  | tgcggtgac  | gctgcgcaac  | gggctgcccg  | 25440 |
| actttatgag | ccaaagcatg | ttgcaaaact  | ttcgctcttt | catcctcgaa  | cgctccggga  | 25500 |
| tcctgccccg | cacctgctcc | gcgctgccct  | cggacttcgt | gccgctgacc  | ttccgcgagt  | 25560 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |             |            |            |       |
|------------|-------------|-------------|-------------|------------|------------|-------|
| gccccccgcc | gctctggagc  | cactgctacc  | tgctgcgct   | ggccaactac | ctggcctacc | 25620 |
| actcggacgt | gatcgaggac  | gtcagcggcg  | agggcctgct  | cgagtgccac | tgccgctgca | 25680 |
| acctctgcac | gccgcaccgc  | tccctggcct  | gcaaccccc   | gctgctgagc | gagaccaga  | 25740 |
| tcatcggcac | cttcgagttg  | caaggccccg  | gcgagggcaa  | ggggggtctg | aaactcaccc | 25800 |
| cggggctgtg | gacctcggcc  | tacttgcgca  | agttcgtgcc  | cgaggactac | catcccttcg | 25860 |
| agatcagggt | ctacgaggac  | caatcccagc  | cgcccaaggc  | cgagctgtcg | gcctgcgtca | 25920 |
| tcaccagagg | ggccatcctg  | gccaattgc   | aagccatcca  | gaaatcccg  | caagaatttc | 25980 |
| tgctgaaaaa | gggccacggg  | gtctacttgg  | acccccagac  | cgagaggag  | ctcaaccccc | 26040 |
| gcttccccca | ggatgccccg  | aggaagcagc  | aagaagctga  | aagtggagct | gccgccgccg | 26100 |
| ccggaggatt | tggaggaaga  | ctgggagagc  | agtcaggcag  | aggaggagga | gatggaagac | 26160 |
| tgggacagca | ctcaggcaga  | ggaggacagc  | ctgcaagaca  | gtctggagga | ggaagacgag | 26220 |
| gtggaggagg | cagaggaaga  | agcagccgcc  | gccagaccgt  | cgctctcggc | ggaggaggag | 26280 |
| aaagcaagca | gcacggatac  | catctccgct  | ccgggtcggg  | gtcgcggcgg | ccgggcccac | 26340 |
| agtagatggg | acgagaccgg  | gcgcttcccc  | aacccccacca | cccagaccgg | taagaaggag | 26400 |
| cggcagggat | acaagtccctg | gcggggggcac | aaaaacgcc   | tcgtctcctg | cttgcaagcc | 26460 |
| tgcgggggca | acatctcctt  | cacccggcgc  | tacctgctct  | tccaccgcgg | ggtgaacttc | 26520 |
| ccccgcaaca | tcttgcatta  | ctaccgtcac  | ctccacagcc  | cctactactg | tttccaagaa | 26580 |
| gaggcagaaa | cccagcagca  | gcagcagcag  | cagaaaacca  | gcggcagcag | ctagaaaatc | 26640 |
| cacagcggcg | gcagggtggac | tgaggatcgc  | ggcgaacgag  | ccggcgcaga | cccgggagct | 26700 |
| gaggaaccgg | atcttttccca | ccctctatgc  | catcttccag  | cagagtcggg | ggcaagagca | 26760 |
| ggaactgaaa | gtcaagaacc  | gttctctgcy  | ctcgtctacc  | cgcagttgtc | tgtatcacia | 26820 |
| gagcgaagac | caacttcagc  | gcactctcga  | ggacgccgag  | gctctcttca | acaagtactg | 26880 |
| cgcgctcact | cttaaagagt  | agcccgcgcc  | cgcccacaca  | cggaaaaaag | cggaattac  | 26940 |
| gtcaccacct | gcgcccctcg  | cccgaccatc  | atcatgagca  | aagagattcc | cacgccttac | 27000 |
| atgtggagct | accagcccca  | gatgggcctg  | gccgccggcg  | ccgcccagga | ctactccacc | 27060 |
| cgcatgaact | ggctcagtgc  | cgggcccgcg  | atgatctcac  | gggtgaatga | catccgcgcc | 27120 |
| caccgaaacc | agatactcct  | agaacagtca  | gcgatcaccg  | ccacgccccg | ccatcacctt | 27180 |
| aatccgcgta | attggcccgc  | cgccctgggt  | taccaggaaa  | ttccccagcc | cacgaccgta | 27240 |
| ctacttccgc | gagacgcccc  | ggccgaagtc  | cagctgacta  | actcaggtgt | ccagctggcc | 27300 |
| ggcggcgccg | ccctgtgtcg  | tcaccgcccc  | gtcagggta   | taaagcggct | ggtgatccga | 27360 |
| ggcagaggca | cacagctcaa  | cgacgaggtg  | gtgagctctt  | cgctgggtct | gcgacctgac | 27420 |
| ggagtcttcc | aactcgccgg  | atcggggaga  | tcttcttca   | cgctcgtca  | ggccgtcctg | 27480 |

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|             |             |            |            |            |            |       |
|-------------|-------------|------------|------------|------------|------------|-------|
| actttggaga  | gttcgtcctc  | gcagccccgc | tcgggtggca | tcggcactct | ccagttcgtg | 27540 |
| gaggagttca  | ctccctcggg  | ctacttcaac | cccttctccg | gctcccccg  | ccactacccg | 27600 |
| gacgagttca  | tcccgaactt  | cgacgccatc | agcgagtcgg | tggacggcta | cgattgaatg | 27660 |
| tcccatgggtg | gcgcggctga  | cctagctcgg | cttcgacacc | tggaccactg | ccgccgcttc | 27720 |
| cgctgcttcg  | ctcgggatct  | cgccgagttt | gcctactttg | agctgcccga | ggagcaccct | 27780 |
| cagggcccg   | cccacggagt  | gcggatcgtc | gtcgaagggg | gtctcgactc | ccacctgctt | 27840 |
| cggatcttca  | gccagcgtcc  | gatcctggcc | gagcgcgagc | aaggacagac | ccttctgacc | 27900 |
| ctgtactgca  | tctgcaacca  | ccccggcctg | catgaaagtc | tttgttgtct | gctgtgtact | 27960 |
| gagtataata  | aaagctgaga  | tcagcgacta | ctccggactt | ccgtgtgttc | ctgctatcaa | 28020 |
| ccagtccctg  | ttcttcaccg  | ggaacgagac | cgagctccag | ctccagtgtg | agccccacaa | 28080 |
| gaagtacctc  | acctggctgt  | tccagggctc | tccgatcgcc | gttgtcaacc | actgcgacaa | 28140 |
| cgacggagtc  | ctgtgagcg   | gccctgccaa | ccttactttt | tccacccgca | gaagcaagct | 28200 |
| ccagctcttc  | caacccttcc  | tccccgggac | ctatcagtgc | gtctcgggac | cctgccatca | 28260 |
| caccttccac  | ctgatcccga  | ataccacagc | gtcgtctccc | gctactaaca | accaaactac | 28320 |
| ccaccaacgc  | caccgtcgcg  | accgcggaca | tgtacagagc | tcgagaagta | ctaggccaca | 28380 |
| atacatgccc  | atattagact  | atgaggccga | gccacagcga | cccatgctcc | ccgctattag | 28440 |
| ttacttcaat  | ctaaccggcg  | gagatgactg | acccactggc | caacaacaac | gtcaacgacc | 28500 |
| ttctcctgga  | catggacggc  | cgcgctcgg  | agcagcgact | cgcccaactt | cgcattcgcc | 28560 |
| agcagcagga  | gagagccgtc  | aaggagctgc | aggacggcat | agccatccac | cagtgcaga  | 28620 |
| aaggcatctt  | ctgcctgggtg | aaacaggcca | agatctccta | cgaggtcacc | ccgaccgacc | 28680 |
| atcgctcttc  | ctacgagctc  | ctgcagcagc | gccagaagtt | cacctgcctg | gtcggagtca | 28740 |
| accccatcgt  | catcacccag  | cagtcgggcg | ataccaaggg | gtgcatccac | tgctcctgcy | 28800 |
| actccccga   | ctgcgtccac  | actctgatca | agaccctctg | cggcctccgc | gacctcctcc | 28860 |
| ccatgaacta  | atcacccctt  | tatccagtga | aataaatatc | atattgatga | tgattttaa  | 28920 |
| aaaaaataat  | catttgattt  | gaaataaaga | tacaatcata | ttgatgattt | gagttttaa  | 28980 |
| aaataaagaa  | tcacttactt  | gaaatctgat | accaggctct | tgtccatgtt | ttctgccaac | 29040 |
| accacctcac  | tcccctcttc  | ccagctctgg | tactgcagac | cccgcgggc  | tgcaaaactt | 29100 |
| ctccacacgc  | tgaaggggat  | gtcaaattcc | tcctgtccct | caatcttcat | tttatcttct | 29160 |
| atcagatgtc  | caaaaagcgc  | gtccgggtgg | atgatgactt | cgaccccgtc | tacctctacg | 29220 |
| atgcagacaa  | cgcaccgacc  | gtgcccttca | tcaaccccc  | cttcgtctct | tcagatggat | 29280 |
| tccaagagaa  | gcccctgggg  | gtgctgtccc | tgcgactggc | tgaccccgtc | accaccaaga | 29340 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |            |             |       |
|-------------|-------------|-------------|------------|------------|-------------|-------|
| acgggggaaat | caccctcaag  | ctgggagagg  | gggtggacct | cgactcctcg | ggaaaaactca | 29400 |
| tctccaacac  | ggccaccaag  | gccgccgccc  | ctctcagttt | ttccaacaac | accatttccc  | 29460 |
| ttaacatgga  | taccctcttt  | tataccaaag  | atggaaaatt | atccttacia | gtttctccac  | 29520 |
| cgtaaacaat  | attaaaaatca | accatttctga | acacattagc | tgtagcttat | ggatcagggtt | 29580 |
| taggactgag  | tgggtggcact | gctcttgacg  | tacagtgggc | ctctccactc | actttttgatg | 29640 |
| aaaaaggaaa  | tattaaaatt  | aacctagcca  | gtggtccatt | aacagttgat | gcaagtcgac  | 29700 |
| ttagtatcaa  | ctgcaaaaaga | ggggtcactg  | tcactacctc | aggagatgca | attgaaagca  | 29760 |
| acataagctg  | gcctaaaggt  | ataagatttg  | aaggtaatgg | catagctgca | aacattggca  | 29820 |
| gaggattgga  | atttgggaacc | actagtacag  | agactgatgt | cacagatgca | taccaaatc   | 29880 |
| aagttaaatt  | gggtactggc  | cttacctttg  | acagtacagg | cgccattggt | gcttggaaaca | 29940 |
| aagaggatga  | taaacttaca  | ttatggacca  | cagccgaccc | ctcgccaaat | tgcaaaatat  | 30000 |
| actctgaaaa  | agatgccaaa  | ctcacacttt  | gcttgacaaa | gtgtggaagt | caaattctgg  | 30060 |
| gtactgtgac  | tgtattggca  | gtgaataatg  | gaagtctcaa | cccaatcaca | aacacagtaa  | 30120 |
| gcactgcact  | cgctctccctc | aagtttgatg  | caagtggagt | tttgctaagc | agctccacat  | 30180 |
| tagacaaaga  | atattggaac  | ttcagaaagg  | gagatgttac | acctgctgag | ccctatacta  | 30240 |
| atgctatagg  | ttttatgcct  | aacataaagg  | cctatcctaa | aaacacatct | gcagcttcaa  | 30300 |
| aaagccatat  | tgtcagtcaa  | gtttatctca  | atggggatga | ggccaaacca | ctgatgctga  | 30360 |
| ttattacttt  | taatgaaact  | gaggatgcaa  | cttgcaccta | cagtatcact | tttcaatgga  | 30420 |
| aatgggatag  | tactaagtac  | acaggtgaaa  | cacttgctac | cagctccttc | accttctcct  | 30480 |
| acatcgccca  | agaatgaaca  | ctgtatccca  | ccctgcatgc | caacccttcc | cacccctcctc | 30540 |
| tgtctatgga  | aaaaactctg  | aagcacaaaa  | taaaataaag | ttcaagtgtt | ttattgattc  | 30600 |
| aacagtttta  | caggattcga  | gcagttattt  | ttcctccacc | ctcccaggac | atggaatata  | 30660 |
| ccaccctctc  | cccccgacac  | gccttgaaca  | tctgaatgcc | attggtgatg | gacatgcttt  | 30720 |
| tggctctccac | gttccacaca  | gtttcagagc  | gagccagtct | cgggtcggtc | agggagatga  | 30780 |
| aaccctccgg  | gcactcccg   | atctgcacct  | cacagctcaa | cagctgagga | ttgtcctcgg  | 30840 |
| tggtcgggat  | cacggttatc  | tggagaagc   | agaagagcgg | cggtggaat  | catagtccgc  | 30900 |
| gaacgggatc  | ggccggtggt  | gtcgcacacg  | gccccgcagc | agtcgctgcc | gccgccgctc  | 30960 |
| cgtaagctg   | ctgctcaggg  | ggtccgggtc  | cagggactcc | ctcagcatga | tgccacggc   | 31020 |
| cctcagcatc  | agtcgtctgg  | tgcggcgggc  | gcagcagcgc | atgcggatct | cgctcaggtc  | 31080 |
| gctgcagtac  | gtgcaacaca  | ggaccaccag  | gttggtcaac | agtccatagt | tcaacacgct  | 31140 |
| ccagccgaaa  | ctcatcgcg   | gaaggatgct  | accacgtgg  | ccgtcgtacc | agatcctcag  | 31200 |
| gtaaatcaag  | tggcgctccc  | tccagaacac  | gctgcccacg | tacatgatct | ccttgggcat  | 31260 |



## 368530-7006W01\_SequenceListing\_ST25.txt

```

gtggcggttc accacctccc ggtaccacat caccctctgg ttgaacatgc agccccggat 31320
gatcctgcgg aaccacaggg ccagcaccgc cccgcccgcc atgcagcgaa gagaccccgg 31380
gtccccgcaa tggcaatgga ggacccaccg ctcgtaccgg tggatcatct gggagctgaa 31440
caagtctatg ttggcacagc acaggcatat gctcatgcat ctcttcagca ctctcagctc 31500
ctcgggggtc aaaaccatat cccagggcac ggggaactct tgcaggacag cgaaccccgc 31560
agaacagggc aatcctcgca cataacttac attgtgcatg gacaggggat cgcaatcagg 31620
cagcaccggg tgatcctcca ccagagaagc gcgggtctcg gtctcctcac agcgtggtaa 31680
gggggcccgc cgatacgggt gatggcggga cgcggtgat cgtgttcgcg accgtgtcat 31740
gatgcagttg ctttcggaca ttttcgtact tgctgtagca gaacctgggc cgggcgctgc 31800
acaccgatcg ccggcggcgg tcccggcgct tggaacgctc ggtgttgaaa ttgtaaaaca 31860
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gcctgatagc tctgatcaca tcgaccaccg tggaatgggc cagaccacgc cagatgatgc 31980
aattttgttg ggtttcggtg acggcggggg aggggaagaac aggaagaacc atgattaact 32040
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ccccgctgtg ttggtggaaa ataacagcca ggtcaaaggt gatacggttc tcgagatgtt 32160
ccacggtggc ttccagcaaa gcctccacgc gcacatccag aaacaagaca atagcgaaag 32220
cgggagggtt ctctaattcc tcaatcatca tgttacactc ctgcaccatc cccagataat 32280
tttcattttt ccagccttga atgattcgaa ctagttcctg aggtaaaatcc aagccagcca 32340
tgataaagag ctcgcgcaga gcgccctcca ccggcattct taagcacacc ctcataattc 32400
caagatatct tgctcctggt tcacctgcag cagattgaca agcggaatat caaaatctct 32460
gccgcgatcc ctaagctcct ccctcagcaa taactgtaag tactctttca taccctctcc 32520
gaaattttta gccataggac caccaggaat aagattaggg caagccacag tacagataaa 32580
ccgaagtcct cccagtgag cattgccaaa tgcaagactg ctataagcat gctggctaga 32640
cccgtgata tcttcagat aactggacag aaaatcaccg aggcaatttt taagaaaatc 32700
aacaaaagaa aaatcctcca ggtgcacgtt tagagcctcg ggaacaacga tgaagtaa 32760
gcaagcg 32767

```

```

<210> 4
<211> 32767
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 4

```

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| catcatcaat  | aatataacctc | aaactttttgg | tgcgcgtaa   | tatgcaaatg | agctgtttga  | 60   |
| atttggggag  | ggaggaaggt  | gattggccga  | gagacgggcg  | accgttaggg | gcggggcggg  | 120  |
| tgacgttttg  | atgacgtggc  | cgtgaggcgg  | agccggtttg  | caagttctcg | tgggaaaagt  | 180  |
| gacgtcaaac  | gaggtgtggt  | ttgaacacgg  | aaataactcaa | ttttcccgcg | ctctctgaca  | 240  |
| ggaaatgagg  | tgtttctggg  | cggatgcaag  | tgaaaacggg  | ccattttcgc | gcgaaaactg  | 300  |
| aatgaggaag  | tgaaaatctg  | agtaatttcg  | cgtttatggc  | agggaggagt | atttgccgag  | 360  |
| ggccgagtag  | actttgaccg  | attacgtggg  | ggtttcgatt  | accgtatttt | tcacctaaat  | 420  |
| ttccgcgtac  | ggtgtcaaag  | tccggtgttt  | ttacgtacga  | tatcatttcc | ccgaaaagtgc | 480  |
| cacctgaccg  | taactataac  | ggtcctaagg  | tagcgaaaagc | tcagatctcc | cgatccccta  | 540  |
| tgggtgactc  | tcagtacaat  | ctgctctgat  | gccgcatagt  | taagccagta | tctgctccct  | 600  |
| gcttgtgtgt  | tggaggtcgc  | tgagtagtgc  | gcgagcaaaa  | tttaagctac | aacaaggcaa  | 660  |
| ggcttgaccg  | acaattgcat  | gaagaatctg  | cttaggggta  | ggcgttttgc | gctgcttcgc  | 720  |
| gatgtacggg  | ccagatatac  | gcgttgacat  | tgattattga  | ctagttatta | atagtaatca  | 780  |
| attacggggg  | cattagttca  | tagcccatat  | atggagttcc  | gcgttacata | acttacggta  | 840  |
| aatggcccgc  | ctggctgacc  | gccaacgac   | ccccgccc    | tgacgtcaat | aatgacgtat  | 900  |
| gttcccatag  | taacgccaat  | agggactttc  | cattgacgtc  | aatgggtgga | gtattttacgg | 960  |
| taaactgccc  | acttggcagt  | acatcaagtg  | tatcatatgc  | caagtacgcc | ccctattgac  | 1020 |
| gtcaatgacg  | gtaaatggcc  | cgcttggcat  | tatgccaggt  | acatgacctt | atgggacttt  | 1080 |
| cctacttggc  | agtacatcta  | cgtattagtc  | atcgctatta  | ccatggtgat | gcggttttgg  | 1140 |
| cagtacatca  | atgggctggt  | atagcggttt  | gactcacggg  | gatttccaag | tctccacccc  | 1200 |
| attgacgtca  | atgggagttt  | gttttggcac  | caaaatcaac  | gggactttcc | aaaatgtcgt  | 1260 |
| aacaactccg  | ccccattgac  | gcaaatgggc  | ggtaggcgtg  | tacggtggga | ggtctatata  | 1320 |
| agcagagctc  | gttttagtgaa | ccgtcagatc  | actagaagct  | ttattgcggt | agtttatcac  | 1380 |
| agttaaattg  | ctaacgcagt  | cagtgccttc  | gacacaacag  | tctcgaactt | aagctgcaga  | 1440 |
| agttggtcgt  | gaggcactgg  | gcaggtaagt  | atcaagggtta | caagacaggt | ttaaggagac  | 1500 |
| caatagaaac  | tgggcttgtc  | gagacagaga  | agactccttg  | gtttctgata | ggcacctatt  | 1560 |
| ggtcttactg  | acatccactt  | tgcccttctc  | tccacaggtg  | tccactccca | gttcaattac  | 1620 |
| agctcttaag  | gctagagtac  | ttaatacgac  | tcactatagg  | ctagcgccac | catgggcgcc  | 1680 |
| agagccagcg  | tgctgagcgg  | gggagagctg  | gatcgctggg  | aaaagattag | actgaggccc  | 1740 |
| ggaggggaaga | aaaagtacaa  | gctgaaacac  | atcgtgtggg  | ccagcagggg | gctggagcgc  | 1800 |
| ttcgccgtga  | accccgact   | gctggagacc  | tccgaaggct  | gtcggcagat | cctggggcag  | 1860 |
| ctgcagcctt  | ccctgcagac  | aggctccgag  | gagctgcggt  | ctctgtataa | tacagtggcc  | 1920 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| acactgtact | gtgtgcacca | gcggattgag | gtgaaggata | caaaagaggc  | cctggagaag  | 1980 |
| attgaggagg | agcagaacaa | gagcaagaag | aaagcccagc | aggccgccgc  | cgacaccggc  | 2040 |
| aatagctccc | aggtgagcca | gaactatcca | attgtgcaga | atctgcaggg  | ccagatggtg  | 2100 |
| caccaggcca | tttccccacg | gacactgaac | gcctgggtga | aggtggtgga  | ggagaaggcc  | 2160 |
| ttcagccccg | aagtgatccc | tatgttttcc | gccctgtccg | aaggcgccac  | ccctcaggac  | 2220 |
| ctgaacacca | tgctgaacac | agtgggggga | caccaggccg | ccatgcagat  | gctgaaggaa  | 2280 |
| accatcaacg | aggaggccgc | cgagtgggat | cggctgcacc | ccgtgcacgc  | cgggccaatc  | 2340 |
| gccccctggc | agatgaggga | gcccagaggc | tctgacatcg | ccggcaccac  | atctaccctg  | 2400 |
| caggaacaga | tcgggtggat | gaccaataac | ccaccaatcc | cagtgggcga  | gatctacaag  | 2460 |
| aggtggatta | ttctgggact | gaacaaaatt | gtgcgcatgt | attcccctac  | atccatcctg  | 2520 |
| gacatcaggc | agggccctaa | ggaacctttc | cgcgactacg | tggatcggtt  | ctacaaaacc  | 2580 |
| ctgcgcgccg | agcaggccag | ccaggaagtg | aagaattgga | tgacagagac  | cctgctggtg  | 2640 |
| cagaacgcca | atcctgactg | taaaaccatc | ctgaaggccc | tgggccctgc  | cgccacactg  | 2700 |
| gaggaaatga | tgaccgcctg | ccagggcgtg | ggcggccctg | gccacaaagc  | caggggtgctg | 2760 |
| gccgaggcca | tgtctcaggt | gaccaactct | gccacaatta | tgatgcagcg  | ggggaacttt  | 2820 |
| cggaaccaga | ggaagaccgt | gaagtgcctc | aactgtggca | aggagggaca  | catcgccaag  | 2880 |
| aattgccgcg | ccccacggaa | gaaggggtgt | tggaaatgcg | ggaaggaggg  | ccaccagatg  | 2940 |
| aaagactgca | cagagcggca | ggccaacttt | ctgggcaaga | tttggcccag  | ccacaagggc  | 3000 |
| cgccccggaa | actttctgca | gtccaggcct | gagcctaccg | ccccccctga  | ggaatccttc  | 3060 |
| cggttcggcg | aggagacaac | caccccaagc | cagaagcagg | aacccatcga  | caaagagctg  | 3120 |
| tacccccctg | ccagcctgag | atccctgttc | gggaatgacc | ccagctctca  | gtgatgatct  | 3180 |
| agcgtttaaa | cgggccctct | agagtcgacc | cgggcggcca | aaccgctgat  | cagcctcgac  | 3240 |
| tgtgccttct | agttgccagc | catctgttgt | ttgccctcc  | cccgtgcctt  | ccttgaccct  | 3300 |
| ggaaggtgcc | actcccactg | tcctttccta | ataaaatgag | gaaattgcat  | cgcattgtct  | 3360 |
| gagtaggtgt | cattctattc | tgggggggtg | ggtggggcag | gacagcaagg  | gggaggattg  | 3420 |
| ggaagacaat | agcaggcatg | ctgggggatg | ggtgggctct | atggcttctg  | aggcggaaag  | 3480 |
| aaccagcaga | tctgcagatc | tgaattcatc | tatgtcgggt | gcggagaaaag | aggtaatgaa  | 3540 |
| atggcattat | gggtattatg | ggtctgcatt | aatgaatcgg | ccagatatgc  | tggccaccgt  | 3600 |
| gcatgtgacc | tcgcaccccc | gcaagacatg | gcccaggttc | gagcacaacg  | tcatgaccgg  | 3660 |
| atgcaatgtg | cacctggggg | cccgccgagg | catgttcatg | ccctaccagt  | gcaacatgca  | 3720 |
| atttgtgaag | gtgctgctgg | agccccgatg | catgtccaga | gtgagcctga  | cgggggtgtt  | 3780 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| tgacatgaat  | gtggagctgt | ggaaaaattct | gagatatgat  | gaatccaaga  | ccagggtgccg | 3840 |
| ggcctgcgaa  | tgcggaggca | agcacgccag  | gcttcagccc  | gtgtgtgtgg  | aggtgacgga  | 3900 |
| ggacctgcga  | cccgatcatt | tggtgttgtc  | ctgcaacggg  | acggagttcg  | gctccagcgg  | 3960 |
| ggaagaatct  | gactagagtg | agtagtgttt  | gggggagggtg | gagggcttgt  | atgagggggca | 4020 |
| gaatgactaa  | aatctgtgtt | tttctgtgtg  | ttgcagcagc  | atgagcggaa  | gcgcctcctt  | 4080 |
| tgagggagggg | gtattcagcc | cttatctgac  | ggggcgctct  | ccctcctggg  | cgggagtgcg  | 4140 |
| tcagaatgtg  | atgggatcca | cggtggacgg  | ccggcccgtg  | cagcccgcga  | actcttcaac  | 4200 |
| cctgacctac  | gcgaccctga | gctcctcgtc  | cgtggacgca  | gctgccgccg  | cagctgctgc  | 4260 |
| ttccgccgcc  | agcgccgtgc | gcggaatggc  | cctgggcgcc  | ggctactaca  | gctctctggt  | 4320 |
| ggccaactcg  | acttccacca | ataatcccg   | cagcctgaac  | gaggagaagc  | tgctgctgct  | 4380 |
| gatggcccag  | ctcgaggccc | tgacccagcg  | cctgggcgag  | ctgacccagc  | aggtgggtca  | 4440 |
| gctgcaggcg  | gagacgcggg | ccgcggttgc  | cacggtgaaa  | accaaataaa  | aaatgaatca  | 4500 |
| ataaataaac  | ggagacggtt | gttgatttta  | acacagagtc  | ttgaatcttt  | atttgatttt  | 4560 |
| tcgcgcgcgg  | taggccctgg | accaccggtc  | tcgatcattg  | agcaccgggt  | ggattttttc  | 4620 |
| caggaccggg  | tagagggtgg | cttggatgtt  | gaggtagatg  | ggcatgagcc  | cgtcccgggg  | 4680 |
| gtggaggtag  | ctccattgca | gggcctcgtg  | ctcgggggtg  | gtgttgtaaa  | tcaccagtc   | 4740 |
| atagcagggg  | cgcagggcgt | ggtgctgcac  | gatgtccttg  | aggaggagac  | tgatggccac  | 4800 |
| gggcagcccc  | ttggtgtagg | tggtgacgaa  | cctgttgagc  | tgggagggat  | gcatgcgggg  | 4860 |
| ggagatgaga  | tgcattcttg | cctggatctt  | gagattggcg  | atgttcccg   | ccagatcccg  | 4920 |
| ccggggggtt  | atgttgtgca | ggaccaccag  | cacggtgtat  | ccggcgcaact | tggggaattt  | 4980 |
| gtcatgcaac  | ttggaaggga | aggcgtgaaa  | gaatttgagg  | acgcccttgt  | gaccgcccag  | 5040 |
| gttttccatg  | cactcatcca | tgatgatggc  | gatgggcccg  | tgggcggcgg  | cctgggcaaa  | 5100 |
| gacgtttcgg  | gggtcggaca | catcgtagtt  | gtggtccttg  | gtgagctcgt  | cataggccat  | 5160 |
| tttaatgaat  | ttggggcgga | gggtgcccga  | ctgggggacg  | aagggtgccct | cgatcccggg  | 5220 |
| ggcgtagttg  | ccctcgcaga | tctgcatctc  | ccaggccttg  | agctcggagg  | gggggatcat  | 5280 |
| gtccacctgc  | ggggcgatga | aaaaaacggt  | ttccggggcg  | ggggagatga  | gctgggcccga | 5340 |
| aagcaggttc  | cggagcagct | gggacttgcc  | gcagccggtg  | gggccgtaga  | tgaccccgat  | 5400 |
| gaccggctgc  | aggtggtagt | tgagggagag  | acagctgccg  | tcctcgcgga  | ggaggggggc  | 5460 |
| cacctcgttc  | atcatctcgc | gcacatgcat  | gttctcgcgc  | acgagttccg  | ccaggaggcg  | 5520 |
| ctcgcccccc  | agcgagagga | gctcttgacg  | cgaggcgaag  | tttttcagcg  | gcttgagccc  | 5580 |
| gtcggccatg  | ggcatttttg | agaggggtctg | ttgcaagagt  | tccagacggt  | cccagagctc  | 5640 |
| ggtgatgtgc  | tctagggcat | ctcgaatccag | cagacctcct  | cgtttcgcgg  | gttggggcga  | 5700 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| ctgcgggagt | agggcaccag | gcgatgggcg  | tccagcgagg  | ccaggggtccg | gtccttccag  | 5760 |
| ggtcgcaggg | tccgcgtcag | cgtggtctcc  | gtcacggtga  | aggggtgcgc  | gccgggctgg  | 5820 |
| gcgcttgca  | gggtgcgctt | caggctcatc  | cggctggtcg  | agaaccgctc  | ccggtcggcg  | 5880 |
| ccctgcgcgt | cggccaggta | gcaattgagc  | atgagttcgt  | agttgagcgc  | ctcggccgcg  | 5940 |
| tggcccttgg | cgcggagctt | acctttggaa  | gtgtgtccgc  | agacgggaca  | gaggagggac  | 6000 |
| ttgagggcgt | agagcttggg | ggcgaggaag  | acggactcgg  | gggcgtaggc  | gtccgcgccg  | 6060 |
| cagctggcgc | agacggtctc | gcactccacg  | agccagggtga | ggtcgggccg  | gttgggggtca | 6120 |
| aaaacgaggt | ttcctccgtg | ctttttgatg  | cgtttcttac  | ctctggtctc  | catgagctcg  | 6180 |
| tgtccccgct | gggtgacaaa | gaggctgtcc  | gtgtccccgt  | agaccgactt  | tatggggccg  | 6240 |
| tcctcgagcg | gggtgccgcg | gtcctcgtcg  | tagaggaacc  | ccgcccactc  | cgagacgaag  | 6300 |
| gcccgggtcc | agggcagcac | gaaggaggcc  | acgtgggagg  | ggtagcggtc  | gttgtccacc  | 6360 |
| agcgggtcca | ccttctccag | ggtatgcaag  | cacatgtccc  | cctcgtccac  | atccaggaag  | 6420 |
| gtgattggct | tgtaagtgtg | ggccacgtga  | ccgggggtcc  | cggccggggg  | ggtataaaaag | 6480 |
| ggggcgggcc | cctgctcgtc | ctcactgtct  | tccggatcgc  | tgtccaggag  | cgccagctgt  | 6540 |
| tggggtaggt | attccctctc | gaaggctggc  | ataacctcgg  | cactcagggt  | gtcagtttct  | 6600 |
| agaaacgagg | aggatttgat | attgacggtg  | ccgttggaga  | cgcctttcat  | gagcccctcg  | 6660 |
| tccatctggg | cagaaaagac | gatctttttg  | ttgtcgagct  | tggtggcgaa  | ggagccgtag  | 6720 |
| agggcgttgg | agaggagctt | ggcgatggag  | cgcatggtct  | ggttcttttc  | cttgtcggcg  | 6780 |
| cgctccttgg | cggcgatggt | gagctgcacg  | tactcgcgcg  | ccacgcactt  | ccattcgggg  | 6840 |
| aagacggtgg | tgagctcgtc | gggcacgatt  | ctgacccgcc  | agccgcgggt  | gtgcaggggtg | 6900 |
| atgaggtcca | cgctggtggc | cacctcgccg  | cgcaggggct  | cgttgggtcca | gcagaggcgc  | 6960 |
| ccgcccttgc | gcgagcagaa | ggggggcagc  | gggtccagca  | tgagctcgtc  | gggggggtcg  | 7020 |
| gcgtccacgg | tgaagatgcc | gggcagaagc  | tcggggtcga  | agtagctgat  | gcagggtgtcc | 7080 |
| agatcgtcca | gcgccgcttg | ccagtcgcgc  | acggccagcg  | cgcgctcgta  | ggggctgagg  | 7140 |
| ggcgtgcccc | agggcatggg | gtgcgtgagc  | gcggaggcgt  | acatgccgca  | gatgtcgtag  | 7200 |
| acgtagaggg | gctcctcgag | gacgccgatg  | taggtggggg  | agcagcgccc  | cccgcgggatg | 7260 |
| ctggcgcgca | cgtagtcgta | cagctcgtgc  | gagggcgcga  | ggagccccgt  | gccgaggttg  | 7320 |
| gagcgttgcg | gcttttcggc | gcggtagacg  | atctggcgga  | agatggcgtg  | ggagttggag  | 7380 |
| gagatggtgg | gcctctggaa | gatgttgaa   | tgggcgtggg  | gcaggccgac  | cgagtccctg  | 7440 |
| atgaagtggg | cgtaggagtc | ctgcagcttg  | gcgacgagct  | cggcggtgac  | gaggacgtcc  | 7500 |
| agggcgagct | agtcgagggg | ctcttggtatg | atgtcgtact  | tgagctggcc  | cttctgcttc  | 7560 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| cacagctcgc  | ggttgagaag  | gaactcttcg  | cggtccttcc  | agtactcttc | gagggggaac | 7620 |
| ccgtcctgat  | cggcacggta  | agagcccacc  | atgtagaact  | ggttgacggc | cttgtaggcg | 7680 |
| cagcagccct  | tctccacggg  | gagggcgtaa  | gcttgtgcgg  | ccttgcgag  | ggaggtgtgg | 7740 |
| gtgagggcga  | aggtgtcgcg  | cacatgacc   | ttgaggaact  | ggtgcttgaa | gtcgaggtcg | 7800 |
| tcgcagccgc  | cctgctccca  | gagctggaag  | tccgtgcgct  | tcttgtaggc | ggggttgggc | 7860 |
| aaagcgaaaag | taacatcggt  | gaagaggatc  | ttgcccgcgc  | ggggcatgaa | gttgcgagtg | 7920 |
| atgcggaaaag | gctggggcac  | ctcggcccgg  | ttgttgatga  | cctgggcggc | gaggacgatc | 7980 |
| tcgtcgaagc  | cggtgatggt  | gtgcccgcgc  | atgtagagtt  | ccacgaatcg | cgggcggccc | 8040 |
| ttaacgtggg  | gcagcttctt  | gagctcgtcg  | taggtgagct  | cggcggggtc | gctgagcccg | 8100 |
| tgctgctcga  | gggcccagtc  | ggcgacgtgg  | gggttggcgc  | tgaggaagga | agtccagaga | 8160 |
| tccacggcca  | gggcggtctg  | caagcggtcc  | cggctactgac | ggaactgctg | gcccacggcc | 8220 |
| attttttcgg  | gggtgacgca  | gtagaagggtg | cgggggtcgc  | cgtgccagcg | gtcccacttg | 8280 |
| agctggaggg  | cgaggtcgtg  | ggcgagctcg  | acgagcggcg  | ggtccccgga | gagtttcatg | 8340 |
| accagcatga  | aggggacgag  | ctgcttgccg  | aaggacccca  | tccaggtgta | ggtttccaca | 8400 |
| tcgtaggtga  | ggaagagcct  | ttcggtgcga  | ggatgcgagc  | cgatggggaa | gaactggatc | 8460 |
| tcctgccacc  | agttggagga  | atggctgttg  | atgtgatgga  | agtagaaatg | ccgacggcgc | 8520 |
| gccgagcact  | cgtgcttggtg | tttatacaag  | cgtccgcagt  | gctcgcaacg | ctgcacggga | 8580 |
| tgcacgtgct  | gcacgagctg  | tacctgggtt  | cctttgacga  | ggaatttcag | tgggcagtg  | 8640 |
| agcgtggcg   | gctgcatctg  | gtgctgtact  | acgtcctggc  | catcggcgtg | gccatcgtct | 8700 |
| gcctcgatgg  | tggatcatgct | gacgagccccg | cgcgggaggg  | aggtccagac | ttcggtcgg  | 8760 |
| acgggtcggg  | gagcgaggac  | gagggcgcg   | aggccggagc  | tgtccaggg  | cctgagacgc | 8820 |
| tgcgaggtca  | ggtcagtggtg | cagcggcggc  | gcgcggttga  | cttgcaggag | cttttccagg | 8880 |
| gcgcgcggga  | ggtccagatg  | gtacttgatc  | tccacggcgc  | cgttggtggc | gacgtccacg | 8940 |
| gcttgcaggg  | tcccgtgccc  | ctggggcgcc  | accaccgtgc  | cccgtttctt | cttgggcgct | 9000 |
| gcttccatgc  | cggtcagaag  | cggcggcgag  | gacgcgcgcc  | gggcggcagg | ggcggctcgg | 9060 |
| gacccggagg  | cagggggcggc | aggggacacgt | cggcgccgcg  | cgcgggcagg | ttctggtact | 9120 |
| gcgcccggag  | aagactggcg  | tgagcgacga  | cgcgacgggt  | gacgtcctgg | atctgacgcc | 9180 |
| tctgggtgaa  | ggccacggga  | cccgtgagtt  | tgaacctgaa  | agagagttcg | acagaatcaa | 9240 |
| tctcggtatc  | gttgacggcg  | gcctgccgca  | ggatctcttg  | cacgtcgccc | gagttgtcct | 9300 |
| ggtaggcgat  | ctcggatcatg | aactgctcga  | tctcctcctc  | ctgaaggctc | ccgcggccgg | 9360 |
| cgcgctcgac  | ggtggccgcg  | aggtcggttg  | agatgcggcc  | catgagctgc | gagaaggcgt | 9420 |
| tcatgccggc  | ctcgttccag  | acgcggctgt  | agaccacggc  | tccgtcgggg | tcgcgcgcgc | 9480 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |             |            |            |       |
|-------------|------------|------------|-------------|------------|------------|-------|
| gcatgaccac  | ctgggcgagg | ttgagctcga | cgtggcgcg   | gaagaccgcg | tagttgcaga | 9540  |
| ggcgtggta   | gaggtagttg | agcgtggtgg | cgatgtgctc  | ggtgacgaag | aagtacatga | 9600  |
| tccagcggcg  | gagcggcatc | tcgctgacgt | cgcccagggc  | ttccaagcgc | tccatggcct | 9660  |
| cgtagaagtc  | cacggcgaag | ttgaaaaact | gggagttgcg  | cgccgagacg | gtcaactcct | 9720  |
| cctccagaag  | acggatgagc | tcagcgatgg | tggcgcgcac  | ctcgcgctcg | aaggcccccg | 9780  |
| ggggctcctc  | ttcttccatc | tcttcctcct | ccactaacat  | ctcttctact | tcctcctcag | 9840  |
| gagggcggcg  | cgggggaggg | gccctgcgtc | gccggcggcg  | cacgggcaga | cggtcgatga | 9900  |
| agcgtcgcg   | ggtctccccg | cgccggcgac | gcatggtctc  | ggtgacggcg | cgcccgtcct | 9960  |
| cgcgggggccg | cagcgtgaag | acgccgccgc | gcatctccag  | gtggccgccg | ggggggtctc | 10020 |
| cgttgggcag  | ggagagggcg | ctgacgatgc | atcttatcaa  | ttggcccgtg | gggactccgc | 10080 |
| gcaaggacct  | gagcgtctcg | agatccacgg | gatccgaaaa  | ccgctgaacg | aaggcttcga | 10140 |
| gccagtcgca  | gtcgcaaggt | aggctgagcc | cggtttcttg  | ttcttcgggg | atttcgggag | 10200 |
| gcgggcgggc  | gatgctgctg | gtgatgaagt | tgaagtaggc  | ggtcctgaga | cggcggatgg | 10260 |
| tggcgaggag  | caccaggtcc | ttggggcccg | cttgctggat  | gcgcagacgg | tcggccatgc | 10320 |
| cccaggcgtg  | gtcctgacac | ctggcgagg  | ccttgtagta  | gtcctgcatg | agccgctcca | 10380 |
| cgggcacctc  | ctcctcgccc | gcgcggccgt | gcatgcgcgt  | gagcccgaac | ccgcgctggg | 10440 |
| gctggacgag  | cgccaggtcg | gcgacgacgc | gctcggcgag  | gatggcctgc | tgtatctggg | 10500 |
| tgaggggtgg  | ctggaagtcg | tcgaagtcga | cgaagcggtg  | gtaggctccg | gtgttgatgg | 10560 |
| tataggagca  | gttggccatg | acggaccagt | tgacggtctg  | gtggccgggt | cgcacgagct | 10620 |
| cgtggtactt  | gaggcgcgag | taggcgcgcg | tgtcgaagat  | gtagtcgttg | cagggtgcga | 10680 |
| cgagggtactg | gtatccgacg | aggaagtgcg | gcggcggtcg  | gcggtagagc | ggccatcgct | 10740 |
| cgggtggcggg | ggcgccgggc | gcgaggtcct | cgagcatgag  | gcggtggtag | ccgtagatgt | 10800 |
| acctggacat  | ccaggtgatg | ccggcgggcg | tgggtggaggc | gcgcgggaac | tcgcggacgc | 10860 |
| ggttccagat  | gttgcgacgc | ggcaggaagt | agttcatggt  | ggccgcggtc | tggcccgtga | 10920 |
| ggcgcgcgca  | gtcgtggatg | ctctagacat | acgggcaaaa  | acgaaagcgg | tcagcggctc | 10980 |
| gactccgtgg  | cctggaggct | aagcgaacgg | gttgggctgc  | gcgtgtaccc | cggttcgaat | 11040 |
| ctcgaatcag  | gctggagccg | cagctaactg | ggtactggca  | ctcccgtctc | gacccaagcc | 11100 |
| tgctaacgaa  | acctccagga | tacggaggcg | ggtcgttttt  | tggccttggg | cgctggtcat | 11160 |
| gaaaaactag  | taagcgcgga | aagcgaccgc | ccgcgatggc  | tcgctgccgt | agtctggaga | 11220 |
| aagaatcgcc  | agggttgcgt | tgcggtgtgc | cccggttcga  | gcctcagcgc | tcggcgccgg | 11280 |
| ccggattccg  | cggctaactg | gggcgtgggt | gccccgtcgt  | ttccaagacc | ccttagccag | 11340 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |            |            |             |       |
|------------|------------|------------|------------|------------|-------------|-------|
| ccgacttctc | cagttacgga | gcgagcccct | ctttttcttg | tgtttttgcc | agatgcatcc  | 11400 |
| cgtactgcgg | cagatgcgcc | cccaccctcc | acctcaaccg | cccctaccgc | cgcagcagca  | 11460 |
| gcaacagccg | gcgcttctgc | ccccgcccc  | gcagcagcca | gccactaccg | cggcggccgc  | 11520 |
| cgtgagcgga | gccggcggtc | agtatgacct | ggccttgga  | gagggcgagg | ggctggcgcg  | 11580 |
| gctgggggcg | tcgtcgccgg | agcggcaccc | gcgcgtgcag | atgaaaagg  | acgctcgca   | 11640 |
| ggcctacgtg | cccaagcaga | acctgttcag | agacaggagc | ggcgaggagc | ccgaggagat  | 11700 |
| gcgcgcctcc | cgcttccacg | cggggcggg  | gctgcggcg  | ggcctggacc | gaaagcgggt  | 11760 |
| gctgagggac | gaggatttcg | aggcggacga | gctgacgggg | atcagccccg | cgcgcgcgca  | 11820 |
| cgtggcccg  | gccaacctgg | tcacggcgta | cgagcagacc | gtgaaggagg | agagcaactt  | 11880 |
| ccaaaaatcc | ttcaacaacc | acgtgcgcac | gctgatcgcg | cgcgaggagg | tgaccctggg  | 11940 |
| cctgatgcac | ctgtgggacc | tgctggaggc | catcgtgcag | aacccacga  | gcaagccgct  | 12000 |
| gacggcgag  | ctgtttctgg | tggtgcagca | cagtcgggac | aacgagacgt | tcagggaggc  | 12060 |
| gctgctgaat | atcaccgagc | ccgagggccg | ctggctcctg | gacctggtga | acattctgca  | 12120 |
| gagcatcgtg | gtgcaggagc | gcgggctgcc | gctgtccgag | aagctggcgg | ctatcaactt  | 12180 |
| ctcggtgctg | agcctgggca | agtactacgc | taggaagatc | tacaagacc  | cgtacgtgcc  | 12240 |
| catagacaag | gaggtgaaga | tcgacgggtt | ttacatgcgc | atgaccctga | aagtgtgac   | 12300 |
| cctgagcgac | gatctggggg | tgtaccgcaa | cgacaggatg | caccgcgcgg | tgagcgccag  | 12360 |
| ccgccggcgc | gagctgagcg | accaggagct | gatgcacagc | ctgcagcggg | ccctgaccgg  | 12420 |
| ggccgggacc | gagggggaga | gctactttga | catgggcgcg | gacctgcgct | ggcagcccag  | 12480 |
| ccgccggggc | ttggaagctg | ccggcgggtc | cccctacgtg | gaggagggtg | acgatgagga  | 12540 |
| ggaggagggc | gagtacctgg | aagactgatg | gcgcgaccgt | atttttgcta | gatgcagcaa  | 12600 |
| cagccaccgc | ctcctgatcc | cgcgatgcgg | gcggcgctgc | agagccagcc | gtccggcatt  | 12660 |
| aactcctcgg | acgattggac | ccaggccatg | caacgcatca | tggcgctgac | gacccgcaat  | 12720 |
| cccgaagcct | ttagacagca | gcctcaggcc | aaccggctct | cggccatcct | ggaggccgtg  | 12780 |
| gtgccctcgc | gctcgaacct | cacgcacgag | aagggtgctg | ccatcgtgaa | cgcgctggtg  | 12840 |
| gagaacaagg | ccatccgcgg | cgacgaggcc | gggctggtgt | acaacgcgct | gctggagcgc  | 12900 |
| gtggcccgc  | acaacagcac | caacgtgcag | acgaacctgg | accgcatggt | gaccgacgtg  | 12960 |
| cgcgaggcgg | tgctgcagcg | cgagcggttc | caccgcgagt | cgaacctggg | ctccatggtg  | 13020 |
| gcgctgaacg | ccttcctgag | cacgcagccc | gccaacgtgc | cccggggcca | ggaggactac  | 13080 |
| accaacttca | tcagcgcgct | gcggctgatg | gtggccgagg | tgccccagag | cgagggtgtac | 13140 |
| cagtcggggc | cggactactt | cttccagacc | agtcgccagg | gcttgacagc | cgtgaacctg  | 13200 |
| agccaggctt | tcaagaactt | gcagggactg | tggggcgctg | aggccccggt | cggggaccgc  | 13260 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |             |            |             |       |
|------------|------------|------------|-------------|------------|-------------|-------|
| gcgacggtgt | cgagcctgct | gacgccgaac | tcgcgctgc   | tgctgctgct | ggtggcgccc  | 13320 |
| ttcacggaca | gcggcagcgt | gagccgcgac | tcgtacctgg  | gctacctgct | taacctgtac  | 13380 |
| cgcgaggcca | tcgggcaggc | gcacgtggac | gagcagacct  | accaggagat | caccacgtg   | 13440 |
| agccgcgcgc | tgggccagga | ggacccgggc | aacctggagg  | ccaccctgaa | cttcctgctg  | 13500 |
| accaaccggt | cgcagaagat | cccgcgccag | tacgcgctga  | gcaccgagga | ggagcgcctc  | 13560 |
| ctgcgctacg | tgcagcagag | cgtggggctg | ttcctgatgc  | aggagggggc | cacgcccagc  | 13620 |
| gccgcgctcg | acatgaccgc | gcgcaacatg | gagcccagca  | tgtacgctcg | caaccgcccg  | 13680 |
| ttcatcaata | agctgatgga | ctacttgcct | cgggcggccg  | ccatgaactc | ggactacttt  | 13740 |
| accaacgcca | tcttgaaccc | gcactggctc | ccgccgcccg  | ggttctacac | gggcgagtac  | 13800 |
| gacatgcccg | acccaacga  | cgggttcctg | tgggacgacg  | tggacagcag | cgtgttctcg  | 13860 |
| ccgcgccccg | ccaccaccgt | gtggaagaaa | gagggcgggg  | accggcgggc | gtcctcggcg  | 13920 |
| ctgtccggtc | gcgcgggtgc | tgccgcggcg | gtgcctgagg  | ccgccagccc | cttcccagac  | 13980 |
| ctgccctttt | cgctgaacag | cgtgcgcagc | agcgagctgg  | gtcggctgac | gcggccgcgc  | 14040 |
| ctgctggggc | aggaggagta | cctgaacgac | tccttgttga  | ggcccagagc | cgagaagaac  | 14100 |
| ttccccaata | acgggataga | gagcctgggt | gacaagatga  | gccgctggaa | gacgtacgcg  | 14160 |
| cacgagcaca | gggacgagcc | ccgagctagc | agcagcgcag  | gcaccgtag  | acgccagcga  | 14220 |
| cacgacaggc | agcggggctc | ggtgtggggc | gatgaggatt  | ccgccgacga | cagcagcgtg  | 14280 |
| ttggacttgg | gtgggagtg  | tggtggtaac | ccgttcgctc  | acttgcgccc | ccgtatcggg  | 14340 |
| cgctgatgt  | aagaatctga | aaaaataaaa | aacggtactc  | accaaggcca | tggcgaccag  | 14400 |
| cgtgcgttct | tctctgttgt | ttgtagtagt | atgatgaggc  | gcgtgtaccc | ggagggctct  | 14460 |
| cctccctcgt | acgagagcgt | gatgcagcag | gcggtggcgg  | cgccgatgca | gcccccgctg  | 14520 |
| gaggcgccct | acgtgcccc  | gcggtacctg | gcgcctacgg  | aggggcggaa | cagcattcgt  | 14580 |
| tactcggagc | tggcaccctt | gtacgatacc | acccggttgt  | acctggtgga | caacaagtcg  | 14640 |
| gcggacatcg | cctcgctgaa | ctaccagaac | gaccacagca  | acttcctgac | caccgtgggt  | 14700 |
| cagaacaacg | atttcacccc | cacggaggcc | agcaccacga  | ccatcaactt | tgacgagcgc  | 14760 |
| tcgcggtggg | gcggccagct | gaaaaccatc | atgcacacca  | acatgcccac | cgtgaacgag  | 14820 |
| ttcatgtaca | gcaacaagtt | caaggcgcgg | gtgatggctc  | cgcgcaagac | ccccaatggg  | 14880 |
| gtcgcggtgg | atgagaatta | tgatggtagt | caggacgagc  | tgacttacga | gtgggtggag  | 14940 |
| tttgagctgc | ccgagggcaa | cttctcgggt | accatgacca  | tcgatctgat | gaacaacgcc  | 15000 |
| atcatcgaca | actacttggc | ggtggggcgt | cagaacgggg  | tgctggagag | cgacatcggc  | 15060 |
| gtgaagtctg | acacgcgcaa | cttccggctg | ggctggggacc | ccgtgaccga | gctgggtgatg | 15120 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |             |            |             |       |
|-------------|------------|------------|-------------|------------|-------------|-------|
| ccgggcggtgt | acaccaacga | ggccttccac | cccgcacatcg | tcctgctgcc | cggtgcggc   | 15180 |
| gtggacttca  | ccgagagccg | cctcagcaac | ctgctgggca  | tccgcaagcg | gcagcccttc  | 15240 |
| caggaggggt  | tccagatcct | gtacgaggac | ctggaggggg  | gcaacatccc | cgctctcttg  | 15300 |
| gatgtcgaag  | cctatgagaa | aagcaaggag | gaggccgccg  | cagcggcgac | cgagccgtg   | 15360 |
| gccaccgcct  | ctaccgaggt | gcggggcgat | aattttgcta  | gcgccgcggc | agtggccgag  | 15420 |
| gcggctgaaa  | ccgaaagtaa | gatatgcac  | cagccggtgg  | agaaggacag | caaggacagg  | 15480 |
| agctacaacg  | tgctcgcgga | caagaaaaac | accgcctacc  | gcagctggta | cctggcctac  | 15540 |
| aactacggcg  | accccgagaa | gggcgtgcgc | tcctggacgc  | tgctcaccac | ctcggacgtc  | 15600 |
| acctgcggcg  | tggagcaagt | ctactggtcg | ctgcccagaca | tgatgcaaga | cccggtcacc  | 15660 |
| ttccgctcca  | cgctcaagt  | tagcaactac | ccggtggtgg  | gcgccgagct | cctgcccgtc  | 15720 |
| tactccaaga  | gcttcttcaa | cgagcaggcc | gtctactcgc  | agcagctgcg | cgcttcacc   | 15780 |
| tcgctcacgc  | acgtcttcaa | ccgcttcccc | gagaaccaga  | tcctcgtccg | cccggccgcg  | 15840 |
| cccaccatta  | ccaccgtcag | tgaaaacgtt | cctgctctca  | cagatcacgg | gaccctgccg  | 15900 |
| ctgcgcagca  | gtatccgggg | agtccagcgc | gtgaccgtca  | ctgacgccag | acgccgcacc  | 15960 |
| tgcccctacg  | tctacaaggc | cctgggcgta | gtcgcgccgc  | gcgtcctctc | gagccgcacc  | 16020 |
| ttctaaaaaa  | tgtccattct | catctcgccc | agtaataaca  | ccggttgggg | cctgcgcgcg  | 16080 |
| cccagcaaga  | tgtacggagg | cgctcgccaa | cgctccacgc  | aacaccccgt | gcgcgtgcgc  | 16140 |
| gggcacttcc  | gcgtccctg  | gggcgccttc | aaggccgcg   | tgcgctcgcg | caccaccgtc  | 16200 |
| gacgacgtga  | tcgaccaggt | ggtggccgac | gcgcgcaact  | acacgcccgc | cgccgcgccc  | 16260 |
| gcctccaccg  | tggacgccgt | catcgacagc | gtggtggccg  | atgcgcgccg | gtacgccgcg  | 16320 |
| gccaaagagc  | ggcggcgggc | catcgcccgg | cggcaccgga  | gcacccccgc | catgcgcgcg  | 16380 |
| gcgcgagcct  | tgctgcgcag | ggccaggcgc | acgggacgca  | gggccatgct | cagggcggcc  | 16440 |
| agacgcgcgg  | cctccggcag | cagcagcgcc | ggcaggaccc  | gcagacgcgc | ggccacggcg  | 16500 |
| gcggcgggcg  | ccatcgccag | catgtcccgc | ccgcggcgcg  | gcaacgtgta | ctgggtgcgc  | 16560 |
| gacgccgcca  | ccggtgtgcg | cgtgcccgtg | cgcacccgcc  | cccctcgcac | ttgaagatgc  | 16620 |
| tgacttcgcg  | atgttgatgt | gtcccagcgg | cgaggaggat  | gtccaagcgc | aaatacaagg  | 16680 |
| aagagatgct  | ccaggtcatc | gcgcctgaga | tctacggccc  | cgcggtgaag | gaggaaagaa  | 16740 |
| agccccgcaa  | actgaagcgg | gtcaaaaagg | acaaaaagga  | ggaggaagat | gtggacggac  | 16800 |
| tggtggagtt  | tgtgcgcgag | ttcgcccccc | ggcggcgcg   | gcagtggcgc | gggcggaaaag | 16860 |
| tgaaaccggt  | gctgcggccc | ggcaccacgg | tggtcttcac  | gcccggcgag | cgttccggct  | 16920 |
| ccgcctccaa  | gcgctcctac | gacgaggtgt | acggggacga  | ggacatcctc | gagcaggcgg  | 16980 |
| tcgagcgtct  | gggcgagttt | gcttacggca | agcgcagccg  | ccccgcgccc | ttgaaagagg  | 17040 |

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|             |            |            |            |            |            |       |
|-------------|------------|------------|------------|------------|------------|-------|
| aggcgggtgtc | catccccgtg | gaccacggca | acccacagcc | gagcctgaag | ccggtgaccc | 17100 |
| tgcagcaggt  | gctgccgagc | gcggcgccgc | gccggggctt | caagcgcgag | ggcggcgagg | 17160 |
| atctgtaccc  | gaccatgcag | ctgatgggtc | ccaagcgcca | gaagctggag | gacgtgctgg | 17220 |
| agcacatgaa  | ggtggacccc | gaggtgcagc | ccgaggtcaa | ggtgcggccc | atcaagcagg | 17280 |
| tggccccggg  | cctgggctgt | cagaccgtgg | acatcaagat | ccccacggag | cccatggaaa | 17340 |
| cgcagaccga  | gcccgtgaag | cccagcacca | gcaccatgga | ggtgcagacg | gatccctgga | 17400 |
| tgccggcgcc  | ggcttccacc | actcgccgaa | gacgcaagta | cggcgcggcc | agcctgctga | 17460 |
| tgcccaacta  | cgcgctgcat | ccttccatca | tccccacgcc | gggctaccgc | ggcacgcgct | 17520 |
| tctaccgcgg  | ctacaccagc | agccgcccga | agaccaccac | ccgccgccgc | cgctgctgca | 17580 |
| cccgccgcag  | cagcaccgcg | acttccgccg | ccgccctggt | gcggagagtg | taccgcagcg | 17640 |
| ggcgcgagcc  | tctgacctgt | ccgcgcgcgc | gctaccaccc | gagcatcgcc | atttaactct | 17700 |
| gccgtcgcct  | cctacttgca | gatatggccc | tcacatgccg | cctccgcgtc | cccattacgg | 17760 |
| gctaccgagg  | aagaaagccg | cgccgtagaa | ggctgacggg | gaacgggctg | cgtcgccatc | 17820 |
| accaccggcg  | gcggcgcgcc | atcagcaagc | ggttgggggg | aggcttcctg | cccgcgctga | 17880 |
| tccccatcat  | cgccgcggcg | atcggggcga | tccccggcat | agcttccgtg | gcggtgcagg | 17940 |
| cctctcagcg  | ccactgagac | acagcttgga | aaatttgtaa | taaaaaatg  | gactgacgct | 18000 |
| cctggtcctg  | tgatgtgtgt | ttttagatgg | aagacatcaa | tttttcgtcc | ctggcaccgc | 18060 |
| gacacggcac  | gcggccgttt | atgggcacct | ggagcgacat | cggcaacagc | caactgaacg | 18120 |
| ggggcgccct  | caattggagc | agtctctgga | gcgggcttaa | gaatttcggg | tccacgctca | 18180 |
| aaacctatgg  | caacaaggcg | tggaacagca | gcacagggca | ggcgctgagg | gaaaagctga | 18240 |
| aagagcagaa  | cttccagcag | aaggtggtcg | atggcctggc | ctcgggcata | aacgggggtg | 18300 |
| tggacctggc  | caaccaggcc | gtgcagaaac | agatcaacag | ccgcctggac | gcggtcccg  | 18360 |
| ccgcgggggtc | cgtggagatg | ccccaggtgg | aggaggagct | gcctcccctg | gacaagcgcg | 18420 |
| gcgacaagcg  | accgcgtccc | gacgcggagg | agacgctgct | gacgcacacg | gacgagccgc | 18480 |
| ccccgtacga  | ggaggcggtg | aaactgggtc | tgcccaccac | gcggcccgtg | gcgcctctgg | 18540 |
| ccaccgggggt | gctgaaaccc | agcagcagca | gccagcccgc | gacctggac  | ttgcctccgc | 18600 |
| ctgcttcccc  | cccctccaca | gtggctaagc | ccctgccgcc | ggtggccgtc | gcgtcgcgcg | 18660 |
| ccccccgagg  | ccgccccag  | gcgaactggc | agagcactct | gaacagcata | gtgggtctgg | 18720 |
| gagtgacag   | tgtgaagcgc | cgccgctgct | attaaaagac | actgtagcgc | ttaacttgct | 18780 |
| tgtctgtgtg  | tatatgtatg | tccgccgacc | agaaggagga | agaggcgctg | cgccgagttg | 18840 |
| caagatggcc  | accccatcga | tgctgcccc  | gtgggcgtac | atgcacatcg | ccggacagga | 18900 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |            |            |            |       |
|-------------|------------|------------|------------|------------|------------|-------|
| cgcttcggag  | tacctgagtc | cggttctggt | gcagttcgcc | cgcgccacag | acacctactt | 18960 |
| cagtctgggg  | aacaagttta | ggaacccac  | ggtggcgccc | acgcacgatg | tgaccaccga | 19020 |
| ccgcagccag  | cggtgacgc  | tgcgttcgt  | gcccgtggac | cgcgaggaca | acacctactc | 19080 |
| gtacaaagtg  | cgctacacgc | tggccgtggg | cgacaaccgc | gtgctggaca | tggccagcac | 19140 |
| ctactttgac  | atccgcggcg | tgctggatcg | ggggcccagc | ttcaaaccct | actccggcac | 19200 |
| cgctacaac   | agcctggctc | ccaagggagc | gcccacact  | tgccagtgga | catataaagc | 19260 |
| tggtgatact  | gatacagaaa | aaacctatac | atatggaaat | gcacctgtgc | aaggcattag | 19320 |
| cattacaaag  | gatggtattc | aacttggaac | tgacagcgat | ggtcaggcaa | tctatgcaga | 19380 |
| cgaaacttat  | caaccagagc | ctcaagtggg | tgatgctgaa | tggcatgaca | tcactggtac | 19440 |
| tgatgaaaaa  | tatggaggca | gagctcttaa | gcctgacacc | aaaatgaagc | cttgctatgg | 19500 |
| ttcttttgcc  | aagcctacca | ataaagaagg | agggcaggca | aatgtgaaaa | ccgaaacagg | 19560 |
| cggtaccaaa  | gaatatgaca | ttgacatggc | attcttcgat | aatcgaagtg | cagctgccgc | 19620 |
| cggcctagcc  | ccagaaattg | ttttgtatac | tgagaatgtg | gatctggaaa | ctccagatac | 19680 |
| ccatattgta  | tacaaggcag | gtacagatga | cagtagctct | tctatcaatt | tgggtcagca | 19740 |
| gtccatgccc  | aacagaccca | actacattgg | cttcagagac | aactttatcg | gtctgatgta | 19800 |
| ctacaacagc  | actggcaata | tgggtgtact | ggctggacag | gcctcccagc | tgaatgctgt | 19860 |
| ggtggacttg  | caggacagaa | acaccgaact | gtcctaccag | ctcttgcttg | actctctggg | 19920 |
| tgacagaacc  | aggtatttca | gtatgtggaa | tcaggcggtg | gacagttatg | accccgatgt | 19980 |
| gcgcattatt  | gaaaatcacg | gtgtggagga | tgaacttcct | aactattgct | tccccctgga | 20040 |
| tgctgtgggt  | agaactgata | cttaccaggg | aattaaggcc | aatggtgata | atcaaaccac | 20100 |
| ctggaccaaa  | gatgatactg | ttaatgatgc | taatgaattg | ggcaagggca | atcctttcgc | 20160 |
| catggagatc  | aacatccagg | ccaacctgtg | gcggaacttc | ctctacgcga | acgtggcgct | 20220 |
| gtacctgccc  | gactcctaca | agtacacgcc | ggccaacatc | acgctgcccc | ccaacaccaa | 20280 |
| cacctacgat  | tacatgaacg | gccgcgtggt | ggcgccctcg | ctggtggacg | cctacatcaa | 20340 |
| catcggggcg  | cgctggtcgc | tggaccccat | ggacaacgtc | aacccttca  | accaccaccg | 20400 |
| caacgcgggc  | ctgcgatacc | gctccatgct | cctgggcaac | gggcgctacg | tgcccttcca | 20460 |
| catccagggtg | ccccaaaagt | ttttcgccat | caagagcctc | ctgctcctgc | ccgggtccta | 20520 |
| cacctacgag  | tggaaacttc | gcaaggacgt | caacatgatc | ctgcagagct | ccctcggcaa | 20580 |
| cgacctgctc  | acggacgggg | cctccatcgc | cttcaccagc | atcaacctct | acgccacctt | 20640 |
| cttccccatg  | gcgcacaaca | ccgcctccac | gctcgaggcc | atgctgcgca | acgacaccaa | 20700 |
| cgaccagtcc  | ttcaacgact | acctctcggc | ggccaacatg | ctctacccca | tcccggccaa | 20760 |
| cgccaccaac  | gtgcccctct | ccatcccctc | gcgcaactgg | gccgccttcc | gcggctggtc | 20820 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| cttcacgcgc  | ctcaagaccc  | gcgagacgcc  | ctcgctcggc | tccgggttcg  | acccctactt  | 20880 |
| cgtctactcg  | ggctccatcc  | cctacctcga  | cggcaccttc | tacctcaacc  | acaccttcaa  | 20940 |
| gaagggtctcc | atcaccttcg  | actcctccgt  | cagctggccc | ggcaacgacc  | gcctcctgac  | 21000 |
| gccaacgag   | ttcgaaatca  | agcgcaccgt  | cgacggagag | gggtacaacg  | tggcccagtg  | 21060 |
| caacatgacc  | aaggactggg  | tcctgggtcca | gatgctggcc | cactacaaca  | tcggctacca  | 21120 |
| gggctttctac | gtgcccagag  | gctacaagga  | ccgcatgtac | tcctttcttc  | gcaacttcca  | 21180 |
| gcccattgagc | cgccaggctg  | tggacgaggt  | caactacaag | gactaccagg  | ccgtcacctt  | 21240 |
| ggcctaccag  | cacaacaact  | cgggcttcgt  | cggctacctc | gcgcccacca  | tgcgccaggg  | 21300 |
| ccagccctac  | cccgccaaact | acccctaccc  | gctcatcggc | aagagcgccg  | tcgccagcgt  | 21360 |
| caccagaaa   | aagttcctct  | gcgaccgggt  | catgtggcgc | atcccccttct | ccagcaactt  | 21420 |
| catgtccatg  | ggcgcgctca  | ccgacctcgg  | ccagaacatg | ctctacgcca  | actccgcccc  | 21480 |
| cgcgctagac  | atgaatttcg  | aagtcgaccc  | catggatgag | tccacccttc  | tctatgttgt  | 21540 |
| cttcgaagtc  | ttcgacgtcg  | tccgagtgc   | ccagccccac | cgcggcgtca  | tcgaggccgt  | 21600 |
| ctacctgcgc  | acgcccttct  | cggccggcaa  | cgccaccacc | taagcctctt  | gcttcttgca  | 21660 |
| agatgacggc  | ctgcgcgggc  | tccggcgagc  | aggagctcag | ggccatcctc  | cgcgacctgg  | 21720 |
| gctgcggggc  | ctgcttcctg  | ggcaccttcg  | acaagcgctt | cccgggattc  | atggccccgc  | 21780 |
| acaagctggc  | ctgcgccatc  | gtcaaacagg  | ccggccgcga | gaccggggggc | gagcactggc  | 21840 |
| tggccttcgc  | ctggaacccg  | cgctcccaca  | cctgctacct | cttcgacccc  | ttcgggttct  | 21900 |
| cggacgagcg  | cctcaagcag  | atctaccagt  | tcgagtacga | gggcctgctg  | cgtcgcagcg  | 21960 |
| ccctggccac  | cgaggaccgc  | tgcgtcaccc  | tggaaaagtc | caccagacc   | gtgcagggtc  | 22020 |
| cgcgctcggc  | cgctgcggg   | ctcttctgct  | gcatgttcct | gcacgccttc  | gtgactggc   | 22080 |
| ccgaccgccc  | catggacaag  | aacccacca   | tgaacttgct | gacgggggtg  | ccaacggca   | 22140 |
| tgtccagtc   | gccccagggtg | gaaccaccc   | tgcgccgcaa | ccaggaggcg  | ctctaccgct  | 22200 |
| tcctcaacgc  | ccactccgcc  | tactttcgct  | cccaccgcgc | gcgcatcgag  | aaggccaccg  | 22260 |
| ccttcgaccg  | catgaatcaa  | gacatgtaat  | ccggtgtgtg | tatgtgaatg  | ctttattcat  | 22320 |
| cataataaac  | agcacatgtt  | tatgccacct  | tctctgaggc | tctgacttta  | tttagaaatc  | 22380 |
| gaaggggttc  | tgccggctct  | cggcatggcc  | cgcgggcagg | gatacgttgc  | ggaactggta  | 22440 |
| cttgggcagc  | cacttgaact  | cggggatcag  | cagcttcggc | acggggagggt | cggggaacga  | 22500 |
| gtcgtccac   | agcttgcgcg  | tgagttgcag  | ggcgcccagc | aggtcggggc  | cggagatctt  | 22560 |
| gaaatcgag   | ttgggacccg  | cgttctgcgc  | gcgagagtta | cggtacacgg  | ggttgcagca  | 22620 |
| ctggaacacc  | atcaggggccg | ggtgcttcac  | gctcgccagc | accgtcgcg   | cggatgatgcc | 22680 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |             |            |            |       |
|------------|------------|-------------|-------------|------------|------------|-------|
| ctccacgtcc | agatcctcgg | cgttggccat  | cccgaagggg  | gtcatcttgc | aggtctgccg | 22740 |
| cccatgctg  | ggcacgcagc | cgggcttggtg | gttgcaatcg  | cagtgcaggg | ggatcagcat | 22800 |
| catctggggc | tgctcggagc | tcatgcccgg  | gtacatggcc  | ttcatgaaag | cctccagctg | 22860 |
| gcggaaggcc | tgctgcgcct | tgccgcccctc | ggtgaagaag  | accccgaggg | acttgctaga | 22920 |
| gaactgggtg | gtggcgcagc | cagcgtcgtg  | cacgcagcag  | cgcgcgctcg | tggtggccag | 22980 |
| ctgcaccacg | ctgcgcccc  | agcggttctg  | ggtgatcttg  | gcccggtcgg | ggttctcctt | 23040 |
| cagcgcgcg  | tgcccgttct | cgctcgccac  | atccatctcg  | atcgtgtgct | ccttctggat | 23100 |
| catcacggtc | ccgtgcaggc | accgcagctt  | gccctcggcc  | tcggtgcacc | cgtcagcca  | 23160 |
| cagcgcgag  | ccggtgctct | cccagttctt  | gtgggcgagc  | tgggagtcg  | agtcagcaa  | 23220 |
| gccctgcagg | aagcggccca | tcatcgtggt  | cagggctctg  | ttgctggtga | aggtcagcgg | 23280 |
| aatgccgcgg | tgctcctcgt | tcacatacag  | gtggcagata  | cggcggtaca | cctcgccctg | 23340 |
| ctcgggcatc | agctggaagg | cggacttcag  | gtcgtctctc  | acgcggtacc | ggtccatcag | 23400 |
| cagcgtcatc | acttccatgc | ccttctccca  | ggccgaaacg  | atcggcaggc | tcaggggggt | 23460 |
| cttcaccgtt | gtcatcttag | tcgcccgcgc  | cgaagtcagg  | gggtcgttct | cgccagggt  | 23520 |
| ctcaaact   | cgcttgccgt | ccttctcggg  | gatgcgcagc  | gggggaaagc | tgaagccac  | 23580 |
| ggccgccagc | tcctcctcgg | cctgcctttc  | gtcctcgtg   | tcctggctga | tgtcttgcaa | 23640 |
| aggcacatgc | ttggtcttgc | ggggtttctt  | tttgggcggc  | agaggcggcg | gcggagacgt | 23700 |
| gctgggcgag | cgcgagttct | cgctcaccac  | gactatttct  | tctccttggc | cgctcgcga  | 23760 |
| gaccacgcgg | cggtaggcat | gcctcttctg  | gggcagaggc  | ggaggcgacg | ggctctcgcg | 23820 |
| gttcggcggg | cggtggcag  | agccccttcc  | gcgttcgggg  | gtgcgctcct | ggcggcgctg | 23880 |
| ctctgactga | cttcctccgc | ggccggccat  | tgtgttctcc  | tagggagcaa | gcatggagac | 23940 |
| tcagccatcg | tcgccaacat | cgccatctgc  | ccccgccgcc  | gccgacgaga | accagcagca | 24000 |
| gcagaatgaa | agcttaaccg | ccccgccgcc  | cagccccacc  | tccgacgccg | cagccccaga | 24060 |
| catgcaagag | atggaggaat | ccatcgagat  | tgacctgggc  | tacgtgacgc | ccgcggagca | 24120 |
| cgaggaggag | ctggcagcgc | gcttttcagc  | cccgggaagag | aaccaccaag | agcagccaga | 24180 |
| gcaggaagca | gagagcgagc | agaaccaggc  | tgggctcgag  | catggcgact | acctgagcgg | 24240 |
| ggcagaggac | gtgctcatca | agcatctggc  | ccgccaatgc  | atcatcgtca | aggacgcgct | 24300 |
| gctcgaccgc | gccgaggtgc | ccctcagcgt  | ggcggagctc  | agccgcgcct | acgagcgcaa | 24360 |
| cctcttctcg | ccgcgcgtgc | cccccaagcg  | ccagcccaac  | ggcacctgcg | agcccaaccc | 24420 |
| gcgcctcaac | ttctacccgg | tcttcgcggg  | gcccgaggcc  | ctggccacct | accacctctt | 24480 |
| tttcaagaac | caaaggatcc | ccgtctcctg  | ccgcgccaac  | cgcacccgcg | ccgacgccct | 24540 |
| gctcaacctg | ggccccggcg | cccgccctacc | tgatatcgcc  | tccttggaag | aggttcccaa | 24600 |

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|             |             |             |             |            |             |       |
|-------------|-------------|-------------|-------------|------------|-------------|-------|
| gatcttcgag  | ggtctgggca  | gcgacgagac  | tcgggccgcg  | aacgctctgc | aaggaagcgg  | 24660 |
| agaggagcat  | gagcaccaca  | gcgccctggt  | ggagttggaa  | ggcgacaacg | cgcgccctggc | 24720 |
| ggtcctcaag  | cgcacggtcg  | agctgaccca  | cttcgcctac  | ccggcgctca | acctgcccc   | 24780 |
| caaggatcatg | agcgccgtca  | tggaccaggt  | gctcatcaag  | cgcgccctcg | ccctctcgga  | 24840 |
| ggaggagatg  | caggacccccg | agagctcgga  | cgagggcaag  | cccgtggtca | gcgacgagca  | 24900 |
| gctggcgcg   | tggctgggag  | cgagtagcac  | ccccagagc   | ctggaagagc | ggcgcaagct  | 24960 |
| catgatggcc  | gtggtcctgg  | tgaccgtgga  | gctggagtgt  | ctgcgccgct | tcttcgccga  | 25020 |
| cgcgagagacc | ctgcgcaagg  | tcgaggagaa  | cctgcactac  | ctcttcagac | acgggttcgt  | 25080 |
| gcgccaggcc  | tgcaagatct  | ccaacgtgga  | gctgaccaac  | ctggtctcct | acatgggcat  | 25140 |
| cctgcacgag  | aaccgcctgg  | ggcagaacgt  | gctgcacacc  | accctgcgcg | gggaggccccg | 25200 |
| ccgcgactac  | atccgcgact  | gcgtctacct  | gtacctctgc  | cacacctggc | agacgggcat  | 25260 |
| gggcgtgtgg  | cagcagtgcc  | tggaggagca  | gaacctgaaa  | gagctctgca | agctcctgca  | 25320 |
| gaagaacctc  | aaggccctgt  | ggaccggggt  | cgacgagcgc  | accaccgccg | cggacctggc  | 25380 |
| cgacctcatc  | ttccccgagc  | gcctgcggct  | gacgctgcgc  | aacgggctgc | ccgactttat  | 25440 |
| gagccaaaagc | atgttgcaaa  | actttcgctc  | tttcatcctc  | gaacgctccg | ggatcctgcc  | 25500 |
| cgccacctgc  | tccgcgctgc  | cctcggactt  | cgtgccgctg  | accttccgcg | agtgccccc   | 25560 |
| gccgctctgg  | agccactgct  | acctgctgcg  | cctggccaac  | tacctggcct | accactcgga  | 25620 |
| cgtgatcgag  | gacgtcagcg  | gcgagggcct  | gctcgagtgc  | cactgccgct | gcaacctctg  | 25680 |
| cacgccgcac  | cgctccctgg  | cctgcaaccc  | ccagctgctg  | agcgagaccc | agatcatcgg  | 25740 |
| caccttcgag  | ttgcaaggcc  | ccggcgaggg  | caaggggggt  | ctgaaactca | ccccggggct  | 25800 |
| gtggacctcg  | gcctacttgc  | gcaagttcgt  | gcccgaggac  | taccatccct | tcgagatcag  | 25860 |
| gttctacgag  | gaccaatccc  | agccgcccaa  | ggccgagctg  | tcggcctgcg | tcatcaccca  | 25920 |
| ggggggccatc | ctggcccaat  | tgcaagccat  | ccagaaatcc  | cgccaagaat | ttctgctgaa  | 25980 |
| aaagggccac  | ggggtctact  | tggacccccca | gaccggagag  | gagctcaacc | ccagcttccc  | 26040 |
| ccaggatgcc  | ccgaggaagc  | agcaagaagc  | tgaaagtgga  | gctgccgccg | ccgccggagg  | 26100 |
| atttggagga  | agactgggag  | agcagtcagg  | cagaggagga  | ggagatggaa | gactgggaca  | 26160 |
| gcactcaggc  | agaggaggac  | agcctgcaag  | acagtctgga  | ggaggaagac | gaggtggagg  | 26220 |
| aggcagagga  | agaagcagcc  | gccgccagac  | cgctcgtcctc | ggcggaggag | gagaaagcaa  | 26280 |
| gcagcacgga  | taccatctcc  | gctccgggtc  | ggggtcgcgg  | cggccggggc | cacagtagat  | 26340 |
| gggacgagac  | cgggcgcttc  | ccgaacccca  | ccaccagac   | cggtaagaag | gagcggcagg  | 26400 |
| gatacaagtc  | ctggcggggg  | cacaaaaacg  | ccatcgtctc  | ctgcttgcaa | gcctgcgggg  | 26460 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |            |             |       |
|-------------|-------------|-------------|------------|------------|-------------|-------|
| gcaacatctc  | cttcacccgg  | cgctacctgc  | tcttccaccg | cggggtgaac | ttcccccgca  | 26520 |
| acatcttgca  | ttactaccgt  | cacctccaca  | gcccctacta | ctgtttccaa | gaagaggcag  | 26580 |
| aaaccagca   | gcagcagcag  | cagcagaaaa  | ccagcggcag | cagctagaaa | atccacagcg  | 26640 |
| gcggcaggtg  | gactgaggat  | cgcggcgaac  | gagccggcgc | agacccggga | gctgaggaac  | 26700 |
| cggatctttc  | ccaccctcta  | tgccatcttc  | cagcagagtc | gggggcaaga | gcaggaaactg | 26760 |
| aaagtcaaga  | accgttctct  | gcgctcgctc  | acccgcagtt | gtctgtatca | caagagcgaa  | 26820 |
| gaccaacttc  | agcgcaactct | cgaggacgcc  | gaggctctct | tcaacaagta | ctgcgcgctc  | 26880 |
| actcttaaag  | agtagcccg   | gcccgcacc   | acacggaaaa | aggcgggaat | tacgtcacca  | 26940 |
| cctgcgccct  | tcgcccagacc | atcatcatga  | gcaaagagat | tcccacgcct | tacatgtgga  | 27000 |
| gctaccagcc  | ccagatgggc  | ctggccgccg  | gcgccgcca  | ggactactcc | acccgcagta  | 27060 |
| actggctcag  | tgccggggcc  | gcgatgatct  | cacgggtgaa | tgacatccgc | gcccaccgaa  | 27120 |
| accagatact  | cctagaacag  | tcagcgatca  | ccgccacgcc | ccgccatcac | cttaatccgc  | 27180 |
| gtaattggcc  | cgccgccctg  | gtgtaccagg  | aaattcccca | gcccacgacc | gtactacttc  | 27240 |
| cgcgagacgc  | ccaggccgaa  | gtccagctga  | ctaactcagg | tgtccagctg | gccggcggcg  | 27300 |
| ccgccctgtg  | tcgtcaccgc  | cccgtcagg   | gtataaagcg | gctggtgatc | cgaggcagag  | 27360 |
| gcacacagct  | caacgacgag  | gtggtgagct  | cttcgctggg | tctgcgacct | gacggagtct  | 27420 |
| tccaactcgc  | cggatcgggg  | agatcttcct  | tcacgcctcg | tcaggccgtc | ctgactttgg  | 27480 |
| agagttcgtc  | ctcgcagccc  | cgctcgggtg  | gcacgcggac | tctccagttc | gtggaggagt  | 27540 |
| tactccctc   | ggtctacttc  | aacccttct   | ccggctcccc | cggccactac | ccggacgagt  | 27600 |
| tcatcccgaa  | cttcgacgcc  | atcagcgagt  | cgggtggacg | ctacgattga | atgtcccatg  | 27660 |
| gtggcgcggc  | tgacctagct  | cggcttcgac  | acctggacca | ctgccgccgc | ttccgctgct  | 27720 |
| tcgctcggga  | tctcgccgag  | tttgccctact | ttgagctgcc | cgaggagcac | cctcagggcc  | 27780 |
| cggcccacgg  | agtgcggtac  | gtcgtcgaag  | ggggtctcga | ctcccacctg | cttcggatct  | 27840 |
| tcagccagcg  | tccgatcctg  | gccgagcgcg  | agcaaggaca | gaccttctg  | accctgtact  | 27900 |
| gcacttgcaa  | ccaccccggc  | ctgcatgaaa  | gtctttgttg | tctgctgtgt | actgagtata  | 27960 |
| ataaaaagctg | agatcagcga  | ctactccgga  | cttccgtgtg | ttcctgctat | caaccagtcc  | 28020 |
| ctgttcttca  | ccgggaacga  | gaccgagctc  | cagctccagt | gtaagcccca | caagaagtac  | 28080 |
| ctcacctggc  | tgttccaggg  | ctctccgac   | gccgttgta  | accactgcga | caacgacgga  | 28140 |
| gtcctgctga  | gcggccctgc  | caaccttact  | ttttccaccc | gcagaagcaa | gctccagctc  | 28200 |
| ttccaaccct  | tcctccccgg  | gacctatcag  | tgctgtctcg | gaccttgcca | tcacaccttc  | 28260 |
| cacctgatcc  | cgaataccac  | agcgtcgctc  | cccgtacta  | acaaccaaac | taccaccaa   | 28320 |
| cgccaccgtc  | gcgaccgcgg  | acatgtacag  | agctcgagaa | gtactaggcc | acaatacatg  | 28380 |



368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |            |            |             |       |
|-------------|------------|-------------|------------|------------|-------------|-------|
| cccatattag  | actatgaggc | cgagccacag  | cgacccatgc | tccccgctat | tagttacttc  | 28440 |
| aatctaaccg  | gcgagatga  | ctgacccact  | ggccaacaac | aacgtcaacg | accttctcct  | 28500 |
| ggacatggac  | ggccgcgcct | cggagcagcg  | actcgcccaa | cttcgcattc | gccagcagca  | 28560 |
| ggagagagcc  | gtcaaggagc | tgcaggacgg  | catagccatc | caccagtgc  | agaaaggcat  | 28620 |
| cttctgcctg  | gtgaaacagg | ccaagatctc  | ctacgaggtc | accccgaccg | accatcgcct  | 28680 |
| ctcctacgag  | ctcctgcagc | agcgccagaa  | gttcacctgc | ctggtcggag | tcaaccccat  | 28740 |
| cgatcatcacc | cagcagtcgg | gcgataccaa  | ggggtgcac  | cactgctcct | gcgactcccc  | 28800 |
| cgactgcgtc  | cacactctga | tcaagaccct  | ctgcggcctc | cgcgacctcc | tccccatgaa  | 28860 |
| ctaataccccc | ccttatccag | tgaataaaat  | atcatattga | tgatgattta | aataaaaaat  | 28920 |
| aatcatttga  | tttgaaataa | agatacaatc  | atattgatga | tttgagtttt | aaaaaataaa  | 28980 |
| gaatcactta  | cttgaaatct | gataccagggt | ctctgtccat | gttttctgcc | aacaccacct  | 29040 |
| cactccccctc | ttcccagctc | tggtagtgca  | gaccccgggc | ggctgcaaac | ttcctccaca  | 29100 |
| cgctgaaggg  | gatgtcaaat | tcctcctgtc  | cctcaatctt | cattttatct | tctatcagat  | 29160 |
| gtccaaaaaag | cgcgtccggg | tggatgatga  | cttcgacccc | gtctaccctc | acgatgcaga  | 29220 |
| caacgcaccg  | accgtgccct | tcatcaaccc  | ccccttcgtc | tcttcagatg | gattccaaga  | 29280 |
| gaagcccctg  | ggggtgctgt | ccctgcgact  | ggctgacccc | gtcaccacca | agaacgggga  | 29340 |
| aatcaccctc  | aagctggggg | aggggggtgga | cctcgactcc | tcgggaaaac | tcctctccaa  | 29400 |
| cacggccacc  | aaggccgccc | cccctctcag  | tttttccaac | aacaccattt | cccttaacat  | 29460 |
| ggatacccct  | ctttatacca | aagatggaaa  | attatcctta | caagtttctc | caccgttaaa  | 29520 |
| catattaaaa  | tcaaccattc | tgaacacatt  | agctgtagct | tatggatcag | gtttaggact  | 29580 |
| gagtgggtggc | actgctcttg | cagtacagtt  | ggcctctcca | ctcacttttg | atgaaaaaagg | 29640 |
| aaatattaaa  | attaacctag | ccagtgggtcc | attaacagtt | gatgcaagtc | gacttagtat  | 29700 |
| caactgcaaa  | agaggggtca | ctgtcactac  | ctcaggagat | gcaattgaaa | gcaacataag  | 29760 |
| ctggccctaaa | ggtataagat | ttgaaggtaa  | tggcatagct | gcaaacattg | gcagaggatt  | 29820 |
| ggaatttgga  | accactagta | cagagactga  | tgtcacagat | gcatacccaa | ttcaagttaa  | 29880 |
| attgggtact  | ggccttacct | ttgacagtac  | aggcgccatt | gttgcttgga | acaaagagga  | 29940 |
| tgataaaactt | acattatgga | ccacagccga  | cccctcgcca | aattgcaaaa | tatactctga  | 30000 |
| aaaagatgcc  | aaactcacac | tttgcttgac  | aaagtgtgga | agtcaaattc | tgggtactgt  | 30060 |
| gactgtattg  | gcagtgaata | atggaagtct  | caacccaatc | acaaacacag | taagcactgc  | 30120 |
| actcgtctcc  | ctcaagtttg | atgcaagtgg  | agttttgcta | agcagctcca | cattagacaa  | 30180 |
| agaatattgg  | aacttcagaa | agggagatgt  | tacacctgct | gagccctata | ctaattgctat | 30240 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |             |             |       |
|-------------|-------------|-------------|-------------|-------------|-------------|-------|
| aggttttatg  | cctaacataa  | aggcctatcc  | taaaaacaca  | tctgcagctt  | caaaaagcca  | 30300 |
| tattgtcagt  | caagtttatc  | tcaatgggga  | tgaggccaaa  | ccactgatgc  | tgattattac  | 30360 |
| ttttaatgaa  | actgaggatg  | caacttgcac  | ctacagtatc  | acttttcaat  | ggaaatggga  | 30420 |
| tagtactaag  | tacacagggtg | aaacacttgc  | taccagctcc  | ttcaccttct  | cctacatcgc  | 30480 |
| ccaagaatga  | acactgtatc  | ccaccctgca  | tgccaaccct  | tcccacccca  | ctctgtctat  | 30540 |
| ggaaaaaact  | ctgaagcaca  | aaataaaaata | aagtccaagt  | gttttattga  | ttcaacagtt  | 30600 |
| ttacaggatt  | cgagcagtta  | tttttcctcc  | accctcccag  | gacatggaat  | acaccaccct  | 30660 |
| ctccccccgc  | acagccttga  | acatctgaat  | gccattgggtg | atggacatgc  | ttttgggtctc | 30720 |
| cacgttccac  | acagtttcag  | agcgagccag  | tctcgggtcg  | gtcagggaga  | tgaaaccctc  | 30780 |
| cgggcactcc  | cgcactctga  | cctcacagct  | caacagctga  | ggattgtcct  | cggtggtcgg  | 30840 |
| gatcacgggtt | atctggaaga  | agcagaagag  | cggcgggtggg | aatcatagtc  | cgcgaaacggg | 30900 |
| atcggccggt  | ggtgtcgcac  | caggccccgc  | agcagtcgct  | gccgccgccg  | ctccgtcaag  | 30960 |
| ctgctgctca  | gggggtccgg  | gtccagggac  | tccctcagca  | tgatgcccac  | ggccctcagc  | 31020 |
| atcagtcgtc  | tgggtgcggcg | ggcgcagcag  | cgcattgcgga | tctcgtcag   | gtcgtgcag   | 31080 |
| tacgtgcaac  | acaggaccac  | cagggtgttc  | aacagtccat  | agttcaacac  | gctccagccg  | 31140 |
| aaactcatcg  | cgggaaggat  | gctaccacag  | tggccgtcgt  | accagatcct  | caggtaaatac | 31200 |
| aagtggcgct  | ccctccagaa  | cacgtgccc   | acgtacatga  | tctccttggg  | catgtggcgg  | 31260 |
| ttcaccacct  | cccgttacca  | catcacctc   | tgggtgaaca  | tgacagccccg | gatgatcctg  | 31320 |
| cgggaaccaca | gggccagcac  | cgccccgcc   | gccatgcagc  | gaagagaccc  | cgggtccccg  | 31380 |
| caatggcaat  | ggaggaccca  | ccgctcgtac  | ccgtggatca  | tctgggagct  | gaacaagtct  | 31440 |
| atgttggcac  | agcacaggca  | tatgctcatg  | catctcttca  | gcactctcag  | ctcctcgggg  | 31500 |
| gtcaaaacca  | tatcccagg   | cacggggaac  | tcttgcagga  | cagcgaaccc  | cgcagaacag  | 31560 |
| ggcaatcctc  | gcacataact  | tacattgtgc  | atggacagg   | tatcgcaatc  | aggcagcacc  | 31620 |
| gggtgatcct  | ccaccagaga  | agcgcgggtc  | tcggtctcct  | cacagcgtgg  | taagggggcc  | 31680 |
| ggccgatacg  | ggtgatggcg  | ggacgcggct  | gatcgtgttc  | gcgaccgtgt  | catgatgcag  | 31740 |
| ttgctttcgg  | acattttcgt  | acttgctgta  | gcagaacctg  | gtccggggcg  | tgacaccga   | 31800 |
| tcgccggcg   | cgggtccggc  | gcttggaaac  | ctcgggtgtg  | aaattgtaaa  | acagccactc  | 31860 |
| tctcagaccg  | tgacgcagat  | ctagggcctc  | aggagtgatg  | aagatcccat  | catgcctgat  | 31920 |
| agctctgatc  | acatcgacca  | ccgtggaatg  | ggccagaccc  | agccagatga  | tgcaattttg  | 31980 |
| ttgggtttcg  | gtgacggcg   | gggaggggaag | aacaggaaga  | accatgatta  | acttttaatac | 32040 |
| caaacggtct  | cggagcactt  | caaaatgaag  | gtcgcggaga  | tggcacctct  | cgcccccgct  | 32100 |
| gtgttggtgg  | aaaataaacag | ccagggtcaaa | ggtgatacgg  | ttctcgagat  | gttccacggt  | 32160 |

## 368530-7006W01\_SequenceListing\_ST25.txt

```

ggcttccagc aaagcctcca cgcgcacatc cagaaacaag acaatagcga aagcgggagg 32220
gttctctaata tcctcaatca tcatgttaca ctctgcacc atccccagat aattttcatt 32280
tttccagcct tgaatgattc gaactagttc ctgaggtaaa tccaagccag ccatgataaa 32340
gagctcgcgc agagcgccct ccaccggcat tcttaagcac accctcataa ttccaagata 32400
ttctgctcct ggttcacctg cagcagattg acaagcggaa tatcaaaatc tctgccgcga 32460
tccctaagct cctccctcag caataactgt aagtactctt tcatactctc tccgaaatct 32520
ttagccatag gaccaccagg aataagatta gggcaagcca cagtacagat aaaccgaagt 32580
cctccccagt gagcattgcc aaatgcaaga ctgctataag catgctggct agaccggtg 32640
atatcttcca gataactgga cagaaaaatca cccaggcaat ttttaagaaa atcaacaaaa 32700
gaaaaatcct ccagggtcac gtttagagcc tcgggaacaa cgatgaagta aatgcaagcg 32760
gtgcggtt 32767

```

```

<210> 5
<211> 32767
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Artificially Synthesized

```

```

<400> 5
catcatcaat aatatacctc aaacttttgg tgcgcgttaa tatgcaaagt agctgtttga 60
atttggggag ggaggaaggt gattggctgc gggagcggcg accgttaggg gcggggcggg 120
tgacgttttg atgacgtggc tatgaggcgg agccggtttg caagtctctg tgggaaaagt 180
gacgtcaaac gaggtgtggt ttgaacacgg aaataactcaa ttttcccgcg ctctctgaca 240
ggaaatgagg tgtttctggg cggatgcaag tgaaaacggg ccattttcgc gcgaaaactg 300
aatgaggaag tgaaaatctg agtaatttcg cgtttatggc agggaggagt atttgccgag 360
ggccgagtag actttgaccg attacgtggg ggtttcgatt accgtatttt tcacctaaat 420
ttccgcgtac ggtgtcaaag tccggtgttt ttacgtacga tatcatttcc ccgaaagtgc 480
cacctgaccg taactataac ggtcctaagg tagcgaaagc tcagatctcc cgatccccta 540
tggtgactc tcagtacaat ctgctctgat gccgcatagt taagccagta tctgctccct 600
gcttgtgtgt tggaggtcgc tgagtagtgc gcgagcaaaa ttttaagctac aacaaggcaa 660
ggcttgaccg acaattgcat gaagaatctg cttaggggta ggcgttttgc gctgcttcgc 720
gatgtacggg ccagatatac gcgttgacat tgattattga ctagtatgcc aagtacgcc 780
cctattgacg tcaatgacgg taaatggccc gcctggcatt atgccagta catgacctta 840
tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac catggtgatg 900

```

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| cggttttggc | agtacatcaa | tgggcgtgga  | tagcggtttg  | actcacgggg | atttccaagt  | 960  |
| ctccacccca | ttgacgtcaa | tgggagtttg  | ttttggcacc  | aaaatcaacg | ggactttcca  | 1020 |
| aaatgtcgta | acaactccgc | cccattgacg  | caaatgggcg  | gtaggcgtgt | acggtgggag  | 1080 |
| gtctatataa | gcagagctcg | tttagtgaac  | cgtcagatca  | ctagaagctt | tattgcggta  | 1140 |
| gtttatcaca | gttaaattgc | taacgcagtc  | agtgccttctg | acacaacagt | ctcgaactta  | 1200 |
| aggctagagt | acttaatacg | actcactata  | ggctagttaa  | ggctagagtt | cgacgccacc  | 1260 |
| atgcgcgtga | tgggcatcct | gcgctcctac  | cagcagtggg  | ggatctgggg | catcctgggc  | 1320 |
| ttctggatgc | tgatgatctg | caacgtgtgg  | ggcaacctgt  | gggtgaccgt | gtactacggc  | 1380 |
| gtgcccgtgt | ggaaggaggc | caagaccacc  | ctgttctcg   | cctccgacgc | caaggccac   | 1440 |
| aaggaggagg | tgcacaacat | ctgggccacc  | cacgcctgcg  | tggccaccga | ccccaacccc  | 1500 |
| caggagatcg | tgctgaagaa | cgtagccgag  | aacttcaaca  | tgtggaagaa | cgacatgggtg | 1560 |
| gaccagatgc | acgaggacat | catctccctg  | tgggaccagt  | ccctgaagcc | ctgcgtgaag  | 1620 |
| ctgaccccc  | tgtgcgtgac | cctgaactgc  | tccgacgtga  | agatcaaggg | caccaacgcc  | 1680 |
| acctacaaca | acgccaccta | caacaacaac  | aacaccatct  | ccgacatgaa | gaactgctcc  | 1740 |
| ttcaacacca | ccaccgagat | caccgacaag  | aagaagaagg  | agtacgccct | gttctacaag  | 1800 |
| ctggacgtgg | tggccctgga | cggcaaggag  | accaactcca  | ccaactcctc | cgagtaccgc  | 1860 |
| ctgatcaact | gcaacacctc | cgccgtgacc  | caggcctgcc  | ccaaggtgtc | cttcgacccc  | 1920 |
| atccccatcc | actactgcgc | ccccgccggc  | tacgccatcc  | tgaagtgcaa | caacaagacc  | 1980 |
| ttcaacggca | ccggcccctg | caacaacgtg  | tccaccgtgc  | agtgcaccca | cggcatcaag  | 2040 |
| cccgtggtgt | ccaccagct  | gctgctgaac  | ggctccctgg  | ccgaggagga | ggtggtgac   | 2100 |
| cgcttcgaga | acctgaccaa | caacgccaa   | atcatcatcg  | tgcacctgaa | cgagtccgtg  | 2160 |
| gagatcaact | gcacccgccc | ctccaacaac  | acccgcaagt  | ccgtgcgcat | cggccccggc  | 2220 |
| cagaccttct | tcgccaccgg | cgacatcatc  | ggcgacatcc  | gccaggccca | ctgcaacatc  | 2280 |
| tcccgcaaga | agtggaacac | cacctgcag   | cgcgtgaagg  | agaagctgaa | ggagaagttc  | 2340 |
| cccaacaaga | ccatccagtt | cgccccctcc  | tccggcggcg  | acctggagat | caccaccac   | 2400 |
| tccttcaact | gccgcggcga | gttctttctac | tgctacacct  | ccgacctgtt | caactccacc  | 2460 |
| tacatgtcca | acaacaccgg | cggcgccaac  | atcacctgc   | agtgccgcat | caagcagatc  | 2520 |
| atccgcatgt | ggcagggcgt | gggccaggcc  | atgtacgcc   | cccccatcgc | cggcaacatc  | 2580 |
| acctgcaagt | ccaacatcac | cggcctgctg  | ctgacccgcg  | acggcggcaa | ggagaagaac  | 2640 |
| gacaccgaga | ccttccgccc | cggcgggcgg  | gacatgcgcg  | acaactggcg | ctccgagctg  | 2700 |
| tacaagtaca | aggtggtgga | gatcaagccc  | ctgggcatcg  | cccccgacaa | ggccaagcgc  | 2760 |
| cgcggtggtg | agcgcgagaa | gcgcgccgtg  | ggcatcgggc  | ccgtgttcct | gggcttcctg  | 2820 |

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|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| ggcgccgccc | gcagcaccat  | ggcgccgcc   | agcatgaccc  | tgaccgtgca | ggcccgccag  | 2880 |
| ctgctgagcg | gcatcgtgca  | gcagcagagc  | aacctgctgc  | gcgccatcga | ggcccagcag  | 2940 |
| cacatgctgc | agctgaccgt  | gtggggcatc  | aagcagctgc  | agacccgcgt | gctggccatc  | 3000 |
| gagcgctacc | tgaaggacca  | gcagctgctg  | ggcatctggg  | gctgcagcgg | caagctgac   | 3060 |
| tgcaccaccg | ccgtgccctg  | gaacgccagc  | tggagcaaca  | agagctacga | ggagatctgg  | 3120 |
| ggcaacatga | cctggatgca  | gtgggaccgc  | gagatcaaca  | actacaccaa | caccatctac  | 3180 |
| agcctgctgg | aggagagcca  | gaaccagcag  | gagaagaacg  | agaaggacct | gctggccctg  | 3240 |
| gacagctggg | agagcctgtg  | gagctggttc  | aacatcacca  | actggctgtg | gtacatccgc  | 3300 |
| atcttcatca | tcatcgtggg  | cggcctgac   | ggcctgcgca  | tcatcttcgc | cgtgctgagc  | 3360 |
| atcgtgaacc | gcgtgcgcca  | gggctacagc  | cccctgagct  | tccagaccct | gacccccagc  | 3420 |
| ccccgcgagc | ccgaccgcct  | ggggccgcatc | gaggaggagg  | gcggcgagca | ggaccgcgcc  | 3480 |
| cgagcgctgc | gcctggtgaa  | cggcttcctg  | gccctggcct  | gggaggacct | gcgcagcctg  | 3540 |
| tgctgttca  | gctaccaccg  | cctgcgcgac  | ctgatcctga  | tcgccgcccg | cgccgccgcc  | 3600 |
| ctgctggggc | gcagcagcct  | gtggggcctg  | cagaagggct  | gggaggccct | gaagtacctg  | 3660 |
| ggcagcctgg | tgcagtactg  | gggcctggag  | ctgaagaaga  | gcgccatcag | cctgttcgac  | 3720 |
| gccatcgcca | tcaccgtggc  | cgagggcacc  | gaccgcatca  | tcaacatcgt | gcagcgcac   | 3780 |
| agccgcgcct | tctacaacat  | ccccgcgcgc  | atccgccagg  | gcttcgaggc | caccctgcag  | 3840 |
| taaggtagct | ctagagtcga  | cccgggcggc  | caaaccgctg  | atcagcctcg | actgtgcctt  | 3900 |
| ctagttgcca | gccatctgtt  | gtttgcccct  | ccccgtgcc   | ttccttgacc | ctggaagggtg | 3960 |
| ccactcccac | tgtcctttcc  | taataaaatg  | aggaaaattgc | atcgcattgt | ctgagtaggt  | 4020 |
| gtcattctat | tctgggggggt | ggggtggggc  | aggacagcaa  | gggggaggat | tgggaagaca  | 4080 |
| atagcaggca | tgctggggat  | gcggtgggct  | ctatggcttc  | tgaggcgga  | agaaccagca  | 4140 |
| gatctgcaga | tctgaattca  | tctatgtcgg  | gtgcggagaa  | agaggtaatg | aaatggcatt  | 4200 |
| atgggtatta | tgggtctgca  | ttaatgaatc  | ggtcagatat  | cgacatatgc | tggccaccgt  | 4260 |
| gcatgtggcc | tcgcaccccc  | gcaagacatg  | gcccaggttc  | gagcacaacg | tcatgaccgc  | 4320 |
| ctgcaatgtg | cacctgggct  | cccgcggagg  | catgttcacg  | ccctaccagt | gcaacatgca  | 4380 |
| atgtgtgaag | gtgctgctgg  | agccccgatgc | catgtccaga  | gtgagcctga | cgggggtgtt  | 4440 |
| tgacatgaat | gtggagctgt  | ggaaaattct  | gagatatgat  | gaatccaaga | ccagggtgccg | 4500 |
| ggcctgcgaa | tgcgagggca  | agcacgccag  | gcttcagccc  | gtgtgtgtgg | aggtgacgga  | 4560 |
| ggacctgcga | cccgatcatt  | tgggtgtgtc  | ctgcaacggg  | acggagtctg | gctccagcgg  | 4620 |
| ggaagaatct | gactagagtg  | agtagtggtt  | ggggctgggt  | gtgagcctgc | atgaggggca  | 4680 |

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|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| gaatgactaa | aatctgtggt | tttctgtgtg  | ttgcagcagc  | atgagcggaa  | gcgccctcctt | 4740 |
| tgagggaggg | gtattcagcc | cttatctgac  | ggggcgtctc  | ccctcctggg  | cgggagtgcg  | 4800 |
| tcagaatgtg | atgggatcca | cggtggacgg  | ccggcccgtg  | cagcccgcga  | actcttcaac  | 4860 |
| cctgacctac | gcgaccctga | gctcctcgtc  | cgtggacgca  | gctgccgccg  | cagctgctgc  | 4920 |
| ttccgccgcc | agcgccgtgc | gcggaatggc  | cctgggcgcc  | ggctactaca  | gctctctggt  | 4980 |
| ggccaactcg | agttccacca | ataatcccgc  | cagcctgaac  | gaggagaagc  | tgctgctgct  | 5040 |
| gatggcccag | ctcgaggccc | tgaccacagc  | cctgggcgag  | ctgaccacagc | aggtgggtca  | 5100 |
| gctgcaggcg | gagacgcggg | ccgcggttgc  | cacggtgaaa  | accaaataaa  | aaatgaatca  | 5160 |
| ataaataaac | ggagacggtt | gttgatttta  | acacagagtc  | ttgaatcttt  | atttgatttt  | 5220 |
| tcgcgcgcgg | taggccctgg | accaccggtc  | tcgatcattg  | agcacccggt  | ggatcttttc  | 5280 |
| caggaccccg | tagaggtggg | cttggatggt  | gaggtacatg  | ggcatgagcc  | cgtcccgggg  | 5340 |
| gtggaggtag | ctccattgca | gggcctcgtg  | ctcggggatg  | gtgttgtaaa  | tcaccacagtc | 5400 |
| atagcagggg | cgcagggcgt | ggtgctgcac  | gatgtccttg  | aggaggagac  | tgatggccac  | 5460 |
| gggcagcccc | ttggtgtagg | tgttgacgaa  | cctgttgagc  | tgggagggat  | gcatgcgggg  | 5520 |
| ggagatgaga | tgcatcttgg | cctggatctt  | gagattggcg  | atgttcccgc  | ccagatcccg  | 5580 |
| ccgggggttc | atgttgtagc | ggaccaccag  | cacggtgtat  | ccggtgcact  | tggggaattt  | 5640 |
| gtcatgcaac | ttggaaggga | aggcgtgaaa  | gaatttgagg  | acgcccttgt  | gaccgcccag  | 5700 |
| gttttccatg | cactcatcca | tgatgatggc  | gatgggcccg  | tgggcggcgg  | cctgggcaaa  | 5760 |
| gacgtttcgg | gggtcggaca | catcgtagtt  | gtggtcctgg  | gtgagctcgt  | cataggccat  | 5820 |
| tttaatgaat | ttggggcgga | gggtgcccga  | ctgggggacg  | aagggtgccct | cgatcccggg  | 5880 |
| ggcgtagttg | ccctcgcaga | tctgcatctc  | ccaggccttg  | agctcggagg  | gggggatcat  | 5940 |
| gtccacctgc | ggggcgatga | aaaaaacggt  | ttccggggcg  | ggggagatga  | gctgggccga  | 6000 |
| aagcaggttc | cggagcagct | gggacttgcc  | gcaaccggtg  | gggccgtaga  | tgaccccgat  | 6060 |
| gaccggctgc | aggtggtagt | tgagggagag  | acagctgccg  | tcctcgcgga  | ggaggggggc  | 6120 |
| cacctcgttc | atcatctcgc | gcacatgcat  | gttctcgcgc  | acgagttccg  | ccaggaggcg  | 6180 |
| ctcgcccccc | agcgagagga | gctcttgacg  | cgaggcgaa   | tttttcagcg  | gcttgagtcc  | 6240 |
| gtcggccatg | ggcatttttg | agaggggtctg | ttgcaagagt  | tccagacggt  | cccagagctc  | 6300 |
| ggtgatgtgc | tctagggcat | ctcgatccag  | cagacctcct  | cgtttcgcgg  | gttggggcga  | 6360 |
| ctgcgggagt | agggcaccag | gcgatgggcg  | tccagcgagg  | ccagggtccg  | gtccttccag  | 6420 |
| ggccgcaggg | tccgcgtcag | cgtggtctcc  | gtcacgggtga | aggggtgcgc  | gccgggctgg  | 6480 |
| gcgcttgca  | gggtgcgctt | caggctcatc  | cggctggtcg  | agaaccgctc  | ccggtcggcg  | 6540 |
| ccctgcgcgt | cggccaggta | gcaattgagc  | atgagttcgt  | agttgagcgc  | ctcggccgcg  | 6600 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| tggcccttgg | cgcgagctt  | acctttgaa   | gtgtgtccgc  | agacgggaca  | gaggagggac  | 6660 |
| ttgagggcgt | agagcttggg | ggcgaggaag  | acggactcgg  | gggcgtaggc  | gtccgcgccg  | 6720 |
| cagctggcgc | agacggtctc | gcactccacg  | agccagggtga | ggtcggggcg  | gttgggggtca | 6780 |
| aaaacgaggt | ttcctccgtg | ctttttgatg  | cgtttcttac  | ctctggtctc  | catgagctcg  | 6840 |
| tgtccccgct | gggtgacaaa | gaggctgtcc  | gtgtccccgt  | agaccgactt  | tatggggccgg | 6900 |
| tcctcgagcg | gggtgccgcg | gtcctcgtcg  | tagaggaacc  | ccgcccactc  | cgagacgaag  | 6960 |
| gcccgggtcc | aggccagcac | gaaggaggcc  | acgtgggagg  | ggtagcggtc  | gttgtccacc  | 7020 |
| agcgggtcca | ccttctccag | ggtatgcaag  | cacatgtccc  | cctcgtcac   | atccaggaag  | 7080 |
| gtgattggct | tgtaagtgtg | ggccacgtga  | ccgggggtcc  | cggccggggg  | ggtataaaag  | 7140 |
| ggggcgggcc | cctgctcgtc | ctcactgtct  | tccggatcgc  | tgtccaggag  | cgccagctgt  | 7200 |
| tggggtaggt | attccctctc | gaaggcgggc  | atgacctcgg  | cactcaggtt  | gtcagtttct  | 7260 |
| agaaacgagg | aggatttgat | attgacggtg  | ccgttggaga  | cgcctttcat  | gagcccctcg  | 7320 |
| tccatttggg | cagaaaagac | gatctttttg  | ttgtcgagct  | tgggtggcgaa | ggagccgtag  | 7380 |
| agggcggttg | agagcagctt | ggcgatggag  | cgcaggtgtc  | ggttcttttc  | cttgtcggcg  | 7440 |
| cgctccttgg | cggcgatgtt | gagctgcacg  | tactcgcgcg  | ccacgcactt  | ccattcgggg  | 7500 |
| aagacggtgg | tgagctcgtc | gggcacgatt  | ctgaccgcgc  | agccgcggtt  | gtgcaggggtg | 7560 |
| atgaggtcca | cgctggtggc | cacctcgccg  | cgcagggggt  | cgttgggtcca | gcagaggcgc  | 7620 |
| ccgcccttgc | gcgagcagaa | ggggggcagc  | gggtccagca  | tgagctcgtc  | gggggggtcg  | 7680 |
| gcgtccacgg | tgaagatgcc | gggcaggagc  | tcggggtcga  | agtagctgat  | gcaggtgccc  | 7740 |
| agattgtcca | gcgccgcttg | ccagtcgcgc  | acggccagcg  | cgcgctcgta  | ggggctgagg  | 7800 |
| ggcgtgcccc | agggcatggg | gtgcgtgagc  | gcggaggcgt  | acatgccgca  | gatgtcgtag  | 7860 |
| acgtagaggg | gctcctcgag | gacgccgatg  | taggtggggg  | agcagcgccc  | cccgcggatg  | 7920 |
| ctggcgcgca | cgtagtcgta | cagctcgtgc  | gagggcgcga  | ggagccccgt  | gccgaggttg  | 7980 |
| gagcgttgcg | gcttttcggc | gcggtagacg  | atctggcgga  | agatggcgtg  | ggagttggag  | 8040 |
| gagatgggtg | gccttttgaa | gatgttgaag  | tgggcgtggg  | gcaggccgac  | cgagtccctg  | 8100 |
| atgaagtggg | cgtaggagtc | ctgcagcttg  | gcgacgagct  | cggcggtgac  | gaggacgtcc  | 8160 |
| agggcgagct | agtcgagggg | ctcttggtatg | atgtcatact  | tgagctggcc  | cttctgcttc  | 8220 |
| cacagctcgc | ggttgagaag | gaactcttcg  | cggtccttcc  | agtactcttc  | gagggggaac  | 8280 |
| ccgtcctgat | cggcacggta | agagcccacc  | atgtagaact  | ggttgacggc  | ctttagggcg  | 8340 |
| cagcagccct | tctccacggg | gagggcgtaa  | gcttgcgcgg  | ccttgcgcag  | ggaggtgtgg  | 8400 |
| gtgagggcga | aggtgtcgcg | caccatgacc  | ttgaggaact  | ggtgcttgaa  | gtcgaggtcg  | 8460 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |            |            |       |
|-------------|-------------|-------------|-------------|------------|------------|-------|
| tcgcagccgc  | cctgctccca  | gagttggaag  | tccgtgcgct  | tcttgtaggc | ggggtaggc  | 8520  |
| aaagcgaaaag | taacatcggt  | gaagaggatc  | ttgcccgcgc  | ggggcatgaa | gttgcgagtg | 8580  |
| atgcggaaaag | gctggggcac  | ctcggcccgg  | ttgttgatga  | cctgggcggc | gaggacgatc | 8640  |
| tcgtcgaagc  | cgttgatgtt  | gtgcccgcgc  | atgtagagtt  | ccacgaatcg | cgggcggccc | 8700  |
| ttgacgtggg  | gcagcttctt  | gagctcgtcg  | taggtgagct  | cggcggggtc | gctgagcccg | 8760  |
| tgctgctcga  | ggggccagtc  | ggcgacgtgg  | gggttggcgc  | tgaggaagga | agtccagaga | 8820  |
| tccacggcca  | gggcggtctg  | caagcggtcc  | cggtagctgac | ggaactgttg | gcccacggcc | 8880  |
| atTTTTTCgg  | gggtgacgca  | gtagaagggtg | cgggggtcgc  | cgtgccagcg | gtcccacttg | 8940  |
| agctggaggg  | cgaggtcgtg  | ggcgagctcg  | acgagcggcg  | ggtccccgga | gagtttcagt | 9000  |
| accagcatga  | aggggacgag  | ctgcttgccg  | aaggacccca  | tccaggtgta | ggtttccaca | 9060  |
| tcgtagggtga | ggaagagcct  | ttcggtgcgga | ggatgcgagc  | cgatggggaa | gaactggatc | 9120  |
| tcttgccacc  | agttggagga  | atggctgttg  | atgtgatgga  | agtagaaatg | ccgacggcgc | 9180  |
| gccgagcact  | cgtgcttggt  | tttatacaag  | cgtccgcagt  | gctcgcaacg | ctgcacggga | 9240  |
| tgcacgtgct  | gcacgagctg  | tacctgggtt  | cctttggcga  | ggaatttcag | tgggcagtgg | 9300  |
| agcgctggcg  | gctgcacttc  | gtgctgtact  | acgtcttggc  | catcggcgtg | gccatcgtct | 9360  |
| gcctcgatgg  | tggtcatgct  | gacgagcccc  | cgcgggaggg  | aggtccagac | ctcggctcgg | 9420  |
| acgggtcgga  | gagcgaggac  | gagggcgcgc  | aggccggagc  | tgtccagggt | cctgagacgc | 9480  |
| tgcggagtca  | ggtcagtggg  | cagcggcggc  | gcgcggttga  | cttgcaggag | cttttccagg | 9540  |
| gcgcgcggga  | ggtccagatg  | gtacttgatc  | tccacggcgc  | cgttggtggc | tacgtccacg | 9600  |
| gcttgacagg  | tgccgtgccc  | ctggggcgcc  | accaccgtgc  | cccgtttctt | cttgggcgct | 9660  |
| gcttccatgt  | cggtcagaag  | cggcggcgag  | gacgcgcgcc  | gggcggcagg | ggcggctcgg | 9720  |
| ggcccggagg  | caggggcggc  | aggggcacgt  | cggcgccgcg  | cgcgggcagg | ttctggtact | 9780  |
| gcgcccggag  | aagactggcg  | tgagcgacga  | cgcgacggtt  | gacgtcctgg | atctgacgcc | 9840  |
| tctgggtgaa  | ggccacggga  | cccgtgagtt  | tgaacctgaa  | agagagttcg | acagaatcaa | 9900  |
| tctcggtatc  | gttgacggcg  | gcctgccgca  | ggatctcttg  | cacgtcgccc | gagttgtcct | 9960  |
| ggtaggcgat  | ctcggtcagt  | aactgctcga  | tctcctcctc  | ctgaaggctt | ccgcggccgg | 10020 |
| cgcgctcgac  | ggtagccgcg  | aggctggttg  | agatgcggcc  | catgagctgc | gagaaggcgt | 10080 |
| tcatgccggc  | ctcgttccag  | acgcggctgt  | agaccacggc  | tccgtcgggg | tcgcgcgcgc | 10140 |
| gcatgaccac  | ctgggcgagg  | ttgagctcga  | cgtggcgcgt  | gaagaccgcg | tagttgcaga | 10200 |
| ggcgtgggta  | gaggtagttg  | agcgtggtgg  | cgatgtgctc  | ggtgacgaag | aagtacatga | 10260 |
| tccagcggcg  | gagcggcatc  | tcgctgacgt  | cgcccagggc  | ttccaagcgt | tccatggcct | 10320 |
| cgtagaagtc  | cacggcgaaag | ttgaaaaact  | gggagttgcg  | cgccgagacg | gtcaactcct | 10380 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |            |            |            |       |
|------------|------------|-------------|------------|------------|------------|-------|
| cctccagaag | acggatgagc | tcggcgatgg  | tggcgcgcac | ctcgcgctcg | aaggccccgg | 10440 |
| ggggctcctc | ttccatctcc | tcctcttctc  | cctccactaa | catctcttct | acttcctcct | 10500 |
| caggaggcgg | tggcggggga | ggggccctgc  | gtcgccggcg | gcgcacgggc | agacggtcga | 10560 |
| tgaagcgctc | gatggtctcc | ccgcgccggc  | gacgcatggt | ctcggtgacg | gcgcgcccgt | 10620 |
| cctcgcgggg | ccgcagcatg | aagacgccgc  | cgcgcatctc | caggtggccg | ccgggggggt | 10680 |
| ctccgttggg | cagggagagg | gcgctgacga  | tgcattctat | caattgacct | gtagggactc | 10740 |
| cgcgcaagga | cctgagcgtc | tcgagatcca  | cgggatccga | aaaccgctga | acgaaggctt | 10800 |
| cgagccagtc | gcagtcgcaa | ggtaggctga  | gcccggtttc | ttgttcttcg | ggtatttggt | 10860 |
| cgggaggcgg | gcgggcatg  | ctgctggtga  | tgaagttgaa | gtaggcggtc | ctgagacggc | 10920 |
| ggatggtggc | gaggagcacc | aggtccttgg  | gcccggcttg | ctggatgcgc | agacggtcgg | 10980 |
| ccatgcccc  | ggcgtggtcc | tgacacctgg  | cgaggtcctt | gtagtagtcc | tgcatgagcc | 11040 |
| gctccacggg | cacctcctcc | tcgcccgcgc  | ggccgtgcat | gcgcgtgagc | ccgaacccgc | 11100 |
| gctgcggctg | gacgagcgcc | aggtcggcga  | cgacgcgctc | ggtgaggatg | gcctgctgga | 11160 |
| tctgggtgag | ggtggtctgg | aagtcgtcga  | agtcgacgaa | gcggtggtag | gctccggtgt | 11220 |
| tgatggtgta | ggagcagttg | gccatgacgg  | accagttgac | ggtctggtgg | ccgggtcgca | 11280 |
| cgagctcgtg | gtacttgagg | cgcgagtagg  | cgcgcggtgc | gaagatgtag | tcgttgagg  | 11340 |
| cgcgcacgag | gtactggtat | ccgacgagga  | agtgcggcgg | cggctggcgg | tagagcggcc | 11400 |
| atcgctcgg  | ggcggggg   | ccgggcgca   | ggtcctcgag | catgaggcgg | tggtagccgt | 11460 |
| agatgtacct | ggacatccag | gtgatgccgg  | cggcggtggt | ggaggcgcg  | gggaactcgc | 11520 |
| ggacgcggtt | ccagatgttg | cgcagcggca  | ggaagtagtt | catggtggcc | gcggtctggc | 11580 |
| ccgtgaggcg | cgcgcagtcg | tggatgctct  | agacatacgg | gcaaaaacga | aagcggtcag | 11640 |
| cggctcgact | ccgtggcctg | gaggctaagc  | gaacgggttg | ggctgcgcgt | gtaccccggt | 11700 |
| tcgaatctcg | aatcaggctg | gagccgcagc  | taacgtggta | ctggcactcc | cgtctcgacc | 11760 |
| caagcctgct | aacgaaacct | ccaggatacg  | gaggcgggtc | gttttttggc | cttggtcgct | 11820 |
| ggtcatgaaa | aactagtaag | cgcggaagc   | ggccgcccgc | gatggctcgc | tgccgtagtc | 11880 |
| tggagaaaga | atcgccagg  | ttgcgttgcg  | gtgtgccccg | gttcgagcct | cagcgctcgg | 11940 |
| cgccggccgg | attccgcggc | taacgtgggc  | gtggctgccc | cgctcgtttc | aagacccctt | 12000 |
| agccagccga | cttctccagt | tacggagcga  | gcccctcttt | ttttttcttg | tgtttttgcc | 12060 |
| agatgcatcc | cgtactgcgg | cagatgcgcc  | cccaccctcc | accacaaccg | cccctaccgc | 12120 |
| agcagcagca | acagccggcg | cttctgcccc  | cgccccagca | gcagccagcc | actaccgcgg | 12180 |
| cggccgccgt | gagcggagcc | ggcggttcagt | atgacctggc | cttgaagag  | ggcgaggggc | 12240 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |            |             |       |
|-------------|-------------|-------------|------------|------------|-------------|-------|
| tggcgcggtct | gggggcggtcg | tcgccggagc  | ggcaccgcg  | cgtgcagatg | aaaagggacg  | 12300 |
| ctcgcgaggc  | ctacgtgccc  | aagcagaacc  | tgttcagaga | caggagcggc | gaggagcccg  | 12360 |
| aggagatgcg  | cgcctcccgc  | ttccacgcgg  | ggcgggagct | gcggcgcggc | ctggaccgaa  | 12420 |
| agcgggtgct  | gagggacgag  | gatttcgagg  | cggacgagct | gacggggatc | agccccgcgc  | 12480 |
| gcgcgcacgt  | ggccgcggcc  | aacctggtca  | cggcgtacga | gcagaccgtg | aaggaggaga  | 12540 |
| gcaacttcca  | aaaatccttc  | aacaaccacg  | tgcgcacgct | gatcgcgcg  | gaggaggtga  | 12600 |
| ccctgggcct  | gatgcacctg  | tgggacctgc  | tggaggccat | cgtgcagaac | cccacgagca  | 12660 |
| agccgctgac  | ggcgcagctg  | tttctggtgg  | tgcagcacag | tcgggacaac | gagacgttca  | 12720 |
| gggaggcgct  | gctgaatatc  | accgagcccc  | agggccgctg | gctcctggac | ctggtgaaca  | 12780 |
| ttttgcagag  | catcgtggtg  | caggagcgcg  | ggctgccgct | gtccgagaag | ctggcggcca  | 12840 |
| tcaacttctc  | ggtgctgagt  | ctgggcaagt  | actacgctag | gaagatctac | aagaccccgt  | 12900 |
| acgtgcccac  | agacaaggag  | gtgaagatcg  | acgggtttta | catgcgcatg | accctgaaag  | 12960 |
| tgctgaccct  | gagcgacgat  | ctgggggtgt  | accgcaacga | caggatgcac | cgcgcggtga  | 13020 |
| gcgccagccg  | ccggcgcgag  | ctgagcgacc  | aggagctgat | gcacagcctg | cagcggggcc  | 13080 |
| tgaccggggc  | cgggaccgag  | ggggagagct  | actttgacat | gggcgcggac | ctgcgctggc  | 13140 |
| agcccagccg  | ccgggccttg  | gaagctgccg  | gcggttcccc | ctacgtggag | gaggtggacg  | 13200 |
| atgaggagga  | ggagggcgag  | tacctggaag  | actgatggcg | cgaccgtatt | tttgctagat  | 13260 |
| gcagcaacag  | ccaccgccgc  | cgcctcctga  | tcccgcgatg | cgggcggcgc | tgcagagcca  | 13320 |
| gccgtccggc  | attaactcct  | cggacgattg  | gaccagggcc | atgcaacgca | tcatggcgct  | 13380 |
| gacgacccgc  | aatcccgaag  | ccttttagaca | gcagcctcag | gccaaccggc | tctcggccat  | 13440 |
| cctggaggcc  | gtggtgccct  | cgcgctcgaa  | ccccacgcac | gagaagggtc | tggccatcgt  | 13500 |
| gaacgcgctg  | gtggagaaca  | aggccatccg  | cggtgacgag | gccgggctgg | tgtacaacgc  | 13560 |
| gctgctggag  | cgcgtagccc  | gctacaacag  | caccaacgtg | cagacgaacc | tggaccgcat  | 13620 |
| ggtgaccgac  | gtgcgcgagg  | cgggtgctga  | gcgcgagcgg | ttccaccgcg | agtcgaacct  | 13680 |
| gggctccatg  | gtggcgctga  | acgccttcct  | gagcacgcag | cccgccaacg | tgccccgggg  | 13740 |
| ccaggaggac  | tacaccaact  | tcatcagcgc  | gctgcggctg | atggtggccg | aggtgccccca | 13800 |
| gagcgagggtg | taccagtcgg  | ggccggacta  | cttcttccag | accagtcgcc | agggcttgca  | 13860 |
| gaccgtgaac  | ctgagccagg  | ctttcaagaa  | cttgacggga | ctgtggggcg | tgcaggcccc  | 13920 |
| ggtcggggac  | cgcgcgacgg  | tgtcgagcct  | gctgacgccg | aactcgcgcc | tgctgctgct  | 13980 |
| gctggtggcg  | cccttcacgg  | acagcggcag  | cgtgagccgc | gactcgtacc | tgggctacct  | 14040 |
| gcttaacctg  | taccgcgagg  | ccatcggaca  | ggcgcacgtg | gacgagcaga | cctaccagga  | 14100 |
| gatcaccac   | gtgagccgcg  | cgctggggcca | ggaggaccgg | ggcaacctgg | aggccaccct  | 14160 |

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|            |             |            |            |            |            |       |
|------------|-------------|------------|------------|------------|------------|-------|
| gaacttcctg | ctgaccaacc  | ggtcgcagaa | gatccccgcc | cagtacgcgc | tgagcaccga | 14220 |
| ggaggagcgc | atcctgcgct  | acgtgcagca | gagcgtgggg | ctgttcctga | tgcaggaggg | 14280 |
| ggccacgccc | agcgcggcgc  | tcgacatgac | cgcgcgcaac | atggagccca | gcatgtacgc | 14340 |
| ccgcaaccgc | ccgttcatca  | ataagctgat | ggactacttg | catcgggcgg | ccgccatgaa | 14400 |
| ctcggactac | tttaccaacg  | ccatcttgaa | cccgcactgg | ctccccccgc | ccgggttcta | 14460 |
| cacgggcgag | tacgacatgc  | ccgaccccaa | cgacgggttc | ctgtgggacg | acgtggacag | 14520 |
| cagcgtgttc | tcgccgcgtc  | caggaaccaa | tgccgtgtgg | aagaaagagg | gcggggaccg | 14580 |
| gcggccgtcc | tcggcgctgt  | ccggtcgcgc | gggtgctgcc | gcggcggtgc | ccgaggccgc | 14640 |
| cagccccctt | ccgagcctgc  | ccttttcgct | gaacagcgtg | cgcagcagcg | agctgggtcg | 14700 |
| gctgacgcga | ccgcgcctgc  | tgggcgagga | ggagtacctg | aacgactcct | tgttgaggcc | 14760 |
| cgagcgcgag | aagaacttcc  | ccaataacgg | gatagagagc | ctggtggaca | agatgagccg | 14820 |
| ctggaagacg | tacgcgcacg  | agcacaggga | cgagccccga | gctagcagcg | caggcacccg | 14880 |
| tagacgccag | cggcacgaca  | ggcagcgggg | actggtgtgg | gacgatgagg | attccgccga | 14940 |
| cgacagcagc | gtgttggaact | tgggtgggag | tgggtgtaac | ccgttcgctc | acctgcgccc | 15000 |
| ccgtatcggg | cgcctgatgt  | aagaatctga | aaaaataaaa | gacggtactc | accaaggcca | 15060 |
| tggcgaccag | cgtgcgttct  | tctctgttgt | ttgtagtagt | atgatgaggc | gcgtgtaccc | 15120 |
| ggagggtcct | cctccctcgt  | acgagagcgt | gatgcagcag | gcggtggcgg | cggcgatgca | 15180 |
| gcccccgctg | gaggcgcctt  | acgtgcccc  | gcggtacctg | gcgcctacgg | aggggcggaa | 15240 |
| cagcattcgt | tactcggagc  | tggcacccct | gtacgatacc | acccggttgt | acctggtgga | 15300 |
| caacaagtcg | gcagacatcg  | cctcgctgaa | ctaccagaac | gaccacagca | acttcctgac | 15360 |
| caccgtggtg | cagaacaacg  | atttcacccc | cacggaggcc | agcacccaga | ccatcaactt | 15420 |
| tgacgagcgc | tcgcggtggg  | gcggccagct | gaaaaccatc | atgcacacca | acatgcccaa | 15480 |
| cgtgaacgag | ttcatgtaca  | gcaacaagtt | caaggcgcgg | gtgatggtct | cgcgcaagac | 15540 |
| ccccaacggg | gtggatgatg  | attatgatgg | tagtcaggac | gagctgacct | acgagtgggt | 15600 |
| ggagtttgag | ctgcccagag  | gcaacttctc | ggtgaccatg | accatcgatc | tgatgaacaa | 15660 |
| cgccatcatc | gacaactact  | tggcggtggg | gcggcagaac | ggggtgctgg | agagcgacat | 15720 |
| cggcgtgaag | ttcgacacgc  | gcaacttccg | gctgggctgg | gaccccgta  | ccgagctggt | 15780 |
| gatgccgggc | gtgtacacca  | acgaggcctt | ccaccccgac | atcgtcctgc | tgcccggctg | 15840 |
| cggcgtggac | ttcaccgaga  | gccgcctcag | caacctgctg | ggcatccgca | agcggcagcc | 15900 |
| cttccaggag | ggcttccaga  | tcctgtacga | ggacctggag | gggggcaaca | tccccgcgct | 15960 |
| cttggatgtc | gaagcctacg  | agaaaagcaa | ggaggatagc | accgccgcgg | cgaccgcagc | 16020 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |                                                         |       |
|------------|---------------------------------------------------------|-------|
| cgtagcgctg | cggcagcggc                                              | 16080 |
| cgaggcggct | gaaaccgaaa gtaagatagt catccagccg gtggagaagg acagcaagga  | 16140 |
| caggagctac | aacgtgctcg cggacaagaa aaacaccgcc taccgcagct ggtacctggc  | 16200 |
| ctacaactac | ggcgaccccc agaagggcgt gcgctcctgg acgctgctca ccacctcgga  | 16260 |
| cgtcacctgc | ggcgtggagc aagtctactg gtcgctgccc gacatgatgc aagaccgggt  | 16320 |
| caccttccgc | tccacgcgtc aagttagcaa ctaccgggtg gtgggcgccg agctcctgcc  | 16380 |
| cgtctactcc | aagagcttct tcaacgagca ggccgtctac tcgcagcagc tgcgcgcctt  | 16440 |
| cacctcgctc | acgcacgtct tcaaccgctt ccccgagaac cagatcctcg tccgcccgcc  | 16500 |
| cgcgcccacc | attaccaccg tcagtgtaaa cgttcctgct ctcacagatc acgggaccct  | 16560 |
| gccgctgcgc | agcagtatcc ggggagtcca gcgctgacc gtcactgacg ccagacgccg   | 16620 |
| cacctgcccc | tacgtctaca aggccctggg cgtagtcgcg ccgcgcgtcc tctcgagccg  | 16680 |
| caccttctaa | aaaatgtcca ttctcatctc gcccagtaat aacaccgggtt ggggcctgcg | 16740 |
| cgcgcccagc | aagatgtacg gaggcgctcg ccaacgctcc acgcaacacc ccgtagcgct  | 16800 |
| gcgcgggcac | ttccgcgctc cctggggcgc cctcaagggc cgcgtgcgct cgcgaccac   | 16860 |
| cgtcgacgac | gtgatcgacc aggtgggtgg cgacgcgcgc aactacacgc ccgccgccg   | 16920 |
| gcccgtctcc | accgtggacg ccgtcatcga cagcgtggtg gccgacgcgc gccggtacgc  | 16980 |
| ccgcaccaag | agccggcggc ggcgcatcgc ccggcggcac cggagcacc ccgccatgcg   | 17040 |
| cgcggcgcga | gccttgctgc gcagggccag gcgcacggga cgcagggccca tgctcagggc | 17100 |
| ggccagacgc | gcggcctccg gcagcagcag cgccggcagg acccgagac gcgcggccac   | 17160 |
| ggcggcggcg | gcggccatcg ccagcatgtc ccgcccgcgg cgcggcaacg tgtactgggt  | 17220 |
| gcgcgacgcc | gccaccgggtg tgcgcgtgcc cgtgcgcacc cgccccctc gcacttgaag  | 17280 |
| atgctgactt | cgcgatgttg atgtgtccca gcggcgagga ggatgtccaa gcgcaaatac  | 17340 |
| aaggaagaga | tgctccaggt catcgcgctt gagatctacg gccccgcggc ggcggtgaag  | 17400 |
| gaggaaagaa | agccccgcaa actgaagcgg gtcaaaaagg acaaaaagga ggaggaagat  | 17460 |
| gacggactgg | tggagtttgt gcgcgagttc gccccccggc ggcgctgca gtggcgggg    | 17520 |
| cggaaagtga | aaccggtgct gcggcccggc accacggtgg tcttcacgcc cggcgagcgt  | 17580 |
| tccggctccg | cctccaagcg ctctacgac gaggtgtacg gggacgagga catcctcgag   | 17640 |
| caggcggtcg | agcgtctggg cgagtttgcg tacggcaagc gcagccgcc cgcgcccttg   | 17700 |
| aaagaggagg | cgggtgtccat cccgctggac cacggcaacc ccacgccgag cctgaagccg | 17760 |
| gtgaccctgc | agcaggtgct accgagcgcg gcgccgcgcc ggggcttcaa gcgcgagggc  | 17820 |
| ggcgaggatc | tgtaccgcac catgcagctg atggtgcca agcgccagaa gctggaggac   | 17880 |
| gtgctggagc | acatgaaggt ggaccccag gtgcagcccg aggtcaaggt gcggcccatc   | 17940 |

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|             |            |             |            |             |             |       |
|-------------|------------|-------------|------------|-------------|-------------|-------|
| aagcaggtgg  | ccccgggcct | gggcgtgcag  | accgtggaca | tcaagatccc  | cacggagccc  | 18000 |
| atggaaaacgc | agaccgagcc | cgtgaagccc  | agcaccagca | ccatggaggt  | gcagacggat  | 18060 |
| ccctggatgc  | cagcaccagc | ttccaccagc  | actcgccgaa | gacgcaagta  | cggcgcggcc  | 18120 |
| agcctgctga  | tgcccaacta | cgcgctgcat  | ccttccatca | tccccacgcc  | gggctaccgc  | 18180 |
| ggcacgcgct  | tctaccgcgg | ctacaccagc  | agccgccgcc | gcaagaccac  | cacccgccgc  | 18240 |
| cgtcgtcgca  | gccgccgcag | cagcaccgcg  | acttccgcct | tggtgcggag  | agtgtatcgc  | 18300 |
| agcgggcgcg  | agcctctgac | cctgccgcgc  | gcgcgctacc | acccgagcat  | cgccatttaa  | 18360 |
| ctaccgcctc  | ctacttgag  | atatggccct  | cacatgccgc | ctccgcgtcc  | ccattacggg  | 18420 |
| ctaccgagga  | agaaagccgc | gccgtagaag  | gctgacgggg | aacgggctgc  | gtcgccatca  | 18480 |
| ccaccggcgg  | cggcgcgcca | tcagcaagcg  | gttgggggga | ggcttcctgc  | ccgcgctgat  | 18540 |
| ccccatcatc  | gccgcggcga | tcggggcgat  | ccccggcata | gcttcctgtg  | cgggtgcaggc | 18600 |
| ctctcagcgc  | cactgagaca | caaaaaagca  | tggatttgta | ataaaaaaaaa | aaatggactg  | 18660 |
| acgctcctgg  | tcctgtgatg | tgtgttttta  | gatggaagac | atcaattttt  | cgtccctggc  | 18720 |
| accgcgacac  | ggcacgcggc | cgtttatggg  | cacctggagc | gacatcggca  | acagccaact  | 18780 |
| gaacgggggc  | gccttcaatt | ggagcagtct  | ctggagcggg | cttaagaatt  | tcgggtccac  | 18840 |
| gctcaaaacc  | tatggcaaca | aggcgtggaa  | cagcagcaca | gggcaggcgc  | tgagggaaaa  | 18900 |
| gctgaaaagaa | cagaacttcc | agcagaaggt  | ggttgatggc | ctggcctcag  | gcatcaacgg  | 18960 |
| ggtggttgac  | ctggccaacc | aggccgtgca  | gaaacagatc | aacagccgcc  | tggacgcggt  | 19020 |
| cccgcgcgcg  | gggtccgtgg | agatgcccc   | ggtggaggag | gagctgcctc  | ccctggacaa  | 19080 |
| gcgcggcgac  | aagcgaccgc | gtcccgacgc  | ggaggagacg | ctgctgacgc  | acacggacga  | 19140 |
| gccgcccccg  | tacgaggagg | cggtgaaaact | gggcctgccc | accacgcggc  | ccgtggcgcc  | 19200 |
| tctggccacc  | ggagtgctga | aaccagcag   | cagccagccc | gcgaccctgg  | acttgcctcc  | 19260 |
| gcctcgcccc  | tccacagtgg | ctaagcccct  | gccgccggtg | gccgtcgcgt  | cgcgcgcccc  | 19320 |
| ccgaggccgc  | ccccaggcga | actggcagag  | cactctgaac | agcatcgtgg  | gtctgggagt  | 19380 |
| gcagagtgtg  | aagcgccgcc | gctgctatta  | aaagacactg | tagcgcttaa  | cttgcttgtc  | 19440 |
| tgtgtgtata  | tgtatgtccg | ccgaccagaa  | ggaggagtgt | gaagaggcgc  | gtcgccgagt  | 19500 |
| tgcaagatgg  | ccaccccatc | gatgctgccc  | cagtgggcgt | acatgcacat  | cgccggacag  | 19560 |
| gacgcttcgg  | agtacctgag | tccgggtctg  | gtgcagttcg | cccgcgccac  | agacacctac  | 19620 |
| ttcagtctgg  | ggaacaagtt | taggaacccc  | acggtggcgc | ccacgcacga  | tgtgaccacc  | 19680 |
| gaccgcagcc  | agcggctgac | gctgcgcttc  | gtgcccgtgg | accgcgagga  | caacacctac  | 19740 |
| tcgtacaaag  | tgcgctacac | gctggccgtg  | ggcgacaacc | gcgtgctgga  | catggccagc  | 19800 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |             |            |             |       |
|------------|-------------|-------------|-------------|------------|-------------|-------|
| acctactttg | acatccgcgg  | cggtgctggac | cggggcccta  | gcttcaaacc | ctactctggc  | 19860 |
| accgcctaca | acagcctagc  | tcccaagggga | gctcccaatt  | ccagccagtg | ggagcaagca  | 19920 |
| aaaacaggca | atgggggaac  | tatggaaaca  | cacacatatg  | gtgtggcccc | aatgggcgga  | 19980 |
| gagaatatta | caaaagatgg  | tcttcaaatt  | ggaactgacg  | ttacagcgaa | tcagaataaaa | 20040 |
| ccaatttatg | ccgacaaaac  | atttcaacca  | gaaccgcaag  | taggagaaga | aaattggcaa  | 20100 |
| gaaactgaaa | acttttatgg  | cggtagagct  | cttaaaaaag  | acacaaacat | gaaaccttgc  | 20160 |
| tatggctcct | atgctagacc  | caccaatgaa  | aaaggaggctc | aagctaaact | taaagttgga  | 20220 |
| gatgatggag | ttccaaccaa  | agaattcgac  | atagacctgg  | ctttctttga | tactcccgggt | 20280 |
| ggcaccgtga | acggtcaaga  | cgagtataaa  | gcagacattg  | tcatgtatac | cgaaaacacg  | 20340 |
| tatttgga   | ctccagacac  | gcatgtggta  | tacaaaccag  | gcaaggatga | tgcaagttct  | 20400 |
| gaaattaacc | tggttcagca  | gtctatgccc  | aacagaccca  | actacattgg | gttcagggac  | 20460 |
| aactttatcg | gtcttatgta  | ctacaacagc  | actggcaata  | tgggtgtgct | tgctggtcag  | 20520 |
| gcctcccagc | tgaatgctgt  | ggttgatttg  | caagacagaa  | acaccgagct | gtcctaccag  | 20580 |
| ctcttgcttg | actctttggg  | tgacagaacc  | cggtatttca  | gtatgtggaa | ccaggcgggtg | 20640 |
| gacagttatg | accccgatgt  | gcgcatcatc  | gaaaaccatg  | gtgtggagga | tgaattgcc   | 20700 |
| aactattgct | tccccttgg   | cggtctctggc | actaacgccg  | cataccaagg | tgtgaaagta  | 20760 |
| aaagatggct | aagatgggtga | tggtgagagt  | gaatgggaaa  | atgacgatac | tggtgcagct  | 20820 |
| cgaaatcaat | tatgtaaagg  | taacattttc  | gccatggaga  | ttaatctcca | ggctaacctg  | 20880 |
| tggagaagtt | tcctctactc  | gaacgtggcc  | ctgtacctgc  | ccgactccta | caagtacacg  | 20940 |
| ccgaccaacg | tcacgtgcc   | gaccaacacc  | aacacctacg  | attacatgaa | tggcagagt   | 21000 |
| acacctccct | cgctggtaga  | cgctacctc   | aacatcgggg  | cgcgctggct | gctggacccc  | 21060 |
| atggacaacg | tcaaccctt   | caaccaccac  | cgcaacgcgg  | gcctgcgcta | ccgctccatg  | 21120 |
| ctcctgggca | acgggcgcta  | cggtgccctt  | cacatccagg  | tgccccaaaa | gtttttcgcc  | 21180 |
| atcaagagcc | tcctgctcct  | gcccgggtcc  | tacacctacg  | agtggaaact | ccgcaaggac  | 21240 |
| gtcaacatga | tcctgcagag  | ctccctaggc  | aacgacctgc  | gcacggacgg | ggcctccatc  | 21300 |
| gccttcacca | gcatcaacct  | ctacgccacc  | ttcttcccca  | tggcgcacaa | caccgcctcc  | 21360 |
| acgctcgagg | ccatgctgcy  | caacgacacc  | aacgaccagt  | ccttcaacga | ctacctctcg  | 21420 |
| gcggccaaca | tgctctaccc  | catcccggcc  | aacgccacca  | acgtgccc   | ctccatcccc  | 21480 |
| tcgcgcaact | gggccgcctt  | ccgcggatgg  | tccttcacgc  | gcctgaagac | ccgcgagacg  | 21540 |
| ccctcgctcg | gctccgggtt  | cgaccctac   | ttcgctctact | cgggctccat | cccctaccta  | 21600 |
| gacggcacct | tctacctcaa  | ccacaccttc  | aagaaggctct | ccatcacctt | cgactcctcc  | 21660 |
| gtcagctggc | ccggcaacga  | ccgcctcctg  | acgcccacg   | agttcgaaat | caagcgcacc  | 21720 |

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|            |            |            |            |            |            |       |
|------------|------------|------------|------------|------------|------------|-------|
| gtcgacggag | agggatacaa | cgtggcccag | tgcaacatga | ccaaggactg | gttcctggtc | 21780 |
| cagatgctgg | cccactacaa | catcggctac | cagggcttct | acgtgcccga | gggctacaag | 21840 |
| gaccgcatgt | actccttctt | ccgcaacttc | cagcccatga | gccgccaggt | cgtggacgag | 21900 |
| gtcaactaca | aggactacca | ggccgtcacc | ctggcctacc | agcacaacaa | ctcgggcttc | 21960 |
| gtcggctacc | tcgcgcccac | catgcgccag | ggccagccct | accccgccaa | ctacccttac | 22020 |
| ccgctcatcg | gcaagagcgc | cgtcgccagc | gtcaccaga  | aaaagttcct | ctgcgaccgg | 22080 |
| gtcatgtggc | gcatccccct | ctccagcaac | ttcatgtcca | tgggcgcgct | caccgacctc | 22140 |
| ggccagaaca | tgctctacgc | caactccgcc | cacgcgctag | acatgaattt | cgaagtcgac | 22200 |
| cccatggatg | agtccaccct | tctctatgtt | gtcttcgaag | tcttcgacgt | cgtccgagtg | 22260 |
| caccagcccc | accgcggcgt | catcgaagcc | gtctacctgc | gcacgccctt | ctcggccggc | 22320 |
| aacgccacca | cctaagccgc | tcttgcttct | tgcaagatga | cggcgggctc | cggcgagcag | 22380 |
| gagctcaggg | ccatcctccg | cgacctgggc | tgccggccct | gcttcctggg | caccttcgac | 22440 |
| aagcgcttcc | ctggattcat | ggccccgcac | aagctggcct | gcgccatcgt | gaacacggcc | 22500 |
| ggccgcgaga | ccggggggcg | gacttggtcg | gccttcgcct | ggaacccgcg | ctcccacaca | 22560 |
| tgctacctct | tcgacccctt | cggtttctcg | gacgagcgcc | tcaagcagat | ctaccagttc | 22620 |
| gagtacgagg | gcctgctgcg | tcgcagcgcc | ctggccaccg | aggaccgctg | cgtcaccctg | 22680 |
| gaaaagtcca | cccagaccgt | gcagggtccg | cgctcggccg | cctgcgggct | cttctgctgc | 22740 |
| atgttcctgc | acgccttcgt | gacttggtcc | gaccgcccc  | tggacaagaa | ccccaccatg | 22800 |
| aacttactga | cgggggtgcc | caacggcatg | ctccagtcgc | cccagggtga | accaccctg  | 22860 |
| cgccgcaacc | aggaagcgct | ctaccgttcc | ctcaatgccc | actccgccta | ctttcgctcc | 22920 |
| caccgcgcgc | gcatcgagaa | ggccaccgcc | ttcgaccgca | tgaatcaaga | catgtaaaaa | 22980 |
| accggtgtgt | gtatgtgaat | gctttattca | taataaacag | cacatgttta | tgccaccttc | 23040 |
| tctgaggctc | tgactttatt | tagaaatcga | aggggttctg | ccggctctcg | gcatggcccg | 23100 |
| cgggcaggga | tacgttgctg | aactggtact | tgggcagcca | cttgaactcg | gggatcagca | 23160 |
| gcttgggcac | ggggaggctg | gggaacgagt | cgctccacag | cttgcgcgtg | agttgcaggg | 23220 |
| cgcccagcag | gtcgggcgcg | gagatcttga | aatcgcagtt | gggacccgcg | ttctgcgcgc | 23280 |
| gagagttgcg | gtacacgggg | ttgcagcact | ggaacaccat | cagggccggg | tgcttcacgc | 23340 |
| ttgccagcac | cgtcgcgtcg | gtgatgccct | ccacgtccag | atcctcggcg | ttggccatcc | 23400 |
| cgaagggggg | catcttgcat | gtctgccgcc | ccatgctggg | cacgcagccg | ggcttggtgt | 23460 |
| tgcaatcgca | gtgcaggggg | atcagcatca | tctgggcctg | ctcggagctc | atgcccgggt | 23520 |
| acatggcctt | catgaaagcc | tccagctggc | ggaaggcctg | ctgcgccttg | ccgccctcgg | 23580 |

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|            |            |            |            |            |             |       |
|------------|------------|------------|------------|------------|-------------|-------|
| tgaagaagac | cccgcaggac | ttgctagaga | actggttgg  | ggcgcagccg | gcgtcgtgca  | 23640 |
| cgagcagcg  | cggtcgttg  | ttggccagct | gcaccacgct | gcgccccag  | cggttctggg  | 23700 |
| tgatcttggc | ccggttgggg | ttctccttca | gcgcgcgctg | cccgttctcg | ctcgccacat  | 23760 |
| ccatctcgat | agtgtgctcc | ttctggatca | tcacggtccc | gtgcaggcac | cgagcttgc   | 23820 |
| cctcggttc  | ggtgcagccg | tgcagccaca | gcgcgcagcc | ggtgcactcc | cagttcttgt  | 23880 |
| gggcgatctg | ggagtgcgag | tgcacgaagc | cctgcaggaa | gcggcccatc | atcgcggtca  | 23940 |
| gggtcttgtt | gctggtgaag | gtcagcgga  | tgccgcggtg | ctcctcgttc | acatacaggt  | 24000 |
| ggcagatgcg | gcggtacacc | tcgccctgct | cgggcatcag | ctggaaggcg | gacttcaggt  | 24060 |
| cgctctccac | gcggtaccgg | tccatcagca | gcgtcatcac | ttccatgccc | ttctcccagg  | 24120 |
| ccgaaacgat | cggcaggctc | agggggttct | tcaccgccat | tgtcatctta | gtcgccgccg  | 24180 |
| ccgaggtcag | ggggtcgttc | tcgtccaggg | tctcaaacac | tcgcttgccg | tccttctcga  | 24240 |
| tgatgcgcac | ggggggaaag | ctgaagccca | cggccgccag | ctcctcctcg | gcctgccttt  | 24300 |
| cgctcctgct | gtcctggctg | atgtcttgca | aaggcacatg | cttggctctg | cggggtttct  | 24360 |
| ttttgggcgg | cagaggcggc | ggcgatgtgc | tgggagagcg | cgagttctcg | ttcaccacga  | 24420 |
| ctatttcttc | ttcttggccg | tcgtccgaga | ccacgcggcg | gtaggcagtc | ctcttctggg  | 24480 |
| gcagaggcgg | aggcgacggg | ctctcgcggt | tcggcgggcg | gctggcagag | ccccttccgc  | 24540 |
| gttcgggggt | gcgtccttgg | cggcgctgct | ctgactgact | tcctccgcgg | ccggccattg  | 24600 |
| tgttctccta | gggagcaaca | acaagcatgg | agactcagcc | atcgtcgcca | acatcgccat  | 24660 |
| ctgccccgc  | cgccaccgcc | gacgagaacc | agcagcagaa | tgaaagctta | accgccccgc  | 24720 |
| cgcccagccc | cacctccgac | gccgcggccc | cagacatgca | agagatggag | gaatccatcg  | 24780 |
| agattgacct | gggtacgtg  | acgcccgcgg | agcacgagga | ggagctggca | gcgcgctttt  | 24840 |
| cagccccgga | agagaaccac | caagagcagc | cagagcagga | agcagagAAC | gagcagaacc  | 24900 |
| aggctgggca | cgagcatggc | gactacctga | gcggggcaga | ggacgtgctc | atcaagcatc  | 24960 |
| tggcccgcca | atgcatcatc | gtcaaggacg | cgctgctcga | ccgcgccgag | gtgcccctca  | 25020 |
| gcgtggcgga | gctcagccgc | gcctacgagc | gcaacctctt | ctcgccgcgc | gtgccccca   | 25080 |
| agcgccagcc | caacggcacc | tgtgagccca | acccgcgcct | caacttctac | ccggtcttctg | 25140 |
| cggtgcccga | ggccctggcc | acctaccacc | tctttttcaa | gaaccaaagg | atccccgtct  | 25200 |
| cctgccgcgc | caaccgcacc | cgcgccgacg | ccctgtctaa | cctgggcccc | ggcgcccgcc  | 25260 |
| tacctgatat | cacctccttg | gaagaggttc | ccaagatctt | cgagggtctg | ggcagcgacg  | 25320 |
| agactcgggc | cgcaacgct  | ctgcaaggaa | gcggagagga | gcatgagcac | cacagcgccc  | 25380 |
| tggtgaggtt | ggaaggcgac | aacgcgcgcc | tggcggtcct | caagcgcacg | gtcgagctga  | 25440 |
| cccacttcgc | ctaccggcg  | ctcaacctgc | cccccaaggt | catgagcgcc | gtcatggacc  | 25500 |



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|             |            |            |            |            |             |       |
|-------------|------------|------------|------------|------------|-------------|-------|
| aggtgctcat  | caagcgcgcc | tcgcccctct | cggaggagga | gatgcaggac | cccagagatt  | 25560 |
| cggacgaggg  | caagcccgtg | gtcagcgacg | agcagctggc | gcgctggctg | ggagcgagta  | 25620 |
| gcacccccca  | gagcctggaa | gagcggcgca | agctcatgat | ggccgtggtc | ctggtgaccg  | 25680 |
| tggagctgga  | gtgtctgcgc | cgcttctttg | ccgacgcgga | gaccctgcgc | aaggctgagg  | 25740 |
| agaacctgca  | ctacctcttc | aggcacgggt | tcgtgcgcca | ggcctgcaag | atctccaacg  | 25800 |
| tggagctgac  | caacctggtc | tcctacatgg | gcatcctgca | cgagaaccgc | ctggggcaaa  | 25860 |
| acgtgctgca  | caccaccctg | cgcggggagg | cccgccgcga | ctacatccgc | gactgcgtct  | 25920 |
| acctgtacct  | ctgccacacc | tggcagacgg | gcatgggcgt | gtggcagcag | tgcctggagg  | 25980 |
| agcagaacct  | gaaagagctc | tgcaagctcc | tgcagaagaa | cctcaaggcc | ctgtggaccg  | 26040 |
| ggttcgacga  | gcgtaccacc | gcctcggacc | tggccgacct | catcttcccc | gagcgcctgc  | 26100 |
| ggctgacgct  | gcgcaacggg | ctgcccgact | ttatgagcca | aagcatgttg | caaaactttc  | 26160 |
| gctctttcat  | cctcgaacgc | tccgggatcc | tgcccgccac | ctgctccgcg | ctgccctcgg  | 26220 |
| acttcgtgcc  | gctgaccttc | cgcgagtgcc | ccccgccgct | ctggagccac | tgctacttgc  | 26280 |
| tgcgctggc   | caactacctg | gcctaccact | cggacgtgat | cgaggacgtc | agcggcgagg  | 26340 |
| gtctgctgga  | gtgccactgc | cgctgcaacc | tctgcacgcc | gcaccgctcc | ctggcctgca  | 26400 |
| acccccagct  | gctgagcgag | accagatca  | tcggcacctt | cgagttgcaa | ggccccggcg  | 26460 |
| acggcgaggg  | caaggggggt | ctgaaactca | ccccggggct | gtggacctcg | gcctacttgc  | 26520 |
| gcaagttcgt  | gcccgaggac | taccatccct | tcgagatcag | gttctacgag | gaccaatccc  | 26580 |
| agccgcccaa  | ggccgagctg | tcggcctgcg | tcatcaccca | gggggcatc  | ctggcccaat  | 26640 |
| tgcaagccat  | ccagaaatcc | cgccaagaat | ttctgctgaa | aaagggccac | gggttctact  | 26700 |
| tggacccccca | gaccggagag | gagctcaacc | ccagcttccc | ccaggatgcc | ccgaggaagc  | 26760 |
| agcaagaagc  | tgaaagtgga | gctgccgccg | ccggaggatt | tggaggaaga | ctgggagagc  | 26820 |
| agtcaggcag  | aggaggagga | gatggaagac | tgggacagca | ctcaggcaga | ggaggacagc  | 26880 |
| ctgcaagaca  | gtctggagga | ggaagacgag | gtggaggagg | cagaggaaga | agcagccgcc  | 26940 |
| gccagaccgt  | cgctctcggc | ggagaaagca | agcagcacgg | ataccatctc | cgctccgggt  | 27000 |
| cggggtcgcg  | gcggccgggc | ccacagtagg | tgggacgaga | ccgggcgctt | cccgaacccc  | 27060 |
| accacccaga  | ccggtaaaga | ggagcggcag | ggatacaagt | cctggcgggg | gcacaaaaaac | 27120 |
| gccatcgtct  | cctgcttgca | agcctgcggg | ggcaacatct | ccttcacccg | gcgctacctg  | 27180 |
| ctcttccacc  | gcggggtgaa | cttccccgcg | aacatcttgc | attactaccg | tcacctccac  | 27240 |
| agcccctact  | actgtttcca | agaagaggca | gaaacccagc | agcagcagaa | aaccagcggc  | 27300 |
| agcagcagct  | agaaaatcca | cagcggcggc | aggtggactg | aggatcgcgg | cgaacgagcc  | 27360 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |            |             |             |       |
|------------|-------------|-------------|------------|-------------|-------------|-------|
| ggcgcagacc | cgggagctga  | ggaaccggat  | ctttccacc  | ctctatgcca  | tcttccagca  | 27420 |
| gagtcggggg | caggagcagg  | aactgaaagt  | caagaaccgt | tctctgcgct  | cgctcaccgc  | 27480 |
| cagttgtctg | tatcacaaga  | gcgaagacca  | acttcagcgc | actctcgagg  | acgccgaggc  | 27540 |
| tctcttcaac | aagtactgcg  | cgctcactct  | taaagagtag | cccgcgccc   | cccacacacg  | 27600 |
| gaaaaaggcg | ggaattacgt  | caccacctgc  | gcccttcgcc | cgaccatcat  | gagcaaagag  | 27660 |
| attcccacgc | cttacatgtg  | gagctaccag  | ccccagatgg | gcctggccgc  | cggcgccgcc  | 27720 |
| caggactact | ccacccgcat  | gaactggctc  | agtgccgggc | ccgcgatgat  | ctcacgggtg  | 27780 |
| aatgacatcc | gcgcccaccg  | aaaccagata  | ctcctagaac | agtcagcgat  | caccgccacg  | 27840 |
| ccccgccatc | accttaatcc  | gcgtaattgg  | cccgccgcc  | tggtgtacca  | ggaaattccc  | 27900 |
| cagcccacga | ccgtactact  | tccgcgagac  | gcccaggccg | aagtccagct  | gactaactca  | 27960 |
| ggtgtccagc | tggccggcgg  | cgccgccctg  | tgtcgtcacc | gccccgctca  | gggtataaag  | 28020 |
| cggctggtga | tccgaggcag  | aggcacacag  | ctcaacgacg | agggtggtgag | ctcttcgctg  | 28080 |
| ggtctgcgac | ctgacggagt  | cttccaactc  | gccggatcgg | ggagatcttc  | cttcacgcct  | 28140 |
| cgtcaggccg | tcctgacttt  | ggagagttcg  | tcctcgcagc | cccgtcggg   | cggcatcggc  | 28200 |
| actctccagt | tcgtggagga  | gttcaactcc  | tcggtctact | tcaacccctt  | ctccggctcc  | 28260 |
| cccggccact | acccggacga  | gttcatcccc  | aacttcgacg | ccatcagcga  | gtcgggtggac | 28320 |
| ggctacgatt | gaatgtccca  | tggtggcgca  | gctgacctag | ctcggcttcg  | acacctggac  | 28380 |
| cactgccgcc | gcttccgctg  | cttcgctcgg  | gatctcgcg  | agtttgcccta | ctttgagctg  | 28440 |
| cccgaggagc | accctcaggg  | cccagcccac  | ggagtgcgga | tcatcgtcga  | agggggcctc  | 28500 |
| gactcccacc | tgcttcggat  | cttcagccag  | cgaccgatcc | tggtcgagcg  | cgaacaagga  | 28560 |
| cagacccttc | ttactttgta  | ctgcatctgc  | aaccaccccg | gcctgcatga  | aagtctttgt  | 28620 |
| tgtctgctgt | gtactgagta  | taataaaaagc | tgagatcagc | gactactccg  | gactcgattg  | 28680 |
| tgggtttcct | gctatcaacc  | ggtccctggt  | cttcaccggg | aacgagaccg  | agctccagct  | 28740 |
| ccagtgtaa  | ccccacaaga  | agtacctcac  | ctggctgttc | cagggctccc  | cgatcgccgt  | 28800 |
| tgtcaaccac | tgcgacaacg  | acggagtcct  | gctgagcggc | cctgccaacc  | ttactttttc  | 28860 |
| cacccgcaga | agcaagctcc  | agctctttcca | acccttcctc | cccgggacct  | atcagtgcgt  | 28920 |
| ctcaggaccc | tgccatcaca  | ccttcacact  | gatcccgaat | accacagcgc  | cgctccccgc  | 28980 |
| tactaacaac | caaactaccc  | accaacgcca  | ccgtcgcgac | ctttcctctg  | aatctaatac  | 29040 |
| cactaccgga | ggtggcttct  | gctgttagtg  | ctccccgcgc | ccgtcgaccc  | ccggtccccc  | 29100 |
| actcagtccc | ccgaggaggt  | tcgcaaatgc  | aaattccaag | aacctgggaa  | attcctcaaa  | 29160 |
| tgctaccgcc | aaaaatcaga  | catgcatccc  | agctggatca | tgatcattgg  | gatcgtgaac  | 29220 |
| attctggcct | gcacccctcat | ctcctttgtg  | atttaccctt | gctttgactt  | tggttggaac  | 29280 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |            |             |       |
|-------------|-------------|-------------|------------|------------|-------------|-------|
| tcgccagagg  | cgctctatct  | cccgccctgaa | cctgacacac | caccacagca | gcaacctcag  | 29340 |
| gcacacgcac  | taccaccacc  | acagcctagg  | ccacaataca | tgcccatatt | agactatgag  | 29400 |
| gccgagccac  | agcgacccat  | gctccccgct  | attagttact | tcaatctaac | cggcggagat  | 29460 |
| gactgaccca  | ctggccaata  | acaacgtcaa  | cgaccttctc | ctggacatgg | acggccgcgc  | 29520 |
| ctcggagcag  | cgactcgccc  | aacttcgcat  | tcgtcagcag | caggagagag | ccgtcaagga  | 29580 |
| gctgcaggac  | ggcatagcca  | tccaccagtg  | caagagaggc | atcttctgcc | tggtgaaaca  | 29640 |
| ggccaagatc  | tcctacgagg  | tcaccagac   | cgaccatcgc | ctctcctacg | agctcctgca  | 29700 |
| gcagcgccag  | aagttcacct  | gcctggctcg  | agtcaacccc | atcgtcatca | cccagcagtc  | 29760 |
| gggcgatacc  | aaggggtgca  | tccactgctc  | ctgcgactcc | cccgactgcg | tccacactct  | 29820 |
| gatcaagacc  | ctctgcggcc  | tccgcgacct  | cctccccatg | aactaatcac | ccccttatcc  | 29880 |
| agtgaataa   | agatcatatt  | gatgatgatt  | taaaataaaa | aaataatcat | ttgatttgaa  | 29940 |
| ataaagatac  | aatcatattg  | atgatttgag  | tttaacaaaa | ataaagaatc | acttacttga  | 30000 |
| aatctgatac  | caggctctctg | tccatgtttt  | ctgccaacac | cacctcactc | ccctcttccc  | 30060 |
| agctctggta  | ctgcaggccc  | cggcgggctg  | caaacttcct | ccacacgctg | aaggggatgt  | 30120 |
| caaattcctc  | ctgtccctca  | atcttcattt  | tatcttctat | cagatgtcca | aaaagcgcgt  | 30180 |
| ccgggtggat  | gatgacttcg  | accccgctca  | cccctacgat | gcagacaacg | caccgaccgt  | 30240 |
| gcccttcac   | aacccccct   | tcgtctcttc  | agatggattc | caagagaagc | ccctgggggt  | 30300 |
| gttgtccctg  | cgactggctg  | accccgtcac  | caccaagaac | ggggaaatca | ccctcaagct  | 30360 |
| gggagagggg  | gtggacctcg  | actcgtcggg  | aaaactcatc | tccaacacgg | ccaccaaggc  | 30420 |
| cgcgcgccct  | ctcagtattt  | caaacaacac  | catttccctt | aaaactgctg | cccctttcta  | 30480 |
| caacaacaat  | ggaacttta   | gcctcaatgt  | ctccacacca | ttagcagtat | ttccacatt   | 30540 |
| taacacttta  | ggcataagtc  | ttggaaacgg  | tcttcagact | tcaaataagt | tgttgactgt  | 30600 |
| acaactaact  | catcctctta  | cattcagctc  | aaatagcatc | acagtaaaaa | cagacaaaagg | 30660 |
| gctatatatt  | aactccagtg  | gaaacagagg  | acttgaggct | aatataagcc | taaaaagagg  | 30720 |
| actagttttt  | gacggtaatg  | ctattgcaac  | atatattgga | aatggcttag | actatggatc  | 30780 |
| ttatgatagt  | gatggaaaaa  | caagaccgt   | aattaccaa  | attggagcag | gattaaattt  | 30840 |
| tgatgctaac  | aaagcaatag  | ctgtcaaaact | aggcacagg  | ttaagttttg | actccgctgg  | 30900 |
| tgcccttgaca | gctggaaaca  | aacaggatga  | caagctaaca | ctttggacta | cccctgaccc  | 30960 |
| aagcccta    | tgtcaattac  | tttcagacag  | agatgccaaa | tttactctct | gtcttacaaa  | 31020 |
| atgcggtagt  | caaataactag | gcactgtggc  | agtggcggct | gttactgtag | gatcagcact  | 31080 |
| aaatccaatt  | aatgacacag  | tcaaaagcgc  | catagttttc | cttagatttg | attccgatgg  | 31140 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |             |            |       |
|-------------|------------|-------------|-------------|-------------|------------|-------|
| tgtactcatg  | tcaaactcat | caatggtagg  | tgattactgg  | aacttttaggg | agggacagac | 31200 |
| cactcaaagt  | gtagcctata | caaatgctgt  | gggattcatg  | ccaaatatag  | gtgcatatcc | 31260 |
| aaaaacccaa  | agtaaaacac | ctaaaaaatag | catagtcagt  | caggtatatt  | taactggaga | 31320 |
| aactactatg  | ccaatgacac | taaccataac  | tttcaatggc  | actgatgaaa  | aagacacaac | 31380 |
| cccagttagc  | acctactcta | tgactttttac | atggcagtgg  | actggagact  | ataaggacaa | 31440 |
| aaatattacc  | tttgctacca | actcattctc  | tttttcctac  | atcgcccagg  | aataatccca | 31500 |
| cccagcaagc  | caaccccttt | tcccaccacc  | tttgtctata  | tggaaaactct | gaaacagaaa | 31560 |
| aataaagttc  | aagtgtttta | ttgaatcaac  | agtttttacag | gactcgagca  | gttatttttc | 31620 |
| ctccaccctc  | ccaggacatg | gaatacacca  | ccctctcccc  | ccgcacagcc  | ttgaacatct | 31680 |
| gaatgccatt  | ggtgatggac | atgcttttgg  | tctccacgtt  | ccacacagtt  | tcagagcgag | 31740 |
| ccagtctcgg  | atcggtcagg | gagatgaaac  | cctccgggca  | ctcccgcac   | tgcacctcac | 31800 |
| agctcaacag  | ctgaggattg | tcctcgggtg  | tcgggatcac  | ggttatctgg  | aagaagcaga | 31860 |
| agagcggcgg  | tgggaatcat | agtccgcgaa  | cgggatcggc  | cggtggtgtc  | gcatcaggcc | 31920 |
| ccgcagcagt  | cgctgccgcc | gccgctccgt  | caagctgctg  | ctcagggggt  | tcgggtccag | 31980 |
| ggactccctc  | agcatgatgc | ccacggccct  | cagcatcagt  | cgtctggtgc  | ggcgggcgca | 32040 |
| gcagcgcagt  | cgaatctcgc | tcaggtcact  | gcagtacgtg  | caacacagga  | ccaccagggt | 32100 |
| gttcaacagt  | ccatagttca | acacgctcca  | gccgaaactc  | atcgcgggaa  | ggatgctacc | 32160 |
| cacgtggccg  | tcgtaccaga | tcctcaggta  | aatcaagtgg  | cgctccctcc  | agaagacgct | 32220 |
| gcccattgtac | atgatctcct | tgggcatgtg  | gcggttcacc  | acctcccggg  | accacatcac | 32280 |
| cctctgggtg  | aacatgcagc | cccggatgat  | cctgcggaac  | cacagggcca  | gcaccgcccc | 32340 |
| gcccgccatg  | cagcgaagag | accccgatc   | ccggcaatga  | caatggagga  | cccaccgctc | 32400 |
| gtacccgtgg  | atcatctggg | agctgaacaa  | gtctatgttg  | gcacagcaca  | ggcatatgct | 32460 |
| catgcatctc  | ttcagcactc | tcagctcctc  | gggggtcaaa  | accatatccc  | agggcacggg | 32520 |
| gaactcttgc  | aggacagcga | accccgagc   | acagggcaat  | cctcgcacat  | aacttacatt | 32580 |
| gtgcatggac  | agggtatcgc | aatcaggcag  | caccgggtga  | tcctccacca  | gagaagcgcg | 32640 |
| ggtctcggtc  | tcctcacagc | gtggtaaggg  | ggccggccga  | tacgggtgat  | ggcgggacgc | 32700 |
| ggctgatcgt  | gttctcgacc | gtgtcatgat  | gcagttgctt  | tcggacattt  | tcgtacttgc | 32760 |
| tgtagca     |            |             |             |             |            | 32767 |

<210> 6  
 <211> 32767  
 <212> DNA  
 <213> Artificial Sequence

<220>

&lt;223&gt; Artificially Synthesized

&lt;400&gt; 6

|                                                                    |      |
|--------------------------------------------------------------------|------|
| catcatcaat aatatacctc aaacttttgg tgcgcgttaa tatgcaaatg agctgtttga  | 60   |
| atttggggag ggaggaaggt gattggctgc gggagcggcg accgttaggg gcggggcggg  | 120  |
| tgacgttttg atgacgtggc tatgaggcgg agccggtttg caagttctcg tgggaaaagt  | 180  |
| gacgtcaaac gaggtgtggt ttgaacacgg aaataactcaa ttttcccgcg ctctctgaca | 240  |
| ggaaatgagg tgtttctggg cggatgcaag tgaaaacggg ccattttcgc gcgaaaactg  | 300  |
| aatgaggaag tgaaaatctg agtaatttcg cgtttatggc agggaggagt atttgccgag  | 360  |
| ggccgagtag actttgaccg attacgtggg ggtttcgatt accgtatttt tcacctaaat  | 420  |
| ttccgcgtac ggtgtcaaag tccggtgttt ttacgtacga tatcatttcc ccgaaagtgc  | 480  |
| cacctgaccg taactataac ggtcctaagg tagcgaaagc tcagatctcc cgatccccta  | 540  |
| tggtgactc tcagtacaat ctgctctgat gccgcatagt taagccagta tctgctccct   | 600  |
| gcttgtgtgt tggaggtcgc tgagtagtgc gcgagcaaaa tttaagctac aacaaggcaa  | 660  |
| ggcttgaccg acaattgcat gaagaatctg cttaggggta ggcgttttgc gctgcttcgc  | 720  |
| gatgtacggg ccagatatac gcgttgacat tgattattga ctagtatgcc aagtacgccc  | 780  |
| cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta catgacctta  | 840  |
| tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac catggtgatg  | 900  |
| cggttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg atttccaagt  | 960  |
| ctccacccca ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg ggactttcca  | 1020 |
| aaatgtcgta acaactccgc ccattgacg caaatgggcg gtaggcgtgt acggtgggag   | 1080 |
| gtctatataa gcagagctcg tttagtgaac cgtcagatca ctagaagctt tattgcggta  | 1140 |
| gtttatcaca gttaaattgc taacgcagtc agtgcttctg acacaacagt ctcgaactta  | 1200 |
| aggctagagt tcgacgccac catgcgcgtg cgcggcatcc cccgcaactg gccccagtgg  | 1260 |
| tggatctggg gcacctctgg cttctggatg atcatcatct gccgcgtggg gggcaacctg  | 1320 |
| gacctgtggg tgaccgtgta ctacggcgtg cccgtgtgga aggaggccaa gaccaccctg  | 1380 |
| ttctgcgctt ccgacgcaa ggcctacgac aaggagggtg acaacgtgtg ggccaccac    | 1440 |
| gcctgcgtgc ccaccgaccc caacccccag gagatcgtgc tggagaacgt gaccgagaac  | 1500 |
| ttcaacatgt ggaagaacga catggtggac cagatgcacg aggacatcat ctccctgtgg  | 1560 |
| gaccagtccc tgaagccctg cgtgaagctg acccccctgt gcgtgaccct gaactgcaag  | 1620 |
| aacgtgaaca tctccgcaa cgccaacgcc accgccaccc tgaactcctc catgaacggc   | 1680 |
| gagatcaaga actgctcctt caacaccacc accgagctgc gcgacaagaa gcagaagggtg | 1740 |
| tacgccctgt tctacaagcc cgacgtgggtg cccctgaacg gcggcgagca caacgagacc | 1800 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| ggcgagtaca  | tcctgatcaa | ctgcaactcc  | tccaccatca  | cccaggcctg  | ccccaagggtg | 1860 |
| tccttcgacc  | ccatccccc  | ccactactgc  | gcccccgccg  | gctacgccat  | cctgaagtgc  | 1920 |
| aacaacaaga  | ccttcaacgg | caccggcccc  | tgcaacaacg  | tgtccaccgt  | gcagtgcacc  | 1980 |
| cacggcatca  | agcccgtggt | gtccacccag  | ctgctgctga  | acggctccct  | ggccgaggag  | 2040 |
| gagatcatcg  | tgcgctccga | gaacctgacc  | aacaacatca  | agaccatcat  | cgtgcacctg  | 2100 |
| aacaagtccg  | tggagatcaa | gtgcacccgc  | cccaacaaca  | acaccgcaa   | gtccgtgcgc  | 2160 |
| atcggccccg  | gccagacctt | ctacgccacc  | ggcgagatca  | tcggcgacat  | ccgcgaggcc  | 2220 |
| cactgcaaca  | tctcccgcga | gacctggaac  | tccaccctga  | tccaggtgaa  | ggagaagctg  | 2280 |
| cgcgagcact  | acaacaagac | catcaagttc  | gagccctcct  | ccggcggcga  | cctggagggtg | 2340 |
| accacccact  | ccttcaactg | ccgcggcgag  | ttcttctact  | gcgacaccac  | caagctgttc  | 2400 |
| aacgagacca  | agctgttcaa | cgagtccgag  | tacgtggaca  | acaagaccat  | catcctgccc  | 2460 |
| tgccgcatca  | agcagatcat | caacatgtgg  | caggagggtg  | gccgcgccat  | gtacgcccc   | 2520 |
| cccatcgagg  | gcaacatcac | ctgcaagtcc  | aacatcacccg | gcctgctgct  | gacctgggac  | 2580 |
| ggcggcgaga  | actccaccga | gggcgtgttc  | cgccccggcg  | gcggcaacat  | gaaggacaac  | 2640 |
| tggcgctccg  | agctgtacaa | gtacaagggtg | gtggagatca  | agccccctggg | cgtggcccc   | 2700 |
| accaagagca  | agcgcaaggt | ggtgggccgc  | gagaagcgcg  | ccgtgggcct  | gggcgccgtg  | 2760 |
| ctgctgggct  | tcctgggcgc | cgccggcagc  | accatgggcg  | ccgccagcat  | caccctgacc  | 2820 |
| gtgcaggccc  | gccagctgct | gagcggcatc  | gtgcagcagc  | agagcaacct  | gctgcgcgcc  | 2880 |
| atcgaggccc  | agcagcacct | gctgcagctg  | accgtgtggg  | gcatcaagca  | gctgcagacc  | 2940 |
| cgctgtgctg  | ccatcgagcg | ctacctgaag  | gaccagcagc  | tgctgggcct  | gtggggctgc  | 3000 |
| agcggcaagc  | tgatctgcgc | caccgccgtg  | ccctggaaca  | gcagctggag  | caacaagagc  | 3060 |
| ctgggcgaca  | tctgggacaa | catgacctgg  | atgcagtggg  | accgcgagat  | cagcaactac  | 3120 |
| accaaacacca | tcttccgcct | gctggaggac  | agccagaacc  | agcaggagaa  | gaacgagaag  | 3180 |
| gacctgctgg  | ccctggacag | ctggaagaac  | ctgtggaact  | ggttcgacat  | caccaactgg  | 3240 |
| ctgtggtaca  | tcaagatctt | catcatgata  | gtgggcggcc  | tgatcggcct  | gcgcatcatc  | 3300 |
| ttcggcgtgc  | tggccatcgt | gaagcgcgtg  | cgccagggct  | acagccccct  | gagcttccag  | 3360 |
| accctgatcc  | ccaacccccg | cggccccgac  | cgctggggcc  | gcatcgagga  | ggagggcggc  | 3420 |
| gagcaggaca  | aggaccgcag | catccgcctg  | gtgagcggct  | tcctggccct  | ggcctgggac  | 3480 |
| gacctgcgca  | gcctgtgcct | gttcagctac  | caccagctgc  | gcgacttcat  | cctgaccgcc  | 3540 |
| gccccgcgcc  | ccgagctgct | gggccgcagc  | agcctgcgcg  | gcctgcagcg  | cggctgggag  | 3600 |
| gtgctgaagt  | acctgggcaa | cctggtgcag  | tactggggcc  | tggagctgaa  | gcgcagcgcc  | 3660 |
| atcaacctgt  | tcgacaccat | cgccatcgcc  | gtggccgagg  | gcaccgaccg  | catcatcgag  | 3720 |

368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| gtgatccagc  | gcatctgccg | cgccatccgc  | tacatcccca  | cccgcacccg  | ccagggcttc | 3780 |
| gaggccgccc  | tgctgtaagg | tacctctaga  | gtcgaccccg  | gcggccaaac  | cgctgatcag | 3840 |
| cctcgactgt  | gccttctagt | tgccagccat  | ctgttgtttg  | cccctcccc   | gtgccttcct | 3900 |
| tgaccctgga  | aggtgccact | cccactgtcc  | tttcctaata  | aaatgaggaa  | attgcatcgc | 3960 |
| attgtctgag  | taggtgtcat | tctattctgg  | gggggtgggg  | ggggcaggac  | agcaaggggg | 4020 |
| aggattggga  | agacaatagc | aggcatgctg  | gggatgcggt  | gggctctatg  | gcttctgagg | 4080 |
| cggaaagaac  | cagcagatct | gcagatctga  | attcatctat  | gtcgggtgcg  | gagaaagagg | 4140 |
| taatgaaatg  | gcattatggg | tattatgggt  | ctgcattaat  | gaatcgggtca | gatatcgaca | 4200 |
| tatgctggcc  | accgtgcatg | tggcctcgca  | cccccgcaag  | acatggcccc  | agttcgagca | 4260 |
| caacgtcatg  | acccgctgca | atgtgcacct  | gggctcccg   | cgaggcatgt  | tcatgcccta | 4320 |
| ccagtgaac   | atgcaatttg | tgaagggtgct | gctggagccc  | gatgccatgt  | ccagagtga  | 4380 |
| cctgacgggg  | gtgtttgaca | tgaatgtgga  | gctgtggaaa  | attctgagat  | atgatgaatc | 4440 |
| caagaccagg  | tgccgggcct | gcgaatgcgg  | aggcaagcac  | gccaggcttc  | agcccgtgtg | 4500 |
| tgtggagggtg | acggaggacc | tgcgaccgca  | tcatttggtg  | ttgtcctgca  | acgggacgga | 4560 |
| gttcggctcc  | agcggggaag | aatctgacta  | gagtgaagtag | tggttggggc  | tgggtgtgag | 4620 |
| cctgcatgag  | gggcagaatg | actaaaatct  | gtggttttct  | gtgtgttgca  | gcagcatgag | 4680 |
| cggaaagcgc  | tcctttgagg | gaggggtatt  | cagcccttat  | ctgacggggc  | gtctcccctc | 4740 |
| ctgggcggga  | gtgcgtcaga | atgtgatggg  | atccacggtg  | gacggccggc  | ccgtgcagcc | 4800 |
| cgcgaaactct | tcaaccctga | cctacgcgac  | cctgagctcc  | tcgtccgtgg  | acgcagctgc | 4860 |
| cgccgcagct  | gctgcttccg | ccgccagcgc  | cgtgcgcgga  | atggccctgg  | gcgccggcta | 4920 |
| ctacagctct  | ctggtggcca | actcgagttc  | caccaataat  | cccgccagcc  | tgaacgagga | 4980 |
| gaagctgctg  | ctgctgatgg | cccagctcga  | ggccctgacc  | cagcgcctgg  | gcgagctgac | 5040 |
| ccagcagggtg | gctcagctgc | aggcggagac  | gcgggccgcg  | gttgccacgg  | tgaaaaccaa | 5100 |
| ataaaaaaatg | aatcaataaa | taaacggaga  | cggttggtga  | ttttaacaca  | gagtcttgaa | 5160 |
| tctttatttg  | atttttcgcg | cgcggtaggc  | cctggaccac  | cggtctcgat  | cattgagcac | 5220 |
| ccggtggatc  | ttttccagga | cccggtagag  | gtgggcttgg  | atgttgaggt  | acatgggcat | 5280 |
| gagcccgtcc  | cgggggtgga | ggtagctcca  | ttgcagggcc  | tcgtgctcgg  | ggatggtgtt | 5340 |
| gtaaatacacc | cagtcatagc | aggggcgag   | ggcgtggtgc  | tgacagatgt  | ccttgaggag | 5400 |
| gagactgatg  | gccacgggca | gccccttggg  | gtagggtgtg  | acgaacctgt  | tgagctggga | 5460 |
| gggatgcatg  | cggggggaga | tgagatgcat  | cttggcctgg  | atcttgagat  | tggcgtgtt  | 5520 |
| cccgcccgaga | tcccgcggg  | ggttcatgtt  | gtgcaggacc  | accagcacgg  | tgtatccggt | 5580 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| gcacttgagg | aatttgtcat  | gcaacttgga  | aggggaaggcg | tgaagaatt   | tggagacgcc  | 5640 |
| cttgtgaccg | cccaggtttt  | ccatgcactc  | atccatgatg  | atggcgatgg  | gcccgtgggc  | 5700 |
| ggcggcctgg | gcaaagacgt  | ttcgggggtc  | ggacacatcg  | tagttgtggt  | cctgggtgag  | 5760 |
| ctcgtcatag | gccattttaa  | tgaatttggg  | gcggaggggtg | cccgactggg  | ggacgaaggt  | 5820 |
| gccctcgatc | ccggggggcgt | agttgccctc  | gcagatctgc  | atctcccagg  | ccttgagctc  | 5880 |
| ggaggggggg | atcatgtcca  | cctgcggggc  | gatgaaaaaa  | acggtttccg  | gggcggggga  | 5940 |
| gatgagctgg | gccgaaagca  | ggttccggag  | cagctggggac | ttgccgcaac  | cggtggggcc  | 6000 |
| gtagatgacc | ccgatgaccg  | gctgcagggtg | gtagttgagg  | gagagacagc  | tgccgtcctc  | 6060 |
| gcggaggagg | ggggccacct  | cgttcatcat  | ctcgcgcaca  | tgcattgtct  | cgcgacagag  | 6120 |
| ttccgccagg | aggcgctcgc  | ccccagcga   | gaggagctct  | tgcagcgagg  | cgaagttttt  | 6180 |
| cagcggcttg | agtcgctcgg  | ccatgggcat  | tttgagagg   | gtctgttgca  | agagttccag  | 6240 |
| acggttccag | agctcgggtg  | tgtgctctag  | ggcatctcga  | tccagcagac  | ctcctcgttt  | 6300 |
| cgcggttg   | ggcgactcg   | ggagtagggc  | accaggcgat  | ggcggtccag  | cgaggccagg  | 6360 |
| gtccggctct | tccaggggcg  | cagggtccgc  | gtcagcgtgg  | tctccgtcac  | ggtgaagggg  | 6420 |
| tgcgcgccgg | gctgggcgct  | tgcgagggtg  | cgcttcaggc  | tcatccggct  | ggtcgagaac  | 6480 |
| cgctcccgtt | cggcgccctg  | cgcgctcgcc  | aggtagcaat  | tgagcatgag  | ttcgtagtgt  | 6540 |
| agcgcctcgg | ccgcgtggcc  | cttggcgcgg  | agcttacctt  | tggaaagtgt  | tccgcagacg  | 6600 |
| ggacagagga | gggacttgag  | ggcgtagagc  | ttggggggcga | ggaagacgga  | ctcggggggcg | 6660 |
| taggcgtccg | cgccgcagct  | ggcgacagac  | gtctcgcact  | ccacgagcca  | ggtgaggtcg  | 6720 |
| ggcggttg   | ggtcaaaaaac | gaggtttcct  | ccgtgctttt  | tgatgcgttt  | cttacctctg  | 6780 |
| gtctccatga | gctcgtgtcc  | ccgctgggtg  | acaaagaggc  | tgtccgtgtc  | cccgtagacc  | 6840 |
| gactttatgg | gccggctcctc | gagcgggggtg | ccgcggctcct | cgctcgtagag | gaaccccgcc  | 6900 |
| cactccgaga | cgaaggccccg | ggtccaggcc  | agcacgaagg  | aggccacgtg  | ggaggggtag  | 6960 |
| cggtcgttgt | ccaccagcgg  | gtccaccttc  | tccagggtat  | gcaagcacat  | gtccccctcg  | 7020 |
| tccacatcca | ggaagggtgat | tggcttgtaa  | gtgtaggcca  | cgtgaccggg  | ggtcccggcc  | 7080 |
| gggggggtat | aaaaggggggc | gggcccctgc  | tcgtcctcac  | tgtcttccgg  | atcgctgtcc  | 7140 |
| aggagcgcca | gctgttgggg  | taggtattcc  | ctctcgaagg  | cgggcatgac  | ctcggcactc  | 7200 |
| aggttgtcag | tttctagaaa  | cgaggaggat  | ttgatattga  | cggtgccgtt  | ggagacgcct  | 7260 |
| ttcatgagcc | cctcgtccat  | ttggtcagaa  | aagacgatct  | ttttgtgttc  | gagcttgggtg | 7320 |
| gcgaaggagc | cgtagagggc  | gttgagagac  | agcttggcga  | tggagcgcat  | ggtctggttc  | 7380 |
| ttttccttgt | cggcgcgctc  | cttggcggcg  | atgttgagct  | gcacgtactc  | gcgcgccacg  | 7440 |
| cacttccatt | cggggaagac  | ggtggtgagc  | tcgtcgggca  | cgattctgac  | ccgccagccg  | 7500 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| cggttggtgca | gggtgatgag | gtccacgctg  | gtggccacct  | cgccgcgcag | gggtcgttg  | 7560 |
| gtccagcaga  | ggcgcccgcc | cttgcgcgag  | cagaaggggg  | gcagcgggtc | cagcatgagc | 7620 |
| tcgtcggggg  | ggtcggcgtc | cacggtgaag  | atgccgggca  | ggagctcggg | gtcgaagtag | 7680 |
| ctgatgcagg  | tgcccagatt | gtccagcgcc  | gcttgccagt  | cgcgcacggc | cagcgcgcg  | 7740 |
| tcgtaggggc  | tgaggggctg | gccccagggc  | atgggggtgcg | tgagcgcgga | ggcgtacatg | 7800 |
| ccgcagatgt  | cgtagacgta | gaggggctcc  | tcgaggacgc  | cgatgtaggt | ggggtagcag | 7860 |
| cgccccccgc  | ggatgctggc | gcgcacgtag  | tcgtacagct  | cgtgcgaggg | cgcgaggagc | 7920 |
| cccgtgccga  | ggttgaggcg | ttgcggcttt  | tcggcgcggt  | agacgatctg | gcggaagatg | 7980 |
| gcgtgggagt  | tggaggagat | ggtgggcctt  | tgaagatgt   | tgaagtgggc | gtggggcagg | 8040 |
| ccgaccgagt  | ccctgatgaa | gtgggcgtag  | gagtcctgca  | gcttggcgac | gagctcggcg | 8100 |
| gtgacgagga  | cgtccagggc | gcagtagtcg  | agggctctct  | ggatgatgtc | atacttgagc | 8160 |
| tggcccttct  | gcttccacag | ctcgcggttg  | agaaggaact  | cttcgcggtc | cttccagtac | 8220 |
| tcttcgaggg  | ggaacccgtc | ctgatcggca  | cggtaaagagc | ccaccatgta | gaactggttg | 8280 |
| acggccttgt  | agggcgagca | gcccttctcc  | acggggaggg  | cgtaagcttg | cgcggccttg | 8340 |
| cgcagggagg  | tgtgggtgag | ggcgaagggtg | tcgcgcacca  | tgaccttgag | gaactggtgc | 8400 |
| ttgaagtcga  | ggtcgtcgca | gccgccctgc  | tcccagagtt  | ggaagtccgt | gcgcttcttg | 8460 |
| taggcggggg  | taggcaaagc | gaaagtaaca  | tcgttgaaga  | ggatcttgcc | cgcgcggggc | 8520 |
| atgaagttgc  | gagtgatgag | gaaaggctgg  | ggcacctcgg  | cccggttggt | gatgacctgg | 8580 |
| gcggcgagga  | cgatctcgtc | gaagccgttg  | atgttggtgc  | cgacgatgta | gagttccacg | 8640 |
| aatcgcgggc  | ggcccttgac | gtggggcagc  | ttcttgagct  | cgctgtaggt | gagctcggcg | 8700 |
| gggtcgctga  | gcccgtgctg | ctcgagggcc  | cagtcggcga  | cgtgggggtt | ggcgctgagg | 8760 |
| aaggaagtcc  | agagatccac | ggccagggcg  | gtctgcaagc  | ggtcccggta | ctgacggaac | 8820 |
| tgttgggcca  | cggccatttt | ttcgggggtg  | acgcagtaga  | aggtgcgggg | gtcgccgtgc | 8880 |
| cagcgggtccc | acttgagctg | gagggcgagg  | tcgtgggcga  | gctcgacgag | cggcgggtcc | 8940 |
| ccggagagtt  | tcatgaccag | catgaagggg  | acgagctgct  | tgccgaagga | ccccatccag | 9000 |
| gtgtaggttt  | ccacatcgta | ggtgaggaag  | agcctttcgg  | tgcgaggatg | cgagccgatg | 9060 |
| gggaagaact  | ggatctcctg | ccaccagttg  | gaggaatggc  | tgttgatgtg | atggaagtag | 9120 |
| aaatgccgac  | ggcgcgccga | gcactcgctg  | ttgtgtttat  | acaagcgctc | gcagtgctcg | 9180 |
| caacgctgca  | cgggatgcac | gtgctgcacg  | agctgtacct  | gggttccttt | ggcgaggaat | 9240 |
| ttcagtgggc  | agtggagcgc | tggcggctgc  | atctcgtgct  | gtactacgtc | ttggccatcg | 9300 |
| gcgtggccat  | cgtctgcctc | gatggtgggtc | atgctgacga  | gcccgcgcgg | gaggcaggtc | 9360 |

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|             |            |             |             |             |             |       |
|-------------|------------|-------------|-------------|-------------|-------------|-------|
| cagacctcgg  | ctcggacggg | tcggagagcg  | aggacgaggg  | cgcgaggcc   | ggagctgtcc  | 9420  |
| agggctctga  | gacgctgcgg | agtcagggtca | gtgggcagcg  | gcggcgcgcg  | gttgacttgc  | 9480  |
| aggagctttt  | ccagggcgcg | cgggaggtcc  | agatggtact  | tgatctccac  | ggcgccgttg  | 9540  |
| gtggctacgt  | ccacggcttg | cagggtgccg  | tgcccctggg  | gcgccaccac  | cggtccccgt  | 9600  |
| ttcttcttgg  | gcgctgcttc | catgtcggtc  | agaagcggcg  | gcgaggacgc  | gcgccgggcg  | 9660  |
| gcagggggcg  | ctcggggccc | ggaggcaggg  | gcggcagggg  | cacgtcggcg  | ccgcgcgcgg  | 9720  |
| gcaggttctg  | gtactgcgcc | cggagaagac  | tggcgtgagc  | gacgacgcga  | cggttgacgt  | 9780  |
| cctggatctg  | acgcctctgg | gtgaaggcca  | cgggacccgt  | gagtttgaac  | ctgaaagaga  | 9840  |
| gttcgacaga  | atcaatctcg | gtatcgttga  | cggcggcctg  | ccgcaggatc  | tcttgacagt  | 9900  |
| cgcccgagtt  | gtcctggtag | gcgatctcgg  | tcatgaactg  | ctcgatctcc  | tcctcctgaa  | 9960  |
| ggtctccgcg  | gccggcgcg  | tcgacggtgg  | ccgcgaggtc  | gttgagagatg | cgccccatga  | 10020 |
| gctgcgagaa  | ggcgttcatg | ccggcctcgt  | tccagacgcg  | gctgtagacc  | acggctccgt  | 10080 |
| cggggtcgcg  | cgcgcgcatg | accacctggg  | cgaggttgag  | ctcgacgtgg  | cgcgtaaga   | 10140 |
| ccgcgtagtt  | gcagaggcgc | tggtagaggt  | agttgagcgt  | ggtggcgatg  | tgctcggtga  | 10200 |
| cgaagaagta  | catgatccag | cggcggagcg  | gcctctcgct  | gacgtcgccc  | agggcttcca  | 10260 |
| agcgttccat  | ggcctcgtag | aagtccacgg  | cgaagttgaa  | aaactgggag  | ttgcgcgccg  | 10320 |
| agacgggtcaa | ctcctcctcc | agaagacgga  | tgagctcggc  | gatggtggcg  | cgcacctcgc  | 10380 |
| gctcgaaggc  | cccggggggc | tcctcttcca  | tctcctcctc  | ttcctcctcc  | actaacatct  | 10440 |
| cttctacttc  | ctcctcagga | ggcgggtggcg | ggggaggggc  | cctgcgtcgc  | cggcggcgca  | 10500 |
| cgggcagacg  | gtcgatgaag | cgctcgatgg  | tctccccgcg  | ccggcgacgc  | atggtctcgg  | 10560 |
| tgacggcgcg  | cccgtcctcg | cggggccgca  | gcataagac   | gccgccgcgc  | atctccaggt  | 10620 |
| ggccgccggg  | ggggtctccg | ttgggcaggg  | agagggcgct  | gacgatgcat  | cttatcaatt  | 10680 |
| gacccgtagg  | gactccgcgc | aaggacctga  | gcgtctcgag  | atccacggga  | tccgaaaacc  | 10740 |
| gctgaacgaa  | ggcttcgagc | cagtcgcagt  | cgcaaggtag  | gctgagcccg  | gtttcttgtt  | 10800 |
| cttcgggtat  | ttggtcggga | ggcgggcggg  | cgatgctgct  | ggtgatgaag  | ttgaagtagg  | 10860 |
| cggtcctgag  | acggcggatg | gtggcgagga  | gcaccaggtc  | cttgggcccg  | gcttgctgga  | 10920 |
| tgcgagacg   | gtcggccatg | ccccaggcgt  | ggtcctgaca  | cctggcgagg  | tcctttagt   | 10980 |
| agtcctgcat  | gagccgctcc | acgggcacct  | cctcctcgcc  | cgcgcgggcg  | tgcctgcgcg  | 11040 |
| tgagcccgaa  | cccgcgctgc | ggctggacga  | gcgccaggtc  | ggcgacgacg  | cgctcgggtga | 11100 |
| ggatggcctg  | ctggatctgg | gtgaggggtg  | tctggaagtc  | gtcgaagtcg  | acgaagcggg  | 11160 |
| ggtaggctcc  | ggtgttgatg | gtgtaggagc  | agttggccat  | gacggaccag  | ttgacgggtct | 11220 |
| ggtggccggg  | tcgcacgagc | tcgtggtact  | tgaggcgcgga | gtaggcgcgc  | gtgtcgaaga  | 11280 |

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|            |             |            |            |            |            |       |
|------------|-------------|------------|------------|------------|------------|-------|
| tgtagtcggt | gcaggcgcg   | acgaggtact | ggtatccgac | gaggaagtgc | ggcggcggct | 11340 |
| ggcggtagag | cggccatcgc  | tcggtggcgg | gggcgccggg | cgcgaggtcc | tcgagcatga | 11400 |
| ggcggtagta | gccgtagatg  | tacctggaca | tccaggtgat | gccggcggcg | gtggtggagg | 11460 |
| cgcgcgggaa | ctcgcggacg  | cggttccaga | tgttgcgcag | cggcaggaag | tagttcatgg | 11520 |
| tggccgcggt | ctggcccgtg  | aggcgcgcg  | agtcgtggat | gctctagaca | tacgggcaaa | 11580 |
| aacgaaagcg | gtcagcggtc  | cgactccgtg | gcctggaggc | taagcgaacg | ggttgggctg | 11640 |
| cgcggtgacc | ccggttcgaa  | tctcgaatca | ggctggagcc | gcagctaacg | tggtactggc | 11700 |
| actcccgtct | cgacccaagc  | ctgctaacga | aacctccagg | atacggaggc | gggtcgtttt | 11760 |
| ttggccttgg | tcgctgggtc  | tgaaaaacta | gtaagcgcg  | aaagcggccg | cccgcgatgg | 11820 |
| ctcgtgccc  | tagtctggag  | aaagaatcgc | cagggttgcg | ttgcggtgtg | ccccggttcg | 11880 |
| agcctcagcg | ctcggcgccg  | gccggattcc | gcggctaacg | tgggcgtggc | tgccccgtcg | 11940 |
| ttccaagac  | cccttagcca  | gccgacttct | ccagttacgg | agcgagcccc | tctttttttt | 12000 |
| tcttgtgttt | ttgccagatg  | catcccgtac | tgcggcagat | gcgccccac  | cctccaccac | 12060 |
| aaccgcccct | accgcagcag  | cagcaacagc | cggcgcttct | gcccccgccc | cagcagcagc | 12120 |
| cagccactac | cgcggcggcc  | gccgtgagcg | gagccggcgt | tcagtatgac | ctggccttgg | 12180 |
| aagagggcga | ggggctggcg  | cggctggggg | cgctgctgcc | ggagcggcac | ccgcgcgtgc | 12240 |
| agatgaaaag | ggacgctcgc  | gaggcctacg | tgcccaagca | gaacctgttc | agagacagga | 12300 |
| gcggcgagga | gcccagaggag | atgcgcgcct | cccgttcca  | cgcggggagg | gagctgcggc | 12360 |
| gcggcctgga | ccgaaagcgg  | gtgctgaggg | acgaggattt | cgaggcggac | gagctgacgg | 12420 |
| ggatcagccc | cgcgcgcgcg  | cacgtggccg | cggccaacct | ggtcacggcg | tacgagcaga | 12480 |
| ccgtgaagga | ggagagcaac  | ttccaaaaat | ccttcaacaa | ccacgtgcgc | acgctgatcg | 12540 |
| cgcgcgagga | ggtgaccctg  | ggcctgatgc | acctgtggga | cctgctggag | gccatcgtgc | 12600 |
| agaaccccac | gagcaagccg  | ctgacggcgc | agctgtttct | ggtggtgcag | cacagtcggg | 12660 |
| acaacgagac | gttcagggag  | gcgctgctga | atatcaccga | gcccaggggc | cgctggctcc | 12720 |
| tggacctggt | gaacattttg  | cagagcatcg | tggtgcagga | gcgcgggctg | ccgctgtccg | 12780 |
| agaagctggc | ggccatcaac  | ttctcggtgc | tgagtctggg | caagtactac | gctaggaaga | 12840 |
| tctacaagac | cccgtacgtg  | cccatagaca | aggaggtgaa | gatcgacggg | ttttacatgc | 12900 |
| gcatgaccct | gaaagtgtctg | accctgagcg | acgatctggg | ggtgtaccgc | aacgacagga | 12960 |
| tgcaccgcgc | ggtgagcgcc  | agccgccggc | gcgagctgag | cgaccaggag | ctgatgcaca | 13020 |
| gcctgcagcg | ggccctgacc  | ggggccggga | ccgaggggga | gagctacttt | gacatgggcg | 13080 |
| cggacctgcg | ctggcagccc  | agccgccggg | ccttgaagc  | tgccggcggt | tccccctacg | 13140 |

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|             |            |            |             |            |            |       |
|-------------|------------|------------|-------------|------------|------------|-------|
| tggaggaggt  | ggacgatgag | gaggaggagg | gcgagtacct  | ggaagactga | tggcgcgacc | 13200 |
| gtatTTTTgc  | tagatgcagc | aacagccacc | gccgccgcct  | cctgatcccc | cgatgcgggc | 13260 |
| ggcgtgcag   | agccagccgt | ccggcattaa | ctcctcggac  | gattggaccc | aggccatgca | 13320 |
| acgcatcatg  | gcgctgacga | cccgcaatcc | cgaagccttt  | agacagcagc | ctcaggccaa | 13380 |
| ccggctctcg  | gccatcctgg | aggccgtggt | gccctcgcgc  | tcgaacccca | cgcacgagaa | 13440 |
| ggtgctggcc  | atcgtgaacg | cgctggtgga | gaacaaggcc  | atccgcggtg | acgaggccgg | 13500 |
| gctggtgtac  | aacgcgctgc | tggagcgcgt | ggcccgtac   | aacagcacca | acgtgcagac | 13560 |
| gaacctggac  | cgcatggtga | ccgacgtgcg | cgaggcgggtg | tcgcagcgcg | agcggttcca | 13620 |
| ccgcgagtcg  | aacctgggct | ccatggtggc | gctgaacgcc  | ttcctgagca | cgcagcccg  | 13680 |
| caacgtgccc  | cggggccagg | aggactacac | caacttcac   | agcgcgctgc | ggctgatggt | 13740 |
| ggccgagggtg | ccccagagcg | aggtgtacca | gtcggggccg  | gactacttct | tccagaccag | 13800 |
| tcgccagggc  | ttgcagaccg | tgaacctgag | ccaggctttc  | aagaacttgc | agggactgtg | 13860 |
| gggcgtgcag  | gccccggtcg | gggaccgcgc | gacggtgtcg  | agcctgctga | cgccgaactc | 13920 |
| gcgcctgctg  | ctgctgctgg | tggcgccctt | cacggacagc  | ggcagcgtga | gccgcgactc | 13980 |
| gtacctgggc  | tacctgctta | acctgtaccg | cgaggccatc  | ggacaggcgc | acgtggacga | 14040 |
| gcagacctac  | caggagatca | cccacgtgag | ccgcgcgctg  | ggccaggagg | acccgggcaa | 14100 |
| cctggaggcc  | accctgaact | tcctgctgac | caaccggctc  | cagaagatcc | cgccccagta | 14160 |
| cgcgtgagc   | accgaggagg | agcgcacctc | gcgctacgtg  | cagcagagcg | tggggctgtt | 14220 |
| cctgatgcag  | gagggggcca | cgcccagcgc | ggcgtcgcac  | atgaccgcgc | gcaacatgga | 14280 |
| gcccagcatg  | tacgcccgca | accgcccgtt | catcaataag  | ctgatggact | acttgcacgc | 14340 |
| ggcggccgcc  | atgaactcgg | actactttac | caacgccatc  | ttgaacccgc | actggctccc | 14400 |
| gccgcccggg  | ttctacacgg | gcgagtacga | catgcccgc   | cccaacgacg | ggttcctgtg | 14460 |
| ggacgacgtg  | gacagcagcg | tgttctcgcc | gcgtccagga  | accaatgccg | tgtggaagaa | 14520 |
| agagggcggg  | gaccggcggc | cgctcctcgg | gctgtccggt  | cgcgcgggtg | ctgccgcggc | 14580 |
| ggtgcccag   | gccgccagcc | ccttcccag  | cctgcccttt  | tcgctgaaca | gcgtgcgcag | 14640 |
| cagcgagctg  | ggtcggctga | cgcgaccgcg | cctgctgggc  | gaggaggagt | acctgaacga | 14700 |
| ctccttgttg  | aggcccagc  | gcgagaagaa | cttcccgaat  | aacgggatag | agagcctggt | 14760 |
| ggacaagatg  | agccgctgga | agacgtacgc | gcacgagcac  | agggacgagc | cccagctag  | 14820 |
| cagcgcaggc  | acccgtagac | gccagcggca | cgacaggcag  | cggggactgg | tgtgggacga | 14880 |
| tgaggattcc  | gccgacgaca | gcagcgtggt | ggacttgggt  | gggagtgggt | gtaaccggtt | 14940 |
| cgctcacctg  | cgccccgta  | tcgggcgcct | gatgtaagaa  | tctgaaaaaa | taaaagacgg | 15000 |
| tactaccaa   | ggccatggcg | accagcgtgc | gttcttctct  | gttgtttgta | gtagtatgat | 15060 |

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|             |            |             |             |            |             |       |
|-------------|------------|-------------|-------------|------------|-------------|-------|
| gagggcgcgtg | tacccggagg | gtcctcctcc  | ctcgtacgag  | agcgtgatgc | agcaggcggt  | 15120 |
| ggcggcgggcg | atgcagcccc | cgctggaggc  | gccttacgtg  | cccccgcggt | acctggcgcc  | 15180 |
| tacggagggg  | cggaacagca | ttcgttactc  | ggagctggca  | cccttgtagc | ataccacccg  | 15240 |
| gttgtagctg  | gtggacaaca | agtcggcaga  | catcgccctg  | ctgaactacc | agaacgacca  | 15300 |
| cagcaacttc  | ctgaccaccg | tgggtgcagaa | caacgatttc  | acccccacgg | aggccagcac  | 15360 |
| ccagaccatc  | aactttgacg | agcgctcgcg  | gtggggcggc  | cagctgaaaa | ccatcatgca  | 15420 |
| caccaacatg  | cccaacgtga | acgagttcat  | gtacagcaac  | aagttcaagg | cgcggtgat   | 15480 |
| ggtctcgcg   | aagaccccc  | acggggtgga  | tgatgattat  | gatggtagtc | aggacgagct  | 15540 |
| gacctacgag  | tgggtggagt | ttgagctgcc  | cgagggaac   | ttctcggtga | ccatgaccat  | 15600 |
| cgatctgatg  | aacaacgcca | tcatcgacaa  | ctacttggcg  | gtggggcggc | agaacggggt  | 15660 |
| gctggagagc  | gacatcgggc | tgaagttcga  | cacgcgcaac  | ttccggctgg | gctgggaccc  | 15720 |
| cgtgaccgag  | ctggtgatgc | cgggcggtga  | caccaacgag  | gccttccacc | ccgacatcgt  | 15780 |
| cctgctgccc  | ggctgcggcg | tggacttcac  | cgagagccgc  | ctcagcaacc | tgctgggcat  | 15840 |
| ccgcaagcgg  | cagcccttcc | aggagggctt  | ccagatcctg  | tacgaggacc | tggagggggg  | 15900 |
| caacatcccc  | gcgctcttgg | atgtcgaagc  | ctacgagaaa  | agcaaggagg | atagcaccgc  | 15960 |
| cgcggcgacc  | gcagccgtgg | ccaccgcctc  | taccgagggtg | cggggcgata | attttgctag  | 16020 |
| cgctgcggca  | gcggccgagg | cggctgaaac  | cgaaagtaag  | atagtcatcc | agccggtgga  | 16080 |
| gaaggacagc  | aaggacagga | gctacaacgt  | gctcgcggac  | aagaaaaaca | ccgcctaccg  | 16140 |
| cagctggtac  | ctggcctaca | actacggcga  | ccccgagaag  | ggcgtgcgct | cctggacgct  | 16200 |
| gctcaccacc  | tcggacgtca | cctgcggcgt  | ggagcaagtc  | tactggtcgc | tgcccgacat  | 16260 |
| gatgcaagac  | ccggtcacct | tccgctccac  | gcgtcaagtt  | agcaactacc | cggtggtggg  | 16320 |
| cgccgagctc  | ctgcccgtct | actccaagag  | cttcttcaac  | gagcaggccg | tctactcgca  | 16380 |
| gcagctgcgc  | gccttcacct | cgctcacgca  | cgtcttcaac  | cgttcccccg | agaaccagat  | 16440 |
| cctcgtccgc  | ccgcccgcgc | ccaccattac  | caccgtcagt  | gaaaacgttc | ctgctctcac  | 16500 |
| agatcacggg  | accctgccgc | tgcgagcag   | tatccgggga  | gtccagcgcg | tgaccgtcac  | 16560 |
| tgacgccaga  | cgccgcacct | gcccctacgt  | ctacaaggcc  | ctgggcgtag | tcgcgccgcg  | 16620 |
| cgctctctcg  | agccgcacct | tctaaaaaat  | gtccattctc  | atctcgccca | gtaataaac   | 16680 |
| cggttggggc  | ctgcgcgcgc | ccagcaagat  | gtacggaggc  | gctcgccaac | gctccacgca  | 16740 |
| acaccccggtg | cgcgtcgcgc | ggcacttccg  | cgctccctgg  | ggcgccctca | agggccgcgt  | 16800 |
| gcgctcgcg   | accaccgtcg | acgacgtgat  | cgaccagggtg | gtggccgacg | cgcgcaacta  | 16860 |
| cacgcccgcc  | gccgcgcccg | tctccaccgt  | ggacgccgtc  | atcgacagcg | tgggtggccga | 16920 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |             |            |             |       |
|-------------|------------|------------|-------------|------------|-------------|-------|
| cgcgcgccgg  | tacgcccgca | ccaagagccg | gcggcgccgc  | atcgcccggc | ggcaccggag  | 16980 |
| cacccccgcc  | atgcgcgcgg | cgcgagcctt | gctgcgcagg  | gccaggcgca | cgggacgcag  | 17040 |
| ggccatgctc  | agggcgccca | gacgcgcggc | ctccggcagc  | agcagcgccg | gcaggacccg  | 17100 |
| cagacgcgcg  | gccacggcgg | cggcggcgcc | catcgccagc  | atgtcccgcc | cgcggcgcgg  | 17160 |
| caacgtgtac  | tgggtgcgcg | acgccgccac | cggtgtgcgc  | gtgcccgtgc | gcacccgccc  | 17220 |
| ccctcgcact  | tgaagatgct | gacttcgcga | tgttgatgtg  | tcccagcggc | gaggaggatg  | 17280 |
| tccaagcgca  | aatacaagga | agagatgctc | caggtcatcg  | cgcttgagat | ctacggcccc  | 17340 |
| gcggcgccgg  | tgaaggagga | aagaaagccc | cgcaaactga  | agcgggtcaa | aaaggacaaa  | 17400 |
| aaggaggagg  | aagatgacgg | actggtggag | tttgtgcgcg  | agttcgcccc | ccggcgccgc  | 17460 |
| gtgcagtggc  | gcgggcggaa | agtgaaccgc | gtgctgcggc  | ccggcaccac | ggtggtcttc  | 17520 |
| acgcccggcg  | agcgttccgg | ctccgcctcc | aagcgctcct  | acgacgaggt | gtacggggac  | 17580 |
| gaggacatcc  | tcgagcaggc | ggtcgagcgt | ctgggcgagt  | ttgcgtacgg | caagcgacgc  | 17640 |
| cgccccgcgc  | ccttgaaaga | ggaggcggtg | tccatcccgc  | tggaccacgg | caacccccacg | 17700 |
| ccgagcctga  | agccggtgac | cctgcagcag | gtgctaccga  | gcgcggcgcc | gcgccggggc  | 17760 |
| ttcaagcgcg  | agggcgccga | ggatctgtac | ccgaccatgc  | agctgatggg | gcccgaagcg  | 17820 |
| cagaagctgg  | aggacgtgct | ggagcacatg | aaggtggacc  | ccgaggtgca | gcccgaagtc  | 17880 |
| aaggtgcggc  | ccatcaagca | ggtggccccg | ggcctgggcg  | tgcagaccgt | ggacatcaag  | 17940 |
| atccccacgg  | agcccatgga | aacgcagacc | gagcccgtga  | agcccagcac | cagcaccatg  | 18000 |
| gaggtgcaga  | cggatccctg | gatgccagca | ccagcttcca  | ccagcactcg | ccgaagacgc  | 18060 |
| aagtacggcg  | cggccagcct | gctgatgccc | aactacgcgc  | tgcacccctc | catcatcccc  | 18120 |
| acgcccgggt  | accgcggcac | gcgcttctac | cgcggtctaca | ccagcagccg | ccgccgcaag  | 18180 |
| accaccaccc  | gccgccgtcg | tcgcagccgc | cgcagcagca  | ccgcgacttc | cgccttggtg  | 18240 |
| cggagagtgt  | atcgcagcgg | gcgcgagcct | ctgaccctgc  | cgcgcgcgcg | ctaccacccg  | 18300 |
| agcatcgcca  | tttaactacc | gcctcctact | tgcagatatg  | gccctcacat | gccgcctccg  | 18360 |
| cgtccccatt  | acgggctacc | gaggaagaaa | gccgcgccgt  | agaaggctga | cggggaacgg  | 18420 |
| gctgcgtcgc  | catcaccacc | ggcggcgccg | cgccatcagc  | aagcggttgg | ggggaggctt  | 18480 |
| cctgcccgcg  | ctgatcccca | tcatcgccgc | ggcgatcggg  | gcgatccccg | gcatagcttc  | 18540 |
| cgtggcggtg  | caggcctctc | agcgccactg | agacacaaaa  | aagcatggat | ttgtaataaa  | 18600 |
| aaaaaaaaatg | gactgacgct | cctggtcctg | tgatgtgtgt  | ttttagatgg | aagacatcaa  | 18660 |
| tttttcgtcc  | ctggcaccgc | gacacggcac | gcggccgttt  | atgggcacct | ggagcgacat  | 18720 |
| cggcaacagc  | caactgaacg | ggggcgccct | caattggagc  | agtctctgga | gcgggcttaa  | 18780 |
| gaatttcggg  | tccacgctca | aaacctatgg | caacaaggcg  | tggaacagca | gcacagggca  | 18840 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |             |            |            |            |       |
|------------|-------------|-------------|------------|------------|------------|-------|
| ggcgctgagg | gaaaagctga  | aagaacagaa  | cttccagcag | aaggtggttg | atggcctggc | 18900 |
| ctcaggcatc | aacgggggtgg | ttgacctggc  | caaccaggcc | gtgcagaaac | agatcaacag | 18960 |
| ccgcctggac | gcggtccccgc | ccgcgggggtc | cgtggagatg | ccccagggtg | aggaggagct | 19020 |
| gcctcccctg | gacaagcgcg  | gcgacaagcg  | accgctccc  | gacgcggagg | agacgtgct  | 19080 |
| gacgcacacg | gacgagccgc  | ccccgtacga  | ggaggcggtg | aaactggggc | tgcccaccac | 19140 |
| gcggcccgtg | gcgcctcttg  | ccaccggagt  | gctgaaaccc | agcagcagcc | agcccgcgac | 19200 |
| cctggacttg | cctccgcctc  | gcccctccac  | agtggctaag | cccctgccgc | cggtggccgt | 19260 |
| cgcgctcgcg | gccccccgag  | gccgccccca  | ggcgaactgg | cagagcactc | tgaacagcat | 19320 |
| cgtgggtctg | ggagtgcaga  | gtgtgaagcg  | ccgccgctgc | tattaaaaga | cactgtagcg | 19380 |
| cttaacttgc | ttgtctgtgt  | gtatatgtat  | gtccgccgac | cagaaggagg | agtgtgaaga | 19440 |
| ggcgctcgcg | cgagttgcaa  | gatggccacc  | ccatcgatgc | tgccccagtg | ggcgtacatg | 19500 |
| cacatcgccg | gacaggacgc  | ttcggagtac  | ctgagtccgg | gtctggtgca | gttcgcccgc | 19560 |
| gccacagaca | cctacttcag  | tctggggaac  | aagtttagga | acccacagg  | ggcgcccacg | 19620 |
| cacgatgtga | ccaccgaccg  | cagccagcgg  | ctgacgctgc | gcttcgtgcc | cgtggaccgc | 19680 |
| gaggacaaca | cctactcgta  | caaagtgcgc  | tacacgctgg | ccgtgggcca | caaccgcgtg | 19740 |
| ctggacatgg | ccagcaccta  | ctttgacatc  | cgcggcgtgc | tggaccgggg | ccctagcttc | 19800 |
| aaaccctact | ctggcaccgc  | ctacaacagc  | ctagctccca | agggagctcc | caattccagc | 19860 |
| cagtgggagc | aagcaaaaac  | aggcaatggg  | ggaactatgg | aaacacacac | atatggtgtg | 19920 |
| gccccaatgg | gcggagagaa  | tattacaaaa  | gatggtcttc | aaattggaac | tgacgttaca | 19980 |
| gcgaatcaga | ataaaccaat  | ttatgccgac  | aaaacatttc | aaccagaacc | gcaagtagga | 20040 |
| gaagaaaatt | ggcaagaaac  | tgaaaacttt  | tatggcggta | gagctcttaa | aaaagacaca | 20100 |
| aacatgaaac | cttgctatgg  | ctcctatgct  | agaccaccca | atgaaaaagg | aggtcaagct | 20160 |
| aaacttaaag | ttggagatga  | tggagttcca  | accaaagaat | tcgacataga | cctggctttc | 20220 |
| tttgatactc | ccggtggcac  | cgtgaacgg   | caagacgagt | ataaagcaga | cattgtcatg | 20280 |
| tataccgaaa | acacgtat    | tgaaactcca  | gacacgcatg | tggtatacaa | accaggcaag | 20340 |
| gatgatgcaa | gttctgaaat  | taacctgggt  | cagcagtcta | tgcccaacag | acccaactac | 20400 |
| attgggttca | gggacaactt  | tatcggctct  | atgtactaca | acagcactgg | caatatgggt | 20460 |
| gtgcttgctg | gtcaggcctc  | ccagctgaat  | gctgtgggtg | atttgcaaga | cagaaacacc | 20520 |
| gagctgtcct | accagctctt  | gcttgactct  | ttgggtgaca | gaaccgggta | tttcagtatg | 20580 |
| tggaaccagg | cggtggacag  | ttatgacccc  | gatgtgcgca | tcatcgaaaa | ccatggtgtg | 20640 |
| gaggatgaat | tgccaaacta  | ttgcttcccc  | ttggacggct | ctggcactaa | cgccgcatac | 20700 |

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|            |             |             |             |             |             |       |
|------------|-------------|-------------|-------------|-------------|-------------|-------|
| caaggtgtga | aagtaaaaaga | tgggtcaagat | ggtgatgttg  | agagtgaatg  | ggaaaaatgac | 20760 |
| gatactgttg | cagctcgaaa  | tcaattatgt  | aaaggttaaca | ttttcgccat  | ggagattaat  | 20820 |
| ctccaggcta | acctgtggag  | aagtttcctc  | tactcgaacg  | tggccctgta  | cctgcccgcac | 20880 |
| tcctacaagt | acacgccgac  | caacgtcacg  | ctgccgacca  | acaccaaacac | ctacgattac  | 20940 |
| atgaatggca | gagtgcacac  | tccctcgctg  | gtagacgcct  | acctcaacat  | cggggcgcgcg | 21000 |
| tggtcgctgg | accccatgga  | caacgtcaac  | cccttcaacc  | accaccgcaa  | cgcgggcctg  | 21060 |
| cgctaccgct | ccatgctcct  | gggcaacggg  | cgctacgtgc  | ccttccacat  | ccaggtgccc  | 21120 |
| caaaagtttt | tcgccatcaa  | gagcctcctg  | ctcctgcccg  | ggctctacac  | ctacgagtgg  | 21180 |
| aacttccgca | aggacgtcaa  | catgatcctg  | cagagctccc  | taggcaacga  | cctgcgcacg  | 21240 |
| gacggggcct | ccatcgccct  | caccagcatc  | aacctctacg  | ccaccttctt  | ccccatggcg  | 21300 |
| cacaacaccg | cctccacgct  | cgaggccatg  | ctgcgcaacg  | acaccaacga  | ccagtccttc  | 21360 |
| aacgactacc | tctcggcggc  | caacatgctc  | taccccatcc  | cggccaacgc  | caccaacgtg  | 21420 |
| cccatctcca | tcccctcgcg  | caactgggcc  | gccttccgcg  | gatggtcctt  | cacgcgcctg  | 21480 |
| aagacccgcg | agacgccctc  | gctcggctcc  | gggttcgacc  | cctacttcgt  | ctactcgggc  | 21540 |
| tccatcccct | acctagacgg  | caccttctac  | ctcaaccaca  | ccttcaagaa  | ggtctccatc  | 21600 |
| accttcgact | cctccgtcag  | ctggcccggc  | aacgaccgcc  | tcctgacgcc  | caacgagttc  | 21660 |
| gaaatcaagc | gcaccgtcga  | cggagaggga  | tacaacgtgg  | cccagtgcaa  | catgaccaag  | 21720 |
| gactgggttc | tgggtccagat | gctggcccac  | tacaacatcg  | gctaccaggg  | cttctacgtg  | 21780 |
| cccgagggct | acaaggaccg  | catgtactcc  | ttcttccgca  | acttccagcc  | catgagccgc  | 21840 |
| caggtcgtgg | acgaggtcaa  | ctacaaggac  | taccaggccg  | tcaccctggc  | ctaccagcac  | 21900 |
| aacaactcgg | gcttcgtcgg  | ctacctcgcg  | cccaccatgc  | gccaggggcca | gccctacccc  | 21960 |
| gccaactacc | cctacccgct  | catcggaag   | agcgccgtcg  | ccagcgtcac  | ccagaaaaag  | 22020 |
| ttcctctgcg | accgggtcat  | gtggcgcac   | cccttctcca  | gcaacttcat  | gtccatgggc  | 22080 |
| gcgctcaccg | acctcgggcca | gaacatgctc  | tacgccaact  | ccgcccacgc  | gctagacatg  | 22140 |
| aatttcgaag | tcgaccccat  | ggatgagtcc  | acccttctct  | atgttgtctt  | cgaagtcttc  | 22200 |
| gacgtcgtcc | gagtgcacca  | gccccaccgc  | ggcgtcatcg  | aagccgtcta  | cctgcgcacg  | 22260 |
| cccttctcgg | ccggcaacgc  | caccacctaa  | gccgctcttg  | cttcttgcaa  | gatgacggcg  | 22320 |
| ggctccggcg | agcaggagct  | cagggccatc  | ctccgcgacc  | tgggctgcgg  | gccctgcttc  | 22380 |
| ctgggacact | tcgacaagcg  | cttccctgga  | ttcatggccc  | cgcacaagct  | ggcctgcgcc  | 22440 |
| atcgtgaaca | cggccggccg  | cgagaccggg  | ggcgagcact  | ggctggcctt  | cgcctggaac  | 22500 |
| ccgcgctccc | acacatgcta  | cctcttcgac  | cccttcgggt  | tctcggaaga  | gcgcctcaag  | 22560 |
| cagatctacc | agttcgagta  | cgagggcctg  | ctgcgtcgca  | gcgccctggc  | caccgaggac  | 22620 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |            |             |             |             |       |
|------------|-------------|------------|-------------|-------------|-------------|-------|
| cgctgcgta  | ccctggaaaa  | gtccacccag | accgtgcagg  | gtccgcgctc  | ggccgcctgc  | 22680 |
| gggctcttct | gctgcatgtt  | cctgcacgcc | ttcgtgcaact | ggcccgaaccg | ccccatggac  | 22740 |
| aagaacccca | ccatgaactt  | actgacgggg | gtgcccacg   | gcatgctcca  | gtcgccccag  | 22800 |
| gtggaacca  | ccctgcgccg  | caaccaggaa | gcgctctacc  | gcttcctcaa  | tgcccactcc  | 22860 |
| gcctactttc | gctcccaccg  | cgcgcgcatc | gagaaggcca  | ccgccttcga  | ccgcatgaat  | 22920 |
| caagacatgt | aaaaaaccgg  | tgtgtgtatg | tgaatgcttt  | attcataata  | aacagcacat  | 22980 |
| gtttatgcca | ccttctctga  | ggctctgact | ttatttagaa  | atcgaagggg  | ttctgccggc  | 23040 |
| tctcggcatg | gcccgcgggc  | agggatacgt | tgcggaactg  | gtacttgggc  | agccacttga  | 23100 |
| actcggggat | cagcagcttg  | ggcacgggga | ggtcggggaa  | cgagtcgctc  | cacagcttgc  | 23160 |
| gcgtgagttg | cagggcgccc  | agcaggtcgg | gcgcggagat  | cttgaaatcg  | cagttgggac  | 23220 |
| ccgcgttctg | cgcgcgagag  | ttgcggtaca | cgggggttga  | gcactggaac  | accatcaggg  | 23280 |
| ccgggtgctt | cacgcttgcc  | agcaccgtcg | cgtcggtgat  | gccctccacg  | tccagatcct  | 23340 |
| cggcgttggc | catcccgaag  | ggggtcatct | tgcaggctctg | ccgccccatg  | ctgggcacgc  | 23400 |
| agccgggctt | gtggttgcaa  | tcgcagtgca | gggggatcag  | catcatctgg  | gcctgctcgg  | 23460 |
| agctcatgcc | cgggtacatg  | gccttcatga | aagcctccag  | ctggcggaag  | gcctgctgcg  | 23520 |
| ccttgccgcc | ctcgggtgaag | aagaccccg  | aggacttgct  | agagaactgg  | ttggtggcgc  | 23580 |
| agccggcgtc | gtgcacgcag  | cagcgcgctg | cgttgttggc  | cagctgcacc  | acgctgcgcc  | 23640 |
| cccagcggtt | ctgggtgatc  | ttggcccgg  | tggggttctc  | cttcagcgcg  | cgctgcccgt  | 23700 |
| tctcgtcgc  | cacatccatc  | tcgatagtgt | gctccttctg  | gatcatcacg  | gtcccgtgca  | 23760 |
| ggcaccgcag | cttgccctcg  | gcttcggtgc | agccgtgcag  | ccacagcgcg  | cagccggtgc  | 23820 |
| actcccagtt | cttgtgggcg  | atctgggagt | gcgagtgcac  | gaagccctgc  | aggaagcggc  | 23880 |
| ccatcatcgc | ggtcagggtc  | ttgttgctgg | tgaaggtcag  | cgggatgccg  | cgggtgctcct | 23940 |
| cgttcacata | cagggtggcag | atgcggcggt | acacctcgcc  | ctgctcgggc  | atcagctgga  | 24000 |
| aggcggactt | caggtcgctc  | tccacgcggt | accggtccat  | cagcagcgtc  | atcacttcca  | 24060 |
| tgcccttctc | ccaggccgaa  | acgatcggca | ggctcagggg  | gttcttcacc  | gccattgtca  | 24120 |
| tcttagtcgc | cgccgccgag  | gtcagggggt | cgttctcgtc  | caggtctca   | aacactcgct  | 24180 |
| tgccgtcctt | ctcgatgatg  | cgcacggggg | gaaagctgaa  | gcccacggcc  | gccagctcct  | 24240 |
| cctcggcctg | cctttcgtcc  | tcgctgtcct | ggctgatgtc  | ttgcaaaggc  | acatgcttgg  | 24300 |
| tcttgcgggg | tttctttttg  | ggcggcagag | gcggcgccga  | tgtgctggga  | gagcgcgagt  | 24360 |
| tctcgttcac | cacgactatt  | tcttcttctt | ggccgtcgtc  | cgagaccacg  | cggcggtagg  | 24420 |
| catgcctctt | ctggggcaga  | ggcggaggcg | acgggctctc  | gcggttcggc  | gggcggctgg  | 24480 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |            |             |       |
|-------------|-------------|-------------|-------------|------------|-------------|-------|
| cagagccccct | tccgcgttcg  | ggggtgcgct  | cctggcggcg  | ctgctctgac | tgacttcctc  | 24540 |
| cgcgggccggc | catttgtgttc | tcctagggag  | caacaacaag  | catggagact | cagccatcgt  | 24600 |
| cgccaacatc  | gccatctgcc  | cccgccgcca  | ccgccgacga  | gaaccagcag | cagaatgaaa  | 24660 |
| gcttaaccgc  | cccgccgccc  | agccccacct  | ccgacgccgc  | ggccccagac | atgcaagaga  | 24720 |
| tggaggaatc  | catcgagatt  | gacctgggct  | acgtgacgcc  | cgcgagcac  | gaggaggagc  | 24780 |
| tggcagcgcg  | cttttcagcc  | ccggaagaga  | accaccaaga  | gcagccagag | caggaagcag  | 24840 |
| agaacgagca  | gaaccaggct  | gggcacgagc  | atggcgacta  | cctgagcggg | gcagaggacg  | 24900 |
| tgctcatcaa  | gcatctggcc  | cgccaatgca  | tcctcgtaaa  | ggacgcgctg | ctcgaccgcg  | 24960 |
| ccgaggtgcc  | cctcagcgtg  | gcggagctca  | gccgcgccta  | cgagcgcaac | ctcttctcgc  | 25020 |
| cgcgcggtgcc | ccccaaagcg  | cagccccaacg | gcacctgtga  | gccccacccg | cgcttcaact  | 25080 |
| tctacccggt  | cttcgcggtg  | cccgaggccc  | tggccaccta  | ccacctcttt | ttcaagaacc  | 25140 |
| aaaggatccc  | cgtctcctgc  | cgcgccaacc  | gcacccgcgc  | cgacgccctg | ctcaacctgg  | 25200 |
| gccccggcgc  | ccgcctacct  | gatatcacct  | ccttgggaaga | ggttcccaag | atcttcgagg  | 25260 |
| gtctgggcag  | cgacgagact  | cgggccgcga  | acgctctgca  | aggaagcgga | gaggagcatg  | 25320 |
| agcaccacag  | cgccctgggtg | gagttggaag  | gcgacaacgc  | gcgcctggcg | gtcctcaagc  | 25380 |
| gcacggtcga  | gctgaccac   | ttcgctacc   | cggcgctcaa  | cctgcccccc | aaggatcatga | 25440 |
| gcgccgtcat  | ggaccagggtg | ctcatcaagc  | gcgcctcgcc  | cctctcgag  | gaggagatgc  | 25500 |
| aggacccga   | gagttcggac  | gagggcaagc  | ccgtggtcag  | cgacgagcag | ctggcgcgct  | 25560 |
| ggctgggagc  | gagtagcacc  | ccccagagcc  | tggaaagagcg | gcgcaagctc | atgatggccg  | 25620 |
| tggtcctggt  | gaccgtggag  | ctggagtgtc  | tgcgccgctt  | ctttgccgac | gcggagaccc  | 25680 |
| tgcgcaagggt | cgaggagaac  | ctgcactacc  | tcttcaggca  | cgggttcgtg | cgccaggcct  | 25740 |
| gcaagatctc  | caacgtggag  | ctgaccaacc  | tggctctccta | catgggcatc | ctgcacgaga  | 25800 |
| accgcctggg  | gcaaaacgtg  | ctgcacacca  | ccctgcgcgg  | ggaggcccg  | cgcgactaca  | 25860 |
| tccgcgactg  | cgtctacctg  | tacctctgcc  | acacctggca  | gacgggcatg | ggcgtgtggc  | 25920 |
| agcagtgcct  | ggaggagcag  | aacctgaaag  | agctctgcaa  | gctcctgcag | aagaacctca  | 25980 |
| aggccctgtg  | gaccgggttc  | gacgagcgta  | ccaccgcctc  | ggacctggcc | gacctcatct  | 26040 |
| tccccgagcg  | cctgcggctg  | acgctgcgca  | acgggctgcc  | cgactttatg | agccaaagca  | 26100 |
| tgttgcaaaa  | ctttcgctct  | ttcatcctcg  | aacgctccgg  | gatcctgccc | gccacctgct  | 26160 |
| ccgcgctgcc  | ctcggaacttc | gtgccgctga  | ccttccgcga  | gtgccccccg | ccgctctgga  | 26220 |
| gccactgcta  | cttgctgcgc  | ctggccaact  | acctggccta  | ccactcgag  | gtgatcgagg  | 26280 |
| acgtcagcgg  | cgaggggtctg | ctggagtgcc  | actgccgctg  | caacctctgc | acgccgcacc  | 26340 |
| gctccctggc  | ctgcaacccc  | cagctgctga  | gcgagaccca  | gatcatcggc | accttcgagt  | 26400 |

368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |            |            |             |       |
|------------|------------|-------------|------------|------------|-------------|-------|
| tgcaaggccc | cggcgacggc | gagggcaagg  | ggggtctgaa | actcaccccg | gggctgtgga  | 26460 |
| cctcggccta | cttgcgcaag | ttcgtgcccc  | aggactacca | tcccttcgag | atcaggttct  | 26520 |
| acgaggacca | atcccagccg | cccaaggccg  | agctgtcggc | ctgcgtcatc | acccaggggg  | 26580 |
| ccatcctggc | ccaattgcaa | gccatccaga  | aatcccgcc  | agaatttctg | ctgaaaaagg  | 26640 |
| gccacggggg | ctacttggac | ccccagaccg  | gagaggagct | caaccccagc | ttcccccagg  | 26700 |
| atgccccgag | gaagcagcaa | gaagctgaaa  | gtggagctgc | cgccgccgga | ggatttggag  | 26760 |
| gaagactggg | agagcagtca | ggcagaggag  | gaggagatgg | aagactggga | cagcactcag  | 26820 |
| gcagaggagg | acagcctgca | agacagtctg  | gaggaggaag | acgaggtgga | ggaggcagag  | 26880 |
| gaagaagcag | ccgccgccag | accgtcgtcc  | tcggcggaga | aagcaagcag | cacggatacc  | 26940 |
| atctccgctc | cgggtcgggg | tcgcgcgggc  | cgggcccaca | gtaggtggga | cgagaccggg  | 27000 |
| cgcttcccga | accccaccac | ccagaccggt  | aagaaggagc | ggcagggata | caagtcctgg  | 27060 |
| cgggggcaca | aaaacgccat | cgtctcctgc  | ttgcaagcct | gcgggggcaa | catctccttc  | 27120 |
| acccggcgct | acctgctctt | ccaccgcggg  | gtgaacttcc | cccgaacat  | cttgcatcatt | 27180 |
| taccgtcacc | tccacagccc | ctactactgt  | ttccaagaag | aggcagaaac | ccagcagcag  | 27240 |
| cagaaaacca | gcggcagcag | cagctagaaa  | atccacagcg | gcggcaggtg | gactgaggat  | 27300 |
| cgcggcgaac | gagccggcgc | agaccgggga  | gctgaggaac | cggatctttc | ccaccctcta  | 27360 |
| tgccatcttc | cagcagagtc | gggggcagga  | gcaggaactg | aaagtcaaga | accgttctct  | 27420 |
| gcgctcgctc | acccgcagtt | gtctgtatca  | caagagcgaa | gaccaacttc | agcgactctt  | 27480 |
| cgaggacgcc | gaggctctct | tcaacaagta  | ctgcgcgctc | actcttaaag | agtagcccg   | 27540 |
| gcccggccac | acacggaaaa | aggcggggaat | tacgtcacca | cctgcgccct | tcggccgacc  | 27600 |
| atcatgagca | aagagattcc | cacgccttac  | atgtggagct | accagcccca | gatgggcctg  | 27660 |
| gccgccggcg | ccgccagga  | ctactccacc  | cgcatgaact | ggctcagtc  | cgggcccgcg  | 27720 |
| atgatctcac | gggtgaatga | catccgcgcc  | caccgaaacc | agatactcct | agaacagtca  | 27780 |
| gcgatcaccg | ccacgccccg | ccatcacctt  | aatccgcgta | attggcccg  | cgccctggtg  | 27840 |
| taccaggaaa | ttccccagcc | cacgaccgta  | ctacttccgc | gagacgcca  | ggccgaagtc  | 27900 |
| cagctgacta | actcaggtgt | ccagctggcc  | ggcggcggcg | ccctgtgtcg | tcaccgcccc  | 27960 |
| gctcagggtg | taaagcggct | ggtgatccga  | ggcagaggca | cacagctcaa | cgacgaggtg  | 28020 |
| gtgagctctt | cgctgggtct | gcgacctgac  | ggagtcttcc | aactcgccgg | atcggggaga  | 28080 |
| tcttccttca | cgctcgtca  | ggccgtcctg  | actttggaga | gttcgtcctc | gcagccccgc  | 28140 |
| tcgggcggca | tcggcactct | ccagttcgtg  | gaggagtcca | ctccctcggt | ctacttcaac  | 28200 |
| cccttctccg | gctcccccg  | ccactaccgc  | gacgagttca | tcccgaactt | cgacgccatc  | 28260 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |            |            |            |             |       |
|------------|-------------|------------|------------|------------|-------------|-------|
| agcgagtcgg | tggacggcta  | cgattgaatg | tcccatggtg | gcgcagctga | cctagctcgg  | 28320 |
| cttcgacacc | tggaccactg  | ccgccgcttc | cgctgcttcg | ctcgggatct | cgccgagttt  | 28380 |
| gcctactttg | agctgcccga  | ggagcaccct | cagggcccag | cccacggagt | gcggatcatc  | 28440 |
| gtcgaagggg | gcctcgactc  | ccacctgctt | cggatcttca | gccagcgacc | gatcctggtc  | 28500 |
| gagcgcaaac | aaggacagac  | ccttcttact | ttgtactgca | tctgcaacca | ccccggcctg  | 28560 |
| catgaaagtc | tttgttgtct  | gctgtgtact | gagtataata | aaagctgaga | tcagcgacta  | 28620 |
| ctccggactc | gatttgtgtg  | ttcctgctat | caaccggtcc | ctgttcttca | ccgggaacga  | 28680 |
| gaccgagctc | cagctccagt  | gtaagcccca | caagaagtac | ctcacctggc | tgttccaggg  | 28740 |
| ctccccgatc | gccgttgtca  | accactgcga | caacgacgga | gtcctgctga | gcggccctgc  | 28800 |
| caaccttact | ttttccaccc  | gcagaagcaa | gctccagctc | ttccaaccct | tcctccccgg  | 28860 |
| gacctatcag | tgcgtctcag  | gaccttgcca | tcacaccttc | cacctgatcc | cgaataccac  | 28920 |
| agcgccgctc | cccgtacta   | acaaccaaac | taccaccaa  | cgccaccgtc | gcgacctttc  | 28980 |
| ctctgaatct | aataccacta  | ccggagggtg | cttctgctgt | tagtgctccc | ccgtcccgtc  | 29040 |
| gacccccggt | ccccactca   | gtcccccgag | gaggttcgca | aatgcaaatt | ccaagaaccc  | 29100 |
| tggaaattcc | tcaaattgcta | ccgccaaaaa | tcagacatgc | atcccagctg | gatcatgatc  | 29160 |
| attgggatcg | tgaacattct  | ggcctgcacc | ctcatctcct | ttgtgattta | cccctgcttt  | 29220 |
| gactttgggt | ggaactcgcc  | agaggcgctc | tatctcccg  | ctgaacctga | cacaccacca  | 29280 |
| cagcagcaac | ctcaggcaca  | cgcactacca | ccaccacagc | ctaggccaca | atacatgccc  | 29340 |
| atattagact | atgaggccga  | gccacagcga | cccattgctc | ccgctattag | ttacttcaat  | 29400 |
| ctaaccggcg | gagatgactg  | acccactggc | caataacaac | gtcaacgacc | ttctcctgga  | 29460 |
| catggacggc | cgcgcctcgg  | agcagcgact | cgcccaactt | cgcattcgtc | agcagcagga  | 29520 |
| gagagccgtc | aaggagctgc  | aggacggcat | agccatccac | cagtgaaga  | gaggcatctt  | 29580 |
| ctgcctgggt | aaacaggcca  | agatctccta | cgaggtcacc | cagaccgacc | atcgctctc   | 29640 |
| ctacgagctc | ctgcagcagc  | gccagaagtt | cacctgcctg | gtcggagtca | accccatcgt  | 29700 |
| catcaccag  | cagtcggg    | ataccaagg  | gtgcatccac | tgtcctgcg  | actccccga   | 29760 |
| ctgcgtccac | actctgatca  | agaccctctg | cggcctccgc | gacctcctcc | ccatgaacta  | 29820 |
| atcaccccct | tatccagtga  | aataaagatc | atattgatga | tgatttaa   | aaaaaaaaata | 29880 |
| atcatttgat | ttgaaataaa  | gatacaatca | tattgatgat | ttgagtttaa | caaaaataaa  | 29940 |
| gaatcactta | cttgaaatct  | gataccaggt | ctctgtccat | gttttctgcc | aacaccacct  | 30000 |
| cactcccctc | ttcccagctc  | tggtactgca | ggccccggcg | ggctgcaa   | aac         | 30060 |
| cgctgaaggg | gatgtcaaat  | tcctcctgtc | cctcaatctt | cattttatct | tctatcagat  | 30120 |
| gtccaaaaag | cgcgtccggg  | tggatgatga | cttcgacccc | gtctacccct | acgatgcaga  | 30180 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |            |            |             |             |       |
|------------|-------------|------------|------------|-------------|-------------|-------|
| caacgcaccg | accgtgccct  | tcatcaaccc | ccccttcgtc | tcttcagatg  | gattccaaga  | 30240 |
| gaagcccctg | ggggtgttgt  | ccctgcgact | ggctgacccc | gtcaccacca  | agaacggggga | 30300 |
| aatcaccctc | aagctgggag  | agggggtgga | cctcgactcg | tcgggaaaac  | tcatctccaa  | 30360 |
| cacggccacc | aaggccgccg  | cccctctcag | tatttcaaac | aacaccattt  | cccttaaaac  | 30420 |
| tgctgcccct | ttctacaaca  | acaatggaac | tttaagcctc | aatgtctcca  | caccattagc  | 30480 |
| agtatttccc | acatttaaca  | ctttaggcat | aagtcttggg | aacggtcttc  | agacttcaaa  | 30540 |
| taagttgttg | actgtacaac  | taactcatcc | tcttacattc | agctcaaata  | gcatcacagt  | 30600 |
| aaaaacagac | aaagggttat  | atattaactc | cagtggaaac | agaggacttg  | aggctaatat  | 30660 |
| aagcctaaaa | agaggactag  | tttttgacgg | taatgctatt | gcaacatata  | ttggaaatgg  | 30720 |
| cttagactat | ggatcttatg  | atagtgatgg | aaaaacaaga | cccgtaatata | ccaaaattgg  | 30780 |
| agcaggatta | aattttgatg  | ctaacaaagc | aatagctgtc | aaactaggca  | caggtttaag  | 30840 |
| ttttgactcc | gctggtgcct  | tgacagctgg | aaacaaacag | gatgacaagc  | taacactttg  | 30900 |
| gactaccctt | gacccaagcc  | ctaattgtca | attactttca | gacagagatg  | ccaaatttac  | 30960 |
| tctctgtctt | acaaaaatgcg | gtagtcaaat | actaggcact | gtggcagtg   | cggctgttac  | 31020 |
| tgtaggatca | gcactaaaac  | caattaatga | cacagtcaaa | agcgccatag  | ttttccttag  | 31080 |
| atttgattcc | gatggtgtac  | tcatgtcaaa | ctcatcaatg | gtaggtgatt  | actggaactt  | 31140 |
| tagggaggga | cagaccactc  | aaagtgtagc | ctatacaaat | gctgtgggat  | tcatgccaaa  | 31200 |
| tataggtgca | tatccaaaaa  | cccaaagtaa | aacaccta   | aatagcatag  | tcagtcaggt  | 31260 |
| atatttaact | ggagaaacta  | ctatgccaat | gacactaacc | ataactttca  | atggcactga  | 31320 |
| tgaaaaagac | acaaccccag  | ttagcaccta | ctctatgact | tttacatggc  | agtggactgg  | 31380 |
| agactataag | gacaaaaata  | ttacctttgc | taccaactca | ttctcttttt  | cctacatcgc  | 31440 |
| ccaggaataa | tcccacccag  | caagccaacc | ccctttccca | ccacctttgt  | ctatatggaa  | 31500 |
| actctgaaac | agaaaaataa  | agttcaagtg | ttttattgaa | tcaacagttt  | tacaggactc  | 31560 |
| gagcagttat | ttttcctcca  | ccctcccagg | acatggaata | caccaccctc  | tccccccgca  | 31620 |
| cagccttgaa | catctgaatg  | ccattggtga | tggacatgct | tttggctctc  | acgttccaca  | 31680 |
| cagtttcaga | gcgagccagt  | ctcggatcgg | tcaggagatg | gaaaccctcc  | gggcactccc  | 31740 |
| gcatctgcac | ctcacagctc  | aacagctgag | gattgtcctc | ggtggtcggg  | atcacggtta  | 31800 |
| tctggaagaa | gcagaagagc  | ggcgggtggg | atcatagtcc | gcgaacggga  | tcggccggtg  | 31860 |
| gtgtcgcac  | agggcccgcg  | gcagtcgctg | ccgcccgcgc | tccgtcaagc  | tgctgctcag  | 31920 |
| ggggttcggg | tccagggact  | ccctcagcat | gatgcccacg | gccctcagca  | tcagtcgtct  | 31980 |
| ggtgcggcgg | gcgcagcagc  | gcatgcgaat | ctcgctcagg | tcactgcagt  | acgtgcaaca  | 32040 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |            |            |             |            |       |
|------------|-------------|------------|------------|-------------|------------|-------|
| caggaccacc | aggttgttca  | acagtccata | gttcaacacg | ctccagccga  | aactcatcgc | 32100 |
| gggaaggatg | ctaccacacgt | ggccgtcgta | ccagatcctc | aggtaaataca | agtggcgctc | 32160 |
| cctccagaag | acgctgccc   | tgtacatgat | ctccttgggc | atgtggcggt  | tcaccacctc | 32220 |
| ccggtaccac | atcaccctct  | ggttgaacat | gcagccccgg | atgatcctgc  | ggaaccacag | 32280 |
| ggccagcacc | gccccgccc   | ccatgcagcg | aagagacccc | ggatcccggc  | aatgacaatg | 32340 |
| gaggaccac  | cgctcgta    | cgtggatcat | ctgggagctg | aacaagtcta  | tgttggcaca | 32400 |
| gcacaggcat | atgctcatgc  | atctcttcag | cactctcagc | tcctcggggg  | tcaaaaccat | 32460 |
| atcccagggc | acggggaact  | cttgcaggac | agcgaacccc | gcagaacagg  | gcaatcctcg | 32520 |
| cacataactt | acattgtgca  | tggacaggg  | atcgcaatca | ggcagcaccg  | ggtgatcctc | 32580 |
| caccagagaa | gcgcgggtct  | cggtctcctc | acagcgtggt | aagggggccg  | gccgatacgg | 32640 |
| gtgatggcgg | gacgcggctg  | atcgtgttct | cgaccgtgtc | atgatgcagt  | tgctttcggg | 32700 |
| cattttcgta | cttgctgtag  | cagaacctgg | tccgggcgct | gcacaccgat  | cgccggcggc | 32760 |
| ggtctcg    |             |            |            |             |            | 32767 |

&lt;210&gt; 7

&lt;211&gt; 32767

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificially Synthesized

&lt;400&gt; 7

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| catcatcaat  | aatatacctc | aaacttttgg  | tgcgcgttaa | tatgcaaata | agctgtttga | 60  |
| atttgggggag | ggaggaaggt | gattggccga  | gagacggggc | accgttaggg | gcggggcggg | 120 |
| tgacgttttg  | atgacgtggc | cgtgaggcgg  | agccggtttg | caagtctctg | tgggaaaagt | 180 |
| gacgtcaaac  | gaggtgtggt | ttgaacacgg  | aaataactca | ttttcccgcg | ctctctgaca | 240 |
| ggaaatgagg  | tgtttctggg | cggatgcaag  | tgaaaacggg | ccattttcgc | gcgaaaactg | 300 |
| aatgaggaag  | tgaaaatctg | agtaatttctg | cgtttatggc | aggaggagg  | atttgccgag | 360 |
| ggccgagtag  | actttgaccg | attacgtggg  | ggtttcgatt | accgtatttt | tcacctaaat | 420 |
| ttccgcgtac  | ggtgtcaaa  | tccggtgttt  | ttacgtacga | tatcatttcc | ccgaaagtgc | 480 |
| cacctgaccg  | taactataac | ggtcctaagg  | tagcgaaagc | tcagatctcc | cgatccccta | 540 |
| tgggtgactc  | tcagtacaat | ctgctctgat  | gccgcatagt | taagccagta | tctgctccct | 600 |
| gcttgtgtgt  | tggaggtcgc | tgagtagtgc  | gcgagcaaaa | tttaagctac | aacaaggcaa | 660 |
| ggcttgaccg  | acaattgcat | gaagaatctg  | cttaggggta | ggcgttttgc | gctgcttcgc | 720 |
| gatgtacggg  | ccagatatac | gcgttgacat  | tgattattga | ctagtatgcc | aagtacgccc | 780 |
| cctattgacg  | tcaatgacgg | taaatggccc  | gcctggcatt | atgccagta  | catgacctta | 840 |

368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| tgggactttc  | ctacttggca | gtacatctac  | gtattagtca | tcgctattac | catggtgatg | 900  |
| cggtttttggc | agtacatcaa | tgggcgtgga  | tagcggtttg | actcacgggg | atttccaagt | 960  |
| ctccaccccca | ttgacgtcaa | tgggagtttg  | ttttggcacc | aaaatcaacg | ggactttcca | 1020 |
| aaatgtcgta  | acaactccgc | cccattgacg  | caaatgggcg | gtaggcgtgt | acggtgggag | 1080 |
| gtctatataa  | gcagagctcg | tttagtgaac  | cgtcagatca | ctagaagctt | tattgcggta | 1140 |
| gtttatcaca  | gttaaattgc | taacgcagtc  | agtgcttctg | acacaacagt | ctcgaactta | 1200 |
| aggctagagt  | acttaatacg | actcactata  | ggctagttaa | ggctagagtt | cgacgccacc | 1260 |
| atgcgcgtga  | tgggcaccc  | gcgctcctac  | cagcagtggt | ggatctgggg | catcctgggc | 1320 |
| ttctggatgc  | tgatgatctg | caacgtgtgg  | ggcaacctgt | gggtgaccgt | gtactacggc | 1380 |
| gtgcccgtgt  | ggaaggaggc | caagaccacc  | ctgttctgcg | cctccgacgc | caaggcccac | 1440 |
| aaggaggagg  | tgcacaacat | ctgggccacc  | cacgcctgcg | tgcccaccga | ccccaacccc | 1500 |
| caggagatcg  | tgctgaagaa | cgtgaccgag  | aacttcaaca | tgtggaagaa | cgacatggtg | 1560 |
| gaccagatgc  | acgaggacat | catctccctg  | tgggaccagt | ccctgaagcc | ctgctgaag  | 1620 |
| ctgaccccc   | tgtgctgac  | cctgaactgc  | tccgacgtga | agatcaagg  | caccaacgcc | 1680 |
| acctacaaca  | acgccaccta | caacaacaac  | aacaccatct | ccgacatgaa | gaactgctcc | 1740 |
| ttcaacacca  | ccaccgagat | caccgacaag  | aagaagaagg | agtacgccct | gttctacaag | 1800 |
| ctggacgtgg  | tggccctgga | cggcaaggag  | accaactcca | ccaactcctc | cgagtaccgc | 1860 |
| ctgatcaact  | gcaacacctc | cgccgtgacc  | caggcctgcc | ccaagggtgc | cttcgacccc | 1920 |
| atccccatcc  | actactgctc | ccccgccggc  | tacgccatcc | tgaagtgcaa | caacaagacc | 1980 |
| ttcaacggca  | ccggccctg  | caacaacgtg  | tccaccgtgc | agtgcacca  | cggcatcaag | 2040 |
| cccgtggtgt  | ccaccagct  | gctgctgaac  | ggctccctgg | ccgaggagga | ggtggtgatc | 2100 |
| cgcttcgaga  | acctgaccaa | caacgccaag  | atcatcatcg | tgcacctgaa | cgagtccgtg | 2160 |
| gagatcaact  | gcacccgccc | ctccaacaac  | acccgcaagt | ccgtgcgcat | cggccccggc | 2220 |
| cagaccttct  | tcgccaccgg | cgacatcatc  | ggcgacatcc | gccaggccca | ctgcaacatc | 2280 |
| tcccgcaaga  | agtggaacac | caccctgcag  | cgcgtgaagg | agaagctgaa | ggagaagttc | 2340 |
| cccaacaaga  | ccatccagtt | cgccccctcc  | tccggcggcg | acctggagat | caccaccac  | 2400 |
| tccttcaact  | gccgcggcga | gttctttctac | tgctacacct | ccgacctgtt | caactccacc | 2460 |
| tacatgtcca  | acaacaccgg | cggcgccaac  | atcacctgc  | agtgccgcat | caagcagatc | 2520 |
| atccgcatgt  | ggcaggcggt | gggccaggcc  | atgtacgcc  | ccccatcgc  | cggcaacatc | 2580 |
| acctgcaagt  | ccaacatcac | cggcctgctg  | ctgacccgcg | acggcggcaa | ggagaagaac | 2640 |
| gacaccgaga  | ccttccgccc | cggcgggcgg  | gacatgcgcg | acaactggcg | ctccgagctg | 2700 |

| 368530-7006W01_SequenceListing_ST25.txt |             |            |            |            |             |      |
|-----------------------------------------|-------------|------------|------------|------------|-------------|------|
| tacaagtaca                              | aggtggtgga  | gatcaagccc | ctgggcatcg | cccccgacaa | ggccaagcgc  | 2760 |
| cgcggtggtg                              | agcgcgagaa  | gcgcgccgtg | ggcatcggcg | ccgtgttcct | gggcttcctg  | 2820 |
| ggcgccgccg                              | gcagcaccat  | gggcgccgcc | agcatgaccc | tgaccgtgca | ggcccgccag  | 2880 |
| ctgctgagcg                              | gcatcgtgca  | gcagcagagc | aacctgctgc | gcgccatcga | ggcccagcag  | 2940 |
| cacatgctgc                              | agctgaccgt  | gtggggcatc | aagcagctgc | agacccgcgt | gctggccatc  | 3000 |
| gagcgctacc                              | tgaaggacca  | gcagctgctg | ggcatctggg | gctgcagcgg | caagctgac   | 3060 |
| tgcaccaccg                              | ccgtgccctg  | gaacgccagc | tggagcaaca | agagctacga | ggagatctgg  | 3120 |
| ggcaacatga                              | cctggatgca  | gtgggaccgc | gagatcaaca | actacaccaa | caccatctac  | 3180 |
| agcctgctgg                              | aggagagcca  | gaaccagcag | gagaagaacg | agaaggacct | gctggccctg  | 3240 |
| gacagctggg                              | agagcctgtg  | gagctggttc | aacatcacca | actggctgtg | gtacatccgc  | 3300 |
| atcttcatca                              | tcatcgtggg  | cggcctgac  | ggcctgcgca | tcatcttcgc | cgctgctgagc | 3360 |
| atcgtgaacc                              | gcgtgcgcca  | gggctacagc | cccctgagct | tccagaccct | gacccccagc  | 3420 |
| ccccgcgagc                              | ccgaccgcct  | gggccgcac  | gaggaggagg | gcggcgagca | ggaccgcgcc  | 3480 |
| cgcagcgtgc                              | gcctggtgaa  | cggttcctg  | gccctggcct | gggaggacct | gcgcagcctg  | 3540 |
| tgctgttca                               | gctaccaccg  | cctgcgcgac | ctgatcctga | tcgccgcccg | cgccgccgcc  | 3600 |
| ctgctgggcc                              | gcagcagcct  | gtggggcctg | cagaagggct | gggaggccct | gaagtacctg  | 3660 |
| ggcagcctgg                              | tgagctactg  | gggcctggag | ctgaagaaga | gcgccatcag | cctgttcgac  | 3720 |
| gccatcgcca                              | tcaccgtggc  | cgagggcacc | gaccgcac   | tcaacatcgt | gcagcgcac   | 3780 |
| agccgcgcct                              | tctacaacat  | ccccgcgc   | atccgccagg | gcttcgaggc | caccctgcag  | 3840 |
| taaggtagct                              | ctagagtcga  | cccgggcggc | caaaccgctg | atcagcctcg | actgtgcctt  | 3900 |
| ctagttgcca                              | gccatctgtt  | gtttgcccct | ccccgtgcc  | ttccttgacc | ctggaagggtg | 3960 |
| ccactcccac                              | tgtcctttcc  | taataaaatg | aggaaattgc | atcgcatgtg | ctgagtaggt  | 4020 |
| gtcattctat                              | tctggggggg  | ggggtggggc | aggacagcaa | gggggaggat | tgggaagaca  | 4080 |
| atagcaggca                              | tgctggggat  | gcggtgggct | ctatggcttc | tgaggcgga  | agaaccagca  | 4140 |
| gatctgcaga                              | tctgaattca  | tctatgtcgg | gtgcggagaa | agaggtaatg | aaatggcatt  | 4200 |
| atgggtatta                              | tgggtctgca  | ttaatgaatc | ggccagatat | cgatatgctg | gccaccgtgc  | 4260 |
| atgtgacctc                              | gcacccccgc  | aagacatggc | ccgagttcga | gcacaacgtc | atgaccgat   | 4320 |
| gcaatgtgca                              | cctgggggtcc | cgccgaggca | tgttcatgcc | ctaccagtgc | aacatgcaat  | 4380 |
| ttgtgaagg                               | gctgctggag  | cccgatgcca | tgtccagagt | gagcctgacg | ggggtgtttg  | 4440 |
| acatgaatgt                              | ggagctgtgg  | aaaattctga | gatatgatga | atccaagacc | aggtgccggg  | 4500 |
| cctgcgaatg                              | cggaggcaag  | cacgccaggc | ttcagcccgt | gtgtgtggag | gtgacggagg  | 4560 |
| acctgcgacc                              | cgatcatttg  | gtgtgttcct | gcaacgggac | ggagttcggc | tccagcgggg  | 4620 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| aagaatctga  | ctagagtga  | tagtgtttg   | gggaggtgga  | gggcttgat   | gaggggcaga | 4680 |
| atgactaaaa  | tctgtgtttt | tctgtgtgtt  | gcagcagcat  | gagcggaagc  | gcctcctttg | 4740 |
| agggaggggt  | attcagccct | tatctgacgg  | ggcgtctccc  | ctcctgggcg  | ggagtgcgtc | 4800 |
| agaatgtgat  | gggatccacg | gtggacggcc  | ggcccgtgca  | gcccgcgaac  | tcttcaaccc | 4860 |
| tgacctacgc  | gaccctgagc | tcctcgtccg  | tggacgcagc  | tgccgccgca  | gctgctgctt | 4920 |
| ccgccgccag  | cgccgtgcgc | ggaatggccc  | tgggcgccgg  | ctactacagc  | tctctggtgg | 4980 |
| ccaactcgac  | ttccaccaat | aatcccgcga  | gcctgaacga  | ggagaagctg  | ctgctgctga | 5040 |
| tggcccagct  | cgaggccctg | accacgcgcc  | tgggcgagct  | gacccagcag  | gtggctcagc | 5100 |
| tgcaggcgga  | gacgcggggc | gcggttgcca  | cggtgaaaac  | caaataaaaa  | atgaatcaat | 5160 |
| aaataaacgg  | agacggttgt | tgattttaac  | acagagtctt  | gaatctttat  | ttgatttttc | 5220 |
| gcgcgcggta  | ggccctggac | caccggtctc  | gatcattgag  | cacccggtgg  | attttttcca | 5280 |
| ggacccggta  | gaggtgggct | tggatgttga  | ggtacatggg  | catgagcccc  | tcccgggggt | 5340 |
| ggaggtagct  | ccattgcagg | gcctcgtgct  | cgggggtggt  | gttgtaaatac | accagtcac  | 5400 |
| agcaggggcg  | cagggcggtg | tgtgcacga   | tgtccttgag  | gaggagactg  | atggccacgg | 5460 |
| gcagcccctt  | ggtgtaggtg | ttgacgaacc  | tgttgagctg  | ggagggatgc  | atgcgggggg | 5520 |
| agatgagatg  | catcttggcc | tggatcttga  | gattggcgat  | gttcccggcc  | agatcccggc | 5580 |
| gggggttcat  | gttgtgcagg | accaccagca  | cgggtgtatcc | ggcgcacttg  | gggaatttgt | 5640 |
| catgcaactt  | ggaagggaag | gcgtgaaaaga | atttgagagac | gcccttgatga | ccgcccaggt | 5700 |
| tttccatgca  | ctcatccatg | atgatggcga  | tgggcccgtg  | ggcggcgggc  | tgggcaaaga | 5760 |
| cgtttcgggg  | gtcggacaca | tcgtagtgtg  | ggtcctgggt  | gagctcgtca  | taggccattt | 5820 |
| taatgaattt  | ggggcgagg  | gtgcccgaact | gggggacgaa  | ggtgccctcg  | atcccggggg | 5880 |
| cgtagtgtcc  | ctcgcagatc | tgcactctcc  | aggccttgag  | ctcggagggg  | gggatcatgt | 5940 |
| ccacctgcgg  | ggcgatgaaa | aaaacggttt  | ccggggcggg  | ggagatgagc  | tgggccgaaa | 6000 |
| gcaggttccg  | gagcagctgg | gacttgccgc  | agccggtggg  | gccgtagatg  | accccgatga | 6060 |
| ccggctgcag  | gtggtagtgt | agggagagac  | agctgccgtc  | ctcgcggagg  | aggggggcca | 6120 |
| cctcgttcat  | catctcgcgc | acatgcatgt  | tctcgcgcac  | gagttccgcc  | aggaggcgct | 6180 |
| cgccccccag  | cgagaggagc | tcttgacgcg  | aggcgaagtt  | tttcagcggc  | ttgagyccgt | 6240 |
| cggccatggg  | cattttggag | agggctctgtt | gcaagagttc  | cagacggtcc  | cagagctcgg | 6300 |
| tgatgtgctc  | tagggcatct | cgatccagca  | gacctcctcg  | tttcgcgggt  | tggggcgact | 6360 |
| gcgggagtag  | ggcaccaggc | gatgggcgtc  | cagcgaggcc  | aggggtccgt  | ccttccaggg | 6420 |
| tcgcaggggtc | cgcgtcagcg | tggctctccgt | cacggtgaag  | gggtgcgcgc  | cgggctgggc | 6480 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| gcttgcgagg  | gtgcgcttca  | ggctcatccg | gctggctcgag | aaccgctccc  | ggtcggcgcc  | 6540 |
| ctgcgcgctc  | gccaggtagc  | aattgagcat | gagttcgtag  | ttgagcgcct  | cggccgcgtg  | 6600 |
| gcccttggcg  | cggagcttac  | ctttggaagt | gtgtccgcag  | acgggacaga  | ggagggactt  | 6660 |
| gagggcgtag  | agcttggggg  | cgaggaagac | ggactcgggg  | gcgtaggcgt  | ccgcgccgca  | 6720 |
| gctggcgtag  | acggtctcgc  | actccacgag | ccaggtagag  | tcgggccggt  | tggggtcaaa  | 6780 |
| aacgaggttt  | cctccgtgct  | ttttgatgcg | tttcttacct  | ctgggtctcca | tgagctcgtg  | 6840 |
| tccccgctgg  | gtgacaaaaga | ggctgtccgt | gtccccgtag  | accgacttta  | tgggccggtc  | 6900 |
| ctcgagcggg  | gtgccgcggt  | cctcgtcgta | gaggaacccc  | gcccactccg  | agacgaaggc  | 6960 |
| ccgggtccag  | gccagcacga  | aggaggccac | gtgggagggg  | tagcggtcgt  | tgtccaccag  | 7020 |
| cgggtccacc  | ttctccaggg  | tatgcaagca | catgtccccc  | tcgtccacat  | ccaggaaggt  | 7080 |
| gattggcttg  | taagtgtagg  | ccacgtgacc | gggggtcccc  | gccggggggg  | tataaaaggg  | 7140 |
| ggcgggcccc  | tgctcgtcct  | cactgtcttc | cggatcgctg  | tccaggagcg  | ccagctgttg  | 7200 |
| gggtaggtat  | tccctctcga  | aggctggcat | aacctcggca  | ctcaggttgt  | cagtttctag  | 7260 |
| aaacgaggag  | gatttgatat  | tgacggtgcc | gttgagagac  | cctttcatga  | gcccctcgtc  | 7320 |
| catctgggtca | gaaaagacga  | tctttttgtt | gtcgagcttg  | gtggcgaagg  | agccgtagag  | 7380 |
| ggcgttggag  | aggagcttgg  | cgatggagcg | catggtcttg  | ttcttttcct  | tgtcggcgcg  | 7440 |
| ctccttggcg  | gcgatgttga  | gctgcacgta | ctcgcgcgcc  | acgcacttcc  | attcggggaa  | 7500 |
| gacggtgggtg | agctcgtcgg  | gcacgattct | gacctgccag  | ccgcggttgt  | gcagggtagat | 7560 |
| gaggtccacg  | ctggtggcca  | cctcgcgcg  | caggggctcg  | ttggtccagc  | agaggcgccc  | 7620 |
| gcccttgcgc  | gagcagaagg  | ggggcagcgg | gtccagcatg  | agctcgtcgg  | gggggtcggc  | 7680 |
| gtccacgggtg | aagatgccgg  | gcagaagctc | ggggtcgaag  | tagctgatgc  | aggtgtccag  | 7740 |
| atcgtccagc  | gccgcttgcc  | agtcgcgcac | ggccagcgcg  | cgctcgtagg  | ggctgagggg  | 7800 |
| cgtgccccag  | ggcatgggg   | gcgtgagcgc | ggaggcgtag  | atgccgcaga  | tgtcgtagac  | 7860 |
| gtagaggggg  | tcctcgagga  | cgccgatgta | ggtggggtag  | cagcgcccc   | cgcggtatgt  | 7920 |
| ggcgcgcacg  | tagtcgtaca  | gctcgtgcga | gggcgcgagg  | agccccgtgc  | cgaggttggg  | 7980 |
| gcgttgcggc  | ttttcggcgc  | ggtagacgat | ctggcggaag  | atggcgtggg  | agttggagga  | 8040 |
| gatggtgggc  | ctctggaaga  | tgttgaagt  | ggcgtggggc  | aggccgaccg  | agtccttgat  | 8100 |
| gaagtggg    | taggagtcct  | gcagcttggc | gacgagctcg  | gcggtgacga  | ggacgtccag  | 8160 |
| ggcgcagtag  | tcgaggggtc  | cttggtgat  | gtcgtacttg  | agctggccct  | tctgcttcca  | 8220 |
| cagctcgcgg  | ttgagaagga  | actcttcgcg | gtccttccag  | tactcttcga  | gggggaaccc  | 8280 |
| gtcctgatcg  | gcacggtaag  | agcccaccat | gtagaactgg  | ttgacggcct  | tgtaggcgca  | 8340 |
| gcagcccttc  | tccacgggga  | gggcgtaagc | ttgtgcggcc  | ttgcgcaggg  | aggtgtgggt  | 8400 |

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|             |             |            |            |             |            |       |
|-------------|-------------|------------|------------|-------------|------------|-------|
| gagggcggaag | gtgtcgcgca  | ccatgacctt | gaggaactgg | tgcttgaagt  | cgaggtcgtc | 8460  |
| gcagccgccc  | tgctcccaga  | gctggaagtc | cgtgcgcttc | ttgtaggcgg  | ggttgggcaa | 8520  |
| agcgaaagta  | acatcgttga  | agaggatctt | gcccgcgcgg | ggcatgaagt  | tgcgagtgat | 8580  |
| gcggaaaggc  | tggggcacct  | cggcccgggt | gttgatgacc | tgggcggcga  | ggacgatctc | 8640  |
| gtcgaagccg  | ttgatgttgt  | gcccgcgcat | gtagagtcc  | acgaatcgcg  | ggcggccctt | 8700  |
| aacgtggggc  | agcttcttga  | gctcgtcgta | ggtgagctcg | gcggggtcgc  | tgagcccgtg | 8760  |
| ctgctcgagg  | gcccagtcgg  | cgacgtgggg | gttggcgctg | aggaaggaag  | tccagagatc | 8820  |
| cacggccagg  | gcggtctgca  | agcgggtccc | gtactgacgg | aactgctggc  | ccacggccat | 8880  |
| tttttcgggg  | gtgacgcagt  | agaaggtgcg | ggggtcgccc | tgccagcggg  | cccacttgag | 8940  |
| ctggagggcg  | aggtcgtggg  | cgagctcgac | gagcggcggg | tccccggaga  | gtttcatgac | 9000  |
| cagcatgaag  | gggacgagct  | gcttgccgaa | ggaccccatc | caggtgtagg  | tttccacatc | 9060  |
| gtaggtgagg  | aagagccctt  | cggtgcgagg | atgcgagccg | atggggaaga  | actggatctc | 9120  |
| ctgccaccag  | ttggaggaat  | ggctgttgat | gtgatggaag | tagaaatgcc  | gacggcgcgc | 9180  |
| cgagcactcg  | tgcttgtgtt  | tatacaagcg | tccgcagtcg | tcgcaacgct  | gcacgggatg | 9240  |
| cacgtgctgc  | acgagctgta  | cctgggttcc | tttgacgagg | aatttcagtg  | ggcagtggag | 9300  |
| cgctggcggc  | tgcatctggt  | gctgtactac | gtcctggcca | tcggcgtggc  | catcgtctgc | 9360  |
| ctcgaatggt  | gtcatgctga  | cgagcccgcg | cgggaggcag | gtccagactt  | cggctcggac | 9420  |
| gggtcggaga  | gcgaggacga  | gggcgcgcag | gccggagctg | tccaggggcc  | tgagacgctg | 9480  |
| cggagtcagg  | tcagtgggca  | gcggcggcgc | gcggttgact | tgaggagct   | tttccagggc | 9540  |
| gcgcgggagg  | tccagatggt  | acttgatctc | cacggcgcgg | ttggtggcga  | cgtccacggc | 9600  |
| ttgcagggtc  | ccgtgcccct  | ggggcgccac | caccgtgccc | cgtttcttct  | tgggcgctgc | 9660  |
| ttccatgccg  | gtcagaagcg  | gcggcgagga | cgcgcgccgg | gcggcagggg  | cggctcggga | 9720  |
| cccggaggca  | ggggcggcag  | gggcacgtcg | gcgccgcgcg | cgggcagggt  | ctggtactgc | 9780  |
| gcccggagaa  | gactggcgtg  | agcgacgacg | cgacggttga | cgctcctggat | ctgacgcctc | 9840  |
| tgggtgaagg  | ccacgggacc  | cgtgagtttg | aacctgaaag | agagttcgac  | agaatcaatc | 9900  |
| tcggtatcgt  | tgacggcggc  | ctgccgcagg | atctcttgca | cgctcgccga  | gttgccttgg | 9960  |
| taggcgatct  | cggatcatgaa | ctgctcgatc | tcctcctcct | gaaggctctcc | gcggccggcg | 10020 |
| cgctcgacgg  | tggccgcgag  | gtcgttggag | atgcggccca | tgagctgcga  | gaaggcgttc | 10080 |
| atgccggcct  | cgttccagac  | gcggctgtag | accacggctc | cgctcggggc  | gcgcgcgcgc | 10140 |
| atgaccacct  | gggcgagggt  | gagctcgacg | tggcgcgtga | agaccgcgta  | gttgacgagg | 10200 |
| cgctggtaga  | ggtagttgag  | cgtgggtggc | atgtgctcgg | tgacgaagaa  | gtacatgatc | 10260 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |              |             |             |            |             |       |
|-------------|--------------|-------------|-------------|------------|-------------|-------|
| cagcggcgga  | gcggcacatctc | gctgacgtcg  | cccagggtctt | ccaagcgctc | catggcctcg  | 10320 |
| tagaagtcca  | cggcgaagtt   | gaaaaactgg  | gagttgcgcg  | ccgagacggt | caactcctcc  | 10380 |
| tccagaagac  | ggatgagctc   | agcgatgggtg | gcgcgcacct  | cgcgctcgaa | ggccccgggg  | 10440 |
| ggctcctctt  | cttccatctc   | ttcctcctcc  | actaacatct  | cttctacttc | ctcctcagga  | 10500 |
| ggcggcgggc  | ggggaggggc   | cctgcgtcgc  | cggcggcgca  | cgggcagacg | gtcgatgaag  | 10560 |
| cgctcgatgg  | tctccccgcg   | ccggcgacgc  | atggtctcgg  | tgacggcgcg | cccgtcctcg  | 10620 |
| cggggccgca  | gcgtgaagac   | gccgccgcgc  | atctccaggt  | ggccgccggg | ggggtctccg  | 10680 |
| ttgggcaggg  | agagggcgct   | gacgatgcat  | cttatcaatt  | ggcccgtagg | gactccgcgc  | 10740 |
| aaggacctga  | gcgtctcgag   | atccacggga  | tccgaaaacc  | gctgaacgaa | ggcttcgagc  | 10800 |
| cagtcgcagt  | cgcaaggtag   | gctgagcccc  | gtttcttgtt  | cttcggggat | ttcgggaggc  | 10860 |
| gggcggggcga | tgctgctggt   | gatgaagttg  | aagtaggcgg  | tcctgagacg | gcggatgggtg | 10920 |
| gcgaggagca  | ccaggtcctt   | gggcccggct  | tgctggatgc  | gcagacggtc | ggccatgccc  | 10980 |
| caggcggtgt  | cctgacacct   | ggcgaggtcc  | ttgtagtagt  | cctgcatgag | ccgctccacg  | 11040 |
| ggcacctcct  | cctcgccccg   | gcggccgtgc  | atgcgcgtga  | gcccgaaccc | gcgctggggc  | 11100 |
| tggacgagcg  | ccaggtcggc   | gacgacgcgc  | tcggcgagga  | tggcctgctg | tatctgggtg  | 11160 |
| aggggtggtct | ggaagtcgtc   | gaagtcgacg  | aagcgggtgt  | aggctccggt | gttgatggta  | 11220 |
| taggagcagt  | tggccatgac   | ggaccagttg  | acggtctggt  | ggccgggtcg | cacgagctcg  | 11280 |
| tggtacttga  | ggcgcgagta   | ggcgcgcgtg  | tcgaagatgt  | agtcgttgca | ggtgcgcacg  | 11340 |
| aggtactggt  | atccgacgag   | gaagtgcggc  | ggcggctggc  | ggtagagcgg | ccatcgctcg  | 11400 |
| gtggcggggg  | cgccggggcg   | gaggtcctcg  | agcatgaggc  | ggtggtagcc | gtagatgtac  | 11460 |
| ctggacatcc  | aggtgatgcc   | ggcggcggtg  | gtggaggcgc  | gcgggaactc | gcggacgcgg  | 11520 |
| ttccagatgt  | tgcgcagcgg   | caggaagtag  | ttcatggtgg  | ccgcggtctg | gcccgtgagg  | 11580 |
| cgcgcgcagt  | cgtggatgct   | ctagacatac  | gggcaaaaac  | gaaagcggtc | agcggctcga  | 11640 |
| ctccgtggcc  | tggaggctaa   | gcgaacgggt  | tgggctgcgc  | gtgtaccccg | gttcgaatct  | 11700 |
| cgaatcaggc  | tggagccgca   | gctaactgtg  | tactggcact  | cccgtctcga | cccaagcctg  | 11760 |
| ctaacgaaac  | ctccaggata   | cggaggcggg  | tcgttttttg  | gccttggtcg | ctggtcatga  | 11820 |
| aaaactagta  | agcgcggaaa   | gcgaccgccc  | gcgatggctc  | gctgccgtag | tctggagaaa  | 11880 |
| gaatcgccag  | ggttgcggtg   | cggtgtgccc  | cggttcgagc  | ctcagcgctc | ggcgccggcc  | 11940 |
| ggattccgcg  | gctaactgtg   | gcgtggctgc  | cccgtcgttt  | ccaagacccc | ttagccagcc  | 12000 |
| gacttctcca  | gttacggagc   | gagcccctct  | ttttcttgtg  | tttttgccag | atgcatcccg  | 12060 |
| tactgcggca  | gatgcgcccc   | caccctccac  | ctcaaccgcc  | cctaccgccg | cagcagcagc  | 12120 |
| aacagccggc  | gcttctgccc   | ccgccccagc  | agcagccagc  | cactaccgcg | gcggccggcg  | 12180 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |             |             |            |       |
|-------------|-------------|------------|-------------|-------------|------------|-------|
| tgagcgggagc | cggcggttcag | tatgacctgg | ccttggaaga  | gggcgagggg  | ctggcgcggc | 12240 |
| tgggggcgtc  | gtcgccggag  | cggcacccgc | gcgtgcagat  | gaaaagggac  | gctcgcgagg | 12300 |
| cctacgtgcc  | caagcagaac  | ctgttcagag | acaggagcgg  | cgaggagccc  | gaggagatgc | 12360 |
| gcgcctccc   | cttcacgcg   | gggcgggagc | tgcggcgcg   | cctggaccga  | aagcgggtgc | 12420 |
| tgagggacga  | ggatttcgag  | gcggacgagc | tgacggggat  | cagccccgcg  | cgcgcgcacg | 12480 |
| tggccgcggc  | caacctggtc  | acggcgtagc | agcagaccgt  | gaaggaggag  | agcaacttcc | 12540 |
| aaaaatcctt  | caacaaccac  | gtgcgcacgc | tgatcgcgcg  | cgaggaggtg  | accctgggcc | 12600 |
| tgatgcacct  | gtgggacctg  | ctggaggcca | tcgtgcagaa  | ccccacgagc  | aagccgctga | 12660 |
| cggcgcgagct | gtttctggtg  | gtgcagcaca | gtcgggacaa  | cgagacgttc  | agggaggcgc | 12720 |
| tgctgaatat  | caccgagccc  | gagggccgct | ggctcctgga  | cctggtgaac  | attctgcaga | 12780 |
| gcacgtggt   | gcaggagcgc  | gggctgccgc | tgtccgagaa  | gctggcggct  | atcaacttct | 12840 |
| cggtgctgag  | cctgggcaag  | tactacgcta | ggaagatcta  | caagaccccc  | tacgtgcccc | 12900 |
| tagacaagga  | ggtgaagatc  | gacgggtttt | acatgcgcat  | gaccctgaaa  | gtgctgaccc | 12960 |
| tgagcgacga  | tctgggggtg  | taccgcaacg | acaggatgca  | ccgcgcggtg  | agcgccagcc | 13020 |
| gccggcgcg   | gctgagcgac  | caggagctga | tgcacagcct  | gcagcgggcc  | ctgaccgggg | 13080 |
| ccgggaccga  | gggggagagc  | tactttgaca | tgggcgcgga  | cctgcgctgg  | cagcccagcc | 13140 |
| gccgggcctt  | ggaagctgcc  | ggcggttccc | cctacgtgga  | ggagggtggac | gatgaggagg | 13200 |
| aggagggcga  | gtacctggaa  | gactgatggc | gcgaccgtat  | ttttgctaga  | tgcagcaaca | 13260 |
| gccaccgcct  | cctgatccc   | cgatgcgggc | ggcgtgcag   | agccagccgt  | ccggcattaa | 13320 |
| ctcctcggac  | gattggaccc  | aggccatgca | acgcatcatg  | gcgctgacga  | cccgcaatcc | 13380 |
| cgaagccttt  | agacagcagc  | ctcaggccaa | ccggctctcg  | gccatcctgg  | aggccgtggt | 13440 |
| gccctcgcgc  | tcgaacccca  | cgcacgagaa | ggtgctggcc  | atcgtgaacg  | cgctggtgga | 13500 |
| gaacaaggcc  | atccgcggcg  | acgaggccgg | gctggtgtac  | aacgcgctgc  | tggagcgctg | 13560 |
| ggcccgtac   | aacagcacca  | acgtgcagac | gaacctggac  | cgcatggtga  | ccgacgtgcg | 13620 |
| cgaggcgggtg | tcgcagcgcg  | agcggttcca | ccgcgagtcg  | aacctgggct  | ccatggtggc | 13680 |
| gctgaacgcc  | ttcctgagca  | cgcagcccgc | caacgtgccc  | cggggccagg  | aggactacac | 13740 |
| caacttcac   | agcgcgctgc  | ggctgatggt | ggccgagggtg | ccccagagcg  | aggtgtacca | 13800 |
| gtcggggccg  | gactacttct  | tccagaccag | tcgccagggc  | ttgcagaccg  | tgaacctgag | 13860 |
| ccaggctttc  | aagaacttgc  | agggactgtg | gggcgtgcag  | gccccggtcg  | gggaccgcgc | 13920 |
| gacggtgtcg  | agcctgctga  | cgccgaactc | gcgcctgctg  | ctgctgctgg  | tggcgccctt | 13980 |
| cacggacagc  | ggcagcgtga  | gccgcgactc | gtacctgggc  | tacctgctta  | acctgtaccg | 14040 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |            |            |             |       |
|-------------|------------|------------|------------|------------|-------------|-------|
| cgaggccatc  | gggcaggcgc | acgtggacga | gcagacctac | caggagatca | cccacgtgag  | 14100 |
| ccgcgcgctg  | ggccaggagg | acccgggcaa | cctggaggcc | accctgaact | tcctgctgac  | 14160 |
| caaccggtcg  | cagaagatcc | cgccccagta | cgcgctgagc | accgaggagg | agcgcatcct  | 14220 |
| gcgctacgtg  | cagcagagcg | tggggctgtt | cctgatgcag | gagggggcca | cgcccagcgc  | 14280 |
| cgcgctcgac  | atgaccgcgc | gcaacatgga | gcccagcatg | tacgctcgca | accgcccgtt  | 14340 |
| catcaataag  | ctgatggact | acttgcacgc | ggcgcccgcc | atgaactcgg | actactttac  | 14400 |
| caacgccatc  | ttgaacccgc | actggctccc | gccgcccggg | ttctacacgg | gcgagtacga  | 14460 |
| catgcccgcg  | cccaacgacg | ggttcctgtg | ggacgacgtg | gacagcagcg | tgttctcgcc  | 14520 |
| gcgccccgcc  | accaccgtgt | ggaagaaaga | gggcggggac | cgcgcccggt | cctcggcgct  | 14580 |
| gtccgggtcg  | gcgggtgctg | ccgcggcggt | gcctgaggcc | gccagcccct | tcccgagcct  | 14640 |
| gcccttttcg  | ctgaacagcg | tgcgcagcag | cgagctgggt | cggtcgacgc | ggccgcgcct  | 14700 |
| gctgggagcg  | gaggagtacc | tgaacgactc | cttgttgagg | cccgagcgcg | agaagaactt  | 14760 |
| ccccaataac  | gggatagaga | gcctggtgga | caagatgagc | cgctggaaga | cgtacgcgca  | 14820 |
| cgagcacagg  | gacgagcccc | gagctagcag | cagcgcaggc | acccgtagac | gccagcgaca  | 14880 |
| cgacaggcag  | cggggctctg | tgtgggacga | tgaggattcc | gccgacgaca | gcagcgtgtt  | 14940 |
| ggacttgggt  | gggagtgggt | gtggtaaccc | gttcgctcac | ttgcgcccc  | gtatcgggcg  | 15000 |
| cctgatgtaa  | gaatctgaaa | aaataaaaaa | cggtactcac | caaggccatg | gcgaccagcg  | 15060 |
| tgcgttcttc  | tctgttgttt | gtagtagtat | gatgaggcgc | gtgtaccggg | agggtcctcc  | 15120 |
| tccctcgtag  | gagagcgtga | tgcagcaggc | ggtggcgggc | gcgatgcagc | ccccgctgga  | 15180 |
| ggcgcccttac | gtgccccgcg | ggtacctggc | gcctacggag | ggcggaaca  | gcattcggtta | 15240 |
| ctcggagctg  | gcacccttgt | acgataccac | ccggttgtag | ctggtggaca | acaagtcggc  | 15300 |
| ggacatcgcc  | tcgctgaact | accagaacga | ccacagcaac | ttcctgacca | ccgtggtgca  | 15360 |
| gaacaacgat  | ttcaccccca | cggaggccag | caccagacc  | atcaactttg | acgagcgctc  | 15420 |
| gcggtggggc  | ggccagctga | aaaccatcat | gcacaccaac | atgcccaacg | tgaacgagtt  | 15480 |
| catgtacagc  | aacaagttca | aggcgcggtt | gatggtctcg | cgcaagaccc | ccaatggggt  | 15540 |
| cgcggtggat  | gagaattatg | atggtagtca | ggacgagctg | acttacgagt | gggtggagtt  | 15600 |
| tgagctgccc  | gagggcaact | tctcggtagc | catgacctac | gatctgatga | acaacgcat   | 15660 |
| catcgacaac  | tacttggcgg | tggggcgtag | gaacgggggt | ctggagagcg | acatcggcgt  | 15720 |
| gaagtctgac  | acgcgcaact | tccggctggg | ctgggacccc | gtgaccgagc | tgggtgatgcc | 15780 |
| gggcgtgtac  | accaacgagg | ccttccaccc | cgacatcgct | ctgctgcccg | gctgcggcgt  | 15840 |
| ggacttcacc  | gagagccgcc | tcagcaacct | gctgggcacg | cgcaagcggc | agcccttcca  | 15900 |
| ggagggcctt  | cagatcctgt | acgaggacct | ggaggggggc | aacatccccg | cgctcttgga  | 15960 |

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|             |            |            |             |            |             |       |
|-------------|------------|------------|-------------|------------|-------------|-------|
| tgctgaagcc  | tatgagaaaa | gcaaggagga | ggccgccgca  | gcggcgaccg | cagccgtggc  | 16020 |
| caccgcctct  | accgaggtgc | ggggcgataa | ttttgctagc  | gccgcggcag | tggccgaggc  | 16080 |
| ggctgaaacc  | gaaagtaaga | tagtcatcca | gccggtggag  | aaggacagca | aggacaggag  | 16140 |
| ctacaacgtg  | ctcgcggaca | agaaaaacac | cgcctaccgc  | agctggtacc | tggcctacaa  | 16200 |
| ctacggcgac  | cccgagaagg | gcgtgcgctc | ctggacgctg  | ctcaccacct | cggacgtcac  | 16260 |
| ctgcggcggtg | gagcaagtct | actggtcgct | gcccgcacatg | atgcaagacc | cggtcacctt  | 16320 |
| ccgctccacg  | cgtcaagtta | gcaactaccc | ggtggtgggc  | gccgagctcc | tgcccgtcta  | 16380 |
| ctccaagagc  | ttcttcaacg | agcaggccgt | ctactcgagc  | cagctgcgcg | ccttcacctc  | 16440 |
| gctcacgcac  | gtcttcaacc | gcttccccga | gaaccagatc  | ctcgtccgcc | cgcccgcgcc  | 16500 |
| caccattacc  | accgtcagtg | aaaacgttcc | tgctctcaca  | gatcacggga | ccctgccgct  | 16560 |
| gcgcagcagt  | atccggggag | tccagcgctg | gaccgtcact  | gacgccagac | gccgcacctg  | 16620 |
| cccctacgtc  | tacaaggccc | tgggcgtagt | cgcgccgcgc  | gtcctctcga | gccgcacctt  | 16680 |
| ctaaaaaatg  | tccattctca | tctcgcccag | taataacacc  | ggttggggcc | tgcgcgcgcc  | 16740 |
| cagcaagatg  | tacggaggcg | ctcgccaacg | ctccacgcaa  | caccccgtgc | gcgtgcgcgg  | 16800 |
| gcacttccgc  | gctccctggg | gcgcccctca | gggccgcgtg  | cgctcgcgca | ccaccgtcga  | 16860 |
| cgacgtgatc  | gaccaggtgg | tggccgacgc | gcgcaactac  | acgcccgcgc | ccgcgcccgc  | 16920 |
| ctccaccgtg  | gacgccgtca | tcgacagcgt | ggtggccgat  | gcgcgccggt | acgcccgcgc  | 16980 |
| caagagccgg  | cggcggcgca | tcgcccggcg | gcaccggagc  | acccccgcca | tgcgcgcggc  | 17040 |
| gcgagccttg  | ctgcgcaggg | ccaggcgcac | gggacgcagg  | gcatgctca  | gggcggccag  | 17100 |
| acgcgcggcc  | tccggcagca | gcagcgccgg | caggacccgc  | agacgcgcgg | ccacggcggc  | 17160 |
| ggcggcgggc  | atcgccagca | tgtcccggcc | gcggcgcggc  | aacgtgtact | gggtgcgcga  | 17220 |
| cgccgccacc  | ggtgtgcgcg | tgcccgtgcg | caccgcgcc   | cctcgcactt | gaagatgctg  | 17280 |
| acttcgcgat  | gttgatgtgt | cccagcggcg | aggaggatgt  | ccaagcgcaa | atacaaggaa  | 17340 |
| gagatgctcc  | aggtcatcgc | gcctgagatc | tacggccccg  | cggtgaagga | ggaaagaaaag | 17400 |
| ccccgcaaac  | tgaagcgggt | caaaaaggac | aaaaaggagg  | aggaagatgt | ggacggactg  | 17460 |
| gtggagtttg  | tgcgcgagtt | cgcccccg   | cggcgcgtgc  | agtggcgcg  | gcggaaagtg  | 17520 |
| aaaccgggtg  | tgcggccccg | caccacggtg | gtcttcacgc  | ccggcgagcg | ttccggctcc  | 17580 |
| gcctccaagc  | gctcctacga | cgaggtgtac | ggggacgagg  | acatcctcga | gcaggcggtc  | 17640 |
| gagcgtctgg  | gcgagtttgc | ttacggcaag | cgcagccgcc  | ccgcgccctt | gaaagaggag  | 17700 |
| gcggtgtcca  | tcccgttga  | ccacggcaac | cccacgccga  | gcctgaagcc | ggtgaccctg  | 17760 |
| cagcaggtgc  | tgccgagcgc | ggcgccgcgc | cggggcttca  | agcgcgaggg | cggcgaggat  | 17820 |

| 368530-7006W01_SequenceListing_ST25.txt |            |             |            |             |             |       |
|-----------------------------------------|------------|-------------|------------|-------------|-------------|-------|
| ctgtacccga                              | ccatgcagct | gatggtgccc  | aagcgccaga | agctggaggga | cgctgctggag | 17880 |
| cacatgaagg                              | tggaccccga | ggtgcagccc  | gaggtcaagg | tgcggcccat  | caagcaggtg  | 17940 |
| gccccgggccc                             | tgggcgtgca | gaccgtggac  | atcaagatcc | ccacggagcc  | catggaaacg  | 18000 |
| cagaccgagc                              | ccgtgaagcc | cagcaccagc  | accatggagg | tgcagacgga  | tccctggatg  | 18060 |
| ccggcgccgg                              | cttccaccac | tcgccgaaga  | cgcaagtacg | gcgcggccag  | cctgctgatg  | 18120 |
| cccaactacg                              | cgctgcatcc | ttccatcatc  | cccacgcccg | gctaccgagg  | cacgcgcttc  | 18180 |
| taccgcggct                              | acaccagcag | ccgccgcaag  | accaccaccc | gccgccgccc  | tcgtcgcacc  | 18240 |
| cgccgcagca                              | gcaccgcgac | ttccgccgcc  | gccctgggtg | ggagagtgtg  | ccgcagcggg  | 18300 |
| cgcgagcctc                              | tgacctgcc  | gcgcgcgcgc  | taccacccga | gcacgcgcat  | ttaactctgc  | 18360 |
| cgctgcctcc                              | tacttgca   | tatggccctc  | acatgccgcc | tccgcgtccc  | cattacgggc  | 18420 |
| taccgaggaa                              | gaaagccgcg | ccgtagaagg  | ctgacgggga | acgggctgcg  | tcgccatcac  | 18480 |
| caccggcggc                              | ggcgcgccat | cagcaagcgg  | ttggggggag | gcttcctgcc  | cgcgctgatc  | 18540 |
| cccatcatcg                              | ccgcggcgat | cggggcgatc  | cccggcatag | cttccgtggc  | ggtgcaggcc  | 18600 |
| tctcagcgcc                              | actgagacac | agcttgga    | atttgtaata | aaaaaatgga  | ctgacgctcc  | 18660 |
| tggtcctgtg                              | atgtgtgttt | ttagatggaa  | gacatcaatt | tttcgtccct  | ggcaccgcga  | 18720 |
| cacggcacgc                              | ggccgtttat | gggcacctgg  | agcgacatcg | gcaacagcca  | actgaacggg  | 18780 |
| ggcgcccttca                             | attggagcag | tctctggagc  | gggcttaaga | atttcgggtc  | cacgctcaaa  | 18840 |
| acctatggca                              | acaaggcgtg | gaacagcagc  | acagggcagg | cgctgagggg  | aaagctgaaa  | 18900 |
| gagcagaact                              | tccagcagaa | ggtggtcgat  | ggcctggcct | cgggcatcaa  | cggggtggtg  | 18960 |
| gacctggcca                              | accaggccgt | gcagaaacag  | atcaacagcc | gcctggacgc  | ggtcccgcgc  | 19020 |
| gcgggggtccg                             | tggagatgcc | ccagggtggag | gaggagctgc | ctcccctgga  | caagcgcggc  | 19080 |
| gacaagcgac                              | cgcgctccga | cgcgaggag   | acgctgctga | cgcacacgga  | cgagccgccc  | 19140 |
| ccgtacgagg                              | aggcggtgaa | actgggtctg  | cccaccacgc | ggcccgtggc  | gcctctggcc  | 19200 |
| accgggggtgc                             | tgaaccccag | cagcagcagc  | cagcccgcga | ccctggactt  | gcctccgcct  | 19260 |
| gcttcccgc                               | cctccacagt | ggctaagccc  | ctgccgcccg | tggccgtcgc  | gtcgcgcgcc  | 19320 |
| ccccgaggcc                              | gcccccaggc | gaactggcag  | agcactctga | acagcatcgt  | gggtctggga  | 19380 |
| gtgcagagt                               | tgaagcgcg  | ccgctgctat  | taaaagacac | tgtagcgctt  | aacttgcttg  | 19440 |
| tctgtgtgta                              | tatgtatgtc | cgccgaccag  | aaggaggaag | aggcgctcg   | ccgagttgca  | 19500 |
| agatggccac                              | cccatcgatg | ctgccccagt  | gggcgtacat | gcacatcgcc  | ggacaggacg  | 19560 |
| cttcggagta                              | cctgagtccg | ggtctgggtg  | agttcgcccc | cgccacagac  | acctacttca  | 19620 |
| gtctggggaa                              | caagtttagg | aacccacagg  | tggcgccac  | gcacgatgtg  | accaccgacc  | 19680 |
| gcagccagcg                              | gctgacgctg | cgcttcgtgc  | ccgtggaccg | cgaggacaac  | acctactcgt  | 19740 |



## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |            |             |       |
|-------------|-------------|-------------|-------------|------------|-------------|-------|
| acaaagtgcg  | ctacacgctg  | gccgtgggcg  | acaaccgcgt  | gctggacatg | gccagcacct  | 19800 |
| actttgacat  | ccgcggcgctg | ctggatcggg  | ggcccagctt  | caaaccctac | tccggcaccg  | 19860 |
| cctacaacag  | cctggctccc  | aagggagcgc  | ccaacacttg  | ccagtggaca | tataaagctg  | 19920 |
| gtgatactga  | tacagaaaaa  | acctatacat  | atggaaatgc  | acctgtgcaa | ggcattagca  | 19980 |
| ttacaaaagga | tggatttcaa  | cttggaaactg | acagcgatgg  | tcaggcaatc | tatgcagacg  | 20040 |
| aaacttatca  | accagagcct  | caagtgggtg  | atgctgaatg  | gcatgacatc | actgggtactg | 20100 |
| atgaaaaata  | tggaggcaga  | gctcttaagc  | ctgacaccaa  | aatgaagcct | tgctatggtt  | 20160 |
| cttttgccaa  | gcctaccaat  | aaagaaggag  | gccaggcaaa  | tgtgaaaacc | gaaacaggcg  | 20220 |
| gtaccaaaga  | atatgacatt  | gacatggcat  | tcttcgataa  | tcgaagtgca | gctgccgccg  | 20280 |
| gcctagcccc  | agaaattggt  | ttgtatactg  | agaatgtgga  | tctggaaact | ccagataccc  | 20340 |
| atattgtata  | caaggcaggt  | acagatgaca  | gtagctcttc  | tatcaatttg | ggtcagcagt  | 20400 |
| ccatgcccga  | cagacccaac  | tacattggct  | tcagagacaa  | ctttatcggg | ctgatgtact  | 20460 |
| acaacagcac  | tggcaatatg  | gggtgtactg  | ctggacaggc  | ctcccagctg | aatgctgtgg  | 20520 |
| tggacttgca  | ggacagaaac  | accgaactgt  | cctaccagct  | cttgcttgac | tctctgggtg  | 20580 |
| acagaaccag  | gtatttcagt  | atgtggaatc  | aggcgggtgga | cagttatgac | cccgatgtgc  | 20640 |
| gcattattga  | aaatcacggt  | gtggaggatg  | aacttcctaa  | ctattgcttc | cccctggatg  | 20700 |
| ctgtgggtag  | aactgatact  | taccagggaa  | ttaaggccaa  | tggtgataat | caaaccacct  | 20760 |
| ggaccaaaga  | tgatactggt  | aatgatgcta  | atgaattggg  | caagggcaat | cctttcgcca  | 20820 |
| tggagatcaa  | catccaggcc  | aacctgtggc  | ggaacttcct  | ctacgcgaac | gtggcgctgt  | 20880 |
| acctgcccga  | ctcctacaag  | tacacgccgg  | ccaacatcac  | gctgcccacc | aacaccaaca  | 20940 |
| cctacgatta  | catgaacggc  | cgcggtggtg  | cgccctcgct  | ggtggacgcc | tacatcaaca  | 21000 |
| tcggggcgcg  | ctggtcgctg  | gaccccatgg  | acaacgtcaa  | ccccttcaac | caccaccgca  | 21060 |
| acgcgggcct  | gcgataccgc  | tccatgctcc  | tgggcaacgg  | gcgctacgtg | cccttcacac  | 21120 |
| tccaggtgcc  | ccaaaagtgt  | ttcgccatca  | agagcctcct  | gctcctgccc | gggtcctaca  | 21180 |
| cctacgagtg  | gaacttccgc  | aaggacgtca  | acatgatcct  | gcagagctcc | ctcggcaacg  | 21240 |
| acctgcgcac  | ggacggggcc  | tccatgcctt  | tcaccagcat  | caacctctac | gccaccttct  | 21300 |
| tccccatggc  | gcacaacacc  | gcctccacgc  | tcgaggccat  | gctgcgcaac | gacaccaacg  | 21360 |
| accagtcctt  | caacgactac  | ctctcgggcg  | ccaacatgct  | ctaccccatc | ccggccaacg  | 21420 |
| ccaccaacgt  | gcccctctcc  | atcccctcgc  | gcaactgggc  | cgccctccgc | ggctgggtcct | 21480 |
| tcacgcgcct  | caagacccgc  | gagacgccct  | cgctcggctc  | cggtttcgac | ccctacttcg  | 21540 |
| tctactcggg  | ctccatcccc  | tacctcgacg  | gcaccttcta  | cctcaaccac | accttcaaga  | 21600 |

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|             |             |             |            |            |             |       |
|-------------|-------------|-------------|------------|------------|-------------|-------|
| aggtctccat  | caccttcgac  | tcctccgtca  | gctggcccgc | caacgaccgc | ctcctgacgc  | 21660 |
| ccaacgagtt  | cgaaatcaag  | cgcaccgtcg  | acggagaggg | gtacaacgtg | gcccagtgca  | 21720 |
| acatgaccaa  | ggactgggtc  | ctgggtccaga | tgctggccca | ctacaacatc | ggctaccagg  | 21780 |
| gcttctacgt  | gcccagagggc | tacaaggacc  | gcatgtactc | cttcttccgc | aacttccagc  | 21840 |
| ccatgagccg  | ccagggtcgtg | gacgaggtca  | actacaagga | ctaccaggcc | gtcacccctgg | 21900 |
| cctaccagca  | caacaactcg  | ggcttcgtcg  | gctacctcgc | gcccaccatg | cgccagggcc  | 21960 |
| agccctaccc  | cgccaactac  | ccctacccgc  | tcatcgga   | gagcgccgtc | gccagcgta   | 22020 |
| cccagaaaaa  | gttcctctgc  | gaccgggtca  | tgtggcgcat | ccccttctcc | agcaacttca  | 22080 |
| tgtccatggg  | cgcgctcacc  | gacctcggcc  | agaacatgct | ctacgccaac | tccgcccacg  | 22140 |
| cgctagacat  | gaatttcgaa  | gtcgacccca  | tggatgagtc | cacccttctc | tatgttgtct  | 22200 |
| tcgaagtctt  | cgacgtcgtc  | cgagtgcacc  | agccccaccg | cggcgtcatc | gaggccgtct  | 22260 |
| acctgcgcac  | gccccttctg  | gccggcaacg  | ccaccaccta | agcctcttgc | ttcttgcaag  | 22320 |
| atgacggcct  | gcgcgggctc  | cggcgagcag  | gagctcaggg | ccatcctccg | cgacctgggc  | 22380 |
| tgcgggccct  | gcttcctggg  | caccttcgac  | aagcgcttcc | cgggattcat | ggccccgcac  | 22440 |
| aagctggcct  | gcgccatcgt  | caacacggcc  | ggccgcgaga | ccgggggga  | gcactggctg  | 22500 |
| gccttcgcct  | ggaacccgcg  | ctcccacacc  | tgctacctct | tcgaccctt  | cgggttctcg  | 22560 |
| gacgagcgcc  | tcaagcagat  | ctaccagttc  | gagtacgagg | gcctgctgcg | tcgcagcgcc  | 22620 |
| ctggccaccg  | aggaccgctg  | cgtaaccctg  | gaaaagtcca | cccagaccgt | gcagggtcgg  | 22680 |
| cgctcggccg  | cctgcgggct  | cttctgctgc  | atgttcctgc | acgccttcgt | gcactggccc  | 22740 |
| gaccgccccca | tggacaagaa  | ccccaccatg  | aacttgctga | cgggggtgcc | caacggcatg  | 22800 |
| ctccagtcgc  | cccagggtga  | acccaccctg  | cgccgcaacc | aggaggcgct | ctaccgcttc  | 22860 |
| ctcaacgccc  | actccgccta  | ctttcgtctc  | caccgcgcgc | gcatcgagaa | ggccaccgcc  | 22920 |
| ttcgaccgca  | tgaatcaaga  | catgtaatcc  | ggtgtgtgta | tgtgaatgct | ttattcatca  | 22980 |
| taataaacag  | cacatgttta  | tgccaccctc  | tctgaggctc | tgactttatt | tagaaatcga  | 23040 |
| aggggttctg  | ccggctctcg  | gcatggcccg  | cgggcagggg | tacgttgccg | aactgggtact | 23100 |
| tgggcagcca  | cttgaactcg  | gggatcagca  | gcttcggcac | ggggaggtcg | gggaacgagt  | 23160 |
| cgctccacag  | cttgccgctg  | agttgcaggg  | cgcccagcag | gtcgggcgcg | gagatcttga  | 23220 |
| aatcgcagtt  | gggacccgcg  | ttctgcgcgc  | gagagttacg | gtacacgggg | ttgcagcact  | 23280 |
| ggaacaccat  | cagggccggg  | tgcttcacgc  | tcgccagcac | cgtcgcgtcg | gtgatgccct  | 23340 |
| ccacgtccag  | atcctcggcg  | ttggccatcc  | cgaagggggg | catcttgag  | gtctgccgcc  | 23400 |
| ccatgctggg  | cacgcagccg  | ggcttggtgt  | tgcaatcgca | gtgcaggggg | atcagcatca  | 23460 |
| tctgggcctg  | ctcggagctc  | atgcccgggt  | acatggcctt | catgaaagcc | tccagctggc  | 23520 |

368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |             |             |             |       |
|-------------|-------------|-------------|-------------|-------------|-------------|-------|
| ggaaggcctg  | ctgcgcccttg | ccgccctcgg  | tgaagaagac  | cccgcaggac  | ttgctagaga  | 23580 |
| actggttggg  | ggcgcagcca  | gcgtcgtgca  | cgagcagcg   | cgcgctcgttg | ttggccagct  | 23640 |
| gcaccacgct  | gcgccccag   | cggttctggg  | tgatcttggc  | ccggtcgggg  | ttctccttca  | 23700 |
| gcgcgcgctg  | cccgttctcg  | ctcgccacat  | ccatctcgat  | cgtgtgctcc  | ttctggatca  | 23760 |
| tcacgggtccc | gtgcaggcac  | cgagccttgc  | cctcggccctc | ggtgcacccg  | tgcagccaca  | 23820 |
| gcgcgcagcc  | ggtgctctcc  | cagttcttgt  | gggcgatctg  | ggagtgcgag  | tgcacgaagc  | 23880 |
| cctgcaggaa  | gcggcccatc  | atcgtggtca  | gggtcttgtt  | gctggtgaag  | gtcagcggaa  | 23940 |
| tgccgcggtg  | ctcctcgttc  | acatacaggt  | ggcagatacg  | gcggtacacc  | tcgccctgct  | 24000 |
| cgggcatcag  | ctggaaggcg  | gacttcaggt  | cgctctccac  | gcggtaccgg  | tccatcagca  | 24060 |
| gcgtcatcac  | ttccatgcc   | ttctcccagg  | ccgaaacgat  | cggcaggctc  | agggggttct  | 24120 |
| tcaccgttgt  | catcttagtc  | gccgccgccg  | aagtcagggg  | gtcgttctcg  | tccaggggtct | 24180 |
| caaacactcg  | cttgccgtcc  | ttctcgggtga | tgcgcacggg  | gggaaagctg  | aagcccacgg  | 24240 |
| ccgccagctc  | ctcctcggcc  | tgcctttcgt  | cctcgtgtc   | ctggctgatg  | tcttgcaaag  | 24300 |
| gcacatgctt  | ggtcttgccg  | ggtttctttt  | tgggcggcag  | aggcggcggc  | ggagacgtgc  | 24360 |
| tgggcgagcg  | cgagttctcg  | ctcaccacga  | ctatttcttc  | tccttgggccg | tcgtccgaga  | 24420 |
| ccacgcggcg  | gtaggcagtc  | ctcttctggg  | gcagaggcgg  | aggcgacggg  | ctctcgcggt  | 24480 |
| tcggcgggcg  | gctggcagag  | ccccttccgc  | gttcgggggt  | gcgctcctgg  | cggcgctgct  | 24540 |
| ctgactgact  | tcctccgcgg  | ccggccattg  | tgttctccta  | gggagcaagc  | atggagactc  | 24600 |
| agccatcgtc  | gccaacatcg  | ccatctgccc  | ccgccgccgc  | cgacgagaac  | cagcagcagc  | 24660 |
| agaatgaaag  | cttaaccgcc  | ccgccgcca   | gccccacctc  | cgacgccgca  | gccccagaca  | 24720 |
| tgcaagagat  | ggaggaatcc  | atcgagattg  | acctgggcta  | cgtgacgccc  | gcggagcacg  | 24780 |
| aggaggagct  | ggcagcgcg   | ttttcagccc  | cggagagaaa  | ccaccaagag  | cagccagagc  | 24840 |
| aggaagcaga  | gagcgagcag  | aaccaggctg  | ggctcgagca  | tggcgactac  | ctgagcgggg  | 24900 |
| cagaggacgt  | gctcatcaag  | catctggccc  | gccaatgcat  | catcgtcaag  | gacgcgctgc  | 24960 |
| tcgaccgcgc  | cgagggtgccc | ctcagcgtgg  | cggagctcag  | ccgcgcctac  | gagcgcaacc  | 25020 |
| tcttctcgcc  | gcgcgtgccc  | cccaagcgcc  | agcccaacgg  | cacctgcgag  | cccaaccgcg  | 25080 |
| gcctcaactt  | ctacccggtc  | ttcgcggtgc  | ccgaggccct  | ggccacctac  | cacctctttt  | 25140 |
| tcaagaacca  | aaggatcccc  | gtctcctgcc  | gcgccaaccg  | caccgcgccc  | gacgccctgc  | 25200 |
| tcaacctggg  | ccccggcgcc  | cgcttacctg  | atatcgcttc  | cttggaagag  | gttcccaaga  | 25260 |
| tcttcgaggg  | tctgggcagc  | gacgagactc  | gggccgcgaa  | cgctctgcaa  | ggaagcggag  | 25320 |
| aggagcatga  | gcaccacagc  | gccctggtgg  | agttggaagg  | cgacaacgcg  | cgccctggcg  | 25380 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |             |            |            |             |            |       |
|------------|-------------|------------|------------|-------------|------------|-------|
| tcctcaagcg | cacggtcgcg  | ctgacccact | tcgcctaccc | ggcgctcaac  | ctgcccccca | 25440 |
| aggtcatgag | cgccgtcatg  | gaccagggtc | tcatcaagcg | cgccctcgccc | ctctcggagg | 25500 |
| aggagatgca | ggacccccgag | agctcggacg | agggcaagcc | cgtggtcagc  | gacgagcagc | 25560 |
| tggcgcgctg | gctgggagcg  | agtagcaccc | cccagagcct | ggaagagcgg  | cgcaagctca | 25620 |
| tgatggccgt | ggtcctggtg  | accgtggagc | tggagtgtct | gcgccgcttc  | ttcgccgacg | 25680 |
| cggagaccct | gcgcaaggtc  | gaggagaacc | tgcactacct | cttcagacac  | gggttcgtgc | 25740 |
| gccaggcctg | caagatctcc  | aacgtggagc | tgaccaacct | ggtctcctac  | atgggcatcc | 25800 |
| tgcacgagaa | ccgcctgggg  | cagaacgtgc | tgcacaccac | cctgcgcggg  | gaggcccgcc | 25860 |
| gcgactacat | ccgcgactgc  | gtctacctgt | acctctgcc  | cacctggcag  | acgggcatgg | 25920 |
| gcgtgtggca | gcagtgcctg  | gaggagcaga | acctgaaaga | gctctgcaag  | ctcctgcaga | 25980 |
| agaacctcaa | ggccctgtgg  | accgggttcg | acgagcgcac | caccgccgcg  | gacctggccg | 26040 |
| acctcatctt | ccccgagcgc  | ctgcggctga | cgctgcgcaa | cgggctgccc  | gactttatga | 26100 |
| gccaaagcat | gttgcaaaac  | tttcgctctt | tcatcctcga | acgctccggg  | atcctgcccg | 26160 |
| ccacctgctc | cgcgctgccc  | tcggacttcg | tgccgctgac | cttccgcgag  | tgccccccgc | 26220 |
| cgctctggag | ccactgctac  | ctgctgcgcc | tggccaacta | cctggcctac  | cactcggacg | 26280 |
| tgatcgagga | cgtcagcggc  | gagggcctgc | tcgagtgcc  | ctgccgctgc  | aacctctgca | 26340 |
| cgccgcaccg | ctccctggcc  | tgcaaccccc | agctgctgag | cgagaccag   | atcatcggca | 26400 |
| ccttcgagtt | gcaaggcccc  | ggcgagggca | aggggggtct | gaaactcacc  | ccggggctgt | 26460 |
| ggacctcggc | ctacttgctc  | aagttcgtgc | ccgaggacta | ccatcccttc  | gagatcaggt | 26520 |
| tctacgagga | ccaatcccag  | ccgcccgaag | ccgagctgtc | ggcctgcgtc  | atcacccagg | 26580 |
| gggccatcct | ggcccaattg  | caagccatcc | agaaatccc  | ccaagaattt  | ctgctgaaaa | 26640 |
| agggccacgg | ggtctacttg  | gacccccaga | ccggagagga | gctcaacccc  | agcttcccc  | 26700 |
| aggatgcccc | gaggaagcag  | caagaagctg | aaagtggagc | tgccgccgcc  | gccggaggat | 26760 |
| ttggaggaag | actgggagag  | cagtcaggca | gaggaggagg | agatggaaga  | ctgggacagc | 26820 |
| actcaggcag | aggaggacag  | cctgcaagac | agtctggagg | aggaagacga  | ggtggaggag | 26880 |
| gcagaggaag | aagcagccgc  | cgccagaccg | tcgtcctcgg | cggaggagga  | gaaagcaagc | 26940 |
| agcacggata | ccatctccgc  | tccgggtcgg | ggtcgcggcg | gccgggcca   | cagtagatgg | 27000 |
| gacgagaccg | ggcgcttccc  | gaaccccacc | accagaccg  | gtaagaagga  | gcggcaggga | 27060 |
| tacaagtctt | ggcgggggca  | caaaaacgcc | atcgtctcct | gcttgcaagc  | ctgcgggggc | 27120 |
| aacatctcct | tcacccggcg  | ctacctgctc | ttccaccgcg | gggtgaactt  | ccccgcaac  | 27180 |
| atcttgcat  | actaccgtca  | cctccacagc | ccctactact | gtttccaaga  | agaggcagaa | 27240 |
| accagcagc  | agcagcagca  | gcagaaaacc | agcggcagca | gctagaaaat  | ccacagcggc | 27300 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |            |            |            |       |
|-------------|------------|------------|------------|------------|------------|-------|
| ggcaggtgga  | ctgaggatcg | cggcgaacga | gccggcgag  | acccgggagc | tgaggaaccg | 27360 |
| gatctttccc  | accctctatg | ccatcttcca | gcagagtcgg | gggcaagagc | aggaactgaa | 27420 |
| agtcaagaac  | cgttctctgc | gctcgctcac | ccgcagttgt | ctgtatcaca | agagcgaaga | 27480 |
| ccaacttcag  | cgcactctcg | aggacgccga | ggctctcttc | aacaagtact | gcgcgctcac | 27540 |
| tcttaaagag  | tagcccgcg  | ccgcccacac | acggaaaaag | gcgggaatta | cgtcaccacc | 27600 |
| tgcgcccttc  | gcccgaccat | catcatgagc | aaagagattc | ccacgcctta | catgtggagc | 27660 |
| taccagcccc  | agatgggcct | ggccgccggc | gccgccagg  | actactccac | ccgcatgaac | 27720 |
| tggtcagtg   | ccggggccgc | gatgatctca | cgggtgaatg | acatccgcgc | ccaccgaaac | 27780 |
| cagatactcc  | tagaacagtc | agcgatcacc | gccacgcccc | gccatcacct | taatccgcgt | 27840 |
| aattggcccc  | ccgccctggt | gtaccaggaa | attccccagc | ccacgaccgt | actacttccg | 27900 |
| cgagacgccc  | agggcgaagt | ccagctgact | aactcaggtg | tccagctggc | cggcggcgcc | 27960 |
| gccctgtgtc  | gtcaccgccc | cgctcagggg | ataaagcggc | tggtgatccg | aggcagaggc | 28020 |
| acacagctca  | acgacgaggt | ggtgagctct | tcgctgggtc | tgcgacctga | cggagtcttc | 28080 |
| caactcgccg  | gatcggggag | atcttccctc | acgcctcgtc | aggccgtcct | gactttggag | 28140 |
| agttcgctct  | cgcagccccg | ctcgggtggc | atcggcactc | tccagttcgt | ggaggagttc | 28200 |
| actccctcgg  | tctacttcaa | ccccttctcc | ggctcccccg | gccactaccc | ggacgagttc | 28260 |
| atcccgaact  | tcgacgccat | cagcgagtcg | gtggacggct | acgattgaat | gtcccatggt | 28320 |
| ggcgcgggctg | acctagctcg | gcttcgacac | ctggaccact | gccgccgctt | ccgctgcttc | 28380 |
| gctcgggatc  | tcgccgagtt | tgcctacttt | gagctgcccc | aggagcacc  | tcaggggccc | 28440 |
| gcccacggag  | tgcggatcgt | cgtcgaaggg | ggtctcgact | cccacctgct | tcggatcttc | 28500 |
| agccagcgtc  | cgatcctggc | cgagcgcgag | caaggacaga | cccttctgac | cctgtactgc | 28560 |
| atctgcaacc  | accccggcct | gcatgaaagt | ctttgttgtc | tgctgtgtac | tgagtataat | 28620 |
| aaaagctgag  | atcagcgact | actccggact | tccgtgtgtt | cctgctatca | accagtccct | 28680 |
| gttcttcacc  | gggaacgaga | ccgagctcca | gctccagtgt | aagccccaca | agaagtacct | 28740 |
| cacctggctg  | ttccagggct | ctccgatcgc | cgttgtcaac | cactgcgaca | acgacggagt | 28800 |
| cctgctgagc  | ggccctgcc  | accttacttt | ttccaccgc  | agaagcaagc | tccagctctt | 28860 |
| ccaacccttc  | ctccccggga | cctatcagtg | cgtctcggg  | ccctgccatc | acaccttcca | 28920 |
| cctgatcccc  | aataccacag | cgtcgctccc | cgctactaac | aaccaaacta | cccaccaacg | 28980 |
| ccaccgtcgc  | gaccgcggac | atgtacagag | ctcgagaagt | actaggccac | aatacatgcc | 29040 |
| catattagac  | tatgaggccg | agccacagcg | acccatgctc | cccgtatta  | gttacttcaa | 29100 |
| tctaaccggc  | ggagatgact | gacccactgg | ccaacaacaa | cgtaacgac  | cttctcctgg | 29160 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| acatggacgg  | ccgcgcctcg  | gagcagcgac  | tcgcccact  | tcgcattcgc  | cagcagcagg  | 29220 |
| agagagccgt  | caaggagctg  | caggacggca  | tagccatcca | ccagtgcaag  | aaaggcatct  | 29280 |
| tctgcctgg   | gaaacaggcc  | aagatctcct  | acgaggtcac | cccgaccgac  | catcgcctct  | 29340 |
| cctacgagct  | cctgcagcag  | cgccagaagt  | tcacctgcct | ggtcggagtc  | aacccccatcg | 29400 |
| tcatacccca  | gcagtcgggc  | gataccaagg  | ggcgcaccca | ctgctcctgc  | gactcccccg  | 29460 |
| actgcgtcca  | cactctgac   | aagacctct   | gcggcctccg | cgacctctc   | cccatgaact  | 29520 |
| aatccccccc  | ttatccagtg  | aaataaatat  | catattgatg | atgatttaaa  | taaaaaataa  | 29580 |
| tcatttgatt  | tgaaataaag  | atacaatcat  | attgatgatt | tgagttttta  | aaaataaaga  | 29640 |
| atcacttact  | tgaaatctga  | taccaggctc  | ctgtccatgt | tttctgcca   | caccacctca  | 29700 |
| ctccccctct  | cccagctctg  | gtactgcaga  | ccccggcggg | ctgcaaaact  | cctccacacg  | 29760 |
| ctgaaggggga | tgtaaaattc  | ctcctgtccc  | tcaatcttca | ttttatcttc  | tatcagatgt  | 29820 |
| ccaaaaagcg  | cgtccgggtg  | gatgatgact  | tcgaccccg  | ctacccctac  | gatgcagaca  | 29880 |
| acgcaccgac  | cgtgcccttc  | atcaaccccc  | ccttcgtctc | ttcagatgga  | ttccaagaga  | 29940 |
| agccccctggg | ggcgtgttcc  | ctgcgactgg  | ctgaccccg  | caccaccaag  | aacgggggaaa | 30000 |
| tcacctcaa   | gctgggagag  | ggggtggacc  | tcgactctc  | gggaaaactc  | atctccaaca  | 30060 |
| cgccaccaaa  | ggccgccgcc  | cctctcagtt  | tttccaacaa | caccatttcc  | cttaacatgg  | 30120 |
| ataccctct   | ttataccaaa  | gatggaaaat  | tatccttaca | agtttctcca  | ccgttaaaca  | 30180 |
| tattaaaatc  | aaccattctg  | aacacattag  | ctgtagctta | tggatcaggt  | ttaggactga  | 30240 |
| gtggtggcac  | tgctcttgca  | gtacagttgg  | cctctccact | cacttttgat  | gaaaaaggaa  | 30300 |
| atattaaaaat | taacctagcc  | agtgggtccat | taacagttga | tgcaagtcga  | cttagtatca  | 30360 |
| actgcaaaaag | aggggtcact  | gtcactacct  | caggagatgc | aattgaaagc  | aacataagct  | 30420 |
| ggcctaaaag  | tataagattt  | gaaggtaatg  | gcatagctgc | aaacattggc  | agaggattgg  | 30480 |
| aatttggaac  | cactagtaca  | gagactgatg  | tcacagatgc | ataccaatt   | caagttaa    | 30540 |
| tgggtactgg  | ccttaccttt  | gacagtacag  | gcgccattgt | tgcttggaac  | aaagaggatg  | 30600 |
| ataaacttac  | attatggacc  | acagccgacc  | cctcgccaaa | ttgcaaaaata | tactctgaaa  | 30660 |
| aagatgccaa  | actcacactt  | tgcttgacaa  | agtgtggaag | tcaaatctg   | ggtactgtga  | 30720 |
| ctgtattggc  | agtgaataat  | ggaagtctca  | acccaatcac | aaacacagta  | agcactgcac  | 30780 |
| tcgtctccct  | caagtttgat  | gcaagtggag  | ttttgctaag | cagctccaca  | ttagacaaaag | 30840 |
| aatattggaa  | cttcagaaaag | ggagatgtta  | cacctgctga | gccctatact  | aatgctatag  | 30900 |
| gttttatgcc  | taacataaag  | gcctatccta  | aaaacacatc | tgacagcttca | aaaagccata  | 30960 |
| ttgtcagtca  | agtttatctc  | aatgggggatg | aggccaaacc | actgatgctg  | attattactt  | 31020 |
| ttaatgaaac  | tgaggatgca  | acttgcacct  | acagtatcac | ttttcaatgg  | aaatgggata  | 31080 |

## 368530-7006W01\_SequenceListing\_ST25.txt

```

gtactaagta cacaggtgaa acacttgcta ccagctcctt caccttctcc tacatcgccc 31140
aagaatgaac actgtatccc accctgcatg ccaacccttc ccaccccaact ctgtctatgg 31200
aaaaaactct gaagcacaaa ataaaataaa gttcaagtgt tttattgatt caacagtttt 31260
acaggattcg agcagttatt tttcctccac cctcccagga catggaatac accaccctct 31320
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cggccggtgg tgtcgcatca ggccccgcag cagtcgctgc cgccgccgct ccgtcaagct 31620
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gggtttcggg gacggcgggg gagggaagaa caggaagaac catgattaac ttttaatcca 32700
aacggtctcg gagcacttca aaatgaaggc cgcgagatg gcacctctcg ccccgctgt 32760
gttggtg 32767

```

```

<210> 8
<211> 32767
<212> DNA

```

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificially Synthesized

&lt;400&gt; 8

|                                                                    |      |
|--------------------------------------------------------------------|------|
| catcatcaat aatatacctc aaacttttgg tgcgcgttaa tatgcaaatg agctgtttga  | 60   |
| atttggggag ggaggaaggt gattggccga gagacgggcg accgtagggg gcggggcggg  | 120  |
| tgacgttttg atgacgtggc cgtgaggcgg agccggtttg caagtctctg tgggaaaagt  | 180  |
| gacgtcaaac gaggtgtggt ttgaacacgg aaataactcaa ttttcccgcg ctctctgaca | 240  |
| ggaaatgagg tgtttctggg cggtatgcaag tgaaaacggg ccattttcgc gcgaaaactg | 300  |
| aatgaggaag tgaaaatctg agtaatttcg cgtttatggc agggaggagt atttgccgag  | 360  |
| ggccgagtag actttgaccg attacgtggg ggtttcgatt accgtatttt tcacctaaat  | 420  |
| ttccgcgtac ggtgtcaaag tccggtgttt ttacgtacga tatcatttcc ccgaaagtgc  | 480  |
| cacctgaccg taactataac ggtcctaagg tagcgaaaagc tcagatctcc cgatccccta | 540  |
| tgggtgactc tcagtacaat ctgctctgat gccgcatagt taagccagta tctgctccct  | 600  |
| gcttgtgtgt tggaggtcgc tgagtagtgc gcgagcaaaa tttaagctac aacaaggcaa  | 660  |
| ggcttgaccg acaattgcat gaagaatctg cttagggtta ggcgttttgc gctgcttcgc  | 720  |
| gatgtacggg ccagatatac gcgttgacat tgattattga ctagtatgcc aagtacgccc  | 780  |
| cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta catgacctta  | 840  |
| tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac catggtgatg  | 900  |
| cggttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg atttccaagt  | 960  |
| ctccacccca ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg ggactttcca  | 1020 |
| aaatgtcgta acaactccgc cccattgacg caaatgggcg gtaggcgtgt acggtgggag  | 1080 |
| gtctatataa gcagagctcg tttagtgaac cgtcagatca ctagaagctt tattgcggta  | 1140 |
| gtttatcaca gttaaattgc taacgcagtc agtgcttctg acacaacagt ctcgaactta  | 1200 |
| aggctagagt tcgacgccac catgcgcgtg cgcggcatcc cccgcaactg gccccagtgg  | 1260 |
| tggatctggg gcatcctggg cttctggatg atcatcatct gccgcgtggt gggcaacctg  | 1320 |
| gacctgtggg tgaccgtgta ctacggcgtg cccgtgtgga aggaggccaa gaccaccctg  | 1380 |
| ttctgcgctt ccgacgcca ggcctacgac aaggagggtg acaacgtgtg ggccaccac    | 1440 |
| gcctgcgtgc ccaccgaccc caacccccag gagatcgtgc tggagaacgt gaccgagaac  | 1500 |
| ttcaacatgt ggaagaacga catggtggac cagatgcacg aggacatcat ctccctgtgg  | 1560 |
| gaccagtccc tgaagccctg cgtgaagctg acccccctgt gcgtgaccct gaactgcaag  | 1620 |
| aacgtgaaca tctccgcca cgccaacgcc accgccaccc tgaactcctc catgaacggc   | 1680 |
| gagatcaaga actgctcctt caacaccacc accgagctgc gcgacaagaa gcagaagggtg | 1740 |



368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| tacgccctgt  | tctacaagcc | cgacgtggtg  | cccctgaacg | gcggcgagca | caacgagacc  | 1800 |
| ggcgagtaca  | tcctgatcaa | ctgcaactcc  | tccaccatca | cccaggcctg | ccccaaggtg  | 1860 |
| tccttcgacc  | ccatccccat | ccactactgc  | gcccccgccg | gctacgccat | cctgaagtgc  | 1920 |
| aacaacaaga  | ccttcaacgg | caccggcccc  | tgcaacaacg | tgtccaccgt | gcagtgcacc  | 1980 |
| cacggcatca  | agcccgtggt | gtccacccag  | ctgtgtctga | acggctccct | ggccgaggag  | 2040 |
| gagatcatcg  | tgcgctccga | gaacctgacc  | aacaacatca | agaccatcat | cgtgcacctg  | 2100 |
| aacaagtccg  | tggagatcaa | gtgcacccgc  | cccaacaaca | acacccgcaa | gtccgtgcgc  | 2160 |
| atcgggccccg | gccagacctt | ctacgccacc  | ggcgagatca | tcggcgacat | ccgcgaggcc  | 2220 |
| cactgcaaca  | tctcccgcga | gacctggaac  | tccaccctga | tccaggtgaa | ggagaagctg  | 2280 |
| cgcgagcact  | acaacaagac | catcaagttc  | gagccctcct | ccggcggcga | cctggagggtg | 2340 |
| accacccact  | ccttcaactg | ccgcggcgag  | ttcttctact | gcgacaccac | caagctgttc  | 2400 |
| aacgagacca  | agctgttcaa | cgagtccgag  | tacgtggaca | acaagaccat | catcctgccc  | 2460 |
| tgccgcatca  | agcagatcat | caacatgtgg  | caggagggtg | gccgcgccat | gtacgcccc   | 2520 |
| cccacgagg   | gcaacatcac | ctgcaagtcc  | aacatcaccg | gcctgtgtgt | gacctgggac  | 2580 |
| ggcggcgaga  | actccaccga | gggcgtgttc  | cgccccggcg | gcggcaacat | gaaggacaac  | 2640 |
| tggcgctccg  | agctgtacaa | gtacaagggtg | gtggagatca | agcccctggg | cgtggcccc   | 2700 |
| accaagagca  | agcgcaaggt | ggtgggccgc  | gagaagcgcg | ccgtgggcct | gggcgccgtg  | 2760 |
| ctgctgggct  | tcctggggcg | cgccggcagc  | accatggggc | ccgccagcat | caccctgacc  | 2820 |
| gtgcaggccc  | gccagctgct | gagcggcatc  | gtgcagcagc | agagcaacct | gctgcgcgcc  | 2880 |
| atcgaggccc  | agcagcacct | gctgcagctg  | accgtgtggg | gcatcaagca | gctgcagacc  | 2940 |
| cgctgtgtgg  | ccatcgagcg | ctacctgaag  | gaccagcagc | tgctgggcct | gtggggctgc  | 3000 |
| agcggcaagc  | tgatctgcgc | caccgccgtg  | ccctggaaca | gcagctggag | caacaagagc  | 3060 |
| ctggggcgaca | tctgggacaa | catgacctgg  | atgcagtggg | accgcgagat | cagcaactac  | 3120 |
| accaacacca  | tcttccgcct | gctggaggac  | agccagaacc | agcaggagaa | gaacgagaag  | 3180 |
| gacctgtgtg  | ccctggacag | ctggaagaac  | ctgtggaact | ggttcgacat | caccaactgg  | 3240 |
| ctgtggtaca  | tcaagatctt | catcatgata  | gtgggcggcc | tgatcggcct | gcgcatcatc  | 3300 |
| ttcggcgctg  | tggccatcgt | gaagcgcgtg  | cgccagggct | acagccccct | gagcttccag  | 3360 |
| accctgatcc  | ccaacccccg | cggccccgac  | cgctggggcc | gcatcgagga | ggagggcggc  | 3420 |
| gagcaggaca  | aggaccgcag | catccgcctg  | gtgagcggct | tcctggccct | ggcctgggac  | 3480 |
| gacctgcgca  | gcctgtgcct | gttcagctac  | caccagctgc | gcgacttcat | cctgaccgcc  | 3540 |
| gccccgcgccg | ccgagctgct | gggccgcagc  | agcctgcgcg | gcctgcagcg | cggctgggag  | 3600 |

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|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| gtgctgaagt  | acctgggcaa  | cctggtgcag | tactggggcc | tggagctgaa | gcgcagcgcc | 3660 |
| atcaacctgt  | tcgacaccat  | cgccatcgcc | gtggccgagg | gcaccgaccg | catcatcgag | 3720 |
| gtgatccagc  | gcattctgcc  | cgccatccgc | tacatcccca | cccgcattcc | ccagggcttc | 3780 |
| gaggccgccc  | tgctgtaagg  | tacctctaga | gtcgacccgg | gcggccaaac | cgctgatcag | 3840 |
| cctcgactgt  | gccttctagt  | tgccagccat | ctgttgtttg | cccctcccc  | gtgccttcct | 3900 |
| tgaccctgga  | aggtgccact  | cccactgtcc | tttcctaata | aaatgaggaa | attgcatcgc | 3960 |
| attgtctgag  | taggtgtcat  | tctattctgg | ggggtgggg  | ggggcaggac | agcaaggggg | 4020 |
| aggattggga  | agacaatagc  | aggcatgctg | gggatgcggt | gggctctatg | gcttctgagg | 4080 |
| cggaaagaac  | cagcagatct  | gcagatctga | attcatctat | gtcgggtgcg | gagaaagagg | 4140 |
| taatgaaatg  | gcattatggg  | tattatgggt | ctgcattaat | gaatcggcca | gatatcgata | 4200 |
| tgctggccac  | cgtgcatgtg  | acctcgcacc | cccgcaagac | atggcccag  | ttcgagcaca | 4260 |
| acgtcatgac  | ccgatgcaat  | gtgcacctgg | ggccccgcg  | aggcatgttc | atgccctacc | 4320 |
| agtgaacat   | gcaatttgtg  | aaggtgctgc | tggagcccga | tgccatgtcc | agagtgcgac | 4380 |
| tgacgggggt  | gtttgacatg  | aatgtggagc | tgtggaaaat | tctgagatat | gatgaatcca | 4440 |
| agaccagggt  | ccgggcctgc  | gaatgcggag | gcaagcacgc | caggcttcag | cccgtgtgtg | 4500 |
| tggagggtgac | ggaggacctg  | cgacccgatc | atttggtgtt | gtcctgcaac | gggacggagt | 4560 |
| tcggctccag  | cggggaagaa  | tctgactaga | gtgagtagtg | tttgggggag | gtggagggct | 4620 |
| tgtatgaggg  | gcagaatgac  | taaaatctgt | gtttttctgt | gtgttgacgc | agcatgagcg | 4680 |
| gaagcgcctc  | ctttgagggg  | ggggtattca | gcccttatct | gacggggcgt | ctcccctcct | 4740 |
| gggcgggagt  | gcgtcagaat  | gtgatgggat | ccacggtgga | cggccggccc | gtgcagcccc | 4800 |
| cgaactcttc  | aaccctgacc  | tacgcgaccc | tgagctcctc | gtccgtggac | gcagctgccg | 4860 |
| ccgcagctgc  | tgcttccgcc  | gccagcgccg | tgcgcggaat | ggccctgggc | gccggctact | 4920 |
| acagctctct  | ggtggccaac  | tcgacttcca | ccaataatcc | cgccagcctg | aacgaggaga | 4980 |
| agctgctgct  | gctgatggcc  | cagctcgagg | ccctgaccca | gcgcctgggc | gagctgaccc | 5040 |
| agcagggtgg  | tcagctgcag  | gcggagacgc | gggccgcggt | tgccacggtg | aaaaccaa   | 5100 |
| aaaaaatgaa  | tcaataaata  | aacggagacg | gttgttgatt | ttaacacaga | gtcttgaatc | 5160 |
| tttatttgat  | ttttcgcgcg  | cggtaggccc | tggaccaccg | gtctcgatca | ttgagcacc  | 5220 |
| ggtggatttt  | ttccaggacc  | cggtagaggt | gggcttggat | gttgaggtag | atgggcatga | 5280 |
| gcccgtcccc  | gggggtggagg | tagctccatt | gcagggcctc | gtgctcgggg | gtggtgttgt | 5340 |
| aaatcaccca  | gtcatagcag  | gggcgcaggg | cggtgtgctg | cacgatgtcc | ttgaggagga | 5400 |
| gactgatggc  | cacgggcagc  | cccttggtgt | aggtgttgac | gaacctgttg | agctgggagg | 5460 |
| gatgcatgcg  | gggggagatg  | agatgcatct | tggcctggat | cttgagattg | gcgatgttcc | 5520 |

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|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| cgcccagatc  | ccgccggggg  | ttcatgttgt | gcaggaccac  | cagcacggtg | tatccggcgc  | 5580 |
| acttggggaa  | tttgtcatgc  | aacttggaag | ggaaggcgtg  | aaagaatttg | gagacgccct  | 5640 |
| tgtgaccgcc  | caggttttcc  | atgcactcat | ccatgatgat  | ggcgatgggc | ccgtgggcgg  | 5700 |
| cggcctgggc  | aaagacgttt  | cgggggtcgg | acacatcgta  | gttgtgttcc | tgggtgagct  | 5760 |
| cgatcataggc | catttttaatg | aatttggggc | ggaggggtgcc | cgactggggg | acgaagggtgc | 5820 |
| cctcgatccc  | gggggcgtag  | ttgccctcgc | agatctgcat  | ctcccaggcc | ttgagctcgg  | 5880 |
| agggggggat  | catgtccacc  | tgcggggcga | tgaaaaaac   | ggtttccggg | gcgggggaga  | 5940 |
| tgagctgggc  | cgaaagcagg  | ttccggagca | gctgggactt  | gccgcagccg | gtggggccgt  | 6000 |
| agatgacccc  | gatgaccggc  | tgcagggtgt | agttgaggga  | gagacagctg | ccgtcctcgc  | 6060 |
| ggaggagggg  | ggccacctcg  | ttcatcatct | cgcgcacatg  | catgttctcg | cgcacgagtt  | 6120 |
| ccgccaggag  | gcgctcgccc  | cccagcgaga | ggagctcttg  | cagcgaggcg | aagtttttca  | 6180 |
| gcggcttgag  | yccgtcggcc  | atgggcattt | tggagagggt  | ctgttgcaag | agttccagac  | 6240 |
| ggtcccagag  | ctcgggtgat  | tgctctaggg | catctcgatc  | cagcagacct | cctcgtttcg  | 6300 |
| cgggttgggg  | cgactgcggg  | agtagggcac | caggcgatgg  | gcgtccagcg | aggccagggt  | 6360 |
| ccggtccttc  | cagggtcgca  | gggtccgcgt | cagcgtggtc  | tccgtcacgg | tgaaggggtg  | 6420 |
| cgcgccgggc  | tgggcgcttg  | cgagggtgcg | cttcaggctc  | atccggctgg | tcgagaaccg  | 6480 |
| ctcccggtcg  | gcgccctgcg  | cgtcggccag | gtagcaattg  | agcatgagtt | cgtagttgag  | 6540 |
| cgcctcggcc  | gcgtggccct  | tggcgcgag  | cttacctttg  | gaagtgtgtc | cgcagacggg  | 6600 |
| acagaggagg  | gacttgaggg  | cgtagagctt | gggggcgagg  | aagacggact | cgggggcgta  | 6660 |
| ggcgtccgcg  | ccgcagctgg  | cgcagacggt | ctcgcactcc  | acgagccagg | tgaggtcggg  | 6720 |
| ccggttgggg  | tcaaaaacga  | ggtttcctcc | gtgctttttg  | atgcgtttct | tacctctggt  | 6780 |
| ctccatgagc  | tcgtgtcccc  | gctgggtgac | aaagaggctg  | tccgtgtccc | cgtagaccga  | 6840 |
| ctttatgggc  | cggtcctcga  | gcggggtgcc | gcggtcctcg  | tcgtagagga | accccgccca  | 6900 |
| ctccgagacg  | aaggccccgg  | tccaggccag | cacgaaggag  | gccacgtggg | aggggtagcg  | 6960 |
| gtcgttgtcc  | accagcgggt  | ccaccttctc | cagggtatgc  | aagcacatgt | ccccctcgtc  | 7020 |
| cacatccagg  | aagggtgattg | gcttgtaagt | gtaggccacg  | tgaccggggg | tccgggccgg  | 7080 |
| gggggtataa  | aagggggcgg  | gcccctgctc | gtcctcactg  | tcttccggat | cgctgtccag  | 7140 |
| gagcgccagc  | tggtggggta  | ggtattccct | ctcgaaggct  | ggcataacct | cggcactcag  | 7200 |
| gttgtcagtt  | tctagaaacg  | aggaggattt | gatattgacg  | gtgccgttgg | agacgccttt  | 7260 |
| catgagcccc  | tcgtccatct  | ggtcagaaaa | gacgatcttt  | ttgttgtcga | gcttgggtggc | 7320 |
| gaaggagccg  | tagagggcgt  | tggagaggag | cttggcgatg  | gagcgcatgg | tctggttctt  | 7380 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| ttccttgctg  | gcgcgctcct  | tggcggcgat | gttgagctgc  | acgtactcgc | gcgccacgca | 7440 |
| cttccattcg  | gggaagacgg  | tggtagctc  | gtcgggcacg  | attctgaccc | gccagccgcg | 7500 |
| gttggtcagg  | gtgatgaggt  | ccacgctgg  | ggccacctcg  | ccgcgcagg  | gctcgttgg  | 7560 |
| ccagcagagg  | cgcccgccct  | tgcgcgagca | gaaggggggc  | agcgggtcca | gcatgagctc | 7620 |
| gtcggggggg  | tcggcgctcca | cggtgaagat | gccgggcaga  | agctcggggt | cgaagtagct | 7680 |
| gatgcagggtg | tccagatcgt  | ccacgcgccg | ttgccagtcg  | cgcacggcca | gcgcgcgctc | 7740 |
| gtaggggctg  | aggggcgtgc  | cccagggcat | ggggtgcgtg  | agcgcggagg | cgtacatgcc | 7800 |
| gcagatgtcg  | tagacgtaga  | ggggctcctc | gaggacgccg  | atgtaggtgg | ggtagcagcg | 7860 |
| ccccccgcgg  | atgctggcgc  | gcacgtagtc | gtacagctcg  | tgcgagggcg | cgaggagccc | 7920 |
| cgtgccgagg  | ttggagcgtt  | gcggcttttc | ggcgcggtag  | acgatctggc | ggaagatggc | 7980 |
| gtgggagttg  | gaggagatgg  | tgggcctctg | gaagatgttg  | aagtgggcgt | ggggcaggcc | 8040 |
| gaccgagtcc  | ctgatgaagt  | gggcgtagga | gtcctgcagc  | ttggcgacga | gctcggcggt | 8100 |
| gacgaggacg  | tccagggcgc  | agtagtcgag | ggtctcttgg  | atgatgtcgt | acttgagctg | 8160 |
| gcccttctgc  | ttccacagct  | cgcggttgag | aaggaaactct | tcgcggtcct | tccagtactc | 8220 |
| ttcgaggggg  | aaccctgcct  | gatcggcacg | gtaagagccc  | accatgtaga | actggttgac | 8280 |
| ggccttgtag  | gcgcagcagc  | ccttctccac | ggggagggcg  | taagcttgtg | cggccttgcg | 8340 |
| cagggaggtg  | tgggtgaggg  | cgaagggtgc | gcgcaccatg  | accttgagga | actggtgctt | 8400 |
| gaagtcgagg  | tcgtcgcagc  | cgccctgctc | ccagagctgg  | aagtccgtgc | gcttcttgta | 8460 |
| ggcgggggtg  | ggcaaagcga  | aagtaacatc | gttgaagagg  | atcttgcccg | cgcggggcat | 8520 |
| gaagttgcga  | gtgatgcgga  | aaggctgggg | cacctcggcc  | cggttggtga | tgacctgggc | 8580 |
| ggcgaggacg  | atctcgtcga  | agccgttgat | gttggtgccc  | acgatgtaga | gttccacgaa | 8640 |
| tcgcgggcgg  | cccttaacgt  | ggggcagctt | cttgagctcg  | tcgtaggtga | gctcggcggg | 8700 |
| gtcgtgagc   | ccgtgctgct  | cgagggccca | gtcggcgacg  | tgggggttgg | cgctgaggaa | 8760 |
| ggaagtccag  | agatccacgg  | ccagggcggt | ctgcaagcgg  | tcccgttact | gacggaactg | 8820 |
| ctggcccacg  | gccatttttt  | cgggggtgac | gcagtagaag  | gtgcgggggt | cgccgtgcca | 8880 |
| gcggtcccac  | ttgagctgga  | gggcgaggtc | gtgggcgagc  | tcgacgagcg | gcgggtcccc | 8940 |
| ggagagtttc  | atgaccagca  | tgaaggggac | gagctgcttg  | ccgaaggacc | ccatccaggt | 9000 |
| gtaggtttcc  | acatcgtagg  | tgaggaagag | cctttcggtg  | cgaggatgcg | agccgatggg | 9060 |
| gaagaactgg  | atctcctgcc  | accagttgga | ggaatggctg  | ttgatgtgat | ggaagtagaa | 9120 |
| atgccgacgg  | cgcgccgagc  | actcgtgctt | gtgtttatac  | aagcgtccgc | agtgtctgca | 9180 |
| acgctgcacg  | ggatgcacgt  | gctgcacgag | ctgtacctgg  | gttcctttga | cgaggaattt | 9240 |
| cagtgggcag  | tggagcgctg  | gcggctgcat | ctggtgctgt  | actacgtcct | ggccatcggc | 9300 |

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|            |            |            |            |            |             |       |
|------------|------------|------------|------------|------------|-------------|-------|
| gtggccatcg | tctgcctcga | tgggtggcat | gctgacgagc | ccgcgcggga | ggcaggtcca  | 9360  |
| gacttcggct | cggacgggtc | ggagagcgag | gacgagggcg | cgagggccgg | agctgtccag  | 9420  |
| ggtcctgaga | cgctgcggag | tcaggtcagt | gggcagcggc | ggcgcgcggt | tgacttgacg  | 9480  |
| gagcttttcc | agggcgcgcg | ggaggtccag | atggtacttg | atctccacgg | cgccgttggg  | 9540  |
| ggcgacgtcc | acggcttgca | gggtcccggt | cccctggggc | gccaccaccg | tgccccgttt  | 9600  |
| cttcttgggc | gctgcttcca | tgccggtcag | aagcggcggc | gaggacgcgc | gccgggaggc  | 9660  |
| aggggaggct | cgggacccgg | aggcaggggc | ggcaggggca | cgtcggcgcc | gcgcgcgggc  | 9720  |
| aggttctggg | actgcgcccc | gagaagactg | gcgtgagcga | cgacgcgacg | gttgacgtcc  | 9780  |
| tggatctgac | gcctctgggt | gaaggccacg | ggacccgtga | gtttgaacct | gaaagagagt  | 9840  |
| tcgacagaat | caatctcggt | atcggtgacg | gcggcctgcc | gcaggatctc | ttgcacgtcg  | 9900  |
| cccaggttgt | cctggtaggc | gatctcggtc | atgaactgct | cgatctcctc | ctcctgaagg  | 9960  |
| tctccgcggc | cggcgcgctc | gacgggtggc | gcgaggtcgt | tggagatgag | gccccatgag  | 10020 |
| tgcgagaagg | cgttcatgcc | ggcctcggtc | cagacgcggc | tgtagaccac | ggctccgtcg  | 10080 |
| gggtcgcgcg | cgcgcatgac | cacctggggc | aggttgagct | cgacgtggcg | cgtaagacc   | 10140 |
| gcgtagttgc | agaggcgctg | gtagaggtag | ttgagcgtgg | tggcgatgtg | ctcggtgacg  | 10200 |
| aagaagtaca | tgatccagcg | gcggagcggc | atctcgctga | cgtcgcccag | ggcttccaag  | 10260 |
| cgctccatgg | cctcgtagaa | gtccacggcg | aagttagaaa | actgggagtt | gcgcgccgag  | 10320 |
| acggtcaact | cctcctccag | aagacgggat | agctcagcga | tggtggcgcg | cacctcgcg   | 10380 |
| tcgaaggccc | cgggggggct | ctcttcttcc | atctcttctc | cctccactaa | catctcttct  | 10440 |
| acttctctct | caggaggcgg | cggcggggga | ggggccctgc | gtcgccggcg | gcgcacgggc  | 10500 |
| agacggtcga | tgaagcgctc | gatggtctcc | ccgcgccggc | gacgcatggt | ctcggtgacg  | 10560 |
| gcgcgcccgt | cctcgcgggg | ccgcagcgtg | aagacgccgc | cgcgcatctc | cagggtggcg  | 10620 |
| ccgggggggg | ctccgttggg | caggagagag | gcgctgacga | tgcatttat  | caattggccc  | 10680 |
| gtagggactc | cgcgcaagga | cctgagcgtc | tcgagatcca | cgggatccga | aaaccgctga  | 10740 |
| acgaaggctt | cgagccagtc | gcagtcgcaa | ggtaggctga | gcccgggttc | ttgttcttcg  | 10800 |
| gggatttcgg | gaggcggg   | ggcgatgctg | ctggtgatga | agttgaagta | ggcggctcctg | 10860 |
| agacggcgga | tggtggcgag | gagcaccagg | tccttggggc | cggcttgctg | gatgcgcaga  | 10920 |
| cggtcggcca | tgccccaggc | gtggtcctga | cacctggcga | ggtccttgta | gtagtcctgc  | 10980 |
| atgagccgct | ccacgggcac | ctcctcctcg | cccgcgcggc | cgatgcgacg | cgtagagccc  | 11040 |
| aacccgcgct | ggggctggac | gagcgccagg | tcggcgacga | cgcgctcggc | gaggatggcc  | 11100 |
| tgctgtatct | gggtgagggt | ggtctggaag | tcgtcgaagt | cgacgaagcg | gtggtaggct  | 11160 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |             |       |
|-------------|-------------|-------------|------------|-------------|-------------|-------|
| ccggtgttga  | tggatatagga | gcagttggcc  | atgacggacc | agttgacggt  | ctggtggccg  | 11220 |
| ggtcgcacga  | gctcgtggta  | cttgaggcgc  | gagtaggcgc | gcgtgtcgaa  | gatgtagtcg  | 11280 |
| ttgcaggtgc  | gcacgaggtg  | ctggtatccg  | acgaggaagt | gcggcggcgg  | ctggcggtag  | 11340 |
| agcggccatc  | gctcgggtggc | gggggcccgc  | ggcgcgaggt | cctcgagcat  | gaggcggtgg  | 11400 |
| tagccgtaga  | tgtacctgga  | catccagggtg | atgccggcgg | cggtgggtgga | ggcgcgcggg  | 11460 |
| aactcgcgga  | cgcggttcca  | gatgttgcgc  | agcggcagga | agtagttcat  | ggtggccgcg  | 11520 |
| gtctggccccg | tgaggcgcgc  | gcagtcgtgg  | atgctctaga | catacgggca  | aaaacgaaaag | 11580 |
| cggtcagcgg  | ctcgactccg  | tggcctggag  | gctaagcgaa | cggttggggc  | tgcgcggtga  | 11640 |
| ccccggttcg  | aatctcgaat  | caggctggag  | ccgcagctaa | cgtggtactg  | gcactcccgt  | 11700 |
| ctcgacccaa  | gcctgctaac  | gaaacctcca  | ggatacggag | gcgggtcgtt  | ttttggcctt  | 11760 |
| ggtcgctggg  | catgaaaaac  | tagtaagcgc  | ggaaagcgac | cgcccgcgat  | ggctcgcctgc | 11820 |
| cgtagtctgg  | agaaagaatc  | gccagggttg  | cgttgcggtg | tgccccggtt  | cgagcctcag  | 11880 |
| cgctcggcgc  | cggccggatt  | ccgcggctaa  | cgtgggcgtg | gctgccccgt  | cgtttccaag  | 11940 |
| accccttagc  | cagccgactt  | ctccagttac  | ggagcgagcc | cctctttttc  | ttgtgttttt  | 12000 |
| gccagatgca  | tcccgtactg  | cggcagatgc  | gccccaccc  | tccacctcaa  | ccgcccctac  | 12060 |
| cgccgcagca  | gcagcaacag  | ccggcgcttc  | tgcccccgcc | ccagcagcag  | ccagccacta  | 12120 |
| ccgcggcggc  | cgccgtgagc  | ggagccggcg  | ttcagtatga | cctggccttg  | gaagagggcg  | 12180 |
| aggggctggc  | gcggctgggg  | gcgtcgtcgc  | cggagcggca | cccgcgcgtg  | cagatgaaaa  | 12240 |
| gggacgctcg  | cgaggcctac  | gtgccaagc   | agaacctgtt | cagagacagg  | agcggcgagg  | 12300 |
| agcccagagga | gatgcgcgcc  | tcccgcttcc  | acgcggggcg | ggagctgcgg  | cgcgccctgg  | 12360 |
| accgaaagcg  | ggtgctgagg  | gacgaggatt  | tcgaggcgga | cgagctgacg  | gggatcagcc  | 12420 |
| ccgcgcgcgc  | gcacgtggcc  | gcggccaacc  | tggtcacggc | gtacgagcag  | accgtgaagg  | 12480 |
| aggagagcaa  | cttccaaaaa  | tccttcaaca  | accacgtgcg | cacgctgata  | gcgcgcgagg  | 12540 |
| aggtgaccct  | gggcctgatg  | cacctgtggg  | acctgctgga | ggccatcgtg  | cagaacccca  | 12600 |
| cgagcaagcc  | gctgacggcg  | cagctgtttc  | tggtggtgca | gcacagtcgg  | gacaacgaga  | 12660 |
| cgttcaggga  | ggcgctgctg  | aatatcaccg  | agcccgaggg | ccgctggctc  | ctggacctgg  | 12720 |
| tgaacattct  | gcagagcatc  | gtggtgcagg  | agcgcgggct | gccgctgtcc  | gagaagctgg  | 12780 |
| cggtatcaa   | cttctcgggtg | ctgagcctgg  | gcaagtacta | cgctaggaag  | atctacaaga  | 12840 |
| ccccgtacgt  | gcccatagac  | aaggagggtga | agatcgacgg | gttttacatg  | cgcatgaccc  | 12900 |
| tgaagtgtct  | gaccctgagc  | gacgatctgg  | gggtgtaccg | caacgacagg  | atgcaccgcg  | 12960 |
| cggtgagcgc  | cagccgccgg  | cgcgagctga  | gcgaccagga | gctgatgcac  | agcctgcagc  | 13020 |
| gggccctgac  | cggggccggg  | accgaggggg  | agagctactt | tgacatgggc  | gcggacctgc  | 13080 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |             |             |            |             |       |
|-------------|------------|-------------|-------------|------------|-------------|-------|
| gctggcagcc  | cagccgccgg | gccttggaag  | ctgccggcgg  | ttccccctac | gtggaggagg  | 13140 |
| tggacgatga  | ggaggaggag | ggcgagtacc  | tggaagactg  | atggcgcgac | cgtatttttg  | 13200 |
| ctagatgcag  | caacagccac | cgcctcctga  | tcccgcgatg  | cgggcggcgc | tgcagagcca  | 13260 |
| gccgtccggc  | attaactcct | cggacgattg  | gaccagggcc  | atgcaacgca | tcatggcgct  | 13320 |
| gacgacccgc  | aatcccgaag | ccttttagaca | gcagcctcag  | gccaaccggc | tctcggccat  | 13380 |
| cctggaggcc  | gtggtgccct | cgcgctcgaa  | ccccacgcac  | gagaagggtg | tggccatcgt  | 13440 |
| gaacgcgctg  | gtggagaaca | aggccatccg  | cggcgacgag  | gccgggctgg | tgtacaacgc  | 13500 |
| gctgctggag  | cgcgtggccc | gctacaacag  | caccaacgtg  | cagacgaacc | tggaccgcat  | 13560 |
| ggtgaccgac  | gtgcgcgagg | cggtgtcgca  | gcgcgagcgg  | ttccaccgcg | agtcgaacct  | 13620 |
| gggctccatg  | gtggcgctga | acgccttcct  | gagcacgcag  | cccgccaacg | tgccccgggg  | 13680 |
| ccaggaggac  | tacaccaact | tcatcagcgc  | gctgcggctg  | atggtggccg | aggtgccccca | 13740 |
| gagcgagggtg | taccagtcgg | ggccggacta  | cttcttccag  | accagtcgcc | agggcttgca  | 13800 |
| gaccgtgaac  | ctgagccagg | ctttcaagaa  | cttgcaaggga | ctgtggggcg | tgcaggcccc  | 13860 |
| ggtcgggggac | cgcgcgacgg | tgtcgagcct  | gctgacgccg  | aactcgcgcc | tgctgctgct  | 13920 |
| gctggtggcg  | cccttcacgg | acagcggcag  | cgtgagccgc  | gactcgtacc | tgggctacct  | 13980 |
| gcttaacctg  | taccgcgagg | ccatcgggca  | ggcgcacgtg  | gacgagcaga | cctaccagga  | 14040 |
| gatcacccac  | gtgagccgcg | cgttgggcca  | ggaggaccgg  | ggcaacctgg | aggccaccct  | 14100 |
| gaacttcctg  | ctgaccaacc | ggtcgcagaa  | gatccccgcc  | cagtacgcgc | tgagcaccga  | 14160 |
| ggaggagcgc  | atcctgcgct | acgtgcagca  | gagcgtgggg  | ctgttcctga | tgcaggaggg  | 14220 |
| ggccacgccc  | agcgcgcgcg | tcgacatgac  | cgcgcgcaac  | atggagccca | gcatgtacgc  | 14280 |
| tcgcaaccgc  | ccgttcatca | ataagctgat  | ggactacttg  | catcgggcgg | ccgccatgaa  | 14340 |
| ctcggactac  | tttaccaacg | ccatcttgaa  | cccgcactgg  | ctcccgccgc | ccgggttcta  | 14400 |
| cacgggcgag  | tacgacatgc | ccgaccccaa  | cgacgggttc  | ctgtgggacg | acgtggacag  | 14460 |
| cagcgtgttc  | tcgccgcgcc | ccgccaccac  | cgtgtggaag  | aaagagggcg | gggaccggcg  | 14520 |
| gccgtcctcg  | gcgctgtccg | gtcgcgcggg  | tgctgccgcg  | gcggtgcctg | aggccgccag  | 14580 |
| ccccttcccg  | agcctgccct | tttcgctgaa  | cagcgtgcgc  | agcagcgagc | tgggtcggct  | 14640 |
| gacgcggccc  | cgcctgctgg | gcgaggagga  | gtacctgaac  | gactccttgt | tgaggcccga  | 14700 |
| gcgcgagaag  | aacttcccca | ataacgggat  | agagagcctg  | gtggacaaga | tgagccgctg  | 14760 |
| gaagacgtac  | gcgcacgagc | acagggacga  | gccccgagct  | agcagcagcg | caggcaccgg  | 14820 |
| tagacgccag  | cgacacgaca | ggcagcgggg  | tctggtgtgg  | gacgatgagg | attccgccga  | 14880 |
| cgacagcagc  | gtgttggact | tgggtggggag | tgggtggtgt  | aaccggttcg | ctcacttgcg  | 14940 |

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|             |              |            |            |            |             |       |
|-------------|--------------|------------|------------|------------|-------------|-------|
| cccccgatatc | ggg'gcgcctga | tgtaagaatc | tgaaaaaata | aaaaacggta | ctcaccaagg  | 15000 |
| ccatggcgac  | cagcgtgcgt   | tcttctctgt | tgtttgtagt | agtatgatga | ggcgcgtgta  | 15060 |
| cccggagggg  | cctcctccct   | cgtacgagag | cgtgatgcag | caggcgggtg | cggcggcgat  | 15120 |
| gcagcccccg  | ctggaggcgc   | cttacgtgcc | cccgcggtac | ctggcgccta | cggagggggcg | 15180 |
| gaacagcatt  | cgttactcgg   | agctggcacc | cttgtacgat | accacccggt | tgtacctggt  | 15240 |
| ggacaacaag  | tcggcggaca   | tcgcctcgct | gaactaccag | aacgaccaca | gcaacttcct  | 15300 |
| gaccaccgtg  | gtgcagaaca   | acgatttcac | ccccacggag | gccagcacc  | agaccatcaa  | 15360 |
| ctttgacgag  | cgctcgcggt   | ggggcggcca | gctgaaaacc | atcatgcaca | ccaacatgcc  | 15420 |
| caacgtgaac  | gagttcatgt   | acagcaacaa | gttcaaggcg | cgggtgatgg | tctcgcgcaa  | 15480 |
| gacccccaat  | ggggtcgcgg   | tggatgagaa | ttatgatggt | agtcaggacg | agctgactta  | 15540 |
| cgagtgggtg  | gagtttgagc   | tgcccagagg | caacttctcg | gtgaccatga | ccatcgatct  | 15600 |
| gatgaacaac  | gccatcatcg   | acaactactt | ggcgggtggg | cgtcagaacg | gggtgctgga  | 15660 |
| gagcgacatc  | ggcgtgaagt   | tcgacacgcg | caacttccgg | ctgggctggg | accccgtagc  | 15720 |
| cgagctgggtg | atgccggggcg  | tgtacaccaa | cgaggccttc | caccccgaca | tcgtcctgct  | 15780 |
| gcccggctgc  | ggcgtggact   | tcaccgagag | ccgcctcagc | aacctgctgg | gcatccgcaa  | 15840 |
| gcggcagccc  | ttccaggagg   | gcttccagat | cctgtacgag | gacctggagg | ggggcaacat  | 15900 |
| ccccgcgctc  | ttggatgtcg   | aagcctatga | gaaaagcaag | gaggaggccg | ccgcagcggc  | 15960 |
| gaccgcagcc  | gtggccaccg   | cctctaccga | ggtgcggggc | gataattttg | ctagcgccgc  | 16020 |
| ggcagtggcc  | gaggcggctg   | aaaccgaaa  | taagatagtc | atccagccgg | tggagaagga  | 16080 |
| cagcaaggac  | aggagctaca   | acgtgctcgc | ggacaagaaa | aacaccgcct | accgcagctg  | 16140 |
| gtacctggcc  | tacaactacg   | gcgaccccg  | gaagggcgtg | cgctcctgga | cgctgctcac  | 16200 |
| cacctcggac  | gtcacctcgc   | gcgtggagca | agtctactgg | tcgctgccc  | acatgatgca  | 16260 |
| agacccggtc  | accttccgct   | ccacgcgtca | agttagcaac | tacccggtgg | tgggcgccga  | 16320 |
| gctcctgccc  | gtctactcca   | agagcttctt | caacgagcag | gccgtctact | cgcagcagct  | 16380 |
| gcgcgccttc  | acctcgtcga   | cgcacgtctt | caaccgcttc | cccgagaacc | agatcctcgt  | 16440 |
| ccgcccggcc  | gcgcccacca   | ttaccaccgt | cagtgaaaac | gttcctgctc | tcacagatca  | 16500 |
| cgggaccctg  | ccgctgcgca   | gcagtatccg | gggagtccag | cgcgtgaccg | tcactgacgc  | 16560 |
| cagacgccgc  | acctgcccct   | acgtctacaa | ggccctgggc | gtagtcgcgc | cgcgcgtcct  | 16620 |
| ctcgagccgc  | accttctaaa   | aaatgtccat | tctcatctcg | cccagtaata | acaccggttg  | 16680 |
| gggcctgcgc  | gcgcccagca   | agatgtacgg | aggcgtcgc  | caacgctcca | cgcaacaccc  | 16740 |
| cgtgcgcgtg  | cgcgggcact   | tccgcgtcc  | ctggggcgcc | ctcaagggcc | gcgtgcgctc  | 16800 |
| gcgcaccacc  | gtcgacgacg   | tgatcgacca | ggtgggtggc | gacgcgcgca | actacacgcc  | 16860 |



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|             |             |             |             |             |             |       |
|-------------|-------------|-------------|-------------|-------------|-------------|-------|
| cgccgcccgcg | cccgcctcca  | ccgtggacgc  | cgatcatcgac | agcgtggtgg  | ccgatgcgcg  | 16920 |
| ccggtacgcc  | cgcgccaaga  | gccggcgggcg | gcgcatcgcc  | cggcggcacc  | ggagcacccc  | 16980 |
| cgccatgcgc  | gcggcgcgag  | ccttgctgcg  | cagggccagg  | cgcacgggac  | gcagggccat  | 17040 |
| gctcagggcg  | gccagacgcg  | cggcctccgg  | cagcagcagc  | gccggcagga  | cccgcagacg  | 17100 |
| cgcgggccacg | gcggcgggcg  | cggccatcgc  | cagcatgtcc  | cgcccgcggc  | gcggcaacgt  | 17160 |
| gtactgggtg  | cgcgacgccg  | ccaccggtgt  | gcgcgtgccc  | gtgcgcaccc  | gccccctcg   | 17220 |
| cacttgaaga  | tgctgacttc  | gcgatgttga  | tgtgtcccag  | cggcgaggag  | gatgtccaag  | 17280 |
| cgcaaataca  | aggaagagat  | gctccaggtc  | atcgcgcttg  | agatctacgg  | ccccgcggtg  | 17340 |
| aaggaggaaa  | gaaagccccg  | caaactgaag  | cgggtcaaaa  | aggacaaaaa  | ggaggaggaa  | 17400 |
| gatgtggacg  | gactggtgga  | gtttgtgcgc  | gagttcgccc  | cccggcgggcg | cgtgcagtgg  | 17460 |
| cgcgggcgga  | aagtgaacc   | ggtgctgcgg  | cccggcacca  | cgtggtctt   | cacgccccgc  | 17520 |
| gagcgttccg  | gctccgcctc  | caagcgctcc  | tacgacgagg  | tgtacgggga  | cgaggacatc  | 17580 |
| ctcgagcagg  | cggtcgagcg  | tctgggcgag  | tttgcttacg  | gcaagcgag   | ccgccccgcg  | 17640 |
| cccttgaag   | aggaggcggt  | gtccatcccc  | ctggaccacg  | gcaaccccac  | gccgagcctg  | 17700 |
| aagccggtga  | ccctgcagca  | ggtgctgccg  | agcgcgggcg  | cgcgccgggg  | cttcaagcgc  | 17760 |
| gagggcgggcg | aggatctgta  | cccgaccatg  | cagctgatgg  | tgcccaagcg  | ccagaagctg  | 17820 |
| gaggacgtgc  | tggagcacat  | gaaggtggac  | cccgaggtgc  | agcccagagt  | caaggtgcgg  | 17880 |
| cccatcaagc  | aggtggcccc  | gggcctgggc  | gtgcagaccg  | tggacatcaa  | gatccccacg  | 17940 |
| gagcccatgg  | aaacgcagac  | cgagcccgtg  | aagcccagca  | ccagcaccat  | ggaggtgcag  | 18000 |
| acggatccct  | ggatgccggc  | gccggcttcc  | accactcgcc  | gaagacgcaa  | gtacggcgcg  | 18060 |
| gccagcctgc  | tgatgccccaa | ctacgcgctg  | catccttcca  | tcatccccac  | gccgggctac  | 18120 |
| cgcggcacgc  | gcttctaccg  | cggctacacc  | agcagccgcc  | gcaagaccac  | cacccgcccgc | 18180 |
| cgccgtcgtc  | gcacccgccg  | cagcagcacc  | gcgacttccg  | ccgccgccct  | ggtgcggaga  | 18240 |
| gtgtaccgca  | gcgggcgcga  | gcctctgacc  | ctgccgcgcg  | cgcgctacca  | cccgagcatc  | 18300 |
| gccatttaac  | tctgccgtcg  | cctcctactt  | gcagatatgg  | ccctcacatg  | ccgcctccgc  | 18360 |
| gtccccatta  | cgggctaccg  | aggaagaaaag | ccgcgccgta  | gaaggctgac  | ggggaacggg  | 18420 |
| ctgcgtcgcc  | atcaccaccg  | gcggcgggcg  | gccatcagca  | agcggttggg  | gggaggcttc  | 18480 |
| ctgcccgcgc  | tgatccccat  | catcgccgcg  | gcgatcgggg  | cgatccccgg  | catagcttcc  | 18540 |
| gtggcggtgc  | aggcctctca  | gcgccactga  | gacacagctt  | ggaaaatttg  | taataaaaaa  | 18600 |
| atggactgac  | gctcctggtc  | ctgtgatgtg  | tgtttttaga  | tggaagacat  | caatttttcg  | 18660 |
| tccctggcac  | cgcgacacgg  | cacgcggccg  | tttatgggca  | cctggagcga  | catcggcaac  | 18720 |

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|            |             |            |            |             |            |       |
|------------|-------------|------------|------------|-------------|------------|-------|
| agccaactga | acggggggcgc | cttcaattgg | agcagtctct | ggagcgggct  | taagaatttc | 18780 |
| gggtccacgc | tcaaaaccta  | tggcaacaag | gcgtggaaca | gcagcacagg  | gcaggcgctg | 18840 |
| agggaaaagc | tgaagagca   | gaacttccag | cagaagggtg | tcgatggcct  | ggcctcgggc | 18900 |
| atcaacgggg | tgggtggacct | ggccaaccag | gccgtgcaga | aacagatcaa  | cagccgcctg | 18960 |
| gacgcggtcc | cgcccgcggg  | gtccgtggag | atgccccagg | tggaggagga  | gctgcctccc | 19020 |
| ctggacaagc | gcggcgacaa  | gcgaccgcgt | cccgcgcgg  | aggagacgct  | gctgacgcac | 19080 |
| acggacgagc | cgcccccgta  | cgaggaggcg | gtgaaactgg | gtctgcccac  | cacgcggccc | 19140 |
| gtggcgctc  | tggccaccgg  | ggtgctgaaa | cccagcagca | gcagccagcc  | cgcgaccctg | 19200 |
| gacttgctc  | cgctgcttc   | ccgccccctc | acagtggcta | agccccctgc  | gccggtggcc | 19260 |
| gtcgcgtcg  | gcgccccccg  | aggccgcccc | caggcgaact | ggcagagcac  | tctgaacagc | 19320 |
| atcgtgggtc | tgggagtgca  | gagtgtgaag | cgccgccgct | gctattaaaa  | gacactgtag | 19380 |
| cgcttaactt | gcttgtctgt  | gtgtatatgt | atgtccgccc | accagaagga  | ggaagaggcg | 19440 |
| cgtcgccgag | ttgcaagatg  | gccaccccat | cgatgctgcc | ccagtgggcg  | tacatgcaca | 19500 |
| tcgccggaca | ggacgcttcg  | gagtacctga | gtccgggtct | ggtgcagttc  | gcccgcgcca | 19560 |
| cagacaccta | cttcagtctg  | gggaacaagt | ttaggaaccc | cacggtggcg  | cccacgcacg | 19620 |
| atgtgaccac | cgaccgcagc  | cagcggctga | cgctgcgctt | cgtgcccgtg  | gaccgcgagg | 19680 |
| acaacaccta | ctcgtacaaa  | gtgcgctaca | cgctggccgt | gggcgacaac  | cgctgctgg  | 19740 |
| acatggccag | cacctacttt  | gacatccgcg | gcgtgctgga | tcggggggccc | agcttcaaac | 19800 |
| cctactccgg | caccgcctac  | aacagcctgg | ctcccaaggg | agcgcccaac  | acttgccagt | 19860 |
| ggacatataa | agctggtgat  | actgatacag | aaaaaaccta | tacatatgga  | aatgcacctg | 19920 |
| tgcaaggcat | tagcattaca  | aaggatggta | ttcaacttgg | aactgacagc  | gatggtcagg | 19980 |
| caatctatgc | agacgaaact  | tatcaaccag | agcctcaagt | gggtgatgct  | gaatggcatg | 20040 |
| acatcactgg | tactgatgaa  | aaatatggag | gcagagctct | taagcctgac  | acaaaaatga | 20100 |
| agccttgcta | tggttctttt  | gccaagccta | ccaataaaga | aggaggccag  | gcaaagtgtg | 20160 |
| aaaccgaaac | aggcgttacc  | aaagaatatg | acattgacat | ggcattcttc  | gataatcgaa | 20220 |
| gtgcagctgc | cgccggccta  | gccccagaaa | ttgttttgta | tactgagaat  | gtggatctgg | 20280 |
| aaactccaga | tacccatatt  | gtatacaagg | caggtagaca | tgacagtagc  | tcttctatca | 20340 |
| atttgggtca | gcagtccatg  | cccaacagac | ccaactacat | tggcttcaga  | gacaacttta | 20400 |
| tcggtctgat | gtactacaac  | agcactggca | atatgggtgt | actggctgga  | caggcctccc | 20460 |
| agctgaatgc | tgtggtggac  | ttgcaggaca | gaaacaccga | actgtcctac  | cagctcttgc | 20520 |
| ttgactctct | gggtgacaga  | accaggtatt | tcagtatgtg | gaatcaggcg  | gtggacagtt | 20580 |
| atgaccccga | tgtgcgcatt  | attgaaaatc | acggtgtgga | ggatgaactt  | cctaactatt | 20640 |

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|             |            |             |            |            |            |       |
|-------------|------------|-------------|------------|------------|------------|-------|
| gcttccccct  | ggatgctgtg | ggtagaactg  | atacttacca | gggaattaag | gccaatggtg | 20700 |
| ataatcaaac  | cacctggacc | aaagatgata  | ctgttaatga | tgctaataaa | ttgggcaagg | 20760 |
| gcaatccttt  | cgccatggag | atcaacatcc  | aggccaacct | gtggcggaac | ttcctctacg | 20820 |
| cgaacgtggc  | gctgtacctg | cccgactcct  | acaagtacac | gccggccaac | atcacgctgc | 20880 |
| ccaccaaacac | caacacctac | gattacatga  | acggccgcgt | ggtggcgccc | tcgctggtgg | 20940 |
| acgcctacat  | caacatcggg | gcgcgctggt  | cgctggaccc | catggacaac | gtcaaccctt | 21000 |
| tcaaccacca  | ccgcaacgcg | ggcctgcgat  | accgctccat | gctcctgggc | aacgggcgct | 21060 |
| acgtgccctt  | ccacatccag | gtgccccaaa  | agtttttcgc | catcaagagc | ctcctgctcc | 21120 |
| tgcccgggtc  | ctacacctac | gagtggaaact | tccgcaagga | cgtcaacatg | atcctgcaga | 21180 |
| gctccctcgg  | caacgacctg | cgcacggacg  | gggcctccat | cgccttcacc | agcatcaacc | 21240 |
| tctacgccac  | cttcttcccc | atggcgacac  | acaccgcctc | cacgctcgag | gccatgctgc | 21300 |
| gcaacgacac  | caacgaccag | tccttcaacg  | actacctctc | ggcgccaac  | atgctctacc | 21360 |
| ccatcccggc  | caacgccacc | aacgtgcca   | tctccatccc | ctcgcgcaac | tgggcccgtt | 21420 |
| tccgcggctg  | gtccttcacg | cgcctcaaga  | cccgcgagac | gccctcgctc | ggctccgggt | 21480 |
| tcgacccta   | cttcgtctac | tcgggctcca  | tcccctacct | cgacggcacc | ttctacctca | 21540 |
| accacacctt  | caagaaggct | tccatcacct  | tcgactcctc | cgtcagctgg | cccggcaacg | 21600 |
| accgcctcct  | gacgccaac  | gagttcgaaa  | tcaagcgac  | cgtcgacgga | gaggggtaca | 21660 |
| acgtggccca  | gtgcaacatg | accaaggact  | ggttcctggt | ccagatgctg | gcccactaca | 21720 |
| acatcggcta  | ccagggttc  | tacgtgcccg  | agggtacaa  | ggaccgcatg | tactccttct | 21780 |
| tccgcaactt  | ccagcccata | agccgccagg  | tcgtggacga | ggtcaactac | aaggactacc | 21840 |
| aggccgtcac  | cctggcctac | cagcacaaca  | actcgggctt | cgtcggctac | ctcgcgcca  | 21900 |
| ccatgcgcca  | gggccaagcc | taccccgcca  | actacccta  | cccgtcatc  | ggcaagagcg | 21960 |
| ccgtcgccag  | cgtcacccag | aaaaagtcc   | tctcgcacg  | ggtcatgtgg | cgcacccctt | 22020 |
| tctccagcaa  | cttcatgtcc | atgggcgcgc  | tcaccgacct | cggccagaac | atgctctacg | 22080 |
| ccaactccgc  | ccacgcgcta | gacatgaatt  | tcgaagtcga | ccccatggat | gagtccaccc | 22140 |
| ttctctatgt  | tgtcttcgaa | gtcttcgacg  | tcgtccgagt | gcaccagccc | caccgcggcg | 22200 |
| tcacgcaggc  | cgtctacctg | cgcacgccct  | tctcggccgg | caacgccacc | acctaagcct | 22260 |
| cttgcttctt  | gcaagatgac | ggcctgcgcg  | ggctccggcg | agcaggagct | cagggccatc | 22320 |
| ctccgcgacc  | tgggctgcgg | gccctgcttc  | ctgggcacct | tcgacaagcg | cttcccggga | 22380 |
| ttcatggccc  | cgcacaagct | ggcctgcgcc  | atcgtcaaca | cggccggccg | cgagaccggg | 22440 |
| ggcgagcact  | ggctggcctt | cgcctggaac  | ccgcgctccc | acacctgcta | cctcttcgac | 22500 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |            |       |
|-------------|-------------|-------------|------------|-------------|------------|-------|
| cccttcgggt  | tctcggacga  | gcgcctcaag  | cagatctacc | agttcgagta  | cgagggcctg | 22560 |
| ctgcgtcgca  | gcgccctggc  | caccgaggac  | cgctgcgtca | ccctggaaaa  | gtccacccag | 22620 |
| accgtgcagg  | gtccgcgctc  | ggccgcctgc  | gggtctttct | gctgcatgtt  | cctgcacgcc | 22680 |
| ttcgtgcaact | ggcccgaccg  | ccccatggac  | aagaacccca | ccatgaactt  | gctgacgggg | 22740 |
| gtgccaacg   | gcatgctcca  | gtcgccccag  | gtggaaccca | ccctgcgccg  | caaccaggag | 22800 |
| gcgctctacc  | gcttctctaa  | cgcccactcc  | gcctactttc | gctcccaccg  | cgcgcgcatc | 22860 |
| gagaaggcca  | ccgccttcga  | ccgcatgaat  | caagacatgt | aatccggtgt  | gtgtatgtga | 22920 |
| atgctttatt  | catcataata  | aacagcacat  | gtttatgcc  | ccttctctga  | ggctctgact | 22980 |
| ttatttagaa  | atcgaagggg  | ttctgccggc  | tctcggcatg | gcccgcgggc  | agggatacgt | 23040 |
| tgcggaactg  | gtacttgggc  | agccacttga  | actcggggat | cagcagcttc  | ggcacgggga | 23100 |
| ggtcggggaa  | cgagtcgctc  | cacagcttgc  | gcgtgagttg | cagggcgccc  | agcaggtcgg | 23160 |
| gcgcggagat  | cttgaaatcg  | cagttgggac  | ccgcgttctg | cgcgcgagag  | ttacggtaca | 23220 |
| cggggttgca  | gcaactggaac | accatcaggg  | ccgggtgctt | cacgctcgcc  | agcaccgtcg | 23280 |
| cgtcggtgat  | gccctccacg  | tccagatcct  | cggcgttggc | catcccgaag  | ggggtcatct | 23340 |
| tgcaggctctg | ccgccccatg  | ctgggcacgc  | agccgggctt | gtggttgcaa  | tcgcagtga  | 23400 |
| gggggatcag  | catcatctgg  | gcctgctcgg  | agctcatgcc | cgggtacatg  | gccttcatga | 23460 |
| aagcctccag  | ctggcggaag  | gcctgctgcg  | ccttgccgcc | ctcggtgaa   | aagaccccg  | 23520 |
| aggacttgct  | agagaactgg  | ttggtggcgc  | agccagcgtc | gtgcacgcag  | cagcgcgct  | 23580 |
| cgttggtggc  | cagctgcacc  | acgctgcgcc  | cccagcggtt | ctgggtgatc  | ttggcccgg  | 23640 |
| cggggttctc  | cttcagcgcg  | cgctgcccgt  | tctcgctcgc | cacatccatc  | tcgatcgtgt | 23700 |
| gctccttctg  | gatcatcacg  | gtcccgtgca  | ggcaccgcag | cttgccctcg  | gcctcggcgc | 23760 |
| accggtgcag  | ccacagcgcg  | cagccggtgc  | tctcccagtt | cttgtgggcg  | atctgggagt | 23820 |
| gcgagtgac   | gaagccctgc  | aggaagcggc  | ccatcatcgt | ggtcagggtc  | ttgttgctgg | 23880 |
| tgaaggctcag | cggaatgccg  | cgggtgctcct | cgttcacata | cagggtggcag | atacggcggt | 23940 |
| acacctcgcc  | ctgctcgggc  | atcagctgga  | aggcggactt | caggctcgctc | tccacgcggt | 24000 |
| accggtccat  | cagcagcgtc  | atcaactcca  | tgcccttctc | ccaggccgaa  | acgatcggca | 24060 |
| ggctcagggg  | gttcttcacc  | gttgtcatct  | tagtcgccgc | cgccgaagtc  | agggggcgt  | 24120 |
| tctcgtccag  | ggtctcaaac  | actcgcttgc  | cgctcttctc | ggtgatgcgc  | acggggggaa | 24180 |
| agctgaagcc  | cacggccgcc  | agctcctcct  | cggcctgcct | ttcgtcctcg  | ctgtcctggc | 24240 |
| tgatgtcttg  | caaaggcaca  | tgcttggtct  | tgccgggttt | ctttttgggc  | ggcagaggcg | 24300 |
| gcggcggaga  | cgtgctgggc  | gagcgcgagt  | tctcgctcac | cacgactatt  | tcttctcctt | 24360 |
| ggccgctcgtc | cgagaccacg  | cggcggtagg  | catgcctctt | ctggggcaga  | ggcggaggcg | 24420 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |            |            |             |            |            |       |
|-------------|------------|------------|-------------|------------|------------|-------|
| acgggctctc  | gcggttcggc | gggcggttg  | cagagcccct  | tccgcgttcg | ggggtgcgct | 24480 |
| cctggcggcg  | ctgctctgac | tgacttcctc | cgcgccggcg  | cattgtgttc | tcctagggag | 24540 |
| caagcatgga  | gactcagcca | tcgtcgccaa | catcgccatc  | tgcccccgcc | gccgccgacg | 24600 |
| agaaccagca  | gcagcagaat | gaaagcttaa | ccgccccgcc  | gccagcccc  | acctccgacg | 24660 |
| ccgcagcccc  | agacatgcaa | gagatggagg | aatccatcga  | gattgacctg | ggctacgtga | 24720 |
| cgcccccgga  | gcacgaggag | gagctggcag | cgcgcttttc  | agccccggaa | gagaaccacc | 24780 |
| aagagcagcc  | agagcaggaa | gcagagagcg | agcagaacca  | ggctgggctc | gagcatggcg | 24840 |
| actacctgag  | cggggcagag | gacgtgctca | tcaagcatct  | ggccccgcaa | tgcatcatcg | 24900 |
| tcaaggacgc  | gctgctcgac | cgcgccgagg | tgccccctcag | cgtggcgagg | ctcagccgcg | 24960 |
| cctacgagcg  | caacctcttc | tcgccgcgcg | tgccccccaa  | gcgccagccc | aacggcacct | 25020 |
| gcgagcccaa  | cccgcgcctc | aacttctacc | cggtcttcgc  | ggtgcccag  | gccctggcca | 25080 |
| cctaccacct  | ctttttcaag | aaccaaagga | tccccgtctc  | ctgccgcgcc | aaccgcaccc | 25140 |
| gcgccgacgc  | cctgctcaac | ctgggccccg | gcgccgcct   | acctgatata | gcctccttgg | 25200 |
| aagaggttcc  | caagatcttc | gagggctctg | gcagcgacga  | gactcggggc | gcgaacgctc | 25260 |
| tgcaaggaag  | cggagaggag | catgagcacc | acagcgccct  | ggtggagttg | gaaggcgaca | 25320 |
| acgcgcgcct  | ggcggctctc | aagcgcacgg | tcgagctgac  | ccacttcgcc | taccggcgcg | 25380 |
| tcaacctgcc  | ccccaaggtc | atgagcgccg | tcattggacca | ggtgctcatc | aagcgcgcct | 25440 |
| cgccccctctc | ggaggaggag | atgcaggacc | ccgagagctc  | ggacgagggc | aagcccgtgg | 25500 |
| tcagcgacga  | gcagctggcg | cgctggctgg | gagcgagtag  | cacccccag  | agcctggaag | 25560 |
| agcggcgcaa  | gctcatgatg | gccgtggtcc | tggtgaccgt  | ggagctggag | tgtctgcgcc | 25620 |
| gcttcttcgc  | cgacgcggag | accctgcgca | aggtcgagga  | gaacctgcac | tacctcttca | 25680 |
| gacacggggt  | cgtgcgccag | gcctgcaaga | tctccaacgt  | ggagctgacc | aacctggtct | 25740 |
| cctacatggg  | catcctgcac | gagaaccgcc | tggggcagaa  | cgtgctgcac | accaccctgc | 25800 |
| gcggggaggc  | ccgccgcgac | tacatccgcg | actgcgtcta  | cctgtacctc | tgccacacct | 25860 |
| ggcagacggg  | catgggcgtg | tggcagcagt | gcctggagga  | gcagaacctg | aaagagctct | 25920 |
| gcaagctcct  | gcagaagaac | ctcaaggccc | tgtggaccgg  | gttcgacgag | cgcaccaccg | 25980 |
| ccgcggacct  | ggccgacctc | atcttccccg | agcgcctgcg  | gctgacgctg | cgcaacgggc | 26040 |
| tgccccgactt | tatgagccaa | agcatgttgc | aaaactttcg  | ctctttcatc | ctcgaacgct | 26100 |
| ccgggatcct  | gcccgccacc | tgctccgcgc | tgccctcgga  | cttcgtgccg | ctgaccttcc | 26160 |
| gcgagtggcc  | cccgccgctc | tggagccact | gctacctgct  | gcgcctggcc | aactacctgg | 26220 |
| cctaccactc  | ggacgtgatc | gaggacgtca | gcggcgaggg  | cctgctcgag | tgccactgcc | 26280 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |             |             |             |             |       |
|------------|------------|-------------|-------------|-------------|-------------|-------|
| gctgcaacct | ctgcacgccg | caccgctccc  | tggcctgcaa  | ccccagctg   | ctgagcgaga  | 26340 |
| cccagatcat | cggcaccttc | gagttgcaag  | gccccggcga  | gggcaagggg  | ggtctgaaac  | 26400 |
| tcaccccg   | gctgtggacc | tcggcctact  | tgcgcaagtt  | ctgtcccag   | gactaccatc  | 26460 |
| ccttcgagat | caggttctac | gaggaccaat  | cccagccgcc  | caaggccgag  | ctgtcggcct  | 26520 |
| gcgtcatcac | ccagggggcc | atcctggccc  | aattgcaagc  | catccagaaa  | tcccgccaa   | 26580 |
| aatttctgct | gaaaaagggc | cacggggtct  | acttggaccc  | ccagaccgga  | gaggagctca  | 26640 |
| accccagctt | ccccaggat  | gccccgagga  | agcagcaaga  | agctgaaagt  | ggagctgccg  | 26700 |
| ccgccgccgg | aggatttgga | ggaagactgg  | gagagcagtc  | aggcagagga  | ggaggagatg  | 26760 |
| gaagactggg | acagcactca | ggcagaggag  | gacagcctgc  | aagacagtct  | ggaggaggaa  | 26820 |
| gacgaggtgg | aggaggcaga | ggaagaagca  | gccgccgcca  | gaccgtcgtc  | ctcggcggag  | 26880 |
| gaggagaaa  | caagcagcac | ggataccatc  | tccgctccgg  | gtcggggtcg  | cggcggccgg  | 26940 |
| gcccacagta | gatgggacga | gaccgggctc  | ttcccgaacc  | ccaccacca   | gaccggtaag  | 27000 |
| aaggagcggc | agggatacaa | gtcctggcgg  | gggcacaaaa  | acgccatcgt  | ctcctgcttg  | 27060 |
| caagcctg   | ggggcaacat | ctccttcacc  | cggcgctacc  | tgctcttcca  | ccgcgggggtg | 27120 |
| aacttcccc  | gcaacatctt | gcattactac  | cgtcacctcc  | acagccccta  | ctactgtttc  | 27180 |
| caagaagagg | cagaaacca  | gcagcagcag  | cagcagcaga  | aaaccagcgg  | cagcagctag  | 27240 |
| aaaatccaca | gcggcggcag | gtggactgag  | gatcgcggcg  | aacgagccgg  | cgcagacccg  | 27300 |
| ggagctgagg | aaccggatct | ttcccaccct  | ctatgccatc  | ttccagcaga  | gtcgggggca  | 27360 |
| agagcaggaa | ctgaaagtca | agaaccgttc  | tctgcgctcg  | ctcaccgcga  | gttgtctgta  | 27420 |
| tcacaagagc | gaagaccaac | ttcagcgcac  | tctcgaggac  | gccgaggctc  | tcttcaacaa  | 27480 |
| gtactgcgcg | ctcactctta | aagagtagcc  | cgcgcccgcc  | cacacacgga  | aaaaggcggg  | 27540 |
| aattacgtca | ccacctgcgc | ccttcgcccg  | accatcatca  | tgagcaaaga  | gattcccacg  | 27600 |
| ccttacatgt | ggagctacca | gccccagatg  | ggcctggccg  | ccggcgccgc  | ccaggactac  | 27660 |
| tccacccgca | tgaactggct | cagtgccggg  | cccgcgatga  | tctcacgggt  | gaatgacatc  | 27720 |
| cgcgcccacc | gaaaccagat | actcctagaa  | cagtcagcga  | tcaccgccac  | gccccgcat   | 27780 |
| caccttaatc | cgcgtaattg | gcccgccgcc  | ctggtgtacc  | aggaaaattcc | ccagcccacg  | 27840 |
| accgtactac | ttccgcgaga | cgcccaggcc  | gaagtccagc  | tgactaactc  | aggtgtccag  | 27900 |
| ctggccggcg | gcgccgccct | gtgtcgtcac  | cgccccgctc  | agggtataaa  | gcggctgggtg | 27960 |
| atccgaggca | gaggcacaca | gctcaacgac  | gaggtgggtga | gctcttcgct  | gggtctgcga  | 28020 |
| cctgacggag | tcttccaact | cgccggatcg  | gggagatctt  | ccttcacgcc  | tcgtcaggcc  | 28080 |
| gtcctgactt | tggagagttc | gtcctcgag   | ccccgctcgg  | gtggcatcgg  | cactctccag  | 28140 |
| ttcgtggagg | agttcactcc | ctcgggtctac | ttcaaccctt  | tctccggctc  | ccccggccac  | 28200 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|            |            |            |             |            |            |       |
|------------|------------|------------|-------------|------------|------------|-------|
| tacccggacg | agttcatccc | gaacttcgac | gccatcagcg  | agtcggtgga | cggctacgat | 28260 |
| tgaatgtccc | atggtggcgc | ggctgacct  | gctcggcttc  | gacacctgga | ccactgccgc | 28320 |
| cgcttccgct | gcttcgctcg | ggatctcgcc | gagtttgcct  | actttgagct | gcccgaggag | 28380 |
| caccctcagg | gcccggccca | cggagtgcgg | atcgctcgctg | aagggggtct | cgactccac  | 28440 |
| ctgcttcgga | tcttcagcca | gcgtccgata | ctggccgagc  | gcgagcaagg | acagaccctt | 28500 |
| ctgaccctgt | actgcatctg | caaccacccc | ggcctgcatg  | aaagtctttg | ttgtctgctg | 28560 |
| tgtactgagt | ataataaaa  | ctgagatcag | cgactactcc  | ggacttccgt | gtgttcctgc | 28620 |
| tatcaaccag | tccctgttct | tcaccgggaa | cgagaccgag  | ctccagctcc | agtgtaaagg | 28680 |
| ccacaagaag | tacctcacct | ggctgttcca | gggctctccg  | atcgccgttg | tcaaccactg | 28740 |
| cgacaacgac | ggagtcctgc | tgagcggccc | tgccaacctt  | actttttcca | cccgcagaag | 28800 |
| caagctccag | ctcttccaac | ccttcctccc | cgggacctat  | cagtgcgtct | cgggaccctg | 28860 |
| ccatcacacc | ttccacctga | tcccgaatac | cacagcgtcg  | ctccccgcta | ctaacaacca | 28920 |
| aactaccac  | caacgccacc | gtcgcgaccg | cggacatgta  | cagagctcga | gaagtactag | 28980 |
| gccacaatac | atgcccata  | tagactatga | ggccgagcca  | cagcgaccca | tgctccccgc | 29040 |
| tattagttac | ttcaatctaa | ccggcggaga | tgactgaccc  | actggccaac | aacaacgtca | 29100 |
| acgaccttct | cctggacatg | gacggccgcg | cctcggagca  | gcgactcgcc | caacttcgca | 29160 |
| ttcgccagca | gcaggagaga | gccgtcaagg | agctgcagga  | cggcatagcc | atccaccagt | 29220 |
| gcaagaaaag | catcttctgc | ctggtgaaac | aggccaagat  | ctcctacgag | gtcaccccca | 29280 |
| ccgaccatcg | cctctcctac | gagctcctgc | agcagcgcca  | gaagttcacc | tgcttggtcg | 29340 |
| gagtcaaccc | catcgtcatc | accagcagt  | cgggcgatac  | caaggggtgc | atccactgct | 29400 |
| cctgcgactc | ccccgactgc | gtccacactc | tgatcaagac  | cctctgcggc | ctccgcgacc | 29460 |
| tcctccccat | gaactaatca | cccccttata | cagtgaataa  | aatatcatat | tgatgatgat | 29520 |
| ttaaataaaa | aataatcatt | tgatttgaaa | taaagataca  | atcatattga | tgatttgagt | 29580 |
| tttaaaaaat | aaagaatcac | ttacttgaaa | tctgatacca  | ggtctctgtc | catgttttct | 29640 |
| gccaacacca | cctcactccc | ctcttcccag | ctctggtact  | gcagaccccg | gcgggctgca | 29700 |
| aacttcctcc | acacgctgaa | ggggatgtca | aattcctcct  | gtccctcaat | cttcatttta | 29760 |
| tcttctatca | gatgtccaaa | aagcgcgtcc | gggtggatga  | tgacttcgac | cccgtctacc | 29820 |
| cctacgatgc | agacaacgca | ccgaccgtgc | ccttcatcaa  | cccccccttc | gtctcttcag | 29880 |
| atggattcca | agagaagccc | ctgggggtgc | tgtccctgcg  | actggctgac | cccgtcacca | 29940 |
| ccaagaacgg | ggaaatcacc | ctcaagctgg | gagagggggg  | ggacctcgac | tcctcgggaa | 30000 |
| aactcatctc | caacacggcc | accaaggccg | ccgcccctct  | cagtttttcc | aacaacacca | 30060 |

## 368530-7006W01\_SequenceListing\_ST25.txt

|             |             |             |            |             |            |       |
|-------------|-------------|-------------|------------|-------------|------------|-------|
| tttcccttaa  | catggatacc  | cctctttata  | ccaaagatgg | aaaattatcc  | ttacaagttt | 30120 |
| ctccaccgtt  | aaacatatta  | aaatcaacca  | ttctgaacac | attagctgta  | gcttatggat | 30180 |
| caggtttagg  | actgagtgg   | ggcactgctc  | ttgcagtaca | gttggcctct  | ccactcactt | 30240 |
| ttgatgaaaa  | aggaaaatatt | aaaattaacc  | tagccagtgg | tccattaaca  | gttgatgcaa | 30300 |
| gtcgacttag  | tatcaactgc  | aaaagagggg  | tcactgtcac | tacctcagga  | gatgcaattg | 30360 |
| aaagcaacat  | aagctggcct  | aaaggataaa  | gatttgaagg | taatggcata  | gctgcaaaca | 30420 |
| ttggcagagg  | attggaattt  | ggaaccacta  | gtacagagac | tgatgtcaca  | gatgcatacc | 30480 |
| caattcaagt  | taaattgggt  | actggcctta  | cctttgacag | tacaggcgcc  | attgttgctt | 30540 |
| ggaacaaaga  | ggatgataaa  | cttacattat  | ggaccacagc | cgacccctcg  | ccaaattgca | 30600 |
| aaatatactc  | tgaaaaagat  | gccaaactca  | cactttgctt | gacaaaagtgt | ggaagtcaaa | 30660 |
| ttctgggtac  | tgtgactgta  | ttggcagtga  | ataatggaag | tctcaaccca  | atcacaacaa | 30720 |
| cagtaagcac  | tgcactcgtc  | tccctcaagt  | ttgatgcaag | tggagttttg  | ctaagcagct | 30780 |
| ccacattaga  | caaagaatat  | tggaacttca  | gaaagggaga | tgttacacct  | gctgagccct | 30840 |
| ataactaatgc | tataggtttt  | atgcctaaca  | taaaggccta | tcctaaaaac  | acatctgcag | 30900 |
| cttcaaaaag  | ccatattgtc  | agtcaagttt  | atctcaatgg | ggatgaggcc  | aaaccactga | 30960 |
| tgctgattat  | tacttttaat  | gaaactgagg  | atgcaacttg | cacctacagt  | atcacttttc | 31020 |
| aatggaaatg  | ggatagtact  | aagtacacag  | gtgaaacact | tgctaccagc  | tccttcacct | 31080 |
| tctcctacat  | cgccaagaa   | tgaacactgt  | atcccaccct | gcatgccaac  | ccttcccacc | 31140 |
| ccactctgtc  | tatggaaaaa  | actctgaagc  | acaaaataaa | ataaaagtta  | agtgttttat | 31200 |
| tgattcaaca  | gttttacagg  | attcgagcag  | ttatttttcc | tccaccctcc  | caggacatgg | 31260 |
| aatacaccac  | cctctcccc   | cgcacagcct  | tgaacatctg | aatgccattg  | gtgatggaca | 31320 |
| tgcttttgg   | ctccacgttc  | cacacagttt  | cagagcgagc | cagtctcggg  | tcggtcaggg | 31380 |
| agatgaaacc  | ctccgggcac  | tcccgcactc  | gcacctcaca | gctcaacagc  | tgaggattgt | 31440 |
| cctcgggtgg  | cgggatcacg  | gttatctgga  | agaagcagaa | gagcggcgg   | gggaatcata | 31500 |
| gtccgcgaac  | gggatcggcc  | ggtggtgtcg  | catcaggccc | cgcagcagtc  | gctgccgccg | 31560 |
| ccgctccgtc  | aagctgctgc  | tcaggggggtc | cgggtccagg | gactccctca  | gcatgatgcc | 31620 |
| cacggccctc  | agcatcagtc  | gtctggtgctg | gcgggcgcag | cagcgcagtc  | ggatctcgtc | 31680 |
| caggctcgtg  | cagtacgtgc  | aacacaggac  | caccaggttg | ttcaacagtc  | catagttcaa | 31740 |
| cacgctccag  | ccgaaaactca | tcgcgggaag  | gatgctaccc | acgtggccgt  | cgtaccagat | 31800 |
| cctcaggtaa  | atcaagtggc  | gctccctcca  | gaacacgctg | cccacgtaca  | tgatctcctt | 31860 |
| gggcatgtgg  | cggttcacca  | cctcccggta  | ccacatcacc | ctctggttga  | acatgcagcc | 31920 |
| ccggatgatc  | ctgcggaacc  | acagggccag  | caccgccccg | cccgccatgc  | agcgaagaga | 31980 |



368530-7006W01\_SequenceListing\_ST25.txt

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ccccgggtcc cggcaatggc aatggaggac ccaccgctcg tacccgtgga tcatctggga 32040
gctgaacaag tctatgttgg cacagcacag gcatatgctc atgcatctct tcagcactct 32100
cagctcctcg ggggtcaaaa ccatatccca gggcacgggg aactcttgca ggacagcgaa 32160
ccccgcagaa cagggcaatc ctcgcacata acttacattg tgcattggaca gggatatcgca 32220
atcaggcagc accgggtgat cctccaccag agaagcgcggtgtctcgttct cctcacagcg 32280
tggttaagggg gccggccgat acgggtgatg gcgggacgcg gctgatcgtg ttcgcgaccg 32340
tgtcatgatg cagttgcttt cggacatttt cgtacttgct gtagcagaac ctgggtccggg 32400
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catcatgcct gatagctctg atcacatcga ccaccgtgga atgggcccaga cccagccaga 32580
tgatgcaatt ttgttgggtt tcggtgacgg cgggggaggg aagaacagga agaaccatga 32640
ttaactttta atccaaacgg tctcggagca cttcaaaatg aaggctcgcg agatggcacc 32700
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gatgttc 32767

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<210> 9
<211> 11007
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 9

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His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Cys Gly Ser Gly Asp Arg  
20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Met Arg Arg Ser Arg Phe  
35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg  
50 55 60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
85 90 95

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Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
115 120 125

Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
130 135 140

Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
145 150 155 160

Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
165 170 175

Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
180 185 190

Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
195 200 205

Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
210 215 220

Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
225 230 235 240

Ser Met Pro Ser Thr Pro Pro Ile Asp Val Asn Asp Gly Lys Trp Pro  
245 250 255

Ala Trp His Tyr Ala Gln Tyr Met Thr Leu Trp Asp Phe Pro Thr Trp  
260 265 270

Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile Thr Met Val Met Arg Phe  
275 280 285

Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe Asp Ser Arg Gly Phe Pro  
290 295 300

Ser Leu His Pro Ile Asp Val Asn Gly Ser Leu Phe Trp His Gln Asn  
305 310 315 320

Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn Ser Ala Pro Leu Thr Gln  
325 330 335

Met Gly Gly Arg Arg Val Arg Trp Glu Val Tyr Ile Ser Arg Ala Arg  
340 345 350

368530-7006W01\_SequenceListing\_ST25.txt

Leu Val Asn Arg Gln Ile Thr Arg Ser Phe Ile Ala Val Val Tyr His  
 355 360 365  
 Ser Ile Ala Asn Ala Val Ser Ala Ser Asp Thr Thr Val Ser Asn Leu  
 370 375 380  
 Arg Leu Glu Phe Asp Ala Thr Met Arg Val Arg Gly Ile Pro Arg Asn  
 385 390 395 400  
 Trp Pro Gln Trp Trp Ile Trp Gly Ile Leu Gly Phe Trp Met Ile Ile  
 405 410 415  
 Ile Cys Arg Val Val Gly Asn Leu Asp Leu Trp Val Thr Val Tyr Tyr  
 420 425 430  
 Gly Val Pro Val Trp Lys Glu Ala Lys Thr Thr Leu Phe Cys Ala Ser  
 435 440 445  
 Asp Ala Lys Ala Tyr Asp Lys Glu Val His Asn Val Trp Ala Thr His  
 450 455 460  
 Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu Glu Asn  
 465 470 475 480  
 Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met Val Asp Gln Met  
 485 490 495  
 His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val  
 500 505 510  
 Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Lys Asn Val Asn Ile  
 515 520 525  
 Ser Ala Asn Ala Asn Ala Thr Ala Thr Leu Asn Ser Ser Met Asn Gly  
 530 535 540  
 Glu Ile Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Leu Arg Asp Lys  
 545 550 555 560  
 Lys Gln Lys Val Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu  
 565 570 575  
 Asn Gly Gly Glu His Asn Glu Thr Gly Glu Tyr Ile Leu Ile Asn Cys  
 580 585 590  
 Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro

595

600

605

Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys  
 610 615 620

Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr  
 625 630 635 640

Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu  
 645 650 655

Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Val Arg Ser Glu Asn  
 660 665 670

Leu Thr Asn Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser Val  
 675 680 685

Glu Ile Lys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg  
 690 695 700

Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp  
 705 710 715 720

Ile Arg Glu Ala His Cys Asn Ile Ser Arg Glu Thr Trp Asn Ser Thr  
 725 730 735

Leu Ile Gln Val Lys Glu Lys Leu Arg Glu His Tyr Asn Lys Thr Ile  
 740 745 750

Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Val Thr Thr His Ser  
 755 760 765

Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Thr Lys Leu Phe  
 770 775 780

Asn Glu Thr Lys Leu Phe Asn Glu Ser Glu Tyr Val Asp Asn Lys Thr  
 785 790 795 800

Ile Ile Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu  
 805 810 815

Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys  
 820 825 830

Lys Ser Asn Ile Thr Gly Leu Leu Leu Thr Trp Asp Gly Gly Glu Asn  
 835 840 845

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Ser Thr Glu Gly Val Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn  
 850 855 860

Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu  
 865 870 875 880

Gly Val Ala Pro Thr Lys Ser Lys Leu Thr Val Gln Ala Arg Gln Leu  
 885 890 895

Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu  
 900 905 910

Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu  
 915 920 925

Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu  
 930 935 940

Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys Ala Thr Ala Val  
 945 950 955 960

Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Leu Gly Asp Ile Trp Asp  
 965 970 975

Asn Met Thr Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asn  
 980 985 990

Thr Ile Phe Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn  
 995 1000 1005

Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn  
 1010 1015 1020

Trp Phe Asp Ile Thr Asn Trp Leu Trp Gly Thr Ser Arg Val Asp  
 1025 1030 1035

Pro Gly Gly Gln Thr Ala Asp Gln Pro Arg Leu Cys Leu Leu Val  
 1040 1045 1050

Ala Ser His Leu Leu Phe Ala Pro Pro Pro Cys Leu Pro Pro Trp  
 1055 1060 1065

Lys Val Pro Leu Pro Leu Ser Phe Pro Asn Lys Met Arg Lys Leu  
 1070 1075 1080

His Arg Ile Val Val Gly Val Ile Leu Phe Trp Gly Val Gly Trp  
 1085 1090 1095

## 368530-7006W01\_SequenceListing\_ST25.txt

Gly Arg Thr Ala Arg Gly Arg Ile Gly Lys Thr Ile Ala Gly Met  
 1100 1105 1110  
 Leu Gly Met Arg Trp Ala Leu Trp Leu Leu Arg Arg Lys Glu Pro  
 1115 1120 1125  
 Ala Asp Leu Gln Ile Ile His Leu Cys Arg Val Arg Arg Lys Arg  
 1130 1135 1140  
 Asn Gly Ile Met Gly Ile Met Gly Leu His Ile Gly Gln Ile Ser  
 1145 1150 1155  
 Thr Tyr Ala Gly His Arg Ala Cys Gly Leu Ala Pro Pro Gln Asp  
 1160 1165 1170  
 Met Ala Arg Val Arg Ala Gln Arg His Asp Pro Leu Gln Cys Ala  
 1175 1180 1185  
 Pro Gly Leu Pro Pro Arg His Val His Ala Leu Pro Val Gln His  
 1190 1195 1200  
 Ala Ile Cys Glu Gly Ala Ala Gly Ala Arg Cys His Val Gln Ser  
 1205 1210 1215  
 Glu Pro Asp Gly Gly Val His Glu Cys Gly Ala Val Glu Asn Ser  
 1220 1225 1230  
 Glu Ile Ile Gln Asp Gln Val Pro Gly Leu Arg Met Arg Arg Gln  
 1235 1240 1245  
 Ala Arg Gln Ala Ser Ala Arg Val Cys Gly Gly Asp Gly Gly Pro  
 1250 1255 1260  
 Ala Thr Arg Ser Phe Gly Val Val Leu Gln Arg Asp Gly Val Arg  
 1265 1270 1275  
 Leu Gln Arg Gly Arg Ile Leu Glu Val Val Phe Gly Ala Gly Cys  
 1280 1285 1290  
 Glu Pro Ala Gly Ala Glu Leu Lys Ser Val Val Phe Cys Val Leu  
 1295 1300 1305  
 Gln Gln His Glu Arg Lys Arg Leu Leu Gly Arg Gly Ile Gln Pro  
 1310 1315 1320  
 Leu Ser Asp Gly Ala Ser Pro Leu Leu Gly Gly Ser Ala Ser Glu  
 1325 1330 1335

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Cys Asp Gly Ile His Gly Gly Arg Pro Ala Arg Ala Ala Arg Glu  
 1340 1345 1350  
 Leu Phe Asn Pro Asp Leu Arg Asp Pro Glu Leu Leu Val Arg Gly  
 1355 1360 1365  
 Arg Ser Cys Arg Arg Ser Cys Cys Phe Arg Arg Gln Arg Arg Ala  
 1370 1375 1380  
 Arg Asn Gly Pro Gly Arg Arg Leu Leu Gln Leu Ser Gly Gly Gln  
 1385 1390 1395  
 Leu Glu Phe His Gln Ser Arg Gln Pro Glu Arg Gly Glu Ala Ala  
 1400 1405 1410  
 Ala Ala Asp Gly Pro Ala Arg Gly Pro Asp Pro Ala Pro Gly Arg  
 1415 1420 1425  
 Ala Asp Pro Ala Gly Gly Ser Ala Ala Gly Gly Asp Ala Gly Arg  
 1430 1435 1440  
 Gly Cys His Gly Glu Asn Gln Ile Lys Asn Glu Ser Ile Asn Lys  
 1445 1450 1455  
 Arg Arg Arg Leu Leu Ile Leu Thr Gln Ser Leu Glu Ser Leu Phe  
 1460 1465 1470  
 Asp Phe Ser Arg Ala Val Gly Pro Gly Pro Pro Val Ser Ile Ile  
 1475 1480 1485  
 Glu His Pro Val Asp Leu Phe Gln Asp Pro Val Glu Val Gly Leu  
 1490 1495 1500  
 Asp Val Glu Val His Gly His Glu Pro Val Pro Gly Val Glu Val  
 1505 1510 1515  
 Ala Pro Leu Gln Gly Leu Val Leu Gly Asp Gly Val Val Asn His  
 1520 1525 1530  
 Pro Val Ile Ala Gly Ala Gln Gly Val Val Leu His Asp Val Leu  
 1535 1540 1545  
 Glu Glu Glu Thr Asp Gly His Gly Gln Pro Leu Gly Val Gly Val  
 1550 1555 1560  
 Asp Glu Pro Val Glu Leu Gly Gly Met His Ala Gly Gly Asp Glu

1565

1570

1575

Met His Leu Gly Leu Asp Leu Glu Ile Gly Asp Val Pro Ala Gln  
 1580 1585 1590

Ile Pro Pro Gly Val His Val Val Gln Asp His Gln His Gly Val  
 1595 1600 1605

Ser Gly Ala Leu Gly Glu Phe Val Met Gln Leu Gly Arg Glu Gly  
 1610 1615 1620

Val Lys Glu Phe Gly Asp Ala Leu Val Thr Ala Gln Val Phe His  
 1625 1630 1635

Ala Leu Ile His Asp Asp Gly Asp Gly Pro Val Gly Gly Gly Leu  
 1640 1645 1650

Gly Lys Asp Val Ser Gly Val Gly His Ile Val Val Val Val Leu  
 1655 1660 1665

Gly Glu Leu Val Ile Gly His Phe Asn Glu Phe Gly Ala Glu Gly  
 1670 1675 1680

Ala Arg Leu Gly Asp Glu Gly Ala Leu Asp Pro Gly Gly Val Val  
 1685 1690 1695

Ala Leu Ala Asp Leu His Leu Pro Gly Leu Glu Leu Gly Gly Gly  
 1700 1705 1710

Asp His Val His Leu Arg Gly Asp Glu Lys Asn Gly Phe Arg Gly  
 1715 1720 1725

Gly Gly Asp Glu Leu Gly Arg Lys Gln Val Pro Glu Gln Leu Gly  
 1730 1735 1740

Leu Ala Ala Thr Gly Gly Ala Val Asp Asp Pro Asp Asp Arg Leu  
 1745 1750 1755

Gln Val Val Val Glu Gly Glu Thr Ala Ala Val Leu Ala Glu Glu  
 1760 1765 1770

Gly Gly His Leu Val His His Leu Ala His Met His Val Leu Ala  
 1775 1780 1785

His Glu Phe Arg Gln Glu Ala Leu Ala Pro Gln Arg Glu Glu Leu  
 1790 1795 1800



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Leu Gln Arg Gly Glu Val Phe Gln Arg Leu Glu Ser Val Gly His  
 1805 1810 1815  
  
 Gly His Phe Gly Glu Gly Leu Leu Gln Glu Phe Gln Thr Val Pro  
 1820 1825 1830  
  
 Glu Leu Gly Asp Val Leu Gly Ile Ser Ile Gln Gln Thr Ser Ser  
 1835 1840 1845  
  
 Phe Arg Gly Leu Gly Arg Leu Arg Glu Gly Thr Arg Arg Trp Ala  
 1850 1855 1860  
  
 Ser Ser Glu Ala Arg Val Arg Ser Phe Gln Gly Arg Arg Val Arg  
 1865 1870 1875  
  
 Val Ser Val Val Ser Val Thr Val Lys Gly Cys Ala Pro Gly Trp  
 1880 1885 1890  
  
 Ala Leu Ala Arg Val Arg Phe Arg Leu Ile Arg Leu Val Glu Asn  
 1895 1900 1905  
  
 Arg Ser Arg Ser Ala Pro Cys Ala Ser Ala Arg Gln Leu Ser Met  
 1910 1915 1920  
  
 Ser Ser Leu Ser Ala Ser Ala Ala Trp Pro Leu Ala Arg Ser Leu  
 1925 1930 1935  
  
 Pro Leu Glu Val Cys Pro Gln Thr Gly Gln Arg Arg Asp Leu Arg  
 1940 1945 1950  
  
 Ala Ser Leu Gly Ala Arg Lys Thr Asp Ser Gly Ala Ala Ser Ala  
 1955 1960 1965  
  
 Pro Gln Leu Ala Gln Thr Val Ser His Ser Thr Ser Gln Val Arg  
 1970 1975 1980  
  
 Ser Gly Arg Leu Gly Ser Lys Thr Arg Phe Pro Pro Cys Phe Leu  
 1985 1990 1995  
  
 Met Arg Phe Leu Pro Leu Val Ser Met Ser Ser Cys Pro Arg Trp  
 2000 2005 2010  
  
 Val Thr Lys Arg Leu Ser Val Ser Pro Thr Asp Phe Met Gly Arg  
 2015 2020 2025  
  
 Ser Ser Ser Gly Val Pro Arg Ser Ser Ser Arg Asn Pro Ala His  
 2030 2035 2040

## 368530-7006W01\_SequenceListing\_ST25.txt

Ser Glu Thr Lys Ala Arg Val Gln Ala Ser Thr Lys Glu Ala Thr  
 2045 2050 2055  
 Trp Glu Gly Arg Ser Leu Ser Thr Ser Gly Ser Thr Phe Ser Arg  
 2060 2065 2070  
 Val Cys Lys His Met Ser Pro Ser Ser Thr Ser Arg Lys Val Ile  
 2075 2080 2085  
 Gly Leu Val Ala Thr Pro Gly Val Pro Ala Gly Gly Val Lys Gly  
 2090 2095 2100  
 Ala Gly Pro Cys Ser Ser Ser Leu Ser Ser Gly Ser Leu Ser Arg  
 2105 2110 2115  
 Ser Ala Ser Cys Trp Gly Arg Tyr Ser Leu Ser Lys Ala Gly Met  
 2120 2125 2130  
 Thr Ser Ala Leu Arg Leu Ser Val Ser Arg Asn Glu Glu Asp Leu  
 2135 2140 2145  
 Ile Leu Thr Val Pro Leu Glu Thr Pro Phe Met Ser Pro Ser Ser  
 2150 2155 2160  
 Ile Trp Ser Glu Lys Thr Ile Phe Leu Leu Ser Ser Leu Val Ala  
 2165 2170 2175  
 Lys Glu Pro Arg Ala Leu Glu Ser Ser Leu Ala Met Glu Arg Met  
 2180 2185 2190  
 Val Trp Phe Phe Ser Leu Ser Ala Arg Ser Leu Ala Ala Met Leu  
 2195 2200 2205  
 Ser Cys Thr Tyr Ser Arg Ala Thr His Phe His Ser Gly Lys Thr  
 2210 2215 2220  
 Val Val Ser Ser Ser Gly Thr Ile Leu Thr Arg Gln Pro Arg Leu  
 2225 2230 2235  
 Cys Arg Val Met Arg Ser Thr Leu Val Ala Thr Ser Pro Arg Arg  
 2240 2245 2250  
 Gly Ser Leu Val Gln Gln Arg Arg Pro Pro Leu Arg Glu Gln Lys  
 2255 2260 2265  
 Gly Gly Ser Gly Ser Ser Met Ser Ser Ser Gly Gly Ser Ala Ser  
 2270 2275 2280

368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Val  | Lys | Met | Pro | Gly | Arg  | Ser | Ser | Gly | Ser | Lys  | Leu | Met | Gln |
|     | 2285 |     |     |     |     | 2290 |     |     |     |     | 2295 |     |     |     |
| Val | Pro  | Arg | Leu | Ser | Ser | Ala  | Ala | Cys | Gln | Ser | Arg  | Thr | Ala | Ser |
|     | 2300 |     |     |     |     | 2305 |     |     |     |     | 2310 |     |     |     |
| Ala | Arg  | Ser | Gly | Leu | Arg | Gly  | Val | Pro | Gln | Gly | Met  | Gly | Cys | Val |
|     | 2315 |     |     |     |     | 2320 |     |     |     |     | 2325 |     |     |     |
| Ser | Ala  | Glu | Ala | Tyr | Met | Pro  | Gln | Met | Ser | Thr | Arg  | Gly | Ser | Ser |
|     | 2330 |     |     |     |     | 2335 |     |     |     |     | 2340 |     |     |     |
| Arg | Thr  | Pro | Met | Val | Gly | Gln  | Arg | Pro | Pro | Arg | Met  | Leu | Ala | Arg |
|     | 2345 |     |     |     |     | 2350 |     |     |     |     | 2355 |     |     |     |
| Thr | Ser  | Tyr | Ser | Ser | Cys | Glu  | Gly | Ala | Arg | Ser | Pro  | Val | Pro | Arg |
|     | 2360 |     |     |     |     | 2365 |     |     |     |     | 2370 |     |     |     |
| Leu | Glu  | Arg | Cys | Gly | Phe | Ser  | Ala | Arg | Thr | Ile | Trp  | Arg | Lys | Met |
|     | 2375 |     |     |     |     | 2380 |     |     |     |     | 2385 |     |     |     |
| Ala | Trp  | Glu | Leu | Glu | Glu | Met  | Val | Gly | Leu | Trp | Lys  | Met | Leu | Lys |
|     | 2390 |     |     |     |     | 2395 |     |     |     |     | 2400 |     |     |     |
| Trp | Ala  | Trp | Gly | Arg | Pro | Thr  | Glu | Ser | Leu | Met | Lys  | Trp | Ala | Glu |
|     | 2405 |     |     |     |     | 2410 |     |     |     |     | 2415 |     |     |     |
| Ser | Cys  | Ser | Leu | Ala | Thr | Ser  | Ser | Ala | Val | Thr | Arg  | Thr | Ser | Arg |
|     | 2420 |     |     |     |     | 2425 |     |     |     |     | 2430 |     |     |     |
| Ala | Gln  | Ser | Arg | Val | Ser | Trp  | Met | Met | Ser | Tyr | Leu  | Ser | Trp | Pro |
|     | 2435 |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |
| Phe | Cys  | Phe | His | Ser | Ser | Arg  | Leu | Arg | Arg | Asn | Ser  | Ser | Arg | Ser |
|     | 2450 |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |
| Phe | Gln  | Tyr | Ser | Ser | Arg | Gly  | Asn | Pro | Ser | Ser | Ala  | Arg | Glu | Pro |
|     | 2465 |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |
| Thr | Met  | Asn | Trp | Leu | Thr | Ala  | Leu | Ala | Gln | Gln | Pro  | Phe | Ser | Thr |
|     | 2480 |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Gly | Arg  | Ala | Ala | Cys | Ala | Ala  | Leu | Arg | Arg | Glu | Val  | Trp | Val | Arg |
|     | 2495 |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Ala | Lys  | Val | Ser | Arg | Thr | Met  | Thr | Leu | Arg | Asn | Trp  | Cys | Leu | Lys |

2510

2515

2520

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser | Arg  | Ser | Ser | Gln | Pro | Pro  | Cys | Ser | Gln | Ser | Trp  | Lys | Ser | Val |
|     | 2525 |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Arg | Phe  | Leu | Ala | Gly | Leu | Gly  | Lys | Ala | Lys | Val | Thr  | Ser | Leu | Lys |
|     | 2540 |     |     |     |     | 2545 |     |     |     |     | 2550 |     |     |     |
| Arg | Ile  | Leu | Pro | Ala | Arg | Gly  | Met | Lys | Leu | Arg | Val  | Met | Arg | Lys |
|     | 2555 |     |     |     |     | 2560 |     |     |     |     | 2565 |     |     |     |
| Gly | Trp  | Gly | Thr | Ser | Ala | Arg  | Leu | Leu | Met | Thr | Trp  | Ala | Ala | Arg |
|     | 2570 |     |     |     |     | 2575 |     |     |     |     | 2580 |     |     |     |
| Thr | Ile  | Ser | Ser | Lys | Pro | Leu  | Met | Leu | Cys | Pro | Thr  | Met | Ser | Ser |
|     | 2585 |     |     |     |     | 2590 |     |     |     |     | 2595 |     |     |     |
| Thr | Asn  | Arg | Gly | Arg | Pro | Leu  | Thr | Trp | Gly | Ser | Phe  | Leu | Ser | Ser |
|     | 2600 |     |     |     |     | 2605 |     |     |     |     | 2610 |     |     |     |
| Ser | Val  | Ser | Ser | Ala | Gly | Ser  | Leu | Ser | Pro | Cys | Cys  | Ser | Arg | Ala |
|     | 2615 |     |     |     |     | 2620 |     |     |     |     | 2625 |     |     |     |
| Gln | Ser  | Ala | Thr | Trp | Gly | Leu  | Ala | Leu | Arg | Lys | Glu  | Val | Gln | Arg |
|     | 2630 |     |     |     |     | 2635 |     |     |     |     | 2640 |     |     |     |
| Ser | Thr  | Ala | Arg | Ala | Val | Cys  | Lys | Arg | Ser | Arg | Tyr  | Arg | Asn | Cys |
|     | 2645 |     |     |     |     | 2650 |     |     |     |     | 2655 |     |     |     |
| Trp | Pro  | Thr | Ala | Ile | Phe | Ser  | Gly | Val | Thr | Gln | Lys  | Val | Arg | Gly |
|     | 2660 |     |     |     |     | 2665 |     |     |     |     | 2670 |     |     |     |
| Ser | Pro  | Cys | Gln | Arg | Ser | His  | Leu | Ser | Trp | Arg | Ala  | Arg | Ser | Trp |
|     | 2675 |     |     |     |     | 2680 |     |     |     |     | 2685 |     |     |     |
| Ala | Ser  | Ser | Thr | Ser | Gly | Gly  | Ser | Pro | Glu | Ser | Phe  | Met | Thr | Ser |
|     | 2690 |     |     |     |     | 2695 |     |     |     |     | 2700 |     |     |     |
| Met | Lys  | Gly | Thr | Ser | Cys | Leu  | Pro | Lys | Asp | Pro | Ile  | Gln | Val | Val |
|     | 2705 |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |
| Ser | Thr  | Ser | Val | Arg | Lys | Ser  | Leu | Ser | Val | Arg | Gly  | Cys | Glu | Pro |
|     | 2720 |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |
| Met | Gly  | Lys | Asn | Trp | Ile | Ser  | Cys | His | Gln | Leu | Glu  | Glu | Trp | Leu |
|     | 2735 |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |

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Leu Met Trp Lys Lys Cys Arg Arg Arg Ala Glu His Ser Cys Leu  
 2750 2755 2760  
 Cys Leu Tyr Lys Arg Pro Gln Cys Ser Gln Arg Cys Thr Gly Cys  
 2765 2770 2775  
 Thr Cys Cys Thr Ser Cys Thr Trp Val Pro Leu Ala Arg Asn Phe  
 2780 2785 2790  
 Ser Gly Gln Trp Ser Ala Gly Gly Cys Ile Ser Cys Cys Thr Thr  
 2795 2800 2805  
 Ser Trp Pro Ser Ala Trp Pro Ser Ser Ala Ser Met Val Val Met  
 2810 2815 2820  
 Leu Thr Ser Pro Arg Gly Arg Gln Val Gln Thr Ser Ala Arg Thr  
 2825 2830 2835  
 Gly Arg Arg Ala Arg Thr Arg Ala Arg Arg Pro Glu Leu Ser Arg  
 2840 2845 2850  
 Val Leu Arg Arg Cys Gly Val Arg Ser Val Gly Ser Gly Gly Ala  
 2855 2860 2865  
 Arg Leu Thr Cys Arg Ser Phe Ser Arg Ala Arg Gly Arg Ser Arg  
 2870 2875 2880  
 Trp Tyr Leu Ile Ser Thr Ala Pro Leu Val Ala Thr Ser Thr Ala  
 2885 2890 2895  
 Cys Arg Val Pro Cys Pro Trp Gly Ala Thr Thr Val Pro Arg Phe  
 2900 2905 2910  
 Phe Leu Gly Ala Ala Ser Met Ser Val Arg Ser Gly Gly Glu Asp  
 2915 2920 2925  
 Ala Arg Arg Ala Ala Gly Ala Ala Arg Gly Pro Glu Ala Gly Ala  
 2930 2935 2940  
 Ala Gly Ala Arg Arg Arg Arg Ala Arg Ala Gly Ser Gly Thr Ala  
 2945 2950 2955  
 Pro Gly Glu Asp Trp Arg Glu Arg Arg Arg Asp Gly Arg Pro Gly  
 2960 2965 2970  
 Ser Asp Ala Ser Gly Arg Pro Arg Asp Pro Val Thr Lys Arg Val  
 2975 2980 2985

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Arg Gln Asn Gln Ser Arg Tyr Arg Arg Arg Pro Ala Ala Gly Ser  
2990 2995 3000

Leu Ala Arg Arg Pro Ser Cys Pro Gly Arg Arg Ser Arg Ser Thr  
3005 3010 3015

Ala Arg Ser Pro Pro Pro Glu Gly Leu Arg Gly Arg Arg Ala Arg  
3020 3025 3030

Arg Trp Pro Arg Gly Arg Trp Arg Cys Gly Pro Ala Ala Arg Arg  
3035 3040 3045

Arg Ser Cys Arg Pro Arg Ser Arg Arg Gly Cys Arg Pro Arg Leu  
3050 3055 3060

Arg Arg Gly Arg Ala Arg Ala Pro Pro Gly Arg Gly Ala Arg Arg  
3065 3070 3075

Gly Ala Arg Pro Arg Ser Cys Arg Gly Ala Gly Arg Gly Ser Ala  
3080 3085 3090

Trp Trp Arg Cys Ala Arg Arg Arg Ser Thr Ser Ser Gly Gly Ala  
3095 3100 3105

Ala Ser Arg Arg Arg Pro Gly Leu Pro Ser Val Pro Trp Pro Arg  
3110 3115 3120

Arg Ser Pro Arg Arg Ser Lys Thr Gly Ser Cys Ala Pro Arg Arg  
3125 3130 3135

Ser Thr Pro Pro Pro Glu Asp Gly Ala Arg Arg Trp Trp Arg Ala  
3140 3145 3150

Pro Arg Ala Arg Arg Pro Arg Gly Ala Pro Leu Pro Ser Pro Pro  
3155 3160 3165

Leu Pro Pro Pro Leu Thr Ser Leu Leu Leu Pro Pro Gln Glu Ala  
3170 3175 3180

Val Ala Gly Glu Gly Pro Cys Val Ala Gly Gly Ala Arg Ala Asp  
3185 3190 3195

Gly Arg Ser Ala Arg Trp Ser Pro Arg Ala Gly Asp Ala Trp Ser  
3200 3205 3210

Arg Arg Arg Ala Arg Pro Arg Gly Ala Ala Ala Arg Arg Arg Arg  
3215 3220 3225

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Ala Ser Pro Gly Gly Arg Arg Gly Gly Leu Arg Trp Ala Gly Arg  
3230 3235 3240

Gly Arg Arg Cys Ile Leu Ser Ile Asp Pro Gly Leu Arg Ala Arg  
3245 3250 3255

Thr Ala Ser Arg Asp Pro Arg Asp Pro Lys Thr Ala Glu Arg Arg  
3260 3265 3270

Leu Arg Ala Ser Arg Ser Arg Lys Val Gly Ala Arg Phe Leu Val  
3275 3280 3285

Leu Arg Val Phe Gly Arg Glu Ala Gly Gly Arg Cys Cys Trp Ser  
3290 3295 3300

Ser Arg Arg Ser Asp Gly Gly Trp Trp Arg Gly Ala Pro Gly Pro  
3305 3310 3315

Trp Ala Arg Leu Ala Gly Cys Ala Asp Gly Arg Pro Cys Pro Arg  
3320 3325 3330

Arg Gly Pro Asp Thr Trp Arg Gly Pro Cys Ser Ser Pro Ala Ala  
3335 3340 3345

Ala Pro Arg Ala Pro Pro Pro Arg Pro Arg Gly Arg Ala Cys Ala  
3350 3355 3360

Ala Arg Thr Arg Ala Ala Ala Gly Arg Ala Pro Gly Arg Arg Arg  
3365 3370 3375

Arg Ala Arg Gly Trp Pro Ala Gly Ser Gly Gly Trp Ser Gly Ser  
3380 3385 3390

Arg Arg Ser Arg Arg Ser Gly Gly Arg Leu Arg Cys Trp Cys Arg  
3395 3400 3405

Ser Ser Trp Pro Arg Thr Ser Arg Ser Gly Gly Arg Val Ala Arg  
3410 3415 3420

Ala Arg Gly Thr Gly Ala Ser Arg Arg Ala Cys Arg Arg Cys Ser  
3425 3430 3435

Arg Cys Arg Arg Ala Arg Gly Thr Gly Ile Arg Arg Gly Ser Ala  
3440 3445 3450

Ala Ala Ala Gly Gly Arg Ala Ala Ile Ala Arg Trp Arg Gly Arg

3455

3460

3465

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Ala | Arg | Gly | Pro | Arg | Ala  | Gly | Gly | Gly | Ser | Arg  | Arg | Cys | Thr |
| 3470 |     |     |     |     |     | 3475 |     |     |     |     | 3480 |     |     |     |
| Trp  | Thr | Ser | Arg | Cys | Arg | Arg  | Arg | Trp | Trp | Arg | Arg  | Ala | Gly | Thr |
| 3485 |     |     |     |     |     | 3490 |     |     |     |     | 3495 |     |     |     |
| Arg  | Gly | Arg | Gly | Ser | Arg | Cys  | Cys | Ala | Ala | Ala | Gly  | Ser | Ser | Ser |
| 3500 |     |     |     |     |     | 3505 |     |     |     |     | 3510 |     |     |     |
| Trp  | Trp | Pro | Arg | Ser | Gly | Pro  | Gly | Ala | Arg | Ser | Arg  | Gly | Cys | Ser |
| 3515 |     |     |     |     |     | 3520 |     |     |     |     | 3525 |     |     |     |
| Arg  | His | Thr | Gly | Lys | Asn | Glu  | Ser | Gly | Gln | Arg | Leu  | Asp | Ser | Val |
| 3530 |     |     |     |     |     | 3535 |     |     |     |     | 3540 |     |     |     |
| Ala  | Trp | Arg | Leu | Ser | Glu | Arg  | Val | Gly | Leu | Arg | Val  | Tyr | Pro | Gly |
| 3545 |     |     |     |     |     | 3550 |     |     |     |     | 3555 |     |     |     |
| Ser  | Asn | Leu | Glu | Ser | Gly | Trp  | Ser | Arg | Ser | Arg | Gly  | Thr | Gly | Thr |
| 3560 |     |     |     |     |     | 3565 |     |     |     |     | 3570 |     |     |     |
| Pro  | Val | Ser | Thr | Gln | Ala | Cys  | Arg | Asn | Leu | Gln | Asp  | Thr | Glu | Ala |
| 3575 |     |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
| Gly  | Arg | Phe | Leu | Ala | Leu | Val  | Ala | Gly | His | Glu | Lys  | Leu | Val | Ser |
| 3590 |     |     |     |     |     | 3595 |     |     |     |     | 3600 |     |     |     |
| Ala  | Glu | Ser | Gly | Arg | Pro | Arg  | Trp | Leu | Ala | Ala | Val  | Val | Trp | Arg |
| 3605 |     |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |
| Lys  | Asn | Arg | Gln | Gly | Cys | Val  | Ala | Val | Cys | Pro | Gly  | Ser | Ser | Leu |
| 3620 |     |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
| Ser  | Ala | Arg | Arg | Arg | Pro | Asp  | Ser | Ala | Ala | Asn | Val  | Gly | Val | Ala |
| 3635 |     |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
| Ala  | Pro | Ser | Phe | Pro | Arg | Pro  | Leu | Ser | Gln | Pro | Thr  | Ser | Pro | Val |
| 3650 |     |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
| Thr  | Glu | Arg | Ala | Pro | Leu | Phe  | Phe | Ser | Cys | Val | Phe  | Ala | Arg | Cys |
| 3665 |     |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
| Ile  | Pro | Tyr | Cys | Gly | Arg | Cys  | Ala | Pro | Thr | Leu | His  | His | Asn | Arg |
| 3680 |     |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |



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Pro Tyr Arg Ser Ser Ser Asn Ser Arg Arg Phe Cys Pro Arg Pro  
 3695 3700 3705  
  
 Ser Ser Ser Gln Pro Leu Pro Arg Arg Pro Pro Ala Glu Pro Ala  
 3710 3715 3720  
  
 Phe Ser Met Thr Trp Pro Trp Lys Arg Ala Arg Gly Trp Arg Gly  
 3725 3730 3735  
  
 Trp Gly Arg Arg Arg Arg Ser Gly Thr Arg Ala Cys Arg Lys Gly  
 3740 3745 3750  
  
 Thr Leu Ala Arg Pro Thr Cys Pro Ser Arg Thr Cys Ser Glu Thr  
 3755 3760 3765  
  
 Gly Ala Ala Arg Ser Pro Arg Arg Cys Ala Pro Pro Ala Ser Thr  
 3770 3775 3780  
  
 Arg Gly Gly Ser Cys Gly Ala Ala Trp Thr Glu Ser Gly Cys Gly  
 3785 3790 3795  
  
 Thr Arg Ile Ser Arg Arg Thr Ser Arg Gly Ser Ala Pro Arg Ala  
 3800 3805 3810  
  
 Arg Thr Trp Pro Arg Pro Thr Trp Ser Arg Arg Thr Ser Arg Pro  
 3815 3820 3825  
  
 Arg Arg Arg Ala Thr Ser Lys Asn Pro Ser Thr Thr Thr Cys Ala  
 3830 3835 3840  
  
 Arg Ser Arg Ala Arg Arg Pro Trp Ala Cys Thr Cys Gly Thr Cys  
 3845 3850 3855  
  
 Trp Arg Pro Ser Cys Arg Thr Pro Arg Ala Ser Arg Arg Arg Ser  
 3860 3865 3870  
  
 Cys Phe Trp Trp Cys Ser Thr Val Gly Thr Thr Arg Arg Ser Gly  
 3875 3880 3885  
  
 Arg Arg Cys Ile Ser Pro Ser Pro Arg Ala Ala Gly Ser Trp Thr  
 3890 3895 3900  
  
 Trp Thr Phe Cys Arg Ala Ser Trp Cys Arg Ser Ala Gly Cys Arg  
 3905 3910 3915  
  
 Cys Pro Arg Ser Trp Arg Pro Ser Thr Ser Arg Cys Val Trp Ala  
 3920 3925 3930

368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser | Thr  | Thr | Leu | Gly | Arg | Ser  | Thr | Arg | Pro | Arg | Thr  | Cys | Pro | Thr |
|     | 3935 |     |     |     |     | 3940 |     |     |     |     | 3945 |     |     |     |
| Arg | Arg  | Arg | Ser | Thr | Gly | Phe  | Thr | Cys | Ala | Pro | Lys  | Cys | Pro | Ala |
|     | 3950 |     |     |     |     | 3955 |     |     |     |     | 3960 |     |     |     |
| Thr | Ile  | Trp | Gly | Cys | Thr | Ala  | Thr | Thr | Gly | Cys | Thr  | Ala | Arg | Ala |
|     | 3965 |     |     |     |     | 3970 |     |     |     |     | 3975 |     |     |     |
| Pro | Ala  | Ala | Gly | Ala | Ser | Ala  | Thr | Arg | Ser | Cys | Thr  | Ala | Cys | Ser |
|     | 3980 |     |     |     |     | 3985 |     |     |     |     | 3990 |     |     |     |
| Gly | Pro  | Pro | Gly | Pro | Gly | Pro  | Arg | Gly | Arg | Ala | Thr  | Leu | Thr | Trp |
|     | 3995 |     |     |     |     | 4000 |     |     |     |     | 4005 |     |     |     |
| Ala | Arg  | Thr | Cys | Ala | Gly | Ser  | Pro | Ala | Ala | Gly | Pro  | Trp | Lys | Leu |
|     | 4010 |     |     |     |     | 4015 |     |     |     |     | 4020 |     |     |     |
| Pro | Ala  | Val | Pro | Pro | Thr | Trp  | Arg | Arg | Trp | Thr | Met  | Arg | Arg | Arg |
|     | 4025 |     |     |     |     | 4030 |     |     |     |     | 4035 |     |     |     |
| Arg | Ala  | Ser | Thr | Trp | Lys | Thr  | Asp | Gly | Ala | Thr | Val  | Phe | Leu | Leu |
|     | 4040 |     |     |     |     | 4045 |     |     |     |     | 4050 |     |     |     |
| Asp | Ala  | Ala | Thr | Ala | Thr | Ala  | Ala | Ala | Ser | Ser | Arg  | Asp | Ala | Gly |
|     | 4055 |     |     |     |     | 4060 |     |     |     |     | 4065 |     |     |     |
| Gly | Ala  | Ala | Glu | Pro | Ala | Val  | Arg | His | Leu | Leu | Gly  | Arg | Leu | Asp |
|     | 4070 |     |     |     |     | 4075 |     |     |     |     | 4080 |     |     |     |
| Pro | Gly  | His | Ala | Thr | His | His  | Gly | Ala | Asp | Asp | Pro  | Gln | Ser | Arg |
|     | 4085 |     |     |     |     | 4090 |     |     |     |     | 4095 |     |     |     |
| Ser | Leu  | Thr | Ala | Ala | Ser | Gly  | Gln | Pro | Ala | Leu | Gly  | His | Pro | Gly |
|     | 4100 |     |     |     |     | 4105 |     |     |     |     | 4110 |     |     |     |
| Gly | Arg  | Gly | Ala | Leu | Ala | Leu  | Glu | Pro | His | Ala | Arg  | Glu | Gly | Ala |
|     | 4115 |     |     |     |     | 4120 |     |     |     |     | 4125 |     |     |     |
| Gly | His  | Arg | Glu | Arg | Ala | Gly  | Gly | Glu | Gln | Gly | His  | Pro | Arg | Arg |
|     | 4130 |     |     |     |     | 4135 |     |     |     |     | 4140 |     |     |     |
| Gly | Arg  | Ala | Gly | Val | Gln | Arg  | Ala | Ala | Gly | Ala | Arg  | Gly | Pro | Leu |
|     | 4145 |     |     |     |     | 4150 |     |     |     |     | 4155 |     |     |     |
| Gln | Gln  | His | Gln | Arg | Ala | Asp  | Glu | Pro | Gly | Pro | His  | Gly | Asp | Arg |
|     | 4160 |     |     |     |     | 4165 |     |     |     |     | 4170 |     |     |     |

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Arg Ala Arg Gly Gly Val Ala Ala Arg Ala Val Pro Pro Arg Val  
4175 4180 4185

Glu Pro Gly Leu His Gly Gly Ala Glu Arg Leu Pro Glu His Ala  
4190 4195 4200

Ala Arg Gln Arg Ala Pro Gly Pro Gly Gly Leu His Gln Leu His  
4205 4210 4215

Gln Arg Ala Ala Ala Asp Gly Gly Arg Gly Ala Pro Glu Arg Gly  
4220 4225 4230

Val Pro Val Gly Ala Gly Leu Leu Leu Pro Asp Gln Ser Pro Gly  
4235 4240 4245

Leu Ala Asp Arg Glu Pro Glu Pro Gly Phe Gln Glu Leu Ala Gly  
4250 4255 4260

Thr Val Gly Arg Ala Gly Pro Gly Arg Gly Pro Arg Asp Gly Val  
4265 4270 4275

Glu Pro Ala Asp Ala Glu Leu Ala Pro Ala Ala Ala Ala Gly Gly  
4280 4285 4290

Ala Leu His Gly Gln Arg Gln Arg Glu Pro Arg Leu Val Pro Gly  
4295 4300 4305

Leu Pro Ala Pro Val Pro Arg Gly His Arg Thr Gly Ala Arg Gly  
4310 4315 4320

Arg Ala Asp Leu Pro Gly Asp His Pro Arg Glu Pro Arg Ala Gly  
4325 4330 4335

Pro Gly Gly Pro Gly Gln Pro Gly Gly His Pro Glu Leu Pro Ala  
4340 4345 4350

Asp Gln Pro Val Ala Glu Asp Pro Ala Pro Val Arg Ala Glu His  
4355 4360 4365

Arg Gly Gly Ala His Pro Ala Leu Arg Ala Ala Glu Arg Gly Ala  
4370 4375 4380

Val Pro Asp Ala Gly Gly Gly His Ala Gln Arg Gly Ala Arg His  
4385 4390 4395

Asp Arg Ala Gln His Gly Ala Gln His Val Arg Pro Gln Pro Pro

4400

4405

4410

Val His Gln Ala Asp Gly Leu Leu Ala Ser Gly Gly Arg His Glu  
 4415 4420 4425

Leu Gly Leu Leu Tyr Gln Arg His Leu Glu Pro Ala Leu Ala Pro  
 4430 4435 4440

Ala Ala Arg Val Leu His Gly Arg Val Arg His Ala Arg Pro Gln  
 4445 4450 4455

Arg Arg Val Pro Val Gly Arg Arg Gly Gln Gln Arg Val Leu Ala  
 4460 4465 4470

Ala Ser Arg Asn Gln Cys Arg Val Glu Glu Arg Gly Arg Gly Pro  
 4475 4480 4485

Ala Ala Val Leu Gly Ala Val Arg Ser Arg Gly Cys Cys Arg Gly  
 4490 4495 4500

Gly Ala Arg Gly Arg Gln Pro Leu Pro Glu Pro Ala Leu Phe Ala  
 4505 4510 4515

Glu Gln Arg Ala Gln Gln Arg Ala Gly Ser Ala Asp Ala Thr Ala  
 4520 4525 4530

Pro Ala Gly Arg Gly Gly Val Pro Glu Arg Leu Leu Val Glu Ala  
 4535 4540 4545

Arg Ala Arg Glu Glu Leu Pro Gln Arg Asp Arg Glu Pro Gly Gly  
 4550 4555 4560

Gln Asp Glu Pro Leu Glu Asp Val Arg Ala Arg Ala Gln Gly Arg  
 4565 4570 4575

Ala Pro Ser Gln Arg Arg His Pro Thr Pro Ala Ala Arg Gln Ala  
 4580 4585 4590

Ala Gly Thr Gly Val Gly Arg Gly Phe Arg Arg Arg Gln Gln Arg  
 4595 4600 4605

Val Gly Leu Gly Trp Glu Trp Trp Pro Val Arg Ser Pro Ala Pro  
 4610 4615 4620

Pro Tyr Arg Ala Pro Asp Val Arg Ile Lys Asn Lys Arg Arg Tyr  
 4625 4630 4635

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Ser Pro Arg Pro Trp Arg Pro Ala Cys Val Leu Leu Cys Cys Leu  
 4640 4645 4650  
  
 Tyr Asp Glu Ala Arg Val Pro Gly Gly Ser Ser Ser Leu Val Arg  
 4655 4660 4665  
  
 Glu Arg Asp Ala Ala Gly Gly Gly Gly Gly Asp Ala Ala Pro Ala  
 4670 4675 4680  
  
 Gly Gly Ala Leu Arg Ala Pro Ala Val Pro Gly Ala Tyr Gly Gly  
 4685 4690 4695  
  
 Ala Glu Gln His Ser Leu Leu Gly Ala Gly Thr Leu Val Arg Tyr  
 4700 4705 4710  
  
 His Pro Val Val Pro Gly Gly Gln Gln Val Gly Arg His Arg Leu  
 4715 4720 4725  
  
 Ala Glu Leu Pro Glu Arg Pro Gln Gln Leu Pro Asp His Arg Gly  
 4730 4735 4740  
  
 Ala Glu Gln Arg Phe His Pro His Gly Gly Gln His Pro Asp His  
 4745 4750 4755  
  
 Gln Leu Arg Ala Leu Ala Val Gly Arg Pro Ala Glu Asn His His  
 4760 4765 4770  
  
 Ala His Gln His Ala Gln Arg Glu Arg Val His Val Gln Gln Gln  
 4775 4780 4785  
  
 Val Gln Gly Ala Gly Asp Gly Leu Ala Gln Asp Pro Gln Arg Gly  
 4790 4795 4800  
  
 Gly Leu Trp Ser Gly Arg Ala Asp Leu Arg Val Gly Gly Val Ala  
 4805 4810 4815  
  
 Ala Arg Gly Gln Leu Leu Gly Asp His Asp His Arg Ser Asp Glu  
 4820 4825 4830  
  
 Gln Arg His His Arg Gln Leu Leu Gly Gly Gly Ala Ala Glu Arg  
 4835 4840 4845  
  
 Gly Ala Gly Glu Arg His Arg Arg Glu Val Arg His Ala Gln Leu  
 4850 4855 4860  
  
 Pro Ala Gly Leu Gly Pro Arg Asp Arg Ala Gly Asp Ala Gly Arg  
 4865 4870 4875

368530-7006W01\_SequenceListing\_ST25.txt

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | His | Gln | Arg | Gly | Leu | Pro  | Pro | Arg | His | Arg | Pro  | Ala | Ala | Arg |
| 4880 |     |     |     |     |     | 4885 |     |     |     |     | 4890 |     |     |     |
| Leu  | Arg | Arg | Gly | Leu | His | Arg  | Glu | Pro | Pro | Gln | Gln  | Pro | Ala | Gly |
| 4895 |     |     |     |     |     | 4900 |     |     |     |     | 4905 |     |     |     |
| His  | Pro | Gln | Ala | Ala | Ala | Leu  | Pro | Gly | Gly | Leu | Pro  | Asp | Pro | Val |
| 4910 |     |     |     |     |     | 4915 |     |     |     |     | 4920 |     |     |     |
| Arg  | Gly | Pro | Gly | Gly | Gly | Gln  | His | Pro | Arg | Ala | Leu  | Gly | Cys | Arg |
| 4925 |     |     |     |     |     | 4930 |     |     |     |     | 4935 |     |     |     |
| Ser  | Leu | Arg | Glu | Lys | Gln | Gly  | Gly | His | Arg | Arg | Gly  | Asp | Arg | Ser |
| 4940 |     |     |     |     |     | 4945 |     |     |     |     | 4950 |     |     |     |
| Arg  | Gly | His | Arg | Leu | Tyr | Arg  | Gly | Ala | Gly | Arg | Phe  | Cys | Arg | Cys |
| 4955 |     |     |     |     |     | 4960 |     |     |     |     | 4965 |     |     |     |
| Gly  | Ser | Gly | Arg | Gly | Gly | Asn  | Arg | Lys | Asp | Ser | His  | Pro | Ala | Gly |
| 4970 |     |     |     |     |     | 4975 |     |     |     |     | 4980 |     |     |     |
| Gly  | Glu | Gly | Gln | Gln | Gly | Gln  | Glu | Leu | Gln | Arg | Ala  | Arg | Gly | Gln |
| 4985 |     |     |     |     |     | 4990 |     |     |     |     | 4995 |     |     |     |
| Glu  | Lys | His | Arg | Leu | Pro | Gln  | Leu | Val | Pro | Gly | Leu  | Gln | Leu | Arg |
| 5000 |     |     |     |     |     | 5005 |     |     |     |     | 5010 |     |     |     |
| Arg  | Pro | Arg | Glu | Gly | Arg | Ala  | Leu | Leu | Asp | Ala | Ala  | His | His | Leu |
| 5015 |     |     |     |     |     | 5020 |     |     |     |     | 5025 |     |     |     |
| Gly  | Arg | His | Leu | Arg | Arg | Gly  | Ala | Ser | Leu | Leu | Val  | Ala | Ala | Arg |
| 5030 |     |     |     |     |     | 5035 |     |     |     |     | 5040 |     |     |     |
| His  | Asp | Ala | Arg | Pro | Gly | His  | Leu | Pro | Leu | His | Ala  | Ser | Ser | Gln |
| 5045 |     |     |     |     |     | 5050 |     |     |     |     | 5055 |     |     |     |
| Leu  | Pro | Gly | Gly | Gly | Arg | Arg  | Ala | Pro | Ala | Arg | Leu  | Leu | Gln | Glu |
| 5060 |     |     |     |     |     | 5065 |     |     |     |     | 5070 |     |     |     |
| Leu  | Leu | Gln | Arg | Ala | Gly | Arg  | Leu | Leu | Ala | Ala | Ala  | Ala | Arg | Leu |
| 5075 |     |     |     |     |     | 5080 |     |     |     |     | 5085 |     |     |     |
| His  | Leu | Ala | His | Ala | Arg | Leu  | Gln | Pro | Leu | Pro | Arg  | Glu | Pro | Asp |
| 5090 |     |     |     |     |     | 5095 |     |     |     |     | 5100 |     |     |     |
| Pro  | Arg | Pro | Pro | Ala | Arg | Ala  | His | His | Tyr | His | Arg  | Gln | Lys | Arg |
| 5105 |     |     |     |     |     | 5110 |     |     |     |     | 5115 |     |     |     |

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser | Cys  | Ser | His | Arg | Ser | Arg  | Asp | Pro | Ala | Ala | Ala  | Gln | Gln | Tyr |
|     | 5120 |     |     |     |     | 5125 |     |     |     |     | 5130 |     |     |     |
| Pro | Gly  | Ser | Pro | Ala | Arg | Asp  | Arg | His | Arg | Gln | Thr  | Pro | His | Leu |
|     | 5135 |     |     |     |     | 5140 |     |     |     |     | 5145 |     |     |     |
| Pro | Leu  | Arg | Leu | Gln | Gly | Pro  | Gly | Arg | Ser | Arg | Ala  | Ala | Arg | Pro |
|     | 5150 |     |     |     |     | 5155 |     |     |     |     | 5160 |     |     |     |
| Leu | Glu  | Pro | His | Leu | Leu | Lys  | Asn | Val | His | Ser | His  | Leu | Ala | Gln |
|     | 5165 |     |     |     |     | 5170 |     |     |     |     | 5175 |     |     |     |
| His | Arg  | Leu | Gly | Pro | Ala | Arg  | Ala | Gln | Gln | Asp | Val  | Arg | Arg | Arg |
|     | 5180 |     |     |     |     | 5185 |     |     |     |     | 5190 |     |     |     |
| Ser | Pro  | Thr | Leu | His | Ala | Thr  | Pro | Arg | Ala | Arg | Ala  | Arg | Ala | Leu |
|     | 5195 |     |     |     |     | 5200 |     |     |     |     | 5205 |     |     |     |
| Pro | Arg  | Ser | Leu | Gly | Arg | Pro  | Gln | Gly | Pro | Arg | Ala  | Leu | Ala | His |
|     | 5210 |     |     |     |     | 5215 |     |     |     |     | 5220 |     |     |     |
| His | Arg  | Arg | Arg | Arg | Asp | Arg  | Pro | Gly | Gly | Gly | Arg  | Arg | Ala | Gln |
|     | 5225 |     |     |     |     | 5230 |     |     |     |     | 5235 |     |     |     |
| Leu | His  | Ala | Arg | Arg | Arg | Ala  | Arg | Leu | His | Arg | Gly  | Arg | Arg | His |
|     | 5240 |     |     |     |     | 5245 |     |     |     |     | 5250 |     |     |     |
| Arg | Gln  | Arg | Gly | Gly | Arg | Arg  | Ala | Pro | Val | Arg | Pro  | His | Gln | Glu |
|     | 5255 |     |     |     |     | 5260 |     |     |     |     | 5265 |     |     |     |
| Pro | Ala  | Ala | Ala | His | Arg | Pro  | Ala | Ala | Pro | Glu | His  | Pro | Arg | His |
|     | 5270 |     |     |     |     | 5275 |     |     |     |     | 5280 |     |     |     |
| Ala | Arg  | Gly | Ala | Ser | Leu | Ala  | Ala | Gln | Gly | Gln | Ala  | His | Gly | Thr |
|     | 5285 |     |     |     |     | 5290 |     |     |     |     | 5295 |     |     |     |
| Gln | Gly  | His | Ala | Gln | Gly | Gly  | Gln | Thr | Arg | Gly | Leu  | Arg | Gln | Gln |
|     | 5300 |     |     |     |     | 5305 |     |     |     |     | 5310 |     |     |     |
| Gln | Arg  | Arg | Gln | Asp | Pro | Gln  | Thr | Arg | Gly | His | Gly  | Gly | Gly | Gly |
|     | 5315 |     |     |     |     | 5320 |     |     |     |     | 5325 |     |     |     |
| Gly | His  | Arg | Gln | His | Val | Pro  | Pro | Ala | Ala | Arg | Gln  | Arg | Val | Leu |
|     | 5330 |     |     |     |     | 5335 |     |     |     |     | 5340 |     |     |     |
| Gly | Ala  | Arg | Arg | Arg | His | Arg  | Cys | Ala | Arg | Ala | Arg  | Ala | His | Pro |

5345

5350

5355

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Pro  | Ser | His | Leu | Lys | Met  | Leu | Thr | Ser | Arg | Cys  | Cys | Val | Pro |
|     | 5360 |     |     |     |     | 5365 |     |     |     |     | 5370 |     |     |     |
| Ala | Ala  | Arg | Arg | Met | Ser | Lys  | Arg | Lys | Tyr | Lys | Glu  | Glu | Met | Leu |
|     | 5375 |     |     |     |     | 5380 |     |     |     |     | 5385 |     |     |     |
| Gln | Val  | Ile | Ala | Pro | Glu | Ile  | Tyr | Gly | Pro | Ala | Ala  | Ala | Val | Lys |
|     | 5390 |     |     |     |     | 5395 |     |     |     |     | 5400 |     |     |     |
| Glu | Glu  | Arg | Lys | Pro | Arg | Lys  | Leu | Lys | Arg | Val | Lys  | Lys | Asp | Lys |
|     | 5405 |     |     |     |     | 5410 |     |     |     |     | 5415 |     |     |     |
| Lys | Glu  | Glu | Glu | Asp | Asp | Gly  | Leu | Val | Glu | Phe | Val  | Arg | Glu | Phe |
|     | 5420 |     |     |     |     | 5425 |     |     |     |     | 5430 |     |     |     |
| Ala | Pro  | Arg | Arg | Arg | Val | Gln  | Trp | Arg | Gly | Arg | Lys  | Val | Lys | Pro |
|     | 5435 |     |     |     |     | 5440 |     |     |     |     | 5445 |     |     |     |
| Val | Leu  | Arg | Pro | Gly | Thr | Thr  | Val | Val | Phe | Thr | Pro  | Gly | Glu | Arg |
|     | 5450 |     |     |     |     | 5455 |     |     |     |     | 5460 |     |     |     |
| Ser | Gly  | Ser | Ala | Ser | Lys | Arg  | Ser | Tyr | Asp | Glu | Val  | Tyr | Gly | Asp |
|     | 5465 |     |     |     |     | 5470 |     |     |     |     | 5475 |     |     |     |
| Glu | Asp  | Ile | Leu | Glu | Gln | Ala  | Val | Glu | Arg | Leu | Gly  | Glu | Phe | Ala |
|     | 5480 |     |     |     |     | 5485 |     |     |     |     | 5490 |     |     |     |
| Tyr | Gly  | Lys | Arg | Ser | Arg | Pro  | Ala | Pro | Leu | Lys | Glu  | Glu | Ala | Val |
|     | 5495 |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |
| Ser | Ile  | Pro | Leu | Asp | His | Gly  | Asn | Pro | Thr | Pro | Ser  | Leu | Lys | Pro |
|     | 5510 |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
| Val | Thr  | Leu | Gln | Gln | Val | Leu  | Pro | Ser | Ala | Ala | Pro  | Arg | Arg | Gly |
|     | 5525 |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
| Phe | Lys  | Arg | Glu | Gly | Gly | Glu  | Asp | Leu | Tyr | Pro | Thr  | Met | Gln | Leu |
|     | 5540 |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
| Met | Val  | Pro | Lys | Arg | Gln | Lys  | Leu | Glu | Asp | Val | Leu  | Glu | His | Met |
|     | 5555 |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
| Lys | Val  | Asp | Pro | Glu | Val | Gln  | Pro | Glu | Val | Lys | Val  | Arg | Pro | Ile |
|     | 5570 |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |



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Lys Gln Val Ala Pro Gly Leu Gly Val Gln Thr Val Asp Ile Lys  
 5585 5590 5595  
  
 Ile Pro Thr Glu Pro Met Glu Thr Gln Thr Glu Pro Val Lys Pro  
 5600 5605 5610  
  
 Ser Thr Ser Thr Met Glu Val Gln Thr Asp Pro Trp Met Pro Ala  
 5615 5620 5625  
  
 Pro Ala Ser Thr Ser Thr Arg Arg Arg Arg Lys Tyr Gly Ala Ala  
 5630 5635 5640  
  
 Ser Leu Leu Met Pro Asn Tyr Ala Leu His Pro Ser Ile Ile Pro  
 5645 5650 5655  
  
 Thr Pro Gly Tyr Arg Gly Thr Arg Phe Tyr Arg Gly Tyr Thr Ser  
 5660 5665 5670  
  
 Ser Arg Arg Arg Lys Thr Thr Thr Arg Arg Arg Arg Arg Ser Arg  
 5675 5680 5685  
  
 Arg Ser Ser Thr Ala Thr Ser Ala Leu Val Arg Arg Val Tyr Arg  
 5690 5695 5700  
  
 Ser Gly Arg Glu Pro Leu Thr Leu Pro Arg Ala Arg Tyr His Pro  
 5705 5710 5715  
  
 Ser Ile Ala Ile Leu Pro Pro Pro Thr Cys Arg Tyr Gly Pro His  
 5720 5725 5730  
  
 Met Pro Pro Pro Arg Pro His Tyr Gly Leu Pro Arg Lys Lys Ala  
 5735 5740 5745  
  
 Ala Pro Lys Ala Asp Gly Glu Arg Ala Ala Ser Pro Ser Pro Pro  
 5750 5755 5760  
  
 Ala Ala Ala Arg His Gln Gln Ala Val Gly Gly Arg Leu Pro Ala  
 5765 5770 5775  
  
 Arg Ala Asp Pro His His Arg Arg Gly Asp Arg Gly Asp Pro Arg  
 5780 5785 5790  
  
 His Ser Phe Arg Gly Gly Ala Gly Leu Ser Ala Pro Leu Arg His  
 5795 5800 5805  
  
 Lys Lys Ala Trp Ile Cys Asn Lys Lys Lys Asn Gly Leu Thr Leu  
 5810 5815 5820

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Leu Val 5825    Leu Cys Val Phe 5830    Leu Asp Gly Arg His 5835    Gln Phe Phe Val  
 Pro Gly 5840    Thr Ala Thr Arg His 5845    Ala Ala Val Tyr Gly 5850    His Leu Glu  
 Arg His 5855    Arg Gln Gln Pro Thr 5860    Glu Arg Gly Arg Leu 5865    Gln Leu Glu  
 Gln Ser 5870    Leu Glu Arg Ala Glu 5875    Phe Arg Val His Ala 5880    Gln Asn Leu  
 Trp Gln 5885    Gln Gly Val Glu Gln 5890    Gln His Arg Ala Gly 5895    Ala Glu Gly  
 Lys Ala 5900    Glu Arg Thr Glu Leu 5905    Pro Ala Glu Gly Gly 5910    Trp Pro Gly  
 Leu Arg 5915    His Gln Arg Gly Gly 5920    Pro Gly Gln Pro Gly 5925    Arg Ala Glu  
 Thr Asp 5930    Gln Gln Pro Pro Gly 5935    Arg Gly Pro Ala Arg 5940    Gly Val Arg  
 Gly Asp 5945    Ala Pro Gly Gly Gly 5950    Gly Ala Ala Ser Pro 5955    Gly Gln Ala  
 Arg Arg 5960    Gln Ala Thr Ala Ser 5965    Arg Arg Gly Gly Asp 5970    Ala Ala Asp  
 Ala His 5975    Gly Arg Ala Ala Pro 5980    Val Arg Gly Gly Gly 5985    Glu Thr Gly  
 Pro Ala 5990    His His Ala Ala Arg 5995    Gly Ala Ser Gly His 6000    Arg Ser Ala  
 Glu Thr 6005    Gln Gln Gln Pro Ala 6010    Arg Asp Pro Gly Leu 6015    Ala Ser Ala  
 Ser Pro 6020    Leu His Ser Gly Ala 6025    Pro Ala Ala Gly Gly 6030    Arg Arg Val  
 Ala Arg 6035    Pro Pro Arg Pro Pro 6040    Pro Gly Glu Leu Ala 6045    Glu His Ser  
 Glu Gln 6050    His Arg Gly Ser Gly 6055    Ser Ala Glu Cys Glu 6060    Ala Pro Pro

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu  | Leu | Leu | Lys | Asp | Thr | Val  | Ala | Leu | Asn | Leu | Leu  | Val | Cys | Val |
| 6065 |     |     |     |     |     | 6070 |     |     |     |     | 6075 |     |     |     |
| Tyr  | Met | Tyr | Val | Arg | Arg | Pro  | Glu | Gly | Gly | Val | Arg  | Gly | Ala | Ser |
| 6080 |     |     |     |     |     | 6085 |     |     |     |     | 6090 |     |     |     |
| Pro  | Ser | Cys | Lys | Met | Ala | Thr  | Pro | Ser | Met | Leu | Pro  | Gln | Trp | Ala |
| 6095 |     |     |     |     |     | 6100 |     |     |     |     | 6105 |     |     |     |
| Tyr  | Met | His | Ile | Ala | Gly | Gln  | Asp | Ala | Ser | Glu | Tyr  | Leu | Ser | Pro |
| 6110 |     |     |     |     |     | 6115 |     |     |     |     | 6120 |     |     |     |
| Gly  | Leu | Val | Gln | Phe | Ala | Arg  | Ala | Thr | Asp | Thr | Tyr  | Phe | Ser | Leu |
| 6125 |     |     |     |     |     | 6130 |     |     |     |     | 6135 |     |     |     |
| Gly  | Asn | Lys | Phe | Arg | Asn | Pro  | Thr | Val | Ala | Pro | Thr  | His | Asp | Val |
| 6140 |     |     |     |     |     | 6145 |     |     |     |     | 6150 |     |     |     |
| Thr  | Thr | Asp | Arg | Ser | Gln | Arg  | Leu | Thr | Leu | Arg | Phe  | Val | Pro | Val |
| 6155 |     |     |     |     |     | 6160 |     |     |     |     | 6165 |     |     |     |
| Asp  | Arg | Glu | Asp | Asn | Thr | Tyr  | Ser | Tyr | Lys | Val | Arg  | Tyr | Thr | Leu |
| 6170 |     |     |     |     |     | 6175 |     |     |     |     | 6180 |     |     |     |
| Ala  | Val | Gly | Asp | Asn | Arg | Val  | Leu | Asp | Met | Ala | Ser  | Thr | Tyr | Phe |
| 6185 |     |     |     |     |     | 6190 |     |     |     |     | 6195 |     |     |     |
| Asp  | Ile | Arg | Gly | Val | Leu | Asp  | Arg | Gly | Pro | Ser | Phe  | Lys | Pro | Tyr |
| 6200 |     |     |     |     |     | 6205 |     |     |     |     | 6210 |     |     |     |
| Ser  | Gly | Thr | Ala | Tyr | Asn | Ser  | Leu | Ala | Pro | Lys | Gly  | Ala | Pro | Asn |
| 6215 |     |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Ser  | Ser | Gln | Trp | Glu | Gln | Ala  | Lys | Thr | Gly | Asn | Gly  | Gly | Thr | Met |
| 6230 |     |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Glu  | Thr | His | Thr | Tyr | Gly | Val  | Ala | Pro | Met | Gly | Gly  | Glu | Asn | Ile |
| 6245 |     |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |
| Thr  | Lys | Asp | Gly | Leu | Gln | Ile  | Gly | Thr | Asp | Val | Thr  | Ala | Asn | Gln |
| 6260 |     |     |     |     |     | 6265 |     |     |     |     | 6270 |     |     |     |
| Asn  | Lys | Pro | Ile | Tyr | Ala | Asp  | Lys | Thr | Phe | Gln | Pro  | Glu | Pro | Gln |
| 6275 |     |     |     |     |     | 6280 |     |     |     |     | 6285 |     |     |     |
| Val  | Gly | Glu | Glu | Asn | Trp | Gln  | Glu | Thr | Glu | Asn | Phe  | Tyr | Gly | Gly |

6290

6295

6300

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Ala | Leu | Lys | Lys | Asp | Thr  | Asn | Met | Lys | Pro | Cys  | Tyr | Gly | Ser |
| 6305 |     |     |     |     |     | 6310 |     |     |     |     | 6315 |     |     |     |
| Tyr  | Ala | Arg | Pro | Thr | Asn | Glu  | Lys | Gly | Gly | Gln | Ala  | Lys | Leu | Lys |
| 6320 |     |     |     |     |     | 6325 |     |     |     |     | 6330 |     |     |     |
| Val  | Gly | Asp | Asp | Gly | Val | Pro  | Thr | Lys | Glu | Phe | Asp  | Ile | Asp | Leu |
| 6335 |     |     |     |     |     | 6340 |     |     |     |     | 6345 |     |     |     |
| Ala  | Phe | Phe | Asp | Thr | Pro | Gly  | Gly | Thr | Val | Asn | Gly  | Gln | Asp | Glu |
| 6350 |     |     |     |     |     | 6355 |     |     |     |     | 6360 |     |     |     |
| Tyr  | Lys | Ala | Asp | Ile | Val | Met  | Tyr | Thr | Glu | Asn | Thr  | Tyr | Leu | Glu |
| 6365 |     |     |     |     |     | 6370 |     |     |     |     | 6375 |     |     |     |
| Thr  | Pro | Asp | Thr | His | Val | Val  | Tyr | Lys | Pro | Gly | Lys  | Asp | Asp | Ala |
| 6380 |     |     |     |     |     | 6385 |     |     |     |     | 6390 |     |     |     |
| Ser  | Ser | Glu | Ile | Asn | Leu | Val  | Gln | Gln | Ser | Met | Pro  | Asn | Arg | Pro |
| 6395 |     |     |     |     |     | 6400 |     |     |     |     | 6405 |     |     |     |
| Asn  | Tyr | Ile | Gly | Phe | Arg | Asp  | Asn | Phe | Ile | Gly | Leu  | Met | Tyr | Tyr |
| 6410 |     |     |     |     |     | 6415 |     |     |     |     | 6420 |     |     |     |
| Asn  | Ser | Thr | Gly | Asn | Met | Gly  | Val | Leu | Ala | Gly | Gln  | Ala | Ser | Gln |
| 6425 |     |     |     |     |     | 6430 |     |     |     |     | 6435 |     |     |     |
| Leu  | Asn | Ala | Val | Val | Asp | Leu  | Gln | Asp | Arg | Asn | Thr  | Glu | Leu | Ser |
| 6440 |     |     |     |     |     | 6445 |     |     |     |     | 6450 |     |     |     |
| Tyr  | Gln | Leu | Leu | Leu | Asp | Ser  | Leu | Gly | Asp | Arg | Thr  | Arg | Tyr | Phe |
| 6455 |     |     |     |     |     | 6460 |     |     |     |     | 6465 |     |     |     |
| Ser  | Met | Trp | Asn | Gln | Ala | Val  | Asp | Ser | Tyr | Asp | Pro  | Asp | Val | Arg |
| 6470 |     |     |     |     |     | 6475 |     |     |     |     | 6480 |     |     |     |
| Ile  | Ile | Glu | Asn | His | Gly | Val  | Glu | Asp | Glu | Leu | Pro  | Asn | Tyr | Cys |
| 6485 |     |     |     |     |     | 6490 |     |     |     |     | 6495 |     |     |     |
| Phe  | Pro | Leu | Asp | Gly | Ser | Gly  | Thr | Asn | Ala | Ala | Tyr  | Gln | Gly | Val |
| 6500 |     |     |     |     |     | 6505 |     |     |     |     | 6510 |     |     |     |
| Lys  | Val | Lys | Asp | Gly | Gln | Asp  | Gly | Asp | Val | Glu | Ser  | Glu | Trp | Glu |
| 6515 |     |     |     |     |     | 6520 |     |     |     |     | 6525 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asn | Asp  | Asp | Thr | Val | Ala | Ala  | Arg | Asn | Gln | Leu | Cys  | Lys | Gly | Asn |
|     | 6530 |     |     |     |     | 6535 |     |     |     |     | 6540 |     |     |     |
| Ile | Phe  | Ala | Met | Glu | Ile | Asn  | Leu | Gln | Ala | Asn | Leu  | Trp | Arg | Ser |
|     | 6545 |     |     |     |     | 6550 |     |     |     |     | 6555 |     |     |     |
| Phe | Leu  | Tyr | Ser | Asn | Val | Ala  | Leu | Tyr | Leu | Pro | Asp  | Ser | Tyr | Lys |
|     | 6560 |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Tyr | Thr  | Pro | Thr | Asn | Val | Thr  | Leu | Pro | Thr | Asn | Thr  | Asn | Thr | Tyr |
|     | 6575 |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Asp | Tyr  | Met | Asn | Gly | Arg | Val  | Thr | Pro | Pro | Ser | Leu  | Val | Asp | Ala |
|     | 6590 |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Tyr | Leu  | Asn | Ile | Gly | Ala | Arg  | Trp | Ser | Leu | Asp | Pro  | Met | Asp | Asn |
|     | 6605 |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Val | Asn  | Pro | Phe | Asn | His | His  | Arg | Asn | Ala | Gly | Leu  | Arg | Tyr | Arg |
|     | 6620 |     |     |     |     | 6625 |     |     |     |     | 6630 |     |     |     |
| Ser | Met  | Leu | Leu | Gly | Asn | Gly  | Arg | Tyr | Val | Pro | Phe  | His | Ile | Gln |
|     | 6635 |     |     |     |     | 6640 |     |     |     |     | 6645 |     |     |     |
| Val | Pro  | Gln | Lys | Phe | Phe | Ala  | Ile | Lys | Ser | Leu | Leu  | Leu | Leu | Pro |
|     | 6650 |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |
| Gly | Ser  | Tyr | Thr | Tyr | Glu | Trp  | Asn | Phe | Arg | Lys | Asp  | Val | Asn | Met |
|     | 6665 |     |     |     |     | 6670 |     |     |     |     | 6675 |     |     |     |
| Ile | Leu  | Gln | Ser | Ser | Leu | Gly  | Asn | Asp | Leu | Arg | Thr  | Asp | Gly | Ala |
|     | 6680 |     |     |     |     | 6685 |     |     |     |     | 6690 |     |     |     |
| Ser | Ile  | Ala | Phe | Thr | Ser | Ile  | Asn | Leu | Tyr | Ala | Thr  | Phe | Phe | Pro |
|     | 6695 |     |     |     |     | 6700 |     |     |     |     | 6705 |     |     |     |
| Met | Ala  | His | Asn | Thr | Ala | Ser  | Thr | Leu | Glu | Ala | Met  | Leu | Arg | Asn |
|     | 6710 |     |     |     |     | 6715 |     |     |     |     | 6720 |     |     |     |
| Asp | Thr  | Asn | Asp | Gln | Ser | Phe  | Asn | Asp | Tyr | Leu | Ser  | Ala | Ala | Asn |
|     | 6725 |     |     |     |     | 6730 |     |     |     |     | 6735 |     |     |     |
| Met | Leu  | Tyr | Pro | Ile | Pro | Ala  | Asn | Ala | Thr | Asn | Val  | Pro | Ile | Ser |
|     | 6740 |     |     |     |     | 6745 |     |     |     |     | 6750 |     |     |     |
| Ile | Pro  | Ser | Arg | Asn | Trp | Ala  | Ala | Phe | Arg | Gly | Trp  | Ser | Phe | Thr |
|     | 6755 |     |     |     |     | 6760 |     |     |     |     | 6765 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Leu  | Lys | Thr | Arg | Glu | Thr  | Pro | Ser | Leu | Gly | Ser  | Gly | Phe | Asp |
|     | 6770 |     |     |     |     | 6775 |     |     |     |     | 6780 |     |     |     |
| Pro | Tyr  | Phe | Val | Tyr | Ser | Gly  | Ser | Ile | Pro | Tyr | Leu  | Asp | Gly | Thr |
|     | 6785 |     |     |     |     | 6790 |     |     |     |     | 6795 |     |     |     |
| Phe | Tyr  | Leu | Asn | His | Thr | Phe  | Lys | Lys | Val | Ser | Ile  | Thr | Phe | Asp |
|     | 6800 |     |     |     |     | 6805 |     |     |     |     | 6810 |     |     |     |
| Ser | Ser  | Val | Ser | Trp | Pro | Gly  | Asn | Asp | Arg | Leu | Leu  | Thr | Pro | Asn |
|     | 6815 |     |     |     |     | 6820 |     |     |     |     | 6825 |     |     |     |
| Glu | Phe  | Glu | Ile | Lys | Arg | Thr  | Val | Asp | Gly | Glu | Gly  | Tyr | Asn | Val |
|     | 6830 |     |     |     |     | 6835 |     |     |     |     | 6840 |     |     |     |
| Ala | Gln  | Cys | Asn | Met | Thr | Lys  | Asp | Trp | Phe | Leu | Val  | Gln | Met | Leu |
|     | 6845 |     |     |     |     | 6850 |     |     |     |     | 6855 |     |     |     |
| Ala | His  | Tyr | Asn | Ile | Gly | Tyr  | Gln | Gly | Phe | Tyr | Val  | Pro | Glu | Gly |
|     | 6860 |     |     |     |     | 6865 |     |     |     |     | 6870 |     |     |     |
| Tyr | Lys  | Asp | Arg | Met | Tyr | Ser  | Phe | Phe | Arg | Asn | Phe  | Gln | Pro | Met |
|     | 6875 |     |     |     |     | 6880 |     |     |     |     | 6885 |     |     |     |
| Ser | Arg  | Gln | Val | Val | Asp | Glu  | Val | Asn | Tyr | Lys | Asp  | Tyr | Gln | Ala |
|     | 6890 |     |     |     |     | 6895 |     |     |     |     | 6900 |     |     |     |
| Val | Thr  | Leu | Ala | Tyr | Gln | His  | Asn | Asn | Ser | Gly | Phe  | Val | Gly | Tyr |
|     | 6905 |     |     |     |     | 6910 |     |     |     |     | 6915 |     |     |     |
| Leu | Ala  | Pro | Thr | Met | Arg | Gln  | Gly | Gln | Pro | Tyr | Pro  | Ala | Asn | Tyr |
|     | 6920 |     |     |     |     | 6925 |     |     |     |     | 6930 |     |     |     |
| Pro | Tyr  | Pro | Leu | Ile | Gly | Lys  | Ser | Ala | Val | Ala | Ser  | Val | Thr | Gln |
|     | 6935 |     |     |     |     | 6940 |     |     |     |     | 6945 |     |     |     |
| Lys | Lys  | Phe | Leu | Cys | Asp | Arg  | Val | Met | Trp | Arg | Ile  | Pro | Phe | Ser |
|     | 6950 |     |     |     |     | 6955 |     |     |     |     | 6960 |     |     |     |
| Ser | Asn  | Phe | Met | Ser | Met | Gly  | Ala | Leu | Thr | Asp | Leu  | Gly | Gln | Asn |
|     | 6965 |     |     |     |     | 6970 |     |     |     |     | 6975 |     |     |     |
| Met | Leu  | Tyr | Ala | Asn | Ser | Ala  | His | Ala | Leu | Asp | Met  | Asn | Phe | Glu |
|     | 6980 |     |     |     |     | 6985 |     |     |     |     | 6990 |     |     |     |
| Val | Asp  | Pro | Met | Asp | Glu | Ser  | Thr | Leu | Leu | Tyr | Val  | Val | Phe | Glu |
|     | 6995 |     |     |     |     | 7000 |     |     |     |     | 7005 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | Phe | Asp | Val | Val | Arg | Val  | His | Gln | Pro | His | Arg  | Gly | Val | Ile |
| 7010 |     |     |     |     |     | 7015 |     |     |     |     | 7020 |     |     |     |
| Glu  | Ala | Val | Tyr | Leu | Arg | Thr  | Pro | Phe | Ser | Ala | Gly  | Asn | Ala | Thr |
| 7025 |     |     |     |     |     | 7030 |     |     |     |     | 7035 |     |     |     |
| Thr  | Ala | Ala | Leu | Ala | Ser | Cys  | Lys | Met | Thr | Ala | Gly  | Ser | Gly | Glu |
| 7040 |     |     |     |     |     | 7045 |     |     |     |     | 7050 |     |     |     |
| Gln  | Glu | Leu | Arg | Ala | Ile | Leu  | Arg | Asp | Leu | Gly | Cys  | Gly | Pro | Cys |
| 7055 |     |     |     |     |     | 7060 |     |     |     |     | 7065 |     |     |     |
| Phe  | Leu | Gly | Thr | Phe | Asp | Lys  | Arg | Phe | Pro | Gly | Phe  | Met | Ala | Pro |
| 7070 |     |     |     |     |     | 7075 |     |     |     |     | 7080 |     |     |     |
| His  | Lys | Leu | Ala | Cys | Ala | Ile  | Val | Asn | Thr | Ala | Gly  | Arg | Glu | Thr |
| 7085 |     |     |     |     |     | 7090 |     |     |     |     | 7095 |     |     |     |
| Gly  | Gly | Glu | His | Trp | Leu | Ala  | Phe | Ala | Trp | Asn | Pro  | Arg | Ser | His |
| 7100 |     |     |     |     |     | 7105 |     |     |     |     | 7110 |     |     |     |
| Thr  | Cys | Tyr | Leu | Phe | Asp | Pro  | Phe | Gly | Phe | Ser | Asp  | Glu | Arg | Leu |
| 7115 |     |     |     |     |     | 7120 |     |     |     |     | 7125 |     |     |     |
| Lys  | Gln | Ile | Tyr | Gln | Phe | Glu  | Tyr | Glu | Gly | Leu | Leu  | Arg | Arg | Ser |
| 7130 |     |     |     |     |     | 7135 |     |     |     |     | 7140 |     |     |     |
| Ala  | Leu | Ala | Thr | Glu | Asp | Arg  | Cys | Val | Thr | Leu | Glu  | Lys | Ser | Thr |
| 7145 |     |     |     |     |     | 7150 |     |     |     |     | 7155 |     |     |     |
| Gln  | Thr | Val | Gln | Gly | Pro | Arg  | Ser | Ala | Ala | Cys | Gly  | Leu | Phe | Cys |
| 7160 |     |     |     |     |     | 7165 |     |     |     |     | 7170 |     |     |     |
| Cys  | Met | Phe | Leu | His | Ala | Phe  | Val | His | Trp | Pro | Asp  | Arg | Pro | Met |
| 7175 |     |     |     |     |     | 7180 |     |     |     |     | 7185 |     |     |     |
| Asp  | Lys | Asn | Pro | Thr | Met | Asn  | Leu | Leu | Thr | Gly | Val  | Pro | Asn | Gly |
| 7190 |     |     |     |     |     | 7195 |     |     |     |     | 7200 |     |     |     |
| Met  | Leu | Gln | Ser | Pro | Gln | Val  | Glu | Pro | Thr | Leu | Arg  | Arg | Asn | Gln |
| 7205 |     |     |     |     |     | 7210 |     |     |     |     | 7215 |     |     |     |
| Glu  | Ala | Leu | Tyr | Arg | Phe | Leu  | Asn | Ala | His | Ser | Ala  | Tyr | Phe | Arg |
| 7220 |     |     |     |     |     | 7225 |     |     |     |     | 7230 |     |     |     |
| Ser  | His | Arg | Ala | Arg | Ile | Glu  | Lys | Ala | Thr | Ala | Phe  | Asp | Arg | Met |

7235

7240

7245

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asn  | Gln | Asp | Met | Lys | Thr | Gly  | Val | Cys | Met | Met | Leu  | Tyr | Ser | Thr |
| 7250 |     |     |     |     |     | 7255 |     |     |     |     | 7260 |     |     |     |
| Ala  | His | Val | Tyr | Ala | Thr | Phe  | Ser | Glu | Ala | Leu | Thr  | Leu | Phe | Arg |
| 7265 |     |     |     |     |     | 7270 |     |     |     |     | 7275 |     |     |     |
| Asn  | Arg | Arg | Gly | Ser | Ala | Gly  | Ser | Arg | His | Gly | Pro  | Arg | Ala | Gly |
| 7280 |     |     |     |     |     | 7285 |     |     |     |     | 7290 |     |     |     |
| Ile  | Arg | Cys | Gly | Thr | Gly | Thr  | Trp | Ala | Ala | Thr | Thr  | Arg | Gly | Ser |
| 7295 |     |     |     |     |     | 7300 |     |     |     |     | 7305 |     |     |     |
| Ala  | Ala | Trp | Ala | Arg | Gly | Gly  | Arg | Gly | Thr | Ser | Arg  | Ser | Thr | Ala |
| 7310 |     |     |     |     |     | 7315 |     |     |     |     | 7320 |     |     |     |
| Cys  | Ala | Val | Ala | Gly | Arg | Pro  | Ala | Gly | Arg | Ala | Arg  | Arg | Ser | Asn |
| 7325 |     |     |     |     |     | 7330 |     |     |     |     | 7335 |     |     |     |
| Arg  | Ser | Trp | Asp | Pro | Arg | Ser  | Ala | Arg | Glu | Ser | Cys  | Gly | Thr | Arg |
| 7340 |     |     |     |     |     | 7345 |     |     |     |     | 7350 |     |     |     |
| Gly  | Cys | Ser | Thr | Gly | Thr | Pro  | Ser | Gly | Pro | Gly | Ala  | Ser | Arg | Leu |
| 7355 |     |     |     |     |     | 7360 |     |     |     |     | 7365 |     |     |     |
| Pro  | Ala | Pro | Ser | Arg | Arg | Cys  | Pro | Pro | Arg | Pro | Asp  | Pro | Arg | Arg |
| 7370 |     |     |     |     |     | 7375 |     |     |     |     | 7380 |     |     |     |
| Trp  | Pro | Ser | Arg | Arg | Gly | Ser  | Ser | Cys | Arg | Ser | Ala  | Ala | Pro | Cys |
| 7385 |     |     |     |     |     | 7390 |     |     |     |     | 7395 |     |     |     |
| Trp  | Ala | Arg | Ser | Arg | Ala | Cys  | Gly | Cys | Asn | Arg | Ser  | Ala | Gly | Gly |
| 7400 |     |     |     |     |     | 7405 |     |     |     |     | 7410 |     |     |     |
| Ser  | Ala | Ser | Ser | Gly | Pro | Ala  | Arg | Ser | Ser | Cys | Pro  | Gly | Thr | Trp |
| 7415 |     |     |     |     |     | 7420 |     |     |     |     | 7425 |     |     |     |
| Pro  | Ser | Lys | Pro | Pro | Ala | Gly  | Gly | Arg | Pro | Ala | Ala  | Pro | Cys | Arg |
| 7430 |     |     |     |     |     | 7435 |     |     |     |     | 7440 |     |     |     |
| Pro  | Arg | Arg | Arg | Pro | Arg | Arg  | Thr | Cys | Arg | Thr | Gly  | Trp | Trp | Arg |
| 7445 |     |     |     |     |     | 7450 |     |     |     |     | 7455 |     |     |     |
| Ser  | Arg | Arg | Arg | Ala | Arg | Ser  | Ser | Ala | Arg | Arg | Cys  | Trp | Pro | Ala |
| 7460 |     |     |     |     |     | 7465 |     |     |     |     | 7470 |     |     |     |



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Ala Pro Arg Cys Ala Pro Ser Gly Ser Gly Ser Trp Pro Gly Trp  
7475 7480 7485

Gly Ser Pro Ser Ala Arg Ala Ala Arg Ser Arg Ser Pro His Pro  
7490 7495 7500

Ser Arg Cys Ala Pro Ser Gly Ser Ser Arg Ser Arg Ala Gly Thr  
7505 7510 7515

Ala Ala Cys Pro Arg Leu Arg Cys Ser Arg Ala Ala Thr Ala Arg  
7520 7525 7530

Ser Arg Cys Thr Pro Ser Ser Cys Gly Arg Ser Gly Ser Ala Ser  
7535 7540 7545

Ala Arg Ser Pro Ala Gly Ser Gly Pro Ser Ser Arg Ser Gly Ser  
7550 7555 7560

Cys Cys Trp Arg Ser Ala Gly Cys Arg Gly Ala Pro Arg Ser His  
7565 7570 7575

Thr Gly Gly Arg Cys Gly Gly Thr Pro Arg Pro Ala Arg Ala Ser  
7580 7585 7590

Ala Gly Arg Arg Thr Ser Gly Arg Ser Pro Arg Gly Thr Gly Pro  
7595 7600 7605

Ser Ala Ala Ser Ser Leu Pro Cys Pro Ser Pro Arg Pro Lys Arg  
7610 7615 7620

Ser Ala Gly Ser Gly Gly Ser Ser Pro Pro Leu Ser Ser Ser Pro  
7625 7630 7635

Pro Pro Arg Ser Gly Gly Arg Ser Arg Pro Gly Ser Gln Thr Leu  
7640 7645 7650

Ala Cys Arg Pro Ser Arg Cys Ala Arg Gly Glu Ser Ser Pro Arg  
7655 7660 7665

Pro Pro Ala Pro Pro Arg Pro Ala Phe Arg Pro Arg Cys Pro Gly  
7670 7675 7680

Cys Leu Ala Lys Ala His Ala Trp Ser Cys Gly Val Ser Phe Trp  
7685 7690 7695

Ala Ala Glu Ala Ala Ala Met Cys Trp Glu Ser Ala Ser Ser Arg  
7700 7705 7710

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Ser Pro Arg Leu Phe Leu Leu Leu Gly Arg Arg Pro Arg Pro Arg  
7715 7720 7725

Gly Gly Arg His Ala Ser Ser Gly Ala Glu Ala Glu Ala Thr Gly  
7730 7735 7740

Ser Arg Gly Ser Ala Gly Gly Trp Gln Ser Pro Phe Arg Val Arg  
7745 7750 7755

Gly Cys Ala Pro Gly Gly Ala Ala Leu Thr Asp Phe Leu Arg Gly  
7760 7765 7770

Arg Pro Leu Cys Ser Pro Arg Glu Gln Gln Gln Ala Trp Arg Leu  
7775 7780 7785

Ser His Arg Arg Gln His Arg His Leu Pro Pro Pro Pro Pro Pro  
7790 7795 7800

Thr Arg Thr Ser Ser Arg Met Lys Ala Pro Pro Arg Arg Pro Ala  
7805 7810 7815

Pro Pro Pro Thr Pro Arg Pro Gln Thr Cys Lys Arg Trp Arg Asn  
7820 7825 7830

Pro Ser Arg Leu Thr Trp Ala Thr Arg Pro Arg Ser Thr Arg Arg  
7835 7840 7845

Ser Trp Gln Arg Ala Phe Gln Pro Arg Lys Arg Thr Thr Lys Ser  
7850 7855 7860

Ser Gln Ser Arg Lys Gln Arg Thr Ser Arg Thr Arg Leu Gly Thr  
7865 7870 7875

Ser Met Ala Thr Thr Ala Gly Gln Arg Thr Cys Ser Ser Ser Ile  
7880 7885 7890

Trp Pro Ala Asn Ala Ser Ser Ser Arg Thr Arg Cys Ser Thr Ala  
7895 7900 7905

Pro Arg Cys Pro Ser Ala Trp Arg Ser Ser Ala Ala Pro Thr Ser  
7910 7915 7920

Ala Thr Ser Ser Arg Arg Ala Cys Pro Pro Ser Ala Ser Pro Thr  
7925 7930 7935

Ala Pro Val Ser Pro Thr Arg Ala Ser Thr Ser Thr Arg Ser Ser  
7940 7945 7950

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Cys  | Pro | Arg | Pro | Trp | Pro  | Pro | Thr | Thr | Ser | Phe  | Ser | Arg | Thr |
|     | 7955 |     |     |     |     | 7960 |     |     |     |     | 7965 |     |     |     |
| Lys | Gly  | Ser | Pro | Ser | Pro | Ala  | Ala | Pro | Thr | Ala | Pro  | Ala | Pro | Thr |
|     | 7970 |     |     |     |     | 7975 |     |     |     |     | 7980 |     |     |     |
| Pro | Cys  | Ser | Thr | Trp | Ala | Pro  | Ala | Pro | Ala | Tyr | Leu  | Ile | Ser | Pro |
|     | 7985 |     |     |     |     | 7990 |     |     |     |     | 7995 |     |     |     |
| Pro | Trp  | Lys | Arg | Phe | Pro | Arg  | Ser | Ser | Arg | Val | Trp  | Ala | Ala | Thr |
|     | 8000 |     |     |     |     | 8005 |     |     |     |     | 8010 |     |     |     |
| Arg | Leu  | Gly | Pro | Arg | Thr | Leu  | Cys | Lys | Glu | Ala | Glu  | Arg | Ser | Met |
|     | 8015 |     |     |     |     | 8020 |     |     |     |     | 8025 |     |     |     |
| Ser | Thr  | Thr | Ala | Pro | Trp | Trp  | Ser | Trp | Lys | Ala | Thr  | Thr | Arg | Ala |
|     | 8030 |     |     |     |     | 8035 |     |     |     |     | 8040 |     |     |     |
| Trp | Arg  | Ser | Ser | Ser | Ala | Arg  | Ser | Ser | Pro | Thr | Ser  | Pro | Thr | Arg |
|     | 8045 |     |     |     |     | 8050 |     |     |     |     | 8055 |     |     |     |
| Arg | Ser  | Thr | Cys | Pro | Pro | Arg  | Ser | Ala | Pro | Ser | Trp  | Thr | Arg | Cys |
|     | 8060 |     |     |     |     | 8065 |     |     |     |     | 8070 |     |     |     |
| Ser | Ser  | Ser | Ala | Pro | Arg | Pro  | Ser | Arg | Arg | Arg | Arg  | Cys | Arg | Thr |
|     | 8075 |     |     |     |     | 8080 |     |     |     |     | 8085 |     |     |     |
| Pro | Arg  | Val | Arg | Thr | Arg | Ala  | Ser | Pro | Trp | Ser | Ala  | Thr | Ser | Ser |
|     | 8090 |     |     |     |     | 8095 |     |     |     |     | 8100 |     |     |     |
| Trp | Arg  | Ala | Gly | Trp | Glu | Arg  | Val | Ala | Pro | Pro | Arg  | Ala | Trp | Lys |
|     | 8105 |     |     |     |     | 8110 |     |     |     |     | 8115 |     |     |     |
| Ser | Gly  | Ala | Ser | Ser | Trp | Pro  | Trp | Ser | Trp | Pro | Trp  | Ser | Trp | Ser |
|     | 8120 |     |     |     |     | 8125 |     |     |     |     | 8130 |     |     |     |
| Val | Cys  | Ala | Ala | Ser | Leu | Pro  | Thr | Arg | Arg | Pro | Cys  | Ala | Arg | Ser |
|     | 8135 |     |     |     |     | 8140 |     |     |     |     | 8145 |     |     |     |
| Arg | Arg  | Thr | Cys | Thr | Thr | Ser  | Ser | Gly | Thr | Gly | Ser  | Cys | Ala | Arg |
|     | 8150 |     |     |     |     | 8155 |     |     |     |     | 8160 |     |     |     |
| Pro | Ala  | Arg | Ser | Pro | Thr | Trp  | Ser | Pro | Thr | Trp | Ser  | Pro | Thr | Trp |
|     | 8165 |     |     |     |     | 8170 |     |     |     |     | 8175 |     |     |     |
| Ala | Ser  | Cys | Thr | Arg | Thr | Ala  | Trp | Gly | Lys | Thr | Cys  | Cys | Thr | Pro |

8180

8185

8190

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro  | Cys | Ala | Gly | Arg | Pro | Ala  | Ala | Thr | Thr | Ser | Ala  | Thr | Ala | Ser |
| 8195 |     |     |     |     |     | 8200 |     |     |     |     | 8205 |     |     |     |
| Thr  | Cys | Thr | Ser | Ala | Thr | Pro  | Gly | Arg | Arg | Ala | Trp  | Ala | Cys | Gly |
| 8210 |     |     |     |     |     | 8215 |     |     |     |     | 8220 |     |     |     |
| Ser  | Ser | Ala | Trp | Arg | Ser | Arg  | Thr | Lys | Ser | Ser | Ala  | Ser | Ser | Cys |
| 8225 |     |     |     |     |     | 8230 |     |     |     |     | 8235 |     |     |     |
| Arg  | Arg | Thr | Ser | Arg | Pro | Cys  | Gly | Pro | Gly | Ser | Thr  | Ser | Val | Pro |
| 8240 |     |     |     |     |     | 8245 |     |     |     |     | 8250 |     |     |     |
| Pro  | Pro | Arg | Thr | Trp | Pro | Thr  | Ser | Ser | Ser | Pro | Ser  | Ala | Cys | Gly |
| 8255 |     |     |     |     |     | 8260 |     |     |     |     | 8265 |     |     |     |
| Arg  | Cys | Ala | Thr | Gly | Cys | Pro  | Thr | Leu | Ala | Lys | Ala  | Cys | Cys | Lys |
| 8270 |     |     |     |     |     | 8275 |     |     |     |     | 8280 |     |     |     |
| Thr  | Phe | Ala | Leu | Ser | Ser | Ser  | Asn | Ala | Pro | Gly | Ser  | Cys | Pro | Pro |
| 8285 |     |     |     |     |     | 8290 |     |     |     |     | 8295 |     |     |     |
| Pro  | Ala | Pro | Arg | Cys | Pro | Arg  | Thr | Ser | Cys | Arg | Pro  | Ser | Ala | Ser |
| 8300 |     |     |     |     |     | 8305 |     |     |     |     | 8310 |     |     |     |
| Ala  | Pro | Arg | Arg | Ser | Gly | Ala  | Thr | Ala | Thr | Cys | Cys  | Ala | Trp | Pro |
| 8315 |     |     |     |     |     | 8320 |     |     |     |     | 8325 |     |     |     |
| Thr  | Thr | Trp | Pro | Thr | Thr | Arg  | Thr | Ser | Arg | Thr | Ser  | Ala | Ala | Arg |
| 8330 |     |     |     |     |     | 8335 |     |     |     |     | 8340 |     |     |     |
| Val  | Cys | Trp | Ser | Ala | Thr | Ala  | Ala | Ala | Thr | Ser | Ala  | Arg | Arg | Thr |
| 8345 |     |     |     |     |     | 8350 |     |     |     |     | 8355 |     |     |     |
| Ala  | Pro | Trp | Pro | Ala | Thr | Pro  | Ser | Cys | Ala | Arg | Pro  | Arg | Ser | Ser |
| 8360 |     |     |     |     |     | 8365 |     |     |     |     | 8370 |     |     |     |
| Ala  | Pro | Ser | Ser | Cys | Lys | Ala  | Pro | Ala | Thr | Ala | Arg  | Ala | Arg | Gly |
| 8375 |     |     |     |     |     | 8380 |     |     |     |     | 8385 |     |     |     |
| Val  | Asn | Ser | Pro | Arg | Gly | Cys  | Gly | Pro | Arg | Pro | Thr  | Cys | Ala | Ser |
| 8390 |     |     |     |     |     | 8395 |     |     |     |     | 8400 |     |     |     |
| Ser  | Cys | Pro | Arg | Thr | Thr | Ile  | Pro | Ser | Arg | Ser | Gly  | Ser | Thr | Arg |
| 8405 |     |     |     |     |     | 8410 |     |     |     |     | 8415 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Asn  | Pro | Ser | Arg | Pro | Arg  | Pro | Ser | Cys | Arg | Pro  | Ala | Ser | Ser |
|     | 8420 |     |     |     |     | 8425 |     |     |     |     | 8430 |     |     |     |
| Pro | Arg  | Gly | Pro | Ser | Trp | Pro  | Asn | Cys | Lys | Pro | Ser  | Arg | Asn | Pro |
|     | 8435 |     |     |     |     | 8440 |     |     |     |     | 8445 |     |     |     |
| Ala | Lys  | Asn | Phe | Cys | Lys | Arg  | Ala | Thr | Gly | Ser | Thr  | Trp | Thr | Pro |
|     | 8450 |     |     |     |     | 8455 |     |     |     |     | 8460 |     |     |     |
| Arg | Pro  | Glu | Arg | Ser | Ser | Thr  | Pro | Ala | Ser | Pro | Arg  | Met | Pro | Arg |
|     | 8465 |     |     |     |     | 8470 |     |     |     |     | 8475 |     |     |     |
| Gly | Ser  | Ser | Lys | Lys | Leu | Lys  | Val | Glu | Leu | Pro | Pro  | Pro | Glu | Asp |
|     | 8480 |     |     |     |     | 8485 |     |     |     |     | 8490 |     |     |     |
| Leu | Glu  | Glu | Asp | Trp | Glu | Ser  | Ser | Gln | Ala | Glu | Glu  | Glu | Glu | Met |
|     | 8495 |     |     |     |     | 8500 |     |     |     |     | 8505 |     |     |     |
| Glu | Asp  | Trp | Asp | Ser | Thr | Gln  | Ala | Glu | Glu | Asp | Ser  | Leu | Gln | Asp |
|     | 8510 |     |     |     |     | 8515 |     |     |     |     | 8520 |     |     |     |
| Ser | Leu  | Glu | Glu | Glu | Asp | Glu  | Val | Glu | Glu | Ala | Glu  | Glu | Glu | Ala |
|     | 8525 |     |     |     |     | 8530 |     |     |     |     | 8535 |     |     |     |
| Ala | Ala  | Ala | Arg | Pro | Ser | Ser  | Ser | Ala | Glu | Lys | Ala  | Ser | Ser | Thr |
|     | 8540 |     |     |     |     | 8545 |     |     |     |     | 8550 |     |     |     |
| Asp | Thr  | Ile | Ser | Ala | Pro | Gly  | Arg | Gly | Arg | Gly | Gly  | Arg | Ala | His |
|     | 8555 |     |     |     |     | 8560 |     |     |     |     | 8565 |     |     |     |
| Ser | Arg  | Trp | Asp | Glu | Thr | Gly  | Arg | Phe | Pro | Asn | Pro  | Thr | Thr | Gln |
|     | 8570 |     |     |     |     | 8575 |     |     |     |     | 8580 |     |     |     |
| Thr | Gly  | Lys | Lys | Glu | Arg | Gln  | Gly | Tyr | Lys | Ser | Trp  | Arg | Gly | His |
|     | 8585 |     |     |     |     | 8590 |     |     |     |     | 8595 |     |     |     |
| Lys | Asn  | Ala | Ile | Val | Ser | Cys  | Leu | Gln | Ala | Cys | Gly  | Gly | Asn | Ile |
|     | 8600 |     |     |     |     | 8605 |     |     |     |     | 8610 |     |     |     |
| Ser | Phe  | Thr | Arg | Arg | Tyr | Leu  | Leu | Phe | His | Arg | Gly  | Val | Asn | Phe |
|     | 8615 |     |     |     |     | 8620 |     |     |     |     | 8625 |     |     |     |
| Pro | Arg  | Asn | Ile | Leu | His | Tyr  | Tyr | Arg | His | Leu | His  | Ser | Pro | Tyr |
|     | 8630 |     |     |     |     | 8635 |     |     |     |     | 8640 |     |     |     |
| Tyr | Cys  | Phe | Gln | Glu | Glu | Ala  | Glu | Thr | Gln | Gln | Gln  | Gln | Lys | Thr |
|     | 8645 |     |     |     |     | 8650 |     |     |     |     | 8655 |     |     |     |

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Ser Gly Ser Ser Ser Lys Ile His Ser Gly Gly Arg Trp Thr Glu  
 8660 8665 8670  
 Asp Arg Gly Glu Arg Ala Gly Ala Asp Pro Gly Ala Glu Glu Pro  
 8675 8680 8685  
 Asp Leu Ser His Pro Leu Cys His Leu Pro Ala Glu Ser Gly Ala  
 8690 8695 8700  
 Gly Ala Gly Thr Glu Ser Gln Glu Pro Phe Ser Ala Leu Ala His  
 8705 8710 8715  
 Pro Gln Leu Ser Val Ser Gln Glu Arg Arg Pro Thr Ser Ala His  
 8720 8725 8730  
 Ser Arg Gly Arg Arg Gly Ser Leu Gln Gln Val Leu Arg Ala His  
 8735 8740 8745  
 Ser Arg Val Ala Arg Ala Arg Pro His Thr Glu Lys Gly Gly Asn  
 8750 8755 8760  
 Tyr Val Thr Thr Cys Ala Leu Arg Pro Thr Ile Met Ser Lys Glu  
 8765 8770 8775  
 Ile Pro Thr Pro Tyr Met Trp Ser Tyr Gln Pro Gln Met Gly Leu  
 8780 8785 8790  
 Ala Ala Gly Ala Ala Gln Asp Tyr Ser Thr Arg Met Asn Trp Leu  
 8795 8800 8805  
 Ser Ala Gly Pro Ala Met Ile Ser Arg Val Asn Asp Ile Arg Ala  
 8810 8815 8820  
 His Arg Asn Gln Ile Leu Leu Glu Gln Ser Ala Ile Thr Ala Thr  
 8825 8830 8835  
 Pro Arg His His Leu Asn Pro Arg Asn Trp Pro Ala Ala Leu Val  
 8840 8845 8850  
 Tyr Gln Glu Ile Pro Gln Pro Thr Thr Val Leu Leu Pro Arg Asp  
 8855 8860 8865  
 Ala Gln Ala Glu Val Gln Leu Thr Asn Ser Gly Val Gln Leu Ala  
 8870 8875 8880  
 Gly Gly Ala Ala Leu Cys Arg His Arg Pro Ala Gln Gly Ile Lys  
 8885 8890 8895

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Leu | Val | Ile | Arg | Gly | Arg  | Gly | Thr | Gln | Leu | Asn  | Asp | Glu | Val |
| 8900 |     |     |     |     |     | 8905 |     |     |     |     | 8910 |     |     |     |
| Val  | Ser | Ser | Ser | Leu | Gly | Leu  | Arg | Pro | Asp | Gly | Val  | Phe | Gln | Leu |
| 8915 |     |     |     |     |     | 8920 |     |     |     |     | 8925 |     |     |     |
| Ala  | Gly | Ser | Gly | Arg | Ser | Ser  | Phe | Thr | Pro | Arg | Gln  | Ala | Val | Leu |
| 8930 |     |     |     |     |     | 8935 |     |     |     |     | 8940 |     |     |     |
| Thr  | Leu | Glu | Ser | Ser | Ser | Ser  | Gln | Pro | Arg | Ser | Gly  | Gly | Ile | Gly |
| 8945 |     |     |     |     |     | 8950 |     |     |     |     | 8955 |     |     |     |
| Thr  | Leu | Gln | Phe | Val | Glu | Glu  | Phe | Thr | Pro | Ser | Val  | Tyr | Phe | Asn |
| 8960 |     |     |     |     |     | 8965 |     |     |     |     | 8970 |     |     |     |
| Pro  | Phe | Ser | Gly | Ser | Pro | Gly  | His | Tyr | Pro | Asp | Glu  | Phe | Ile | Pro |
| 8975 |     |     |     |     |     | 8980 |     |     |     |     | 8985 |     |     |     |
| Asn  | Phe | Asp | Ala | Ile | Ser | Glu  | Ser | Val | Asp | Gly | Tyr  | Asp | Met | Ser |
| 8990 |     |     |     |     |     | 8995 |     |     |     |     | 9000 |     |     |     |
| His  | Gly | Gly | Ala | Ala | Asp | Leu  | Ala | Arg | Leu | Arg | His  | Leu | Asp | His |
| 9005 |     |     |     |     |     | 9010 |     |     |     |     | 9015 |     |     |     |
| Cys  | Arg | Arg | Phe | Arg | Cys | Phe  | Ala | Arg | Asp | Leu | Ala  | Glu | Phe | Ala |
| 9020 |     |     |     |     |     | 9025 |     |     |     |     | 9030 |     |     |     |
| Tyr  | Phe | Glu | Leu | Pro | Glu | Glu  | His | Pro | Gln | Gly | Pro  | Ala | His | Gly |
| 9035 |     |     |     |     |     | 9040 |     |     |     |     | 9045 |     |     |     |
| Val  | Arg | Ile | Ile | Val | Glu | Gly  | Gly | Leu | Asp | Ser | His  | Leu | Leu | Arg |
| 9050 |     |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Ile  | Phe | Ser | Gln | Arg | Pro | Ile  | Leu | Val | Glu | Arg | Glu  | Gln | Gly | Gln |
| 9065 |     |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Thr  | Leu | Leu | Thr | Leu | Tyr | Cys  | Ile | Cys | Asn | His | Pro  | Gly | Leu | His |
| 9080 |     |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Glu  | Ser | Leu | Cys | Cys | Leu | Leu  | Cys | Thr | Glu | Tyr | Asn  | Lys | Ser | Asp |
| 9095 |     |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Gln  | Arg | Leu | Leu | Arg | Thr | Arg  | Leu | Trp | Cys | Ser | Cys  | Tyr | Gln | Pro |
| 9110 |     |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Val  | Pro | Val | Leu | His | Arg | Glu  | Arg | Asp | Arg | Ala | Pro  | Ala | Pro | Val |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| 9125 |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Pro | Gln | Glu | Val | Pro | His  | Leu | Ala | Val | Pro | Gly  | Leu | Pro | Asp |
| 9140 |     |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Arg  | Arg | Cys | Gln | Pro | Leu | Arg  | Gln | Arg | Arg | Ser | Pro  | Ala | Glu | Arg |
| 9155 |     |     |     |     |     | 9160 |     |     |     |     | 9165 |     |     |     |
| Pro  | Cys | Gln | Pro | Tyr | Phe | Phe  | His | Pro | Gln | Lys | Gln  | Ala | Pro | Ala |
| 9170 |     |     |     |     |     | 9175 |     |     |     |     | 9180 |     |     |     |
| Leu  | Pro | Thr | Leu | Pro | Pro | Arg  | Asp | Leu | Ser | Val | Arg  | Leu | Arg | Thr |
| 9185 |     |     |     |     |     | 9190 |     |     |     |     | 9195 |     |     |     |
| Leu  | Pro | Ser | His | Leu | Pro | Pro  | Asp | Pro | Glu | Tyr | His  | Ser | Ala | Ala |
| 9200 |     |     |     |     |     | 9205 |     |     |     |     | 9210 |     |     |     |
| Pro  | Arg | Tyr | Gln | Pro | Asn | Tyr  | Pro | Pro | Thr | Pro | Pro  | Ser | Arg | Pro |
| 9215 |     |     |     |     |     | 9220 |     |     |     |     | 9225 |     |     |     |
| Phe  | Leu | Ile | Tyr | His | Tyr | Arg  | Arg | Trp | Leu | Leu | Leu  | Leu | Val | Leu |
| 9230 |     |     |     |     |     | 9235 |     |     |     |     | 9240 |     |     |     |
| Pro  | Arg | Pro | Val | Asp | Pro | Arg  | Ser | Pro | Thr | Gln | Ser  | Pro | Glu | Glu |
| 9245 |     |     |     |     |     | 9250 |     |     |     |     | 9255 |     |     |     |
| Val  | Arg | Lys | Cys | Lys | Phe | Gln  | Glu | Pro | Trp | Lys | Phe  | Leu | Lys | Cys |
| 9260 |     |     |     |     |     | 9265 |     |     |     |     | 9270 |     |     |     |
| Tyr  | Arg | Gln | Lys | Ser | Asp | Met  | His | Pro | Ser | Trp | Ile  | Met | Ile | Ile |
| 9275 |     |     |     |     |     | 9280 |     |     |     |     | 9285 |     |     |     |
| Gly  | Ile | Val | Asn | Ile | Leu | Ala  | Cys | Thr | Leu | Ile | Ser  | Phe | Val | Ile |
| 9290 |     |     |     |     |     | 9295 |     |     |     |     | 9300 |     |     |     |
| Tyr  | Pro | Cys | Phe | Asp | Phe | Gly  | Trp | Asn | Ser | Pro | Glu  | Ala | Leu | Tyr |
| 9305 |     |     |     |     |     | 9310 |     |     |     |     | 9315 |     |     |     |
| Leu  | Pro | Pro | Glu | Pro | Asp | Thr  | Pro | Pro | Gln | Gln | Gln  | Pro | Gln | Ala |
| 9320 |     |     |     |     |     | 9325 |     |     |     |     | 9330 |     |     |     |
| His  | Ala | Leu | Pro | Pro | Pro | Gln  | Pro | Arg | Pro | Gln | Tyr  | Met | Pro | Ile |
| 9335 |     |     |     |     |     | 9340 |     |     |     |     | 9345 |     |     |     |
| Leu  | Asp | Tyr | Glu | Ala | Glu | Pro  | Gln | Arg | Pro | Met | Leu  | Pro | Ala | Ile |
| 9350 |     |     |     |     |     | 9355 |     |     |     |     | 9360 |     |     |     |



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Ser Tyr Phe Asn Leu Thr Gly Gly Asp Asp Pro Thr Gly Gln Gln  
 9365 9370 9375  
  
 Arg Gln Arg Pro Ser Pro Gly His Gly Arg Pro Arg Leu Gly Ala  
 9380 9385 9390  
  
 Ala Thr Arg Pro Thr Ser His Ser Ser Ala Ala Gly Glu Ser Arg  
 9395 9400 9405  
  
 Gln Gly Ala Ala Gly Arg His Ser His Pro Pro Val Gln Glu Arg  
 9410 9415 9420  
  
 His Leu Leu Pro Gly Glu Thr Gly Gln Asp Leu Leu Arg Gly His  
 9425 9430 9435  
  
 Pro Asp Arg Pro Ser Pro Leu Leu Arg Ala Pro Ala Ala Ala Pro  
 9440 9445 9450  
  
 Glu Val His Leu Pro Gly Arg Ser Gln Pro His Arg His His Pro  
 9455 9460 9465  
  
 Ala Val Gly Arg Tyr Gln Gly Val His Pro Leu Leu Leu Arg Leu  
 9470 9475 9480  
  
 Pro Arg Leu Arg Pro His Ser Asp Gln Asp Pro Leu Arg Pro Pro  
 9485 9490 9495  
  
 Arg Pro Pro Pro His Glu Leu Ile Thr Pro Leu Ser Ser Glu Ile  
 9500 9505 9510  
  
 Lys Ile Ile Leu Met Met Ile Ile Lys Lys Ile Ile Ile Phe Glu  
 9515 9520 9525  
  
 Ile Lys Ile Gln Ser Tyr Phe Glu Phe Asn Lys Asn Lys Glu Ser  
 9530 9535 9540  
  
 Leu Thr Asn Leu Ile Pro Gly Leu Cys Pro Cys Phe Leu Pro Thr  
 9545 9550 9555  
  
 Pro Pro His Ser Pro Leu Pro Ser Ser Gly Thr Ala Gly Pro Gly  
 9560 9565 9570  
  
 Gly Leu Gln Thr Ser Ser Thr Arg Arg Gly Cys Gln Ile Pro Pro  
 9575 9580 9585  
  
 Val Pro Gln Ser Ser Phe Tyr Leu Leu Ser Asp Val Gln Lys Ala  
 9590 9595 9600

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Pro  | Gly | Gly | Leu | Arg | Pro  | Arg | Leu | Pro | Leu | Arg  | Cys | Arg | Gln |
|     | 9605 |     |     |     |     | 9610 |     |     |     |     | 9615 |     |     |     |
| Arg | Thr  | Asp | Arg | Ala | Leu | His  | Gln | Pro | Pro | Leu | Arg  | Leu | Phe | Arg |
|     | 9620 |     |     |     |     | 9625 |     |     |     |     | 9630 |     |     |     |
| Trp | Ile  | Pro | Arg | Glu | Ala | Pro  | Gly | Gly | Val | Val | Pro  | Ala | Thr | Gly |
|     | 9635 |     |     |     |     | 9640 |     |     |     |     | 9645 |     |     |     |
| Pro | Arg  | His | His | Gln | Glu | Arg  | Gly | Asn | His | Pro | Gln  | Ala | Gly | Arg |
|     | 9650 |     |     |     |     | 9655 |     |     |     |     | 9660 |     |     |     |
| Gly | Gly  | Gly | Pro | Arg | Leu | Val  | Gly | Lys | Thr | His | Leu  | Gln | His | Gly |
|     | 9665 |     |     |     |     | 9670 |     |     |     |     | 9675 |     |     |     |
| His | Gln  | Gly | Arg | Arg | Pro | Ser  | Gln | Tyr | Phe | Lys | Gln  | His | His | Phe |
|     | 9680 |     |     |     |     | 9685 |     |     |     |     | 9690 |     |     |     |
| Pro | Asn  | Cys | Cys | Pro | Phe | Leu  | Gln | Gln | Gln | Trp | Asn  | Phe | Lys | Pro |
|     | 9695 |     |     |     |     | 9700 |     |     |     |     | 9705 |     |     |     |
| Gln | Cys  | Leu | His | Thr | Ile | Ser  | Ser | Ile | Ser | His | Ile  | His | Phe | Arg |
|     | 9710 |     |     |     |     | 9715 |     |     |     |     | 9720 |     |     |     |
| His | Lys  | Ser | Trp | Lys | Arg | Ser  | Ser | Asp | Phe | Lys | Val  | Val | Asp | Cys |
|     | 9725 |     |     |     |     | 9730 |     |     |     |     | 9735 |     |     |     |
| Thr | Thr  | Asn | Ser | Ser | Ser | Tyr  | Ile | Gln | Leu | Lys | His  | His | Ser | Lys |
|     | 9740 |     |     |     |     | 9745 |     |     |     |     | 9750 |     |     |     |
| Asn | Arg  | Gln | Arg | Ala | Ile | Tyr  | Leu | Gln | Trp | Lys | Gln  | Arg | Thr | Gly |
|     | 9755 |     |     |     |     | 9760 |     |     |     |     | 9765 |     |     |     |
| Tyr | Lys  | Pro | Lys | Lys | Arg | Thr  | Ser | Phe | Arg | Cys | Tyr  | Cys | Asn | Ile |
|     | 9770 |     |     |     |     | 9775 |     |     |     |     | 9780 |     |     |     |
| Tyr | Trp  | Lys | Trp | Leu | Arg | Leu  | Trp | Ile | Leu | Trp | Lys  | Asn | Lys | Thr |
|     | 9785 |     |     |     |     | 9790 |     |     |     |     | 9795 |     |     |     |
| Arg | Asn  | Tyr | Gln | Asn | Trp | Ser  | Arg | Ile | Lys | Phe | Cys  | Gln | Ser | Asn |
|     | 9800 |     |     |     |     | 9805 |     |     |     |     | 9810 |     |     |     |
| Ser | Cys  | Gln | Thr | Arg | His | Arg  | Phe | Lys | Phe | Leu | Arg  | Trp | Cys | Leu |
|     | 9815 |     |     |     |     | 9820 |     |     |     |     | 9825 |     |     |     |
| Asp | Ser  | Trp | Lys | Gln | Thr | Gly  | Gln | Ala | Asn | Thr | Leu  | Asp | Tyr | Pro |
|     | 9830 |     |     |     |     | 9835 |     |     |     |     | 9840 |     |     |     |

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Pro Lys Pro Leu Ser Ile Thr Phe Arg Gln Arg Cys Gln Ile Tyr  
9845 9850 9855

Ser Leu Ser Tyr Lys Met Arg Ser Asn Thr Arg His Cys Gly Ser  
9860 9865 9870

Gly Gly Cys Tyr Cys Arg Ile Ser Thr Lys Ser Asn His Ser Gln  
9875 9880 9885

Lys Arg His Ser Phe Pro Ile Phe Arg Trp Cys Thr His Val Lys  
9890 9895 9900

Leu Ile Asn Gly Arg Leu Leu Glu Leu Gly Gly Thr Asp His Ser  
9905 9910 9915

Lys Cys Ser Leu Tyr Lys Cys Cys Gly Ile His Ala Lys Tyr Arg  
9920 9925 9930

Cys Ile Ser Lys Asn Pro Lys Asn Thr Lys His Ser Gln Ser Gly  
9935 9940 9945

Ile Phe Asn Trp Arg Asn Tyr Tyr Ala Asn Asp Thr Asn His Asn  
9950 9955 9960

Phe Gln Trp His Lys Arg His Asn Pro Ser His Leu Leu Tyr Asp  
9965 9970 9975

Phe Tyr Met Ala Val Asp Trp Arg Leu Gly Gln Lys Tyr Tyr Leu  
9980 9985 9990

Cys Tyr Gln Leu Ile Leu Phe Phe Leu His Arg Pro Gly Ile Ile  
9995 10000 10005

Pro Pro Ser Lys Pro Thr Pro Phe Pro Thr Thr Phe Val Tyr Met  
10010 10015 10020

Glu Thr Leu Lys Gln Lys Asn Lys Val Gln Val Phe Tyr Ile Asn  
10025 10030 10035

Ser Phe Thr Gly Leu Glu Gln Leu Phe Phe Leu His Pro Pro Arg  
10040 10045 10050

Thr Trp Asn Thr Pro Pro Ser Pro Pro Ala Gln Pro Thr Ser Glu  
10055 10060 10065

Cys His Trp Trp Thr Cys Phe Trp Ser Pro Arg Ser Thr Gln Phe

10070

10075

10080

|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Gln   | Ser | Glu | Pro | Val | Ser | Asp   | Arg | Ser | Gly | Arg | Asn   | Pro | Pro | Gly |
| 10085 |     |     |     |     |     | 10090 |     |     |     |     | 10095 |     |     |     |
| Thr   | Pro | Ala | Ser | Ala | Pro | His   | Ser | Ser | Thr | Ala | Glu   | Asp | Cys | Pro |
| 10100 |     |     |     |     |     | 10105 |     |     |     |     | 10110 |     |     |     |
| Arg   | Trp | Ser | Gly | Ser | Arg | Leu   | Ser | Gly | Arg | Ser | Arg   | Arg | Ala | Ala |
| 10115 |     |     |     |     |     | 10120 |     |     |     |     | 10125 |     |     |     |
| Val   | Gly | Ile | Ile | Val | Arg | Glu   | Arg | Asp | Arg | Pro | Val   | Val | Ser | His |
| 10130 |     |     |     |     |     | 10135 |     |     |     |     | 10140 |     |     |     |
| Gln   | Ala | Pro | Gln | Gln | Ser | Leu   | Pro | Pro | Pro | Leu | Arg   | Gln | Ala | Ala |
| 10145 |     |     |     |     |     | 10150 |     |     |     |     | 10155 |     |     |     |
| Ala   | Gln | Gly | Val | Arg | Val | Gln   | Gly | Leu | Pro | Gln | His   | Asp | Ala | His |
| 10160 |     |     |     |     |     | 10165 |     |     |     |     | 10170 |     |     |     |
| Gly   | Pro | Gln | His | Gln | Ser | Ser   | Gly | Ala | Ala | Gly | Ala   | Ala | Ala | His |
| 10175 |     |     |     |     |     | 10180 |     |     |     |     | 10185 |     |     |     |
| Ala   | Asn | Leu | Ala | Gln | Val | Thr   | Ala | Val | Arg | Ala | Thr   | Gln | Asp | His |
| 10190 |     |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| Gln   | Val | Val | Gln | Gln | Ser | Ile   | Val | Gln | His | Ala | Pro   | Ala | Glu | Thr |
| 10205 |     |     |     |     |     | 10210 |     |     |     |     | 10215 |     |     |     |
| His   | Arg | Gly | Lys | Asp | Ala | Thr   | His | Val | Ala | Val | Val   | Pro | Asp | Pro |
| 10220 |     |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |
| Gln   | Val | Asn | Gln | Val | Ala | Leu   | Pro | Pro | Glu | Asp | Ala   | Ala | His | Val |
| 10235 |     |     |     |     |     | 10240 |     |     |     |     | 10245 |     |     |     |
| His   | Asp | Leu | Leu | Gly | His | Val   | Ala | Val | His | His | Leu   | Pro | Val | Pro |
| 10250 |     |     |     |     |     | 10255 |     |     |     |     | 10260 |     |     |     |
| His   | His | Pro | Leu | Val | Glu | His   | Ala | Ala | Pro | Asp | Asp   | Pro | Ala | Glu |
| 10265 |     |     |     |     |     | 10270 |     |     |     |     | 10275 |     |     |     |
| Pro   | Gln | Gly | Gln | His | Arg | Pro   | Ala | Arg | His | Ala | Ala   | Lys | Arg | Pro |
| 10280 |     |     |     |     |     | 10285 |     |     |     |     | 10290 |     |     |     |
| Arg   | Ile | Pro | Ala | Met | Thr | Met   | Glu | Asp | Pro | Pro | Leu   | Val | Pro | Val |
| 10295 |     |     |     |     |     | 10300 |     |     |     |     | 10305 |     |     |     |

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Asp His Leu Gly Ala Glu Gln Val Tyr Val Gly Thr Ala Gln Ala  
 10310 10315 10320  
 Tyr Ala His Ala Ser Leu Gln His Ser Gln Leu Leu Gly Gly Gln  
 10325 10330 10335  
 Asn His Ile Pro Gly His Gly Glu Leu Leu Gln Asp Ser Glu Pro  
 10340 10345 10350  
 Arg Arg Thr Gly Gln Ser Ser His Ile Thr Tyr Ile Val His Gly  
 10355 10360 10365  
 Gln Gly Ile Ala Ile Arg Gln His Arg Val Ile Leu His Gln Arg  
 10370 10375 10380  
 Ser Ala Gly Leu Gly Leu Leu Thr Ala Trp Gly Gly Arg Pro Ile  
 10385 10390 10395  
 Arg Val Met Ala Gly Arg Gly Ser Cys Ser Arg Pro Cys His Asp  
 10400 10405 10410  
 Ala Val Ala Phe Gly His Phe Arg Thr Cys Cys Ser Arg Thr Trp  
 10415 10420 10425  
 Ser Gly Arg Cys Thr Pro Ile Ala Gly Gly Gly Leu Gly Ala Trp  
 10430 10435 10440  
 Asn Ala Arg Cys Ser Cys Lys Thr Ala Thr Leu Ser Asp Arg Ala  
 10445 10450 10455  
 Ala Asp Leu Gly Pro Gln Glu Arg Ser His His Ala Leu Ser His  
 10460 10465 10470  
 Arg Pro Pro Trp Asn Gly Pro Gly Pro Ala Arg Cys Asn Phe Val  
 10475 10480 10485  
 Gly Phe Arg Arg Arg Gly Arg Glu Glu Gln Glu Glu Pro Leu Thr  
 10490 10495 10500  
 Phe Asn Pro Asn Gly Leu Gly Ala Leu Gln Asn Glu Gly His Gly  
 10505 10510 10515  
 Asp Gly Thr Ser Arg Pro Arg Cys Val Gly Gly Lys Gln Pro Gly  
 10520 10525 10530  
 Gln Arg Tyr Gly Ser Arg Asp Val Pro Arg Trp Leu Pro Ala Lys  
 10535 10540 10545

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Pro | Pro   | Arg | Ala | His | Pro | Glu   | Thr | Arg | Gln | Arg | Lys   | Arg | Glu | Gly |
|     | 10550 |     |     |     |     | 10555 |     |     |     |     | 10560 |     |     |     |
| Ser | Leu   | Ile | Pro | Gln | Pro | Ser   | Cys | Tyr | Thr | Pro | Ala   | Pro | Ser | Pro |
|     | 10565 |     |     |     |     | 10570 |     |     |     |     | 10575 |     |     |     |
| Asp | Asn   | Phe | His | Phe | Ser | Ser   | Leu | Glu | Phe | Glu | Leu   | Val | Pro | Glu |
|     | 10580 |     |     |     |     | 10585 |     |     |     |     | 10590 |     |     |     |
| Val | Asn   | Pro | Ser | Gln | Pro | Lys   | Ala | Arg | Ala | Glu | His   | Pro | Pro | Pro |
|     | 10595 |     |     |     |     | 10600 |     |     |     |     | 10605 |     |     |     |
| Ala | Phe   | Leu | Ser | Thr | Pro | Ser   | Phe | Gln | Asp | Ile | Leu   | Leu | Leu | Val |
|     | 10610 |     |     |     |     | 10615 |     |     |     |     | 10620 |     |     |     |
| His | Leu   | Gln | Gln | Ile | Asp | Lys   | Arg | Asn | Ile | Lys | Ile   | Ser | Ala | Ala |
|     | 10625 |     |     |     |     | 10630 |     |     |     |     | 10635 |     |     |     |
| Ile | Pro   | Glu | Leu | Leu | Pro | Gln   | Gln | Leu | Val | Leu | Phe   | His | Ile | Val |
|     | 10640 |     |     |     |     | 10645 |     |     |     |     | 10650 |     |     |     |
| Ser | Glu   | Ile | Phe | Ser | His | Arg   | Thr | Pro | Arg | Asn | Lys   | Arg | Arg | Ala |
|     | 10655 |     |     |     |     | 10660 |     |     |     |     | 10665 |     |     |     |
| Ser | His   | Ile | Thr | Asp | Lys | Pro   | Lys | Ser | Pro | Pro | Val   | Ser | Ile | Ala |
|     | 10670 |     |     |     |     | 10675 |     |     |     |     | 10680 |     |     |     |
| Lys | Cys   | Lys | Ile | Glu | Ile | Ser   | Met | Leu | Ala | Arg | Pro   | Gly | Asp | Ile |
|     | 10685 |     |     |     |     | 10690 |     |     |     |     | 10695 |     |     |     |
| Phe | Gln   | Ile | Thr | Gly | Gln | Lys   | Ile | Gly | Ala | Ile | Phe   | Lys | Lys | Ile |
|     | 10700 |     |     |     |     | 10705 |     |     |     |     | 10710 |     |     |     |
| Asn | Lys   | Arg | Lys | Ile | Phe | Gln   | Val | His | Val | Gly | Leu   | Gly | Asn | Asn |
|     | 10715 |     |     |     |     | 10720 |     |     |     |     | 10725 |     |     |     |
| Asp | Gly   | Val | Ser | Ala | Arg | Gly   | Ala | Phe | Gln | His | Gly   | Leu | Ala | Asp |
|     | 10730 |     |     |     |     | 10735 |     |     |     |     | 10740 |     |     |     |
| Leu | Lys   | Asn | Lys | Lys | Asn | Ile   | Lys | Pro | Cys | Pro | Gly   | Glu | Gln | Val |
|     | 10745 |     |     |     |     | 10750 |     |     |     |     | 10755 |     |     |     |
| Gly | Lys   | Ser | Phe | Ser | Pro | Ala   | Pro | Gly | Arg | Pro | Arg   | Gly | Leu | Arg |
|     | 10760 |     |     |     |     | 10765 |     |     |     |     | 10770 |     |     |     |
| Arg | Asp   | Pro | Arg | Lys | Asn | Cys   | Arg | Tyr | Asp | Lys | Pro   | Ser | Gln | Arg |
|     | 10775 |     |     |     |     | 10780 |     |     |     |     | 10785 |     |     |     |

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|                  |                              |                              |             |
|------------------|------------------------------|------------------------------|-------------|
| Asp Val<br>10790 | Pro Gly Gly Arg Arg<br>10795 | Glu Phe Glu Lys Lys<br>10800 | His Thr Pro |
| Pro Glu<br>10805 | His Trp Ser Pro Val<br>10810 | Lys Lys Ser Gly Arg<br>10815 | Gly Ser Asn |
| Glu Ala<br>10820 | Leu Gln Arg Ser Leu<br>10825 | Ser Ser Pro Ala Lys<br>10830 | Arg Cys His |
| Ala Asp<br>10835 | Glu Ala Gln Asn Phe<br>10840 | Gln Val Arg Lys Lys<br>10845 | Cys Asn Tyr |
| Ser Pro<br>10850 | Pro Ala Gln Ala Ala<br>10855 | Lys Leu Pro Ile Pro<br>10860 | Pro Asp Thr |
| His Thr<br>10865 | Lys Pro Gln Arg Pro<br>10870 | Leu Thr Glu Arg Gln<br>10875 | Gln Gln Arg |
| His Thr<br>10880 | Thr Gly Ala Arg Val<br>10885 | Arg Glu Lys Thr Glu<br>10890 | Leu Pro Val |
| Arg Pro<br>10895 | Leu Ser Ala Gln Tyr<br>10900 | Ile Ala Pro Asp Leu<br>10905 | His Arg Lys |
| Gly Gln<br>10910 | Ser Leu Lys Ile Pro<br>10915 | Ala Lys Ser His Thr<br>10920 | Pro Ser Thr |
| Arg Pro<br>10925 | Glu Thr Gly Asp Thr<br>10930 | Leu Arg Lys Ile Arg<br>10935 | Ala Leu Pro |
| Gln Thr<br>10940 | Ala Lys Leu Pro Ser<br>10945 | Phe Pro Gly Ser His<br>10950 | Ala Thr Ser |
| Ser Lys<br>10955 | His Asp Phe Gln Ile<br>10960 | Pro Ser Thr Val Lys<br>10965 | Asn Ile Thr |
| Arg Pro<br>10970 | Ala Pro Asn Gly Arg<br>10975 | Arg Ser Arg Ser Gln<br>10980 | Ser Pro Ser |
| Ser Leu<br>10985 | Pro Lys Phe Lys Gln<br>10990 | Leu Ile Cys Ile Leu<br>10995 | Thr Arg Thr |
| Lys Ser<br>11000 | Leu Arg Tyr Ile Ile<br>11005 | Asp Asp                      |             |

&lt;210&gt; 10

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&lt;211&gt; 10774

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificially Synthesized

&lt;400&gt; 10

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
 1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Cys Gly Ser Gly Asp Arg  
 20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Met Arg Arg Ser Arg Phe  
 35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg  
 50 55 60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
 65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
 85 90 95

Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
 100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
 115 120 125

Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
 130 135 140

Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
 145 150 155 160

Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
 165 170 175

Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
 180 185 190

Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
 195 200 205

Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
 210 215 220



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Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
225 230 235 240

Ser Tyr Ser Ile Thr Gly Ser Leu Val His Ser Pro Tyr Met Glu Phe  
245 250 255

Arg Val Thr Leu Thr Val Asn Gly Pro Pro Gly Pro Pro Asn Asp Pro  
260 265 270

Arg Pro Leu Thr Ser Ile Met Thr Tyr Val Pro Ile Val Thr Pro Ile  
275 280 285

Gly Thr Phe His Arg Gln Trp Val Glu Tyr Leu Arg Thr Ala His Leu  
290 295 300

Ala Val His Gln Val Tyr His Met Pro Ser Thr Pro Pro Ile Asp Val  
305 310 315 320

Asn Asp Gly Lys Trp Pro Ala Trp His Tyr Ala Gln Tyr Met Thr Leu  
325 330 335

Trp Asp Phe Pro Thr Trp Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile  
340 345 350

Thr Met Val Met Arg Phe Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe  
355 360 365

Asp Ser Arg Gly Phe Pro Ser Leu His Pro Ile Asp Val Asn Gly Ser  
370 375 380

Leu Phe Trp His Gln Asn Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn  
385 390 395 400

Ser Ala Pro Leu Thr Gln Met Gly Gly Arg Arg Val Arg Trp Glu Val  
405 410 415

Tyr Ile Ser Arg Ala Arg Leu Val Asn Arg Gln Ile Thr Arg Ser Phe  
420 425 430

Ile Ala Val Val Tyr His Ser Ile Ala Asn Ala Val Ser Ala Ser Asp  
435 440 445

Thr Thr Val Ser Asn Leu Ser Cys Arg Ser Trp Ser Gly Thr Gly Gln  
450 455 460

Val Ser Ile Lys Val Thr Arg Gln Val Gly Asp Gln Lys Leu Gly Leu

```

465                               470                               475                               480
Ser Arg Gln Arg Arg Leu Leu Arg Phe Ala Pro Ile Gly Leu Thr Asp
                               485                               490                               495
Ile His Phe Ala Phe Leu Ser Thr Gly Val His Ser Gln Phe Asn Tyr
                               500                               505                               510
Ser Ser Gly Ser Thr Tyr Asp Ser Leu Ala Ser Ala Thr Met Gly Ala
                               515                               520                               525
Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
                               530                               535                               540
Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
545                               550                               555                               560
Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
                               565                               570                               575
Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
                               580                               585                               590
Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala
595                               600                               605
Thr Leu Tyr Cys Val His Gln Arg Ile Glu Val Lys Asp Thr Lys Glu
610                               615                               620
Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala
625                               630                               635                               640
Gln Gln Ala Ala Ala Asp Thr Gly Asn Ser Ser Gln Val Ser Gln Asn
645                               650                               655
Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
660                               665                               670
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
675                               680                               685
Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
690                               695                               700
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
705                               710                               715                               720

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## 368530-7006W01\_SequenceListing\_ST25.txt

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu  
                   725                  730                  735

Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln  
                   740                  745                  750

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu  
                   755                  760                  765

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly  
                   770                  775                  780

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg  
                   785                  790                  795                  800

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu  
                   805                  810                  815

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
                   820                  825                  830

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
                   835                  840                  845

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
                   850                  855                  860

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
                   865                  870                  875                  880

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr  
                   885                  890                  895

Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg  
                   900                  905                  910

Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys  
                   915                  920                  925

Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu  
                   930                  935                  940

Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly  
                   945                  950                  955                  960

Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser  
                   965                  970                  975

## 368530-7006W01\_SequenceListing\_ST25.txt

Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg Phe Gly Glu  
 980 985 990  
  
 Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp Lys Glu Leu  
 995 1000 1005  
  
 Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Asn Asp Pro Ser  
 1010 1015 1020  
  
 Ser Gln Ser Ser Val Thr Gly Pro Leu Glu Ser Thr Arg Ala Ala  
 1025 1030 1035  
  
 Lys Pro Leu Ile Ser Leu Asp Cys Ala Phe Leu Pro Ala Ile Cys  
 1040 1045 1050  
  
 Cys Leu Pro Leu Pro Arg Ala Phe Leu Asp Pro Gly Arg Cys His  
 1055 1060 1065  
  
 Ser His Cys Pro Phe Leu Ile Lys Gly Asn Cys Ile Ala Leu Ser  
 1070 1075 1080  
  
 Glu Val Ser Phe Tyr Ser Gly Gly Trp Gly Gly Ala Gly Gln Gln  
 1085 1090 1095  
  
 Gly Gly Gly Leu Gly Arg Gln Gln Ala Cys Trp Gly Cys Gly Gly  
 1100 1105 1110  
  
 Leu Tyr Gly Phe Gly Gly Lys Asn Gln Gln Ile Cys Arg Ser Glu  
 1115 1120 1125  
  
 Phe Ile Tyr Val Gly Cys Gly Glu Arg Gly Asn Glu Met Val Leu  
 1130 1135 1140  
  
 Trp Val Leu Trp Val Cys Ile Asn Glu Ser Val Arg Tyr Arg His  
 1145 1150 1155  
  
 Met Leu Ala Thr Val His Val Ala Ser His Pro Arg Lys Thr Trp  
 1160 1165 1170  
  
 Pro Glu Phe Glu His Asn Val Met Thr Arg Cys Asn Val His Leu  
 1175 1180 1185  
  
 Gly Ser Arg Arg Gly Met Phe Met Pro Tyr Gln Cys Asn Met Gln  
 1190 1195 1200  
  
 Phe Val Lys Val Leu Leu Glu Pro Asp Ala Met Ser Arg Val Ser  
 1205 1210 1215

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu | Thr  | Gly | Val | Phe | Asp | Met  | Asn | Val | Glu | Leu | Trp  | Lys | Ile | Leu |
|     | 1220 |     |     |     |     | 1225 |     |     |     |     | 1230 |     |     |     |
| Arg | Tyr  | Asp | Glu | Ser | Lys | Thr  | Arg | Cys | Arg | Ala | Cys  | Glu | Cys | Gly |
|     | 1235 |     |     |     |     | 1240 |     |     |     |     | 1245 |     |     |     |
| Gly | Lys  | His | Ala | Arg | Leu | Gln  | Pro | Val | Cys | Val | Glu  | Val | Thr | Glu |
|     | 1250 |     |     |     |     | 1255 |     |     |     |     | 1260 |     |     |     |
| Asp | Leu  | Arg | Pro | Asp | His | Leu  | Val | Leu | Ser | Cys | Asn  | Gly | Thr | Glu |
|     | 1265 |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |
| Phe | Gly  | Ser | Ser | Gly | Glu | Glu  | Ser | Asp | Ser | Glu | Cys  | Leu | Gly | Leu |
|     | 1280 |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |
| Gly | Val  | Ser | Leu | His | Glu | Gly  | Gln | Asn | Asp | Asn | Leu  | Trp | Phe | Ser |
|     | 1295 |     |     |     |     | 1300 |     |     |     |     | 1305 |     |     |     |
| Val | Cys  | Cys | Ser | Ser | Met | Ser  | Gly | Ser | Ala | Ser | Phe  | Glu | Gly | Gly |
|     | 1310 |     |     |     |     | 1315 |     |     |     |     | 1320 |     |     |     |
| Val | Phe  | Ser | Pro | Tyr | Leu | Thr  | Gly | Arg | Leu | Pro | Ser  | Trp | Ala | Gly |
|     | 1325 |     |     |     |     | 1330 |     |     |     |     | 1335 |     |     |     |
| Val | Arg  | Gln | Asn | Val | Met | Gly  | Ser | Thr | Val | Asp | Gly  | Arg | Pro | Val |
|     | 1340 |     |     |     |     | 1345 |     |     |     |     | 1350 |     |     |     |
| Gln | Pro  | Ala | Asn | Ser | Ser | Thr  | Leu | Thr | Tyr | Ala | Thr  | Leu | Ser | Ser |
|     | 1355 |     |     |     |     | 1360 |     |     |     |     | 1365 |     |     |     |
| Ser | Ser  | Val | Asp | Ala | Ala | Ala  | Ala | Ala | Ala | Ala | Ala  | Ser | Ala | Ala |
|     | 1370 |     |     |     |     | 1375 |     |     |     |     | 1380 |     |     |     |
| Ser | Ala  | Val | Arg | Gly | Met | Ala  | Leu | Gly | Ala | Gly | Tyr  | Tyr | Ser | Ser |
|     | 1385 |     |     |     |     | 1390 |     |     |     |     | 1395 |     |     |     |
| Leu | Val  | Ala | Asn | Ser | Ser | Ser  | Thr | Asn | Asn | Pro | Ala  | Ser | Leu | Asn |
|     | 1400 |     |     |     |     | 1405 |     |     |     |     | 1410 |     |     |     |
| Glu | Glu  | Lys | Leu | Leu | Leu | Leu  | Met | Ala | Gln | Leu | Glu  | Ala | Leu | Thr |
|     | 1415 |     |     |     |     | 1420 |     |     |     |     | 1425 |     |     |     |
| Gln | Arg  | Leu | Gly | Glu | Leu | Thr  | Gln | Gln | Val | Ala | Gln  | Leu | Gln | Ala |
|     | 1430 |     |     |     |     | 1435 |     |     |     |     | 1440 |     |     |     |
| Glu | Thr  | Arg | Ala | Ala | Val | Ala  | Thr | Val | Lys | Thr | Lys  | Lys | Met | Asn |

1445

1450

1455

Gln Ile Asn Gly Asp Gly Cys Phe His Arg Val Leu Asn Leu Tyr  
 1460 1465 1470

Leu Ile Phe Arg Ala Arg Ala Leu Asp His Arg Ser Arg Ser Leu  
 1475 1480 1485

Ser Thr Arg Trp Ile Phe Ser Arg Thr Arg Arg Trp Ala Trp Met  
 1490 1495 1500

Leu Arg Tyr Met Gly Met Ser Pro Ser Arg Gly Trp Arg Leu His  
 1505 1510 1515

Cys Arg Ala Ser Cys Ser Gly Met Val Leu Ile Thr Gln Ser Gln  
 1520 1525 1530

Gly Arg Arg Ala Trp Cys Cys Thr Met Ser Leu Arg Arg Arg Leu  
 1535 1540 1545

Met Ala Thr Gly Ser Pro Leu Val Val Leu Thr Asn Leu Leu Ser  
 1550 1555 1560

Trp Glu Gly Cys Met Arg Gly Glu Met Arg Cys Ile Leu Ala Trp  
 1565 1570 1575

Ile Leu Arg Leu Ala Met Phe Pro Pro Arg Ser Arg Arg Gly Phe  
 1580 1585 1590

Met Leu Cys Arg Thr Thr Ser Thr Val Tyr Pro Val His Leu Gly  
 1595 1600 1605

Asn Leu Ser Cys Asn Leu Glu Gly Lys Ala Lys Asn Leu Glu Thr  
 1610 1615 1620

Pro Leu Pro Pro Arg Phe Ser Met His Ser Ser Met Met Met Ala  
 1625 1630 1635

Met Gly Pro Trp Ala Ala Ala Trp Ala Lys Thr Phe Arg Gly Ser  
 1640 1645 1650

Asp Thr Ser Leu Trp Ser Trp Val Ser Ser Ser Ala Ile Leu Met  
 1655 1660 1665

Asn Leu Gly Arg Arg Val Pro Asp Trp Gly Thr Lys Val Pro Ser  
 1670 1675 1680

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ile | Pro  | Gly | Ala | Leu | Pro | Ser  | Gln | Ile | Cys | Ile | Ser  | Gln | Ala | Leu |
|     | 1685 |     |     |     |     | 1690 |     |     |     |     | 1695 |     |     |     |
| Ser | Ser  | Glu | Gly | Gly | Ile | Met  | Ser | Thr | Cys | Gly | Ala  | Met | Lys | Lys |
|     | 1700 |     |     |     |     | 1705 |     |     |     |     | 1710 |     |     |     |
| Thr | Val  | Ser | Gly | Ala | Gly | Glu  | Met | Ser | Trp | Ala | Glu  | Ser | Arg | Phe |
|     | 1715 |     |     |     |     | 1720 |     |     |     |     | 1725 |     |     |     |
| Arg | Ser  | Ser | Trp | Asp | Leu | Pro  | Gln | Pro | Val | Gly | Pro  | Met | Thr | Pro |
|     | 1730 |     |     |     |     | 1735 |     |     |     |     | 1740 |     |     |     |
| Met | Thr  | Gly | Cys | Arg | Trp | Leu  | Arg | Glu | Arg | Gln | Leu  | Pro | Ser | Ser |
|     | 1745 |     |     |     |     | 1750 |     |     |     |     | 1755 |     |     |     |
| Arg | Arg  | Arg | Gly | Ala | Thr | Ser  | Phe | Ile | Ile | Ser | Arg  | Thr | Cys | Met |
|     | 1760 |     |     |     |     | 1765 |     |     |     |     | 1770 |     |     |     |
| Phe | Ser  | Arg | Thr | Ser | Ser | Ala  | Arg | Arg | Arg | Ser | Pro  | Pro | Ser | Glu |
|     | 1775 |     |     |     |     | 1780 |     |     |     |     | 1785 |     |     |     |
| Arg | Ser  | Ser | Cys | Ser | Glu | Ala  | Lys | Phe | Phe | Ser | Gly  | Leu | Ser | Pro |
|     | 1790 |     |     |     |     | 1795 |     |     |     |     | 1800 |     |     |     |
| Ser | Ala  | Met | Gly | Ile | Leu | Glu  | Arg | Val | Cys | Cys | Lys  | Ser | Ser | Arg |
|     | 1805 |     |     |     |     | 1810 |     |     |     |     | 1815 |     |     |     |
| Arg | Ser  | Gln | Ser | Ser | Val | Met  | Cys | Ser | Arg | Ala | Ser  | Arg | Ser | Ser |
|     | 1820 |     |     |     |     | 1825 |     |     |     |     | 1830 |     |     |     |
| Arg | Pro  | Pro | Arg | Phe | Ala | Gly  | Trp | Gly | Asp | Cys | Gly  | Ser | Arg | Ala |
|     | 1835 |     |     |     |     | 1840 |     |     |     |     | 1845 |     |     |     |
| Pro | Gly  | Asp | Gly | Arg | Pro | Ala  | Arg | Pro | Gly | Ser | Gly  | Pro | Ser | Arg |
|     | 1850 |     |     |     |     | 1855 |     |     |     |     | 1860 |     |     |     |
| Ala | Ala  | Gly | Ser | Ala | Ser | Ala  | Trp | Ser | Pro | Ser | Arg  | Arg | Gly | Ala |
|     | 1865 |     |     |     |     | 1870 |     |     |     |     | 1875 |     |     |     |
| Arg | Arg  | Ala | Gly | Arg | Leu | Arg  | Gly | Cys | Ala | Ser | Gly  | Ser | Ser | Gly |
|     | 1880 |     |     |     |     | 1885 |     |     |     |     | 1890 |     |     |     |
| Trp | Ser  | Arg | Thr | Ala | Pro | Gly  | Arg | Arg | Pro | Ala | Arg  | Arg | Pro | Gly |
|     | 1895 |     |     |     |     | 1900 |     |     |     |     | 1905 |     |     |     |
| Ser | Asn  | Ala | Val | Arg | Ser | Ala  | Pro | Arg | Pro | Arg | Gly  | Pro | Trp | Arg |
|     | 1910 |     |     |     |     | 1915 |     |     |     |     | 1920 |     |     |     |

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Gly Ala Tyr Leu Trp Lys Cys Val Arg Arg Arg Asp Arg Gly Gly  
1925 1930 1935

Thr Gly Arg Arg Ala Trp Gly Arg Gly Arg Arg Thr Arg Gly Arg  
1940 1945 1950

Arg Arg Pro Arg Arg Ser Trp Arg Arg Arg Ser Arg Thr Pro Arg  
1955 1960 1965

Ala Arg Gly Arg Gly Gly Trp Gly Gln Lys Arg Gly Phe Leu Arg  
1970 1975 1980

Ala Phe Cys Val Ser Tyr Leu Trp Ser Pro Ala Arg Val Pro Ala  
1985 1990 1995

Gly Gln Arg Gly Cys Pro Cys Pro Arg Arg Pro Thr Leu Trp Ala  
2000 2005 2010

Gly Pro Arg Ala Gly Cys Arg Gly Pro Arg Arg Arg Gly Thr Pro  
2015 2020 2025

Pro Thr Pro Arg Arg Arg Pro Gly Ser Arg Pro Ala Arg Arg Arg  
2030 2035 2040

Pro Arg Gly Arg Gly Ser Gly Arg Cys Pro Pro Ala Gly Pro Pro  
2045 2050 2055

Ser Pro Gly Tyr Ala Ser Thr Cys Pro Pro Arg Pro His Pro Gly  
2060 2065 2070

Arg Leu Ala Cys Lys Cys Arg Pro Arg Asp Arg Gly Ser Arg Pro  
2075 2080 2085

Gly Gly Tyr Lys Arg Gly Arg Ala Pro Ala Arg Pro His Cys Leu  
2090 2095 2100

Pro Asp Arg Cys Pro Gly Ala Pro Ala Val Gly Val Gly Ile Pro  
2105 2110 2115

Ser Arg Arg Arg Ala Pro Arg His Ser Gly Cys Gln Phe Leu Glu  
2120 2125 2130

Thr Arg Arg Ile Tyr Arg Cys Arg Trp Arg Arg Leu Ser Ala Pro  
2135 2140 2145

Arg Pro Phe Gly Gln Lys Arg Arg Ser Phe Cys Cys Arg Ala Trp  
2150 2155 2160



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Trp Arg Arg Ser Arg Arg Gly Arg Trp Arg Ala Ala Trp Arg Trp  
2165 2170 2175

Ser Ala Trp Ser Gly Ser Phe Pro Cys Arg Arg Ala Pro Trp Arg  
2180 2185 2190

Arg Cys Ala Ala Arg Thr Arg Ala Pro Arg Thr Ser Ile Arg Gly  
2195 2200 2205

Arg Arg Trp Ala Arg Arg Ala Arg Phe Pro Ala Ser Arg Gly Cys  
2210 2215 2220

Ala Gly Gly Pro Arg Trp Trp Pro Pro Arg Arg Ala Gly Ala Arg  
2225 2230 2235

Trp Ser Ser Arg Gly Ala Arg Pro Cys Ala Ser Arg Arg Gly Ala  
2240 2245 2250

Ala Gly Pro Ala Ala Arg Arg Gly Gly Arg Arg Pro Arg Arg Cys  
2255 2260 2265

Arg Ala Gly Ala Arg Gly Arg Ser Ser Cys Arg Cys Pro Asp Cys  
2270 2275 2280

Pro Ala Pro Leu Ala Ser Arg Ala Arg Pro Ala Arg Ala Arg Arg  
2285 2290 2295

Gly Gly Ala Cys Pro Arg Ala Trp Gly Ala Ala Arg Arg Arg Thr  
2300 2305 2310

Cys Arg Arg Cys Arg Arg Arg Arg Gly Ala Pro Arg Gly Arg Arg  
2315 2320 2325

Cys Arg Trp Gly Ser Ser Ala Pro Arg Gly Cys Trp Arg Ala Arg  
2330 2335 2340

Ser Arg Thr Ala Arg Ala Arg Ala Arg Gly Ala Pro Cys Arg Gly  
2345 2350 2355

Trp Ser Val Ala Ala Phe Arg Arg Gly Arg Arg Ser Gly Gly Arg  
2360 2365 2370

Trp Arg Gly Ser Trp Arg Arg Trp Trp Ala Phe Gly Arg Cys Ser  
2375 2380 2385

Gly Arg Gly Ala Gly Arg Pro Ser Pro Ser Gly Arg Arg Ser Pro

2390

2395

2400

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Ala | Trp | Arg | Arg | Ala | Arg  | Arg | Arg | Gly | Arg | Pro  | Gly | Arg | Ser |
| 2405 |     |     |     |     |     | 2410 |     |     |     |     | 2415 |     |     |     |
| Ser  | Arg | Gly | Ser | Leu | Gly | Cys  | His | Thr | Ala | Gly | Pro  | Ser | Ala | Ser |
| 2420 |     |     |     |     |     | 2425 |     |     |     |     | 2430 |     |     |     |
| Thr  | Ala | Arg | Gly | Glu | Gly | Thr  | Leu | Arg | Gly | Pro | Ser  | Ser | Thr | Leu |
| 2435 |     |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |
| Arg  | Gly | Gly | Thr | Arg | Pro | Asp  | Arg | His | Gly | Lys | Ser  | Pro | Pro | Cys |
| 2450 |     |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |
| Arg  | Thr | Gly | Arg | Pro | Cys | Arg  | Arg | Ser | Ser | Pro | Ser  | Pro | Arg | Gly |
| 2465 |     |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |
| Gly  | Arg | Lys | Leu | Ala | Arg | Pro  | Cys | Ala | Gly | Arg | Cys  | Gly | Gly | Arg |
| 2480 |     |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Arg  | Cys | Arg | Ala | Pro | Pro | Gly  | Thr | Gly | Ala | Ser | Arg  | Gly | Arg | Arg |
| 2495 |     |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Ser  | Arg | Pro | Ala | Pro | Arg | Val  | Gly | Ser | Pro | Cys | Ala  | Ser | Cys | Arg |
| 2510 |     |     |     |     |     | 2515 |     |     |     |     | 2520 |     |     |     |
| Arg  | Gly | Ala | Lys | Arg | Lys | His  | Arg | Arg | Gly | Ser | Cys  | Pro | Arg | Gly |
| 2525 |     |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Ala  | Ser | Cys | Glu | Cys | Gly | Lys  | Ala | Gly | Ala | Pro | Arg  | Pro | Gly | Cys |
| 2540 |     |     |     |     |     | 2545 |     |     |     |     | 2550 |     |     |     |
| Pro  | Gly | Arg | Arg | Gly | Arg | Ser  | Arg | Arg | Ser | Arg | Cys  | Cys | Ala | Arg |
| 2555 |     |     |     |     |     | 2560 |     |     |     |     | 2565 |     |     |     |
| Arg  | Cys | Arg | Val | Pro | Arg | Ile  | Ala | Gly | Gly | Pro | Arg  | Gly | Ala | Ala |
| 2570 |     |     |     |     |     | 2575 |     |     |     |     | 2580 |     |     |     |
| Ser  | Ala | Arg | Arg | Arg | Ala | Arg  | Arg | Gly | Arg | Ala | Arg  | Ala | Ala | Arg |
| 2585 |     |     |     |     |     | 2590 |     |     |     |     | 2595 |     |     |     |
| Gly  | Pro | Ser | Arg | Arg | Arg | Gly  | Gly | Trp | Arg | Gly | Arg  | Lys | Ser | Arg |
| 2600 |     |     |     |     |     | 2605 |     |     |     |     | 2610 |     |     |     |
| Asp  | Pro | Arg | Pro | Gly | Arg | Ser  | Ala | Ser | Gly | Pro | Gly  | Thr | Asp | Gly |
| 2615 |     |     |     |     |     | 2620 |     |     |     |     | 2625 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Val  | Gly | Pro | Arg | Pro | Phe  | Phe | Arg | Gly | Arg | Ser  | Arg | Arg | Cys |
|     | 2630 |     |     |     |     | 2635 |     |     |     |     | 2640 |     |     |     |
| Gly | Gly  | Arg | Arg | Ala | Ser | Gly  | Pro | Thr | Ala | Gly | Gly  | Arg | Gly | Arg |
|     | 2645 |     |     |     |     | 2650 |     |     |     |     | 2655 |     |     |     |
| Gly | Arg  | Ala | Arg | Arg | Ala | Ala  | Gly | Pro | Arg | Arg | Val  | Ser | Pro | Ala |
|     | 2660 |     |     |     |     | 2665 |     |     |     |     | 2670 |     |     |     |
| Arg | Gly  | Arg | Ala | Ala | Cys | Arg  | Arg | Thr | Pro | Ser | Arg  | Cys | Arg | Phe |
|     | 2675 |     |     |     |     | 2680 |     |     |     |     | 2685 |     |     |     |
| Pro | His  | Arg | Arg | Gly | Arg | Ala  | Phe | Arg | Cys | Glu | Asp  | Ala | Ser | Arg |
|     | 2690 |     |     |     |     | 2695 |     |     |     |     | 2700 |     |     |     |
| Trp | Gly  | Arg | Thr | Gly | Ser | Pro  | Ala | Thr | Ser | Trp | Arg  | Asn | Gly | Cys |
|     | 2705 |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |
| Cys | Asp  | Gly | Ser | Arg | Asn | Ala  | Asp | Gly | Ala | Pro | Ser  | Thr | Arg | Ala |
|     | 2720 |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |
| Cys | Val  | Tyr | Thr | Ser | Val | Arg  | Ser | Ala | Arg | Asn | Ala  | Ala | Arg | Asp |
|     | 2735 |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |
| Ala | Arg  | Ala | Ala | Arg | Ala | Val  | Pro | Gly | Phe | Leu | Trp  | Arg | Gly | Ile |
|     | 2750 |     |     |     |     | 2755 |     |     |     |     | 2760 |     |     |     |
| Ser | Val  | Gly | Ser | Gly | Ala | Leu  | Ala | Ala | Ala | Ser | Arg  | Ala | Val | Leu |
|     | 2765 |     |     |     |     | 2770 |     |     |     |     | 2775 |     |     |     |
| Arg | Leu  | Gly | His | Arg | Arg | Gly  | His | Arg | Leu | Pro | Arg  | Trp | Trp | Ser |
|     | 2780 |     |     |     |     | 2785 |     |     |     |     | 2790 |     |     |     |
| Cys | Arg  | Ala | Arg | Ala | Gly | Gly  | Arg | Ser | Arg | Pro | Arg  | Leu | Gly | Arg |
|     | 2795 |     |     |     |     | 2800 |     |     |     |     | 2805 |     |     |     |
| Val | Gly  | Glu | Arg | Gly | Arg | Gly  | Arg | Ala | Gly | Arg | Ser  | Cys | Pro | Gly |
|     | 2810 |     |     |     |     | 2815 |     |     |     |     | 2820 |     |     |     |
| Ser | Asp  | Ala | Ala | Glu | Ser | Gly  | Gln | Trp | Ala | Ala | Ala  | Ala | Arg | Gly |
|     | 2825 |     |     |     |     | 2830 |     |     |     |     | 2835 |     |     |     |
| Leu | Ala  | Gly | Ala | Phe | Pro | Gly  | Arg | Ala | Gly | Gly | Pro  | Asp | Gly | Thr |
|     | 2840 |     |     |     |     | 2845 |     |     |     |     | 2850 |     |     |     |
| Ser | Pro  | Arg | Arg | Arg | Trp | Trp  | Leu | Arg | Pro | Arg | Leu  | Ala | Gly | Cys |
|     | 2855 |     |     |     |     | 2860 |     |     |     |     | 2865 |     |     |     |

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|     |      |     |     |     |     |      |      |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|------|-----|-----|-----|------|-----|-----|-----|
| Arg | Ala  | Pro | Gly | Ala | Pro | Pro  | Pro  | Cys | Pro | Val | Ser  | Ser | Trp | Ala |
|     | 2870 |     |     |     |     |      | 2875 |     |     |     | 2880 |     |     |     |
| Leu | Leu  | Pro | Cys | Arg | Ser | Glu  | Ala  | Ala | Ala | Arg | Thr  | Arg | Ala | Gly |
|     | 2885 |     |     |     |     | 2890 |      |     |     |     | 2895 |     |     |     |
| Arg | Gln  | Gly | Arg | Leu | Gly | Ala  | Arg  | Arg | Gln | Gly | Arg  | Gln | Gly | His |
|     | 2900 |     |     |     |     | 2905 |      |     |     |     | 2910 |     |     |     |
| Val | Gly  | Ala | Ala | Arg | Gly | Gln  | Val  | Leu | Val | Leu | Arg  | Pro | Glu | Lys |
|     | 2915 |     |     |     |     | 2920 |      |     |     |     | 2925 |     |     |     |
| Thr | Gly  | Val | Ser | Asp | Asp | Ala  | Thr  | Val | Asp | Val | Leu  | Asp | Leu | Thr |
|     | 2930 |     |     |     |     | 2935 |      |     |     |     | 2940 |     |     |     |
| Pro | Leu  | Gly | Glu | Gly | His | Gly  | Thr  | Arg | Glu | Phe | Glu  | Pro | Glu | Arg |
|     | 2945 |     |     |     |     | 2950 |      |     |     |     | 2955 |     |     |     |
| Glu | Phe  | Asp | Arg | Ile | Asn | Leu  | Gly  | Ile | Val | Asp | Gly  | Gly | Leu | Pro |
|     | 2960 |     |     |     |     | 2965 |      |     |     |     | 2970 |     |     |     |
| Gln | Asp  | Leu | Leu | His | Val | Ala  | Arg  | Val | Val | Leu | Val  | Gly | Asp | Leu |
|     | 2975 |     |     |     |     | 2980 |      |     |     |     | 2985 |     |     |     |
| Gly | His  | Glu | Leu | Leu | Asp | Leu  | Leu  | Leu | Leu | Lys | Val  | Ser | Ala | Ala |
|     | 2990 |     |     |     |     | 2995 |      |     |     |     | 3000 |     |     |     |
| Gly | Ala  | Leu | Asp | Gly | Gly | Arg  | Glu  | Val | Val | Gly | Asp  | Ala | Ala | His |
|     | 3005 |     |     |     |     | 3010 |      |     |     |     | 3015 |     |     |     |
| Glu | Leu  | Arg | Glu | Gly | Val | His  | Ala  | Gly | Leu | Val | Pro  | Asp | Ala | Ala |
|     | 3020 |     |     |     |     | 3025 |      |     |     |     | 3030 |     |     |     |
| Val | Asp  | His | Gly | Ser | Val | Gly  | Val  | Ala | Arg | Ala | His  | Asp | His | Leu |
|     | 3035 |     |     |     |     | 3040 |      |     |     |     | 3045 |     |     |     |
| Gly | Glu  | Val | Glu | Leu | Asp | Val  | Ala  | Arg | Glu | Asp | Arg  | Val | Val | Ala |
|     | 3050 |     |     |     |     | 3055 |      |     |     |     | 3060 |     |     |     |
| Glu | Ala  | Leu | Val | Glu | Val | Val  | Glu  | Arg | Gly | Gly | Asp  | Val | Leu | Gly |
|     | 3065 |     |     |     |     | 3070 |      |     |     |     | 3075 |     |     |     |
| Asp | Glu  | Glu | Val | His | Asp | Pro  | Ala  | Ala | Glu | Arg | His  | Leu | Ala | Asp |
|     | 3080 |     |     |     |     | 3085 |      |     |     |     | 3090 |     |     |     |
| Val | Ala  | Gln | Gly | Phe | Gln | Ala  | Phe  | His | Gly | Leu | Val  | Glu | Val | His |
|     | 3095 |     |     |     |     | 3100 |      |     |     |     | 3105 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly | Glu  | Val | Glu | Lys | Leu | Gly  | Val | Ala | Arg | Arg | Asp  | Gly | Gln | Leu |
|     | 3110 |     |     |     |     | 3115 |     |     |     |     | 3120 |     |     |     |
| Leu | Leu  | Gln | Lys | Thr | Asp | Glu  | Leu | Gly | Asp | Gly | Gly  | Ala | His | Leu |
|     | 3125 |     |     |     |     | 3130 |     |     |     |     | 3135 |     |     |     |
| Ala | Leu  | Glu | Gly | Pro | Gly | Gly  | Leu | Leu | Phe | His | Leu  | Leu | Leu | Phe |
|     | 3140 |     |     |     |     | 3145 |     |     |     |     | 3150 |     |     |     |
| Leu | Leu  | His | His | Leu | Phe | Tyr  | Phe | Leu | Leu | Arg | Arg  | Arg | Trp | Arg |
|     | 3155 |     |     |     |     | 3160 |     |     |     |     | 3165 |     |     |     |
| Gly | Arg  | Gly | Pro | Ala | Ser | Pro  | Ala | Ala | His | Gly | Gln  | Thr | Val | Asp |
|     | 3170 |     |     |     |     | 3175 |     |     |     |     | 3180 |     |     |     |
| Glu | Ala  | Leu | Asp | Gly | Leu | Pro  | Ala | Pro | Ala | Thr | His  | Gly | Leu | Gly |
|     | 3185 |     |     |     |     | 3190 |     |     |     |     | 3195 |     |     |     |
| Asp | Gly  | Ala | Pro | Val | Leu | Ala  | Gly | Pro | Gln | His | Glu  | Asp | Ala | Ala |
|     | 3200 |     |     |     |     | 3205 |     |     |     |     | 3210 |     |     |     |
| Ala | His  | Leu | Gln | Val | Ala | Ala  | Gly | Gly | Val | Ser | Val  | Gly | Gln | Gly |
|     | 3215 |     |     |     |     | 3220 |     |     |     |     | 3225 |     |     |     |
| Glu | Gly  | Ala | Asp | Asp | Ala | Ser  | Tyr | Gln | Leu | Thr | Arg  | Arg | Asp | Ser |
|     | 3230 |     |     |     |     | 3235 |     |     |     |     | 3240 |     |     |     |
| Ala | Gln  | Gly | Pro | Glu | Arg | Leu  | Glu | Ile | His | Gly | Ile  | Arg | Lys | Pro |
|     | 3245 |     |     |     |     | 3250 |     |     |     |     | 3255 |     |     |     |
| Leu | Asn  | Glu | Gly | Phe | Glu | Pro  | Val | Ala | Val | Ala | Arg  | Ala | Glu | Pro |
|     | 3260 |     |     |     |     | 3265 |     |     |     |     | 3270 |     |     |     |
| Gly | Phe  | Leu | Phe | Phe | Gly | Tyr  | Leu | Val | Gly | Arg | Arg  | Ala | Gly | Asp |
|     | 3275 |     |     |     |     | 3280 |     |     |     |     | 3285 |     |     |     |
| Ala | Ala  | Gly | Asp | Glu | Val | Glu  | Val | Gly | Gly | Pro | Glu  | Thr | Ala | Asp |
|     | 3290 |     |     |     |     | 3295 |     |     |     |     | 3300 |     |     |     |
| Gly | Gly  | Glu | Glu | His | Gln | Val  | Leu | Gly | Pro | Gly | Leu  | Leu | Asp | Ala |
|     | 3305 |     |     |     |     | 3310 |     |     |     |     | 3315 |     |     |     |
| Gln | Thr  | Val | Gly | His | Ala | Pro  | Gly | Val | Val | Leu | Thr  | Pro | Gly | Glu |
|     | 3320 |     |     |     |     | 3325 |     |     |     |     | 3330 |     |     |     |
| Val | Leu  | Val | Val | Val | Leu | His  | Glu | Pro | Leu | His | Gly  | His | Leu | Leu |

3335

3340

3345

Leu Ala Arg Ala Ala Val His Ala Arg Glu Pro Glu Pro Ala Leu  
 3350 3355 3360

Arg Leu Asp Glu Arg Gln Val Gly Asp Asp Ala Leu Gly Glu Asp  
 3365 3370 3375

Gly Leu Leu Asp Leu Gly Glu Gly Gly Leu Glu Val Val Glu Val  
 3380 3385 3390

Asp Glu Ala Val Val Gly Ser Gly Val Asp Gly Val Gly Ala Val  
 3395 3400 3405

Gly His Asp Gly Pro Val Asp Gly Leu Val Ala Gly Ser His Glu  
 3410 3415 3420

Leu Val Val Leu Glu Ala Arg Val Gly Ala Arg Val Glu Asp Val  
 3425 3430 3435

Val Val Ala Gly Ala His Glu Val Leu Val Ser Asp Glu Glu Val  
 3440 3445 3450

Arg Arg Arg Leu Ala Val Glu Arg Pro Ser Leu Gly Gly Gly Gly  
 3455 3460 3465

Ala Gly Arg Glu Val Leu Glu His Glu Ala Val Val Ala Val Asp  
 3470 3475 3480

Val Pro Gly His Pro Gly Asp Ala Gly Gly Gly Gly Gly Gly Ala  
 3485 3490 3495

Arg Glu Leu Ala Asp Ala Val Pro Asp Val Ala Gln Arg Gln Glu  
 3500 3505 3510

Val Val His Gly Gly Arg Gly Leu Ala Arg Glu Ala Arg Ala Val  
 3515 3520 3525

Val Asp Ala Leu Asp Ile Arg Ala Lys Thr Lys Ala Val Ser Gly  
 3530 3535 3540

Ser Thr Pro Trp Pro Gly Gly Ala Asn Gly Leu Gly Cys Ala Cys  
 3545 3550 3555

Thr Pro Val Arg Ile Ser Asn Gln Ala Gly Ala Ala Ala Asn Val  
 3560 3565 3570

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val | Leu  | Ala | Leu | Pro | Ser | Arg  | Pro | Lys | Pro | Ala | Asn  | Glu | Thr | Ser |
|     | 3575 |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg | Ile  | Arg | Arg | Arg | Val | Val  | Phe | Trp | Pro | Trp | Ser  | Leu | Val | Met |
|     | 3590 |     |     |     |     | 3595 |     |     |     |     | 3600 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Lys | Asn  | Ala | Arg | Lys | Ala | Ala  | Ala | Arg | Asp | Gly | Ser  | Leu | Pro | Ser |
|     | 3605 |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly | Glu  | Arg | Ile | Ala | Arg | Val  | Ala | Leu | Arg | Cys | Ala  | Pro | Val | Arg |
|     | 3620 |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala | Ser  | Ala | Leu | Gly | Ala | Gly  | Arg | Ile | Pro | Arg | Leu  | Thr | Trp | Ala |
|     | 3635 |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Trp | Leu  | Pro | Arg | Arg | Phe | Gln  | Asp | Pro | Leu | Ala | Ser  | Arg | Leu | Leu |
|     | 3650 |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gln | Leu  | Arg | Ser | Glu | Pro | Leu  | Phe | Phe | Phe | Leu | Val  | Phe | Leu | Pro |
|     | 3665 |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asp | Ala  | Ser | Arg | Thr | Ala | Ala  | Asp | Ala | Pro | Pro | Pro  | Ser | Thr | Thr |
|     | 3680 |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Thr | Ala  | Pro | Thr | Ala | Ala | Ala  | Ala | Thr | Ala | Gly | Ala  | Ser | Ala | Pro |
|     | 3695 |     |     |     |     | 3700 |     |     |     |     | 3705 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala | Pro  | Ala | Ala | Ala | Ser | His  | Tyr | Arg | Gly | Gly | Arg  | Arg | Glu | Arg |
|     | 3710 |     |     |     |     | 3715 |     |     |     |     | 3720 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser | Arg  | Arg | Ser | Val | Pro | Gly  | Leu | Gly | Arg | Gly | Arg  | Gly | Ala | Gly |
|     | 3725 |     |     |     |     | 3730 |     |     |     |     | 3735 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala | Ala  | Gly | Gly | Val | Val | Ala  | Gly | Ala | Ala | Pro | Ala  | Arg | Ala | Asp |
|     | 3740 |     |     |     |     | 3745 |     |     |     |     | 3750 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Glu | Lys  | Gly | Arg | Ser | Arg | Gly  | Leu | Arg | Ala | Gln | Ala  | Glu | Pro | Val |
|     | 3755 |     |     |     |     | 3760 |     |     |     |     | 3765 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gln | Arg  | Gln | Glu | Arg | Arg | Gly  | Ala | Arg | Gly | Asp | Ala  | Arg | Leu | Pro |
|     | 3770 |     |     |     |     | 3775 |     |     |     |     | 3780 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Leu | Pro  | Arg | Gly | Ala | Gly | Ala  | Ala | Ala | Arg | Pro | Gly  | Pro | Lys | Ala |
|     | 3785 |     |     |     |     | 3790 |     |     |     |     | 3795 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly | Ala  | Glu | Gly | Arg | Gly | Phe  | Arg | Gly | Gly | Arg | Ala  | Asp | Gly | Asp |
|     | 3800 |     |     |     |     | 3805 |     |     |     |     | 3810 |     |     |     |

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Gln Pro Arg Ala Arg Ala Arg Gly Arg Gly Gln Pro Gly His Gly  
 3815 3820 3825  
 Val Arg Ala Asp Arg Glu Gly Gly Glu Gln Leu Pro Lys Ile Leu  
 3830 3835 3840  
 Gln Gln Pro Arg Ala His Leu Asp Arg Ala Arg Gly Gly Asp Pro  
 3845 3850 3855  
 Gly Pro Asp Ala Pro Val Gly Pro Ala Gly Gly His Arg Ala Glu  
 3860 3865 3870  
 Pro His Glu Gln Ala Ala Asp Gly Ala Ala Val Ser Gly Gly Ala  
 3875 3880 3885  
 Ala Gln Ser Gly Gln Arg Asp Val Gln Gly Gly Ala Ala Glu Tyr  
 3890 3895 3900  
 His Arg Ala Arg Gly Pro Leu Ala Pro Gly Pro Gly Glu His Phe  
 3905 3910 3915  
 Ala Glu His Arg Gly Ala Gly Ala Arg Ala Ala Ala Val Arg Glu  
 3920 3925 3930  
 Ala Gly Gly His Gln Leu Leu Gly Ala Glu Ser Gly Gln Val Leu  
 3935 3940 3945  
 Arg Glu Asp Leu Gln Asp Pro Val Arg Ala His Arg Gln Gly Gly  
 3950 3955 3960  
 Glu Asp Arg Arg Val Leu His Ala His Asp Pro Glu Ser Ala Asp  
 3965 3970 3975  
 Pro Glu Arg Arg Ser Gly Gly Val Pro Gln Arg Gln Asp Ala Pro  
 3980 3985 3990  
 Arg Gly Glu Arg Gln Pro Pro Ala Arg Ala Glu Arg Pro Gly Ala  
 3995 4000 4005  
 Asp Ala Gln Pro Ala Ala Gly Pro Asp Arg Gly Arg Asp Arg Gly  
 4010 4015 4020  
 Gly Glu Leu Leu His Gly Arg Gly Pro Ala Leu Ala Ala Gln Pro  
 4025 4030 4035  
 Pro Gly Leu Gly Ser Cys Arg Arg Phe Pro Leu Arg Gly Gly Gly  
 4040 4045 4050



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly  | Arg | Gly | Gly | Gly | Gly | Arg  | Val | Pro | Gly | Arg | Leu  | Met | Ala | Arg |
| 4055 |     |     |     |     |     | 4060 |     |     |     |     | 4065 |     |     |     |
| Pro  | Tyr | Phe | Cys | Met | Gln | Gln  | Gln | Pro | Pro | Pro | Pro  | Pro | Pro | Asp |
| 4070 |     |     |     |     |     | 4075 |     |     |     |     | 4080 |     |     |     |
| Pro  | Ala | Met | Arg | Ala | Ala | Leu  | Gln | Ser | Gln | Pro | Ser  | Gly | Ile | Asn |
| 4085 |     |     |     |     |     | 4090 |     |     |     |     | 4095 |     |     |     |
| Ser  | Ser | Asp | Asp | Trp | Thr | Gln  | Ala | Met | Gln | Arg | Ile  | Met | Ala | Leu |
| 4100 |     |     |     |     |     | 4105 |     |     |     |     | 4110 |     |     |     |
| Thr  | Thr | Arg | Asn | Pro | Glu | Ala  | Phe | Arg | Gln | Gln | Pro  | Gln | Ala | Asn |
| 4115 |     |     |     |     |     | 4120 |     |     |     |     | 4125 |     |     |     |
| Arg  | Leu | Ser | Ala | Ile | Leu | Glu  | Ala | Val | Val | Pro | Ser  | Arg | Ser | Asn |
| 4130 |     |     |     |     |     | 4135 |     |     |     |     | 4140 |     |     |     |
| Pro  | Thr | His | Glu | Lys | Val | Leu  | Ala | Ile | Val | Asn | Ala  | Leu | Val | Glu |
| 4145 |     |     |     |     |     | 4150 |     |     |     |     | 4155 |     |     |     |
| Asn  | Lys | Ala | Ile | Arg | Gly | Asp  | Glu | Ala | Gly | Leu | Val  | Tyr | Asn | Ala |
| 4160 |     |     |     |     |     | 4165 |     |     |     |     | 4170 |     |     |     |
| Leu  | Leu | Glu | Arg | Val | Ala | Arg  | Tyr | Asn | Ser | Thr | Asn  | Val | Gln | Thr |
| 4175 |     |     |     |     |     | 4180 |     |     |     |     | 4185 |     |     |     |
| Asn  | Leu | Asp | Arg | Met | Val | Thr  | Asp | Val | Arg | Glu | Ala  | Val | Ser | Gln |
| 4190 |     |     |     |     |     | 4195 |     |     |     |     | 4200 |     |     |     |
| Arg  | Glu | Arg | Phe | His | Arg | Glu  | Ser | Asn | Leu | Gly | Ser  | Met | Val | Ala |
| 4205 |     |     |     |     |     | 4210 |     |     |     |     | 4215 |     |     |     |
| Leu  | Asn | Ala | Phe | Leu | Ser | Thr  | Gln | Pro | Ala | Asn | Val  | Pro | Arg | Gly |
| 4220 |     |     |     |     |     | 4225 |     |     |     |     | 4230 |     |     |     |
| Gln  | Glu | Asp | Tyr | Thr | Asn | Phe  | Ile | Ser | Ala | Leu | Arg  | Leu | Met | Val |
| 4235 |     |     |     |     |     | 4240 |     |     |     |     | 4245 |     |     |     |
| Ala  | Glu | Val | Pro | Gln | Ser | Glu  | Val | Tyr | Gln | Ser | Gly  | Pro | Asp | Tyr |
| 4250 |     |     |     |     |     | 4255 |     |     |     |     | 4260 |     |     |     |
| Phe  | Phe | Gln | Thr | Ser | Arg | Gln  | Gly | Leu | Gln | Thr | Val  | Asn | Leu | Ser |
| 4265 |     |     |     |     |     | 4270 |     |     |     |     | 4275 |     |     |     |
| Gln  | Ala | Phe | Lys | Asn | Leu | Gln  | Gly | Leu | Trp | Gly | Val  | Gln | Ala | Pro |

4280

4285

4290

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | Gly | Asp | Arg | Ala | Thr | Val  | Ser | Ser | Leu | Leu | Thr  | Pro | Asn | Ser |
| 4295 |     |     |     |     |     | 4300 |     |     |     |     | 4305 |     |     |     |
| Arg  | Leu | Leu | Leu | Leu | Leu | Val  | Ala | Pro | Phe | Thr | Asp  | Ser | Gly | Ser |
| 4310 |     |     |     |     |     | 4315 |     |     |     |     | 4320 |     |     |     |
| Val  | Ser | Arg | Asp | Ser | Tyr | Leu  | Gly | Tyr | Leu | Leu | Asn  | Leu | Tyr | Arg |
| 4325 |     |     |     |     |     | 4330 |     |     |     |     | 4335 |     |     |     |
| Glu  | Ala | Ile | Gly | Gln | Ala | His  | Val | Asp | Glu | Gln | Thr  | Tyr | Gln | Glu |
| 4340 |     |     |     |     |     | 4345 |     |     |     |     | 4350 |     |     |     |
| Ile  | Thr | His | Val | Ser | Arg | Ala  | Leu | Gly | Gln | Glu | Asp  | Pro | Gly | Asn |
| 4355 |     |     |     |     |     | 4360 |     |     |     |     | 4365 |     |     |     |
| Leu  | Glu | Ala | Thr | Leu | Asn | Phe  | Leu | Leu | Thr | Asn | Arg  | Ser | Gln | Lys |
| 4370 |     |     |     |     |     | 4375 |     |     |     |     | 4380 |     |     |     |
| Ile  | Pro | Pro | Gln | Tyr | Ala | Leu  | Ser | Thr | Glu | Glu | Glu  | Arg | Ile | Leu |
| 4385 |     |     |     |     |     | 4390 |     |     |     |     | 4395 |     |     |     |
| Arg  | Tyr | Val | Gln | Gln | Ser | Val  | Gly | Leu | Phe | Leu | Met  | Gln | Glu | Gly |
| 4400 |     |     |     |     |     | 4405 |     |     |     |     | 4410 |     |     |     |
| Ala  | Thr | Pro | Ser | Ala | Ala | Leu  | Asp | Met | Thr | Ala | Arg  | Asn | Met | Glu |
| 4415 |     |     |     |     |     | 4420 |     |     |     |     | 4425 |     |     |     |
| Pro  | Ser | Met | Tyr | Ala | Arg | Asn  | Arg | Pro | Phe | Ile | Asn  | Lys | Leu | Met |
| 4430 |     |     |     |     |     | 4435 |     |     |     |     | 4440 |     |     |     |
| Asp  | Tyr | Leu | His | Arg | Ala | Ala  | Ala | Met | Asn | Ser | Asp  | Tyr | Phe | Thr |
| 4445 |     |     |     |     |     | 4450 |     |     |     |     | 4455 |     |     |     |
| Asn  | Ala | Ile | Leu | Asn | Pro | His  | Trp | Leu | Pro | Pro | Pro  | Gly | Phe | Tyr |
| 4460 |     |     |     |     |     | 4465 |     |     |     |     | 4470 |     |     |     |
| Thr  | Gly | Glu | Tyr | Asp | Met | Pro  | Asp | Pro | Asn | Asp | Gly  | Phe | Leu | Trp |
| 4475 |     |     |     |     |     | 4480 |     |     |     |     | 4485 |     |     |     |
| Asp  | Asp | Val | Asp | Ser | Ser | Val  | Phe | Ser | Pro | Arg | Pro  | Gly | Thr | Asn |
| 4490 |     |     |     |     |     | 4495 |     |     |     |     | 4500 |     |     |     |
| Ala  | Val | Trp | Lys | Lys | Glu | Gly  | Gly | Asp | Arg | Arg | Pro  | Ser | Ser | Ala |
| 4505 |     |     |     |     |     | 4510 |     |     |     |     | 4515 |     |     |     |

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Leu Ser Gly Arg Ala Gly Ala Ala Ala Ala Val Pro Glu Ala Ala  
 4520 4525 4530  
  
 Ser Pro Phe Pro Ser Leu Pro Phe Ser Leu Asn Ser Val Arg Ser  
 4535 4540 4545  
  
 Ser Glu Leu Gly Arg Leu Thr Arg Pro Arg Leu Leu Gly Glu Glu  
 4550 4555 4560  
  
 Glu Tyr Leu Asn Asp Ser Leu Leu Arg Pro Glu Arg Glu Lys Asn  
 4565 4570 4575  
  
 Phe Pro Asn Asn Gly Ile Glu Ser Leu Val Asp Lys Met Ser Arg  
 4580 4585 4590  
  
 Trp Lys Thr Tyr Ala His Glu His Arg Asp Glu Pro Arg Ala Ser  
 4595 4600 4605  
  
 Ser Ala Gly Thr Arg Arg Arg Gln Arg His Asp Arg Gln Arg Gly  
 4610 4615 4620  
  
 Leu Val Trp Asp Asp Glu Asp Ser Ala Asp Asp Ser Ser Val Leu  
 4625 4630 4635  
  
 Asp Leu Gly Gly Ser Gly Gly Asn Pro Phe Ala His Leu Arg Pro  
 4640 4645 4650  
  
 Arg Ile Gly Arg Leu Met Glu Ser Glu Lys Ile Lys Asp Gly Thr  
 4655 4660 4665  
  
 His Gln Gly His Gly Asp Gln Arg Ala Phe Phe Ser Val Val Cys  
 4670 4675 4680  
  
 Ser Ser Met Met Arg Arg Val Tyr Pro Glu Gly Pro Pro Pro Ser  
 4685 4690 4695  
  
 Tyr Glu Ser Val Met Gln Gln Ala Val Ala Ala Ala Met Gln Pro  
 4700 4705 4710  
  
 Pro Leu Glu Ala Pro Tyr Val Pro Pro Arg Tyr Leu Ala Pro Thr  
 4715 4720 4725  
  
 Glu Gly Arg Asn Ser Ile Arg Tyr Ser Glu Leu Ala Pro Leu Tyr  
 4730 4735 4740  
  
 Asp Thr Thr Arg Leu Tyr Leu Val Asp Asn Lys Ser Ala Asp Ile  
 4745 4750 4755

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala | Ser  | Leu | Asn | Tyr | Gln | Asn  | Asp | His | Ser | Asn | Phe  | Leu | Thr | Thr |
|     | 4760 |     |     |     |     | 4765 |     |     |     |     | 4770 |     |     |     |
| Val | Val  | Gln | Asn | Asn | Asp | Phe  | Thr | Pro | Thr | Glu | Ala  | Ser | Thr | Gln |
|     | 4775 |     |     |     |     | 4780 |     |     |     |     | 4785 |     |     |     |
| Thr | Ile  | Asn | Phe | Asp | Glu | Arg  | Ser | Arg | Trp | Gly | Gly  | Gln | Leu | Lys |
|     | 4790 |     |     |     |     | 4795 |     |     |     |     | 4800 |     |     |     |
| Thr | Ile  | Met | His | Thr | Asn | Met  | Pro | Asn | Val | Asn | Glu  | Phe | Met | Tyr |
|     | 4805 |     |     |     |     | 4810 |     |     |     |     | 4815 |     |     |     |
| Ser | Asn  | Lys | Phe | Lys | Ala | Arg  | Val | Met | Val | Ser | Arg  | Lys | Thr | Pro |
|     | 4820 |     |     |     |     | 4825 |     |     |     |     | 4830 |     |     |     |
| Asn | Gly  | Val | Asp | Asp | Asp | Tyr  | Asp | Gly | Ser | Gln | Asp  | Glu | Leu | Thr |
|     | 4835 |     |     |     |     | 4840 |     |     |     |     | 4845 |     |     |     |
| Tyr | Glu  | Trp | Val | Glu | Phe | Glu  | Leu | Pro | Glu | Gly | Asn  | Phe | Ser | Val |
|     | 4850 |     |     |     |     | 4855 |     |     |     |     | 4860 |     |     |     |
| Thr | Met  | Thr | Ile | Asp | Leu | Met  | Asn | Asn | Ala | Ile | Ile  | Asp | Asn | Tyr |
|     | 4865 |     |     |     |     | 4870 |     |     |     |     | 4875 |     |     |     |
| Leu | Ala  | Val | Gly | Arg | Gln | Asn  | Gly | Val | Leu | Glu | Ser  | Asp | Ile | Gly |
|     | 4880 |     |     |     |     | 4885 |     |     |     |     | 4890 |     |     |     |
| Val | Lys  | Phe | Asp | Thr | Arg | Asn  | Phe | Arg | Leu | Gly | Trp  | Asp | Pro | Val |
|     | 4895 |     |     |     |     | 4900 |     |     |     |     | 4905 |     |     |     |
| Thr | Glu  | Leu | Val | Met | Pro | Gly  | Val | Tyr | Thr | Asn | Glu  | Ala | Phe | His |
|     | 4910 |     |     |     |     | 4915 |     |     |     |     | 4920 |     |     |     |
| Pro | Asp  | Ile | Val | Leu | Leu | Pro  | Gly | Cys | Gly | Val | Asp  | Phe | Thr | Glu |
|     | 4925 |     |     |     |     | 4930 |     |     |     |     | 4935 |     |     |     |
| Ser | Arg  | Leu | Ser | Asn | Leu | Leu  | Gly | Ile | Arg | Lys | Arg  | Gln | Pro | Phe |
|     | 4940 |     |     |     |     | 4945 |     |     |     |     | 4950 |     |     |     |
| Gln | Glu  | Gly | Phe | Gln | Ile | Leu  | Tyr | Glu | Asp | Leu | Glu  | Gly | Gly | Asn |
|     | 4955 |     |     |     |     | 4960 |     |     |     |     | 4965 |     |     |     |
| Ile | Pro  | Ala | Leu | Leu | Asp | Val  | Glu | Ala | Tyr | Glu | Lys  | Ser | Lys | Glu |
|     | 4970 |     |     |     |     | 4975 |     |     |     |     | 4980 |     |     |     |
| Asp | Ser  | Thr | Ala | Ala | Ala | Thr  | Ala | Ala | Val | Ala | Thr  | Ala | Ser | Thr |
|     | 4985 |     |     |     |     | 4990 |     |     |     |     | 4995 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Glu  | Val | Arg | Gly | Asp | Asn | Phe  | Ala | Ser | Ala | Ala | Ala  | Ala | Ala | Glu |
| 5000 |     |     |     |     |     | 5005 |     |     |     |     | 5010 |     |     |     |
| Ala  | Ala | Glu | Thr | Glu | Ser | Lys  | Ile | Val | Ile | Gln | Pro  | Val | Glu | Lys |
| 5015 |     |     |     |     |     | 5020 |     |     |     |     | 5025 |     |     |     |
| Asp  | Ser | Lys | Asp | Arg | Ser | Tyr  | Asn | Val | Leu | Ala | Asp  | Lys | Lys | Asn |
| 5030 |     |     |     |     |     | 5035 |     |     |     |     | 5040 |     |     |     |
| Thr  | Ala | Tyr | Arg | Ser | Trp | Tyr  | Leu | Ala | Tyr | Asn | Tyr  | Gly | Asp | Pro |
| 5045 |     |     |     |     |     | 5050 |     |     |     |     | 5055 |     |     |     |
| Glu  | Lys | Gly | Val | Arg | Ser | Trp  | Thr | Leu | Leu | Thr | Thr  | Ser | Asp | Val |
| 5060 |     |     |     |     |     | 5065 |     |     |     |     | 5070 |     |     |     |
| Thr  | Cys | Gly | Val | Glu | Gln | Val  | Tyr | Trp | Ser | Leu | Pro  | Asp | Met | Met |
| 5075 |     |     |     |     |     | 5080 |     |     |     |     | 5085 |     |     |     |
| Gln  | Asp | Pro | Val | Thr | Phe | Arg  | Ser | Thr | Arg | Gln | Val  | Ser | Asn | Tyr |
| 5090 |     |     |     |     |     | 5095 |     |     |     |     | 5100 |     |     |     |
| Pro  | Val | Val | Gly | Ala | Glu | Leu  | Leu | Pro | Val | Tyr | Ser  | Lys | Ser | Phe |
| 5105 |     |     |     |     |     | 5110 |     |     |     |     | 5115 |     |     |     |
| Phe  | Asn | Glu | Gln | Ala | Val | Tyr  | Ser | Gln | Gln | Leu | Arg  | Ala | Phe | Thr |
| 5120 |     |     |     |     |     | 5125 |     |     |     |     | 5130 |     |     |     |
| Ser  | Leu | Thr | His | Val | Phe | Asn  | Arg | Phe | Pro | Glu | Asn  | Gln | Ile | Leu |
| 5135 |     |     |     |     |     | 5140 |     |     |     |     | 5145 |     |     |     |
| Val  | Arg | Pro | Pro | Ala | Pro | Thr  | Ile | Thr | Thr | Val | Ser  | Glu | Asn | Val |
| 5150 |     |     |     |     |     | 5155 |     |     |     |     | 5160 |     |     |     |
| Pro  | Ala | Leu | Thr | Asp | His | Gly  | Thr | Leu | Pro | Leu | Arg  | Ser | Ser | Ile |
| 5165 |     |     |     |     |     | 5170 |     |     |     |     | 5175 |     |     |     |
| Arg  | Gly | Val | Gln | Arg | Val | Thr  | Val | Thr | Asp | Ala | Arg  | Arg | Arg | Thr |
| 5180 |     |     |     |     |     | 5185 |     |     |     |     | 5190 |     |     |     |
| Cys  | Pro | Tyr | Val | Tyr | Lys | Ala  | Leu | Gly | Val | Val | Ala  | Pro | Arg | Val |
| 5195 |     |     |     |     |     | 5200 |     |     |     |     | 5205 |     |     |     |
| Leu  | Ser | Ser | Arg | Thr | Phe | Lys  | Met | Ser | Ile | Leu | Ile  | Ser | Pro | Ser |
| 5210 |     |     |     |     |     | 5215 |     |     |     |     | 5220 |     |     |     |
| Asn  | Asn | Thr | Gly | Trp | Gly | Leu  | Arg | Ala | Pro | Ser | Lys  | Met | Tyr | Gly |

5225

5230

5235

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly  | Ala | Arg | Gln | Arg | Ser | Thr  | Gln | His | Pro | Val | Arg  | Val | Arg | Gly |
| 5240 |     |     |     |     |     | 5245 |     |     |     |     | 5250 |     |     |     |
| His  | Phe | Arg | Ala | Pro | Trp | Gly  | Ala | Leu | Lys | Gly | Arg  | Val | Arg | Ser |
| 5255 |     |     |     |     |     | 5260 |     |     |     |     | 5265 |     |     |     |
| Arg  | Thr | Thr | Val | Asp | Asp | Val  | Ile | Asp | Gln | Val | Val  | Ala | Asp | Ala |
| 5270 |     |     |     |     |     | 5275 |     |     |     |     | 5280 |     |     |     |
| Arg  | Asn | Tyr | Thr | Pro | Ala | Ala  | Ala | Pro | Val | Ser | Thr  | Val | Asp | Ala |
| 5285 |     |     |     |     |     | 5290 |     |     |     |     | 5295 |     |     |     |
| Val  | Ile | Asp | Ser | Val | Val | Ala  | Asp | Ala | Arg | Arg | Tyr  | Ala | Arg | Thr |
| 5300 |     |     |     |     |     | 5305 |     |     |     |     | 5310 |     |     |     |
| Lys  | Ser | Arg | Arg | Arg | Arg | Ile  | Ala | Arg | Arg | His | Arg  | Ser | Thr | Pro |
| 5315 |     |     |     |     |     | 5320 |     |     |     |     | 5325 |     |     |     |
| Ala  | Met | Arg | Ala | Ala | Arg | Ala  | Leu | Leu | Arg | Arg | Ala  | Arg | Arg | Thr |
| 5330 |     |     |     |     |     | 5335 |     |     |     |     | 5340 |     |     |     |
| Gly  | Arg | Arg | Ala | Met | Leu | Arg  | Ala | Ala | Arg | Arg | Ala  | Ala | Ser | Gly |
| 5345 |     |     |     |     |     | 5350 |     |     |     |     | 5355 |     |     |     |
| Ser  | Ser | Ser | Ala | Gly | Arg | Thr  | Arg | Arg | Arg | Ala | Ala  | Thr | Ala | Ala |
| 5360 |     |     |     |     |     | 5365 |     |     |     |     | 5370 |     |     |     |
| Ala  | Ala | Ala | Ile | Ala | Ser | Met  | Ser | Arg | Pro | Arg | Arg  | Gly | Asn | Val |
| 5375 |     |     |     |     |     | 5380 |     |     |     |     | 5385 |     |     |     |
| Tyr  | Trp | Val | Arg | Asp | Ala | Ala  | Thr | Gly | Val | Arg | Val  | Pro | Val | Arg |
| 5390 |     |     |     |     |     | 5395 |     |     |     |     | 5400 |     |     |     |
| Thr  | Arg | Pro | Pro | Arg | Thr | Arg  | Cys | Leu | Arg | Asp | Val  | Asp | Val | Ser |
| 5405 |     |     |     |     |     | 5410 |     |     |     |     | 5415 |     |     |     |
| Gln  | Arg | Arg | Gly | Gly | Cys | Pro  | Ser | Ala | Asn | Thr | Arg  | Lys | Arg | Cys |
| 5420 |     |     |     |     |     | 5425 |     |     |     |     | 5430 |     |     |     |
| Ser  | Arg | Ser | Ser | Arg | Leu | Arg  | Ser | Thr | Ala | Pro | Arg  | Arg | Arg | Arg |
| 5435 |     |     |     |     |     | 5440 |     |     |     |     | 5445 |     |     |     |
| Arg  | Lys | Glu | Ser | Pro | Ala | Asn  | Ser | Gly | Ser | Lys | Arg  | Thr | Lys | Arg |
| 5450 |     |     |     |     |     | 5455 |     |     |     |     | 5460 |     |     |     |

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Arg | Lys | Met | Thr | Asp | Trp  | Trp | Ser | Leu | Cys | Ala  | Ser | Ser | Pro |
| 5465 |     |     |     |     |     | 5470 |     |     |     |     | 5475 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Gly | Gly | Ala | Cys | Ser | Gly  | Ala | Gly | Gly | Lys | Asn  | Arg | Cys | Cys |
| 5480 |     |     |     |     |     | 5485 |     |     |     |     | 5490 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly  | Pro | Ala | Pro | Arg | Trp | Ser  | Ser | Arg | Pro | Ala | Ser  | Val | Pro | Ala |
| 5495 |     |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Pro | Pro | Ser | Ala | Pro | Thr  | Thr | Arg | Cys | Thr | Gly  | Thr | Arg | Thr |
| 5510 |     |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser  | Ser | Ser | Arg | Arg | Ser | Ser  | Val | Trp | Ala | Ser | Leu  | Arg | Thr | Ala |
| 5525 |     |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser  | Ala | Ala | Ala | Pro | Arg | Pro  | Lys | Arg | Arg | Arg | Cys  | Pro | Ser | Arg |
| 5540 |     |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Trp  | Thr | Thr | Ala | Thr | Pro | Arg  | Arg | Ala | Ser | Arg | Pro  | Cys | Ser | Arg |
| 5555 |     |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Cys  | Tyr | Arg | Ala | Arg | Arg | Arg  | Ala | Gly | Ala | Ser | Ser  | Ala | Arg | Ala |
| 5570 |     |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Arg | Ile | Cys | Thr | Arg | Pro  | Cys | Ser | Trp | Cys | Pro  | Ser | Ala | Arg |
| 5585 |     |     |     |     |     | 5590 |     |     |     |     | 5595 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser  | Trp | Arg | Thr | Cys | Trp | Ser  | Thr | Arg | Trp | Thr | Pro  | Arg | Cys | Ser |
| 5600 |     |     |     |     |     | 5605 |     |     |     |     | 5610 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Arg | Ser | Arg | Cys | Gly | Pro  | Ser | Ser | Arg | Trp | Pro  | Arg | Ala | Trp |
| 5615 |     |     |     |     |     | 5620 |     |     |     |     | 5625 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Cys | Arg | Pro | Trp | Thr | Ser  | Arg | Ser | Pro | Arg | Ser  | Pro | Trp | Lys |
| 5630 |     |     |     |     |     | 5635 |     |     |     |     | 5640 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Arg | Pro | Ser | Pro | Ser | Pro  | Ala | Pro | Ala | Pro | Trp  | Arg | Cys | Arg |
| 5645 |     |     |     |     |     | 5650 |     |     |     |     | 5655 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Ile | Pro | Gly | Cys | Gln | His  | Gln | Leu | Pro | Pro | Ala  | Leu | Ala | Glu |
| 5660 |     |     |     |     |     | 5665 |     |     |     |     | 5670 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asp  | Ala | Ser | Thr | Ala | Arg | Pro  | Ala | Cys | Cys | Pro | Thr  | Thr | Arg | Cys |
| 5675 |     |     |     |     |     | 5680 |     |     |     |     | 5685 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ile  | Leu | Pro | Ser | Ser | Pro | Arg  | Arg | Ala | Thr | Ala | Ala  | Arg | Ala | Ser |
| 5690 |     |     |     |     |     | 5695 |     |     |     |     | 5700 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Ala  | Ala | Thr | Pro | Ala | Ala  | Ala | Ala | Ala | Arg | Pro  | Pro | Pro | Ala |
|     | 5705 |     |     |     |     | 5710 |     |     |     |     | 5715 |     |     |     |
| Ala | Val  | Val | Ala | Ala | Ala | Ala  | Ala | Ala | Pro | Arg | Leu  | Pro | Pro | Trp |
|     | 5720 |     |     |     |     | 5725 |     |     |     |     | 5730 |     |     |     |
| Cys | Gly  | Glu | Cys | Ile | Ala | Ala  | Gly | Ala | Ser | Leu | Pro  | Cys | Arg | Ala |
|     | 5735 |     |     |     |     | 5740 |     |     |     |     | 5745 |     |     |     |
| Arg | Ala  | Thr | Thr | Arg | Ala | Ser  | Pro | Phe | Asn | Tyr | Arg  | Leu | Leu | Leu |
|     | 5750 |     |     |     |     | 5755 |     |     |     |     | 5760 |     |     |     |
| Ala | Asp  | Met | Ala | Leu | Thr | Cys  | Arg | Leu | Arg | Val | Pro  | Ile | Thr | Gly |
|     | 5765 |     |     |     |     | 5770 |     |     |     |     | 5775 |     |     |     |
| Tyr | Arg  | Gly | Arg | Lys | Pro | Arg  | Arg | Arg | Arg | Leu | Thr  | Gly | Asn | Gly |
|     | 5780 |     |     |     |     | 5785 |     |     |     |     | 5790 |     |     |     |
| Leu | Arg  | Arg | His | His | His | Arg  | Arg | Arg | Arg | Ala | Ile  | Ser | Lys | Arg |
|     | 5795 |     |     |     |     | 5800 |     |     |     |     | 5805 |     |     |     |
| Leu | Gly  | Gly | Gly | Phe | Leu | Pro  | Ala | Leu | Ile | Pro | Ile  | Ile | Ala | Ala |
|     | 5810 |     |     |     |     | 5815 |     |     |     |     | 5820 |     |     |     |
| Ala | Ile  | Gly | Ala | Ile | Pro | Gly  | Ile | Ala | Ser | Val | Ala  | Val | Gln | Ala |
|     | 5825 |     |     |     |     | 5830 |     |     |     |     | 5835 |     |     |     |
| Ser | Gln  | Arg | His | Asp | Thr | Lys  | Lys | His | Gly | Phe | Val  | Ile | Lys | Lys |
|     | 5840 |     |     |     |     | 5845 |     |     |     |     | 5850 |     |     |     |
| Lys | Met  | Asp | Arg | Ser | Trp | Ser  | Cys | Asp | Val | Cys | Phe  | Met | Glu | Asp |
|     | 5855 |     |     |     |     | 5860 |     |     |     |     | 5865 |     |     |     |
| Ile | Asn  | Phe | Ser | Ser | Leu | Ala  | Pro | Arg | His | Gly | Thr  | Arg | Pro | Phe |
|     | 5870 |     |     |     |     | 5875 |     |     |     |     | 5880 |     |     |     |
| Met | Gly  | Thr | Trp | Ser | Asp | Ile  | Gly | Asn | Ser | Gln | Leu  | Asn | Gly | Gly |
|     | 5885 |     |     |     |     | 5890 |     |     |     |     | 5895 |     |     |     |
| Ala | Phe  | Asn | Trp | Ser | Ser | Leu  | Trp | Ser | Gly | Leu | Lys  | Asn | Phe | Gly |
|     | 5900 |     |     |     |     | 5905 |     |     |     |     | 5910 |     |     |     |
| Ser | Thr  | Leu | Lys | Thr | Tyr | Gly  | Asn | Lys | Ala | Trp | Asn  | Ser | Ser | Thr |
|     | 5915 |     |     |     |     | 5920 |     |     |     |     | 5925 |     |     |     |
| Gly | Gln  | Ala | Leu | Arg | Glu | Lys  | Leu | Lys | Glu | Gln | Asn  | Phe | Gln | Gln |
|     | 5930 |     |     |     |     | 5935 |     |     |     |     | 5940 |     |     |     |



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Lys Val Val Asp Gly Leu Ala Ser Gly Ile Asn Gly Val Val Asp  
 5945 5950 5955  
 Leu Ala Asn Gln Ala Val Gln Lys Gln Ile Asn Ser Arg Leu Asp  
 5960 5965 5970  
 Ala Val Pro Pro Ala Gly Ser Val Glu Met Pro Gln Val Glu Glu  
 5975 5980 5985  
 Glu Leu Pro Pro Leu Asp Lys Arg Gly Asp Lys Arg Pro Arg Pro  
 5990 5995 6000  
 Asp Ala Glu Glu Thr Leu Leu Thr His Thr Asp Glu Pro Pro Pro  
 6005 6010 6015  
 Tyr Glu Glu Ala Val Lys Leu Gly Leu Pro Thr Thr Arg Pro Val  
 6020 6025 6030  
 Ala Pro Leu Ala Thr Gly Val Leu Lys Pro Ser Ser Ser Gln Pro  
 6035 6040 6045  
 Ala Thr Leu Asp Leu Pro Pro Pro Arg Pro Ser Thr Val Ala Lys  
 6050 6055 6060  
 Pro Leu Pro Pro Val Ala Val Ala Ser Arg Ala Pro Arg Gly Arg  
 6065 6070 6075  
 Pro Gln Ala Asn Trp Gln Ser Thr Leu Asn Ser Ile Val Gly Leu  
 6080 6085 6090  
 Gly Val Gln Ser Val Lys Arg Arg Arg Cys Tyr Lys Thr Leu Arg  
 6095 6100 6105  
 Leu Thr Cys Leu Ser Val Cys Ile Cys Met Ser Ala Asp Gln Lys  
 6110 6115 6120  
 Glu Glu Cys Glu Glu Ala Arg Arg Arg Val Ala Arg Trp Pro Pro  
 6125 6130 6135  
 His Arg Cys Cys Pro Ser Gly Arg Thr Cys Thr Ser Pro Asp Arg  
 6140 6145 6150  
 Thr Leu Arg Ser Thr Val Arg Val Trp Cys Ser Ser Pro Ala Pro  
 6155 6160 6165  
 Gln Thr Pro Thr Ser Val Trp Gly Thr Ser Leu Gly Thr Pro Arg

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| 6170 |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Trp  | Arg | Pro | Arg | Thr | Met | Pro  | Pro | Thr | Ala | Ala | Ser  | Gly | Arg | Cys |
| 6185 |     |     |     |     |     | 6190 |     |     |     |     | 6195 |     |     |     |
| Ala  | Ser | Cys | Pro | Trp | Thr | Ala  | Arg | Thr | Thr | Pro | Thr  | Arg | Thr | Lys |
| 6200 |     |     |     |     |     | 6205 |     |     |     |     | 6210 |     |     |     |
| Cys  | Ala | Thr | Arg | Trp | Pro | Trp  | Ala | Thr | Thr | Ala | Cys  | Trp | Thr | Trp |
| 6215 |     |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Pro  | Ala | Pro | Thr | Leu | Thr | Ser  | Ala | Ala | Cys | Trp | Thr  | Gly | Ala | Leu |
| 6230 |     |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Ala  | Ser | Asn | Pro | Thr | Leu | Ala  | Pro | Pro | Thr | Thr | Ala  | Leu | Pro | Arg |
| 6245 |     |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |
| Glu  | Leu | Pro | Ile | Pro | Ala | Ser  | Gly | Ser | Lys | Gln | Lys  | Gln | Ala | Met |
| 6260 |     |     |     |     |     | 6265 |     |     |     |     | 6270 |     |     |     |
| Gly  | Glu | Leu | Trp | Lys | His | Thr  | His | Met | Val | Trp | Pro  | Gln | Trp | Ala |
| 6275 |     |     |     |     |     | 6280 |     |     |     |     | 6285 |     |     |     |
| Glu  | Arg | Ile | Leu | Gln | Lys | Met  | Val | Phe | Lys | Leu | Glu  | Leu | Thr | Leu |
| 6290 |     |     |     |     |     | 6295 |     |     |     |     | 6300 |     |     |     |
| Gln  | Arg | Ile | Arg | Ile | Asn | Gln  | Phe | Met | Pro | Thr | Lys  | His | Phe | Asn |
| 6305 |     |     |     |     |     | 6310 |     |     |     |     | 6315 |     |     |     |
| Gln  | Asn | Arg | Lys | Glu | Lys | Lys  | Ile | Gly | Lys | Lys | Leu  | Lys | Thr | Phe |
| 6320 |     |     |     |     |     | 6325 |     |     |     |     | 6330 |     |     |     |
| Met  | Ala | Val | Glu | Leu | Leu | Lys  | Lys | Thr | Gln | Thr | Asn  | Leu | Ala | Met |
| 6335 |     |     |     |     |     | 6340 |     |     |     |     | 6345 |     |     |     |
| Ala  | Pro | Met | Leu | Asp | Pro | Pro  | Met | Lys | Lys | Glu | Val  | Lys | Leu | Asn |
| 6350 |     |     |     |     |     | 6355 |     |     |     |     | 6360 |     |     |     |
| Leu  | Lys | Leu | Glu | Met | Met | Glu  | Phe | Gln | Pro | Lys | Asn  | Ser | Thr | Thr |
| 6365 |     |     |     |     |     | 6370 |     |     |     |     | 6375 |     |     |     |
| Trp  | Leu | Ser | Leu | Ile | Leu | Pro  | Val | Ala | Pro | Thr | Val  | Lys | Thr | Ser |
| 6380 |     |     |     |     |     | 6385 |     |     |     |     | 6390 |     |     |     |
| Ile  | Lys | Gln | Thr | Leu | Ser | Cys  | Ile | Pro | Lys | Thr | Arg  | Ile | Trp | Lys |
| 6395 |     |     |     |     |     | 6400 |     |     |     |     | 6405 |     |     |     |

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Leu Gln Thr Arg Met Trp Tyr Thr Asn Gln Ala Arg Met Met Gln  
 6410 6415 6420  
  
 Val Leu Lys Leu Thr Trp Phe Ser Ser Leu Cys Pro Thr Asp Pro  
 6425 6430 6435  
  
 Thr Thr Leu Gly Ser Gly Thr Thr Leu Ser Val Leu Cys Thr Thr  
 6440 6445 6450  
  
 Thr Ala Leu Ala Ile Trp Val Cys Leu Leu Val Arg Pro Pro Ser  
 6455 6460 6465  
  
 Met Leu Trp Leu Ile Cys Lys Thr Glu Thr Pro Ser Cys Pro Thr  
 6470 6475 6480  
  
 Ser Ser Cys Leu Thr Leu Trp Val Thr Glu Pro Gly Ile Ser Val  
 6485 6490 6495  
  
 Cys Gly Thr Arg Arg Trp Thr Val Met Thr Pro Met Cys Ala Ser  
 6500 6505 6510  
  
 Ser Lys Thr Met Val Trp Arg Met Asn Cys Gln Thr Ile Ala Ser  
 6515 6520 6525  
  
 Pro Trp Thr Ala Leu Ala Leu Thr Pro His Thr Lys Val Lys Lys  
 6530 6535 6540  
  
 Met Val Lys Met Val Met Leu Arg Val Asn Gly Lys Met Thr Ile  
 6545 6550 6555  
  
 Leu Leu Gln Leu Glu Ile Asn Tyr Val Lys Val Thr Phe Ser Pro  
 6560 6565 6570  
  
 Trp Arg Leu Ile Ser Arg Leu Thr Cys Gly Glu Val Ser Ser Thr  
 6575 6580 6585  
  
 Arg Thr Trp Pro Cys Thr Cys Pro Thr Pro Thr Ser Thr Arg Arg  
 6590 6595 6600  
  
 Pro Thr Ser Arg Cys Arg Pro Thr Pro Thr Pro Thr Ile Thr Met  
 6605 6610 6615  
  
 Ala Glu His Leu Pro Arg Trp Thr Pro Thr Ser Thr Ser Gly Arg  
 6620 6625 6630  
  
 Ala Gly Arg Trp Thr Pro Trp Thr Thr Ser Thr Pro Ser Thr Thr  
 6635 6640 6645

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Ala  | Thr | Arg | Ala | Cys | Ala  | Thr | Ala | Pro | Cys | Ser  | Trp | Ala | Thr |
|     | 6650 |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |
| Gly | Ala  | Thr | Cys | Pro | Ser | Thr  | Ser | Arg | Cys | Pro | Lys  | Ser | Phe | Ser |
|     | 6665 |     |     |     |     | 6670 |     |     |     |     | 6675 |     |     |     |
| Pro | Ser  | Arg | Ala | Ser | Cys | Ser  | Cys | Pro | Gly | Pro | Thr  | Pro | Thr | Ser |
|     | 6680 |     |     |     |     | 6685 |     |     |     |     | 6690 |     |     |     |
| Gly | Thr  | Ser | Ala | Arg | Thr | Ser  | Thr | Ser | Cys | Arg | Ala  | Pro | Ala | Thr |
|     | 6695 |     |     |     |     | 6700 |     |     |     |     | 6705 |     |     |     |
| Thr | Cys  | Ala | Arg | Thr | Gly | Pro  | Pro | Ser | Pro | Ser | Pro  | Ala | Ser | Thr |
|     | 6710 |     |     |     |     | 6715 |     |     |     |     | 6720 |     |     |     |
| Ser | Thr  | Pro | Pro | Ser | Ser | Pro  | Trp | Arg | Thr | Thr | Pro  | Pro | Pro | Arg |
|     | 6725 |     |     |     |     | 6730 |     |     |     |     | 6735 |     |     |     |
| Ser | Arg  | Pro | Cys | Cys | Ala | Thr  | Thr | Pro | Thr | Thr | Ser  | Pro | Ser | Thr |
|     | 6740 |     |     |     |     | 6745 |     |     |     |     | 6750 |     |     |     |
| Thr | Thr  | Ser | Arg | Arg | Pro | Thr  | Cys | Ser | Thr | Pro | Ser  | Arg | Pro | Thr |
|     | 6755 |     |     |     |     | 6760 |     |     |     |     | 6765 |     |     |     |
| Pro | Pro  | Thr | Cys | Pro | Ser | Pro  | Ser | Pro | Arg | Ala | Thr  | Gly | Pro | Pro |
|     | 6770 |     |     |     |     | 6775 |     |     |     |     | 6780 |     |     |     |
| Ser | Ala  | Asp | Gly | Pro | Ser | Arg  | Ala | Arg | Pro | Ala | Arg  | Arg | Pro | Arg |
|     | 6785 |     |     |     |     | 6790 |     |     |     |     | 6795 |     |     |     |
| Ser | Ala  | Pro | Gly | Ser | Thr | Pro  | Thr | Ser | Ser | Thr | Arg  | Ala | Pro | Ser |
|     | 6800 |     |     |     |     | 6805 |     |     |     |     | 6810 |     |     |     |
| Pro | Thr  | Thr | Ala | Pro | Ser | Thr  | Ser | Thr | Thr | Pro | Ser  | Arg | Arg | Ser |
|     | 6815 |     |     |     |     | 6820 |     |     |     |     | 6825 |     |     |     |
| Pro | Ser  | Pro | Ser | Thr | Pro | Pro  | Ser | Ala | Gly | Pro | Ala  | Thr | Thr | Ala |
|     | 6830 |     |     |     |     | 6835 |     |     |     |     | 6840 |     |     |     |
| Ser | Arg  | Pro | Thr | Ser | Ser | Lys  | Ser | Ser | Ala | Pro | Ser  | Thr | Glu | Arg |
|     | 6845 |     |     |     |     | 6850 |     |     |     |     | 6855 |     |     |     |
| Asp | Thr  | Thr | Trp | Pro | Ser | Ala  | Thr | Pro | Arg | Thr | Gly  | Ser | Trp | Ser |
|     | 6860 |     |     |     |     | 6865 |     |     |     |     | 6870 |     |     |     |
| Arg | Cys  | Trp | Pro | Thr | Thr | Thr  | Ser | Ala | Thr | Arg | Ala  | Ser | Thr | Cys |
|     | 6875 |     |     |     |     | 6880 |     |     |     |     | 6885 |     |     |     |

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Pro Arg Ala Thr Arg Thr Ala Cys Thr Pro Ser Ser Ala Thr Ser  
6890 6895 6900

Ser Pro Ala Ala Arg Ser Trp Thr Arg Ser Thr Thr Arg Thr Thr  
6905 6910 6915

Arg Pro Ser Pro Trp Pro Thr Ser Thr Thr Thr Arg Ala Ser Ser  
6920 6925 6930

Ala Thr Ser Arg Pro Pro Cys Ala Arg Ala Ser Pro Thr Pro Pro  
6935 6940 6945

Thr Thr Pro Thr Arg Ser Ser Ala Arg Ala Pro Ser Pro Ala Ser  
6950 6955 6960

Pro Arg Lys Ser Ser Ser Ala Thr Gly Ser Cys Gly Ala Ser Pro  
6965 6970 6975

Ser Pro Ala Thr Ser Cys Pro Trp Ala Arg Ser Pro Thr Ser Ala  
6980 6985 6990

Arg Thr Cys Ser Thr Pro Thr Pro Pro Thr Arg Thr Ile Ser Lys  
6995 7000 7005

Ser Thr Pro Trp Met Ser Pro Pro Phe Ser Met Leu Ser Ser Lys  
7010 7015 7020

Ser Ser Thr Ser Ser Glu Cys Thr Ser Pro Thr Ala Ala Ser Ser  
7025 7030 7035

Lys Pro Ser Thr Cys Ala Arg Pro Ser Arg Pro Ala Thr Pro Pro  
7040 7045 7050

Pro Lys Pro Leu Leu Leu Leu Ala Arg Arg Arg Ala Pro Ala Ser  
7055 7060 7065

Arg Ser Ser Gly Pro Ser Ser Ala Thr Trp Ala Ala Gly Pro Ala  
7070 7075 7080

Ser Trp Ala Pro Ser Thr Ser Ala Ser Leu Asp Ser Trp Pro Arg  
7085 7090 7095

Thr Ser Trp Pro Ala Pro Ser Thr Arg Pro Ala Ala Arg Pro Gly  
7100 7105 7110

Ala Ser Thr Gly Trp Pro Ser Pro Gly Thr Arg Ala Pro Thr His

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| 7115 |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Thr | Ser | Ser | Thr | Pro | Ser  | Gly | Ser | Arg | Thr | Ser  | Ala | Ser | Ser |
| 7130 |     |     |     |     |     | 7135 |     |     |     |     | 7140 |     |     |     |
| Arg  | Ser | Thr | Ser | Ser | Ser | Thr  | Arg | Ala | Cys | Cys | Val  | Ala | Ala | Pro |
| 7145 |     |     |     |     |     | 7150 |     |     |     |     | 7155 |     |     |     |
| Trp  | Pro | Pro | Arg | Thr | Ala | Ala  | Ser | Pro | Trp | Lys | Ser  | Pro | Pro | Arg |
| 7160 |     |     |     |     |     | 7165 |     |     |     |     | 7170 |     |     |     |
| Pro  | Cys | Arg | Val | Arg | Ala | Arg  | Pro | Pro | Ala | Gly | Ser  | Ser | Ala | Ala |
| 7175 |     |     |     |     |     | 7180 |     |     |     |     | 7185 |     |     |     |
| Cys  | Ser | Cys | Thr | Pro | Ser | Cys  | Thr | Gly | Pro | Thr | Ala  | Pro | Trp | Thr |
| 7190 |     |     |     |     |     | 7195 |     |     |     |     | 7200 |     |     |     |
| Arg  | Thr | Pro | Pro | Thr | Tyr | Arg  | Gly | Cys | Pro | Thr | Ala  | Cys | Ser | Ser |
| 7205 |     |     |     |     |     | 7210 |     |     |     |     | 7215 |     |     |     |
| Arg  | Pro | Arg | Trp | Asn | Pro | Pro  | Cys | Ala | Ala | Thr | Arg  | Lys | Arg | Ser |
| 7220 |     |     |     |     |     | 7225 |     |     |     |     | 7230 |     |     |     |
| Thr  | Ala | Ser | Ser | Met | Pro | Thr  | Pro | Pro | Thr | Phe | Ala  | Pro | Thr | Ala |
| 7235 |     |     |     |     |     | 7240 |     |     |     |     | 7245 |     |     |     |
| Arg  | Ala | Ser | Arg | Arg | Pro | Pro  | Pro | Ser | Thr | Ala | Ile  | Lys | Thr | Cys |
| 7250 |     |     |     |     |     | 7255 |     |     |     |     | 7260 |     |     |     |
| Lys  | Lys | Pro | Val | Cys | Val | Cys  | Glu | Cys | Phe | Ile | His  | Asn | Lys | Gln |
| 7265 |     |     |     |     |     | 7270 |     |     |     |     | 7275 |     |     |     |
| His  | Met | Phe | Met | Pro | Pro | Ser  | Leu | Arg | Leu | Leu | Tyr  | Leu | Glu | Ile |
| 7280 |     |     |     |     |     | 7285 |     |     |     |     | 7290 |     |     |     |
| Glu  | Gly | Val | Leu | Pro | Ala | Leu  | Gly | Met | Ala | Arg | Gly  | Gln | Gly | Tyr |
| 7295 |     |     |     |     |     | 7300 |     |     |     |     | 7305 |     |     |     |
| Val  | Ala | Glu | Leu | Val | Leu | Gly  | Gln | Pro | Leu | Glu | Leu  | Gly | Asp | Gln |
| 7310 |     |     |     |     |     | 7315 |     |     |     |     | 7320 |     |     |     |
| Gln  | Leu | Gly | His | Gly | Glu | Val  | Gly | Glu | Arg | Val | Ala  | Pro | Gln | Leu |
| 7325 |     |     |     |     |     | 7330 |     |     |     |     | 7335 |     |     |     |
| Ala  | Arg | Glu | Leu | Gln | Gly | Ala  | Gln | Gln | Val | Gly | Arg  | Gly | Asp | Leu |
| 7340 |     |     |     |     |     | 7345 |     |     |     |     | 7350 |     |     |     |

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Glu Ile Ala Val Gly Thr Arg Val Leu Arg Ala Arg Val Ala Val  
 7355 7360 7365  
  
 His Gly Val Ala Ala Leu Glu His His Gln Gly Arg Val Leu His  
 7370 7375 7380  
  
 Ala Cys Gln His Arg Arg Val Gly Asp Ala Leu His Val Gln Ile  
 7385 7390 7395  
  
 Leu Gly Val Gly His Pro Glu Gly Gly His Leu Ala Gly Leu Pro  
 7400 7405 7410  
  
 Pro His Ala Gly His Ala Ala Gly Leu Val Val Ala Ile Ala Val  
 7415 7420 7425  
  
 Gln Gly Asp Gln His His Leu Gly Leu Leu Gly Ala His Ala Arg  
 7430 7435 7440  
  
 Val His Gly Leu His Glu Ser Leu Gln Leu Ala Glu Gly Leu Leu  
 7445 7450 7455  
  
 Arg Leu Ala Ala Leu Gly Glu Glu Asp Pro Ala Gly Leu Ala Arg  
 7460 7465 7470  
  
 Glu Leu Val Gly Gly Ala Ala Gly Val Val His Ala Ala Ala Arg  
 7475 7480 7485  
  
 Val Val Val Gly Gln Leu His His Ala Ala Pro Pro Ala Val Leu  
 7490 7495 7500  
  
 Gly Asp Leu Gly Pro Val Gly Val Leu Leu Gln Arg Ala Leu Pro  
 7505 7510 7515  
  
 Val Leu Ala Arg His Ile His Leu Asp Ser Val Leu Leu Leu Asp  
 7520 7525 7530  
  
 His His Gly Pro Val Gln Ala Pro Gln Leu Ala Leu Gly Phe Gly  
 7535 7540 7545  
  
 Ala Ala Val Gln Pro Gln Arg Ala Ala Gly Ala Leu Pro Val Leu  
 7550 7555 7560  
  
 Val Gly Asp Leu Gly Val Arg Val His Glu Ala Leu Gln Glu Ala  
 7565 7570 7575  
  
 Ala His His Arg Gly Gln Gly Leu Val Ala Gly Glu Gly Gln Arg  
 7580 7585 7590

## 368530-7006W01\_SequenceListing\_ST25.txt

Asp Ala Ala Val Leu Leu Val His Ile Gln Val Ala Asp Ala Ala  
 7595 7600 7605  
  
 Val His Leu Ala Leu Leu Gly His Gln Leu Glu Gly Gly Leu Gln  
 7610 7615 7620  
  
 Val Ala Leu His Ala Val Pro Val His Gln Gln Arg His His Phe  
 7625 7630 7635  
  
 His Ala Leu Leu Pro Gly Arg Asn Asp Arg Gln Ala Gln Gly Val  
 7640 7645 7650  
  
 Leu His Arg His Cys His Leu Ser Arg Arg Arg Arg Gly Gln Gly  
 7655 7660 7665  
  
 Val Val Leu Val Gln Gly Leu Lys His Ser Leu Ala Val Leu Leu  
 7670 7675 7680  
  
 Asp Asp Ala His Gly Gly Lys Ala Glu Ala His Gly Arg Gln Leu  
 7685 7690 7695  
  
 Leu Leu Gly Leu Pro Phe Val Leu Ala Val Leu Ala Asp Val Leu  
 7700 7705 7710  
  
 Gln Arg His Met Leu Gly Leu Ala Gly Phe Leu Phe Gly Arg Gln  
 7715 7720 7725  
  
 Arg Arg Arg Arg Cys Ala Gly Arg Ala Arg Val Leu Val His His  
 7730 7735 7740  
  
 Asp Tyr Phe Phe Phe Leu Ala Val Val Arg Asp His Ala Ala Val  
 7745 7750 7755  
  
 Gly Met Pro Leu Leu Gly Gln Arg Arg Arg Arg Arg Ala Leu Ala  
 7760 7765 7770  
  
 Val Arg Arg Ala Ala Gly Arg Ala Pro Ser Ala Phe Gly Gly Ala  
 7775 7780 7785  
  
 Leu Leu Ala Ala Leu Leu Leu Thr Ser Ser Ala Ala Gly His Cys  
 7790 7795 7800  
  
 Val Leu Leu Gly Ser Asn Asn Lys His Gly Asp Ser Ala Ile Val  
 7805 7810 7815  
  
 Ala Asn Ile Ala Ile Cys Pro Arg Arg His Arg Arg Arg Glu Pro  
 7820 7825 7830



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Ala | Glu | Lys | Leu | Asn | Arg  | Pro | Ala | Ala | Gln | Pro  | His | Leu | Arg |
| 7835 |     |     |     |     |     | 7840 |     |     |     |     | 7845 |     |     |     |
| Arg  | Arg | Gly | Pro | Arg | His | Ala  | Arg | Asp | Gly | Gly | Ile  | His | Arg | Asp |
| 7850 |     |     |     |     |     | 7855 |     |     |     |     | 7860 |     |     |     |
| Pro  | Gly | Leu | Arg | Asp | Ala | Arg  | Gly | Ala | Arg | Gly | Gly  | Ala | Gly | Ser |
| 7865 |     |     |     |     |     | 7870 |     |     |     |     | 7875 |     |     |     |
| Ala  | Leu | Phe | Ser | Pro | Gly | Arg  | Glu | Pro | Pro | Arg | Ala  | Ala | Arg | Ala |
| 7880 |     |     |     |     |     | 7885 |     |     |     |     | 7890 |     |     |     |
| Gly  | Ser | Arg | Glu | Arg | Ala | Glu  | Pro | Gly | Trp | Ala | Arg  | Ala | Trp | Arg |
| 7895 |     |     |     |     |     | 7900 |     |     |     |     | 7905 |     |     |     |
| Leu  | Pro | Glu | Arg | Gly | Arg | Gly  | Arg | Ala | His | Gln | Ala  | Ser | Gly | Pro |
| 7910 |     |     |     |     |     | 7915 |     |     |     |     | 7920 |     |     |     |
| Pro  | Met | His | His | Arg | Gln | Gly  | Arg | Ala | Ala | Arg | Pro  | Arg | Arg | Gly |
| 7925 |     |     |     |     |     | 7930 |     |     |     |     | 7935 |     |     |     |
| Ala  | Pro | Gln | Arg | Gly | Gly | Ala  | Gln | Pro | Arg | Leu | Arg  | Ala | Gln | Pro |
| 7940 |     |     |     |     |     | 7945 |     |     |     |     | 7950 |     |     |     |
| Leu  | Leu | Ala | Ala | Arg | Ala | Pro  | Gln | Ala | Pro | Ala | Gln  | Arg | His | Leu |
| 7955 |     |     |     |     |     | 7960 |     |     |     |     | 7965 |     |     |     |
| Ala  | Gln | Pro | Ala | Pro | Gln | Leu  | Leu | Pro | Gly | Leu | Arg  | Gly | Ala | Arg |
| 7970 |     |     |     |     |     | 7975 |     |     |     |     | 7980 |     |     |     |
| Gly  | Pro | Gly | His | Leu | Pro | Pro  | Leu | Phe | Gln | Glu | Pro  | Lys | Asp | Pro |
| 7985 |     |     |     |     |     | 7990 |     |     |     |     | 7995 |     |     |     |
| Arg  | Leu | Leu | Pro | Arg | Gln | Pro  | His | Pro | Arg | Arg | Arg  | Pro | Ala | Gln |
| 8000 |     |     |     |     |     | 8005 |     |     |     |     | 8010 |     |     |     |
| Pro  | Gly | Pro | Arg | Arg | Pro | Pro  | Thr | Tyr | His | Leu | Leu  | Gly | Arg | Gly |
| 8015 |     |     |     |     |     | 8020 |     |     |     |     | 8025 |     |     |     |
| Ser  | Gln | Asp | Leu | Arg | Gly | Ser  | Gly | Gln | Arg | Arg | Asp  | Ser | Gly | Arg |
| 8030 |     |     |     |     |     | 8035 |     |     |     |     | 8040 |     |     |     |
| Glu  | Arg | Ser | Ala | Arg | Lys | Arg  | Arg | Gly | Ala | Ala | Pro  | Gln | Arg | Pro |
| 8045 |     |     |     |     |     | 8050 |     |     |     |     | 8055 |     |     |     |
| Gly  | Gly | Val | Gly | Arg | Arg | Gln  | Arg | Ala | Pro | Gly | Gly  | Pro | Gln | Ala |

8060

8065

8070

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| His | Gly  | Arg | Ala | Asp | Pro | Leu  | Arg | Leu | Pro | Gly | Ala  | Gln | Pro | Ala |
|     | 8075 |     |     |     |     | 8080 |     |     |     |     | 8085 |     |     |     |
| Pro | Gln  | Gly | His | Glu | Arg | Arg  | His | Gly | Pro | Gly | Ala  | His | Gln | Ala |
|     | 8090 |     |     |     |     | 8095 |     |     |     |     | 8100 |     |     |     |
| Arg | Leu  | Ala | Pro | Leu | Gly | Gly  | Gly | Asp | Ala | Gly | Pro  | Arg | Glu | Phe |
|     | 8105 |     |     |     |     | 8110 |     |     |     |     | 8115 |     |     |     |
| Gly | Arg  | Gly | Gln | Ala | Arg | Gly  | Gln | Arg | Arg | Ala | Ala  | Gly | Ala | Leu |
|     | 8120 |     |     |     |     | 8125 |     |     |     |     | 8130 |     |     |     |
| Ala | Gly  | Ser | Glu | His | Pro | Pro  | Glu | Pro | Gly | Arg | Ala  | Ala | Gln | Ala |
|     | 8135 |     |     |     |     | 8140 |     |     |     |     | 8145 |     |     |     |
| His | Asp  | Gly | Arg | Gly | Pro | Gly  | Asp | Arg | Gly | Ala | Gly  | Val | Ser | Ala |
|     | 8150 |     |     |     |     | 8155 |     |     |     |     | 8160 |     |     |     |
| Pro | Leu  | Leu | Cys | Arg | Arg | Gly  | Asp | Pro | Ala | Gln | Gly  | Arg | Gly | Glu |
|     | 8165 |     |     |     |     | 8170 |     |     |     |     | 8175 |     |     |     |
| Pro | Ala  | Leu | Pro | Leu | Gln | Ala  | Arg | Val | Arg | Ala | Pro  | Gly | Leu | Gln |
|     | 8180 |     |     |     |     | 8185 |     |     |     |     | 8190 |     |     |     |
| Asp | Leu  | Gln | Arg | Gly | Ala | Asp  | Gln | Pro | Gly | Leu | Leu  | His | Gly | His |
|     | 8195 |     |     |     |     | 8200 |     |     |     |     | 8205 |     |     |     |
| Pro | Ala  | Arg | Glu | Pro | Pro | Gly  | Ala | Lys | Arg | Ala | Ala  | His | His | Pro |
|     | 8210 |     |     |     |     | 8215 |     |     |     |     | 8220 |     |     |     |
| Ala | Arg  | Gly | Gly | Pro | Pro | Arg  | Leu | His | Pro | Arg | Leu  | Arg | Leu | Pro |
|     | 8225 |     |     |     |     | 8230 |     |     |     |     | 8235 |     |     |     |
| Val | Pro  | Leu | Pro | His | Leu | Ala  | Asp | Gly | His | Gly | Arg  | Val | Ala | Ala |
|     | 8240 |     |     |     |     | 8245 |     |     |     |     | 8250 |     |     |     |
| Val | Pro  | Gly | Gly | Ala | Glu | Pro  | Glu | Arg | Ala | Leu | Gln  | Ala | Pro | Ala |
|     | 8255 |     |     |     |     | 8260 |     |     |     |     | 8265 |     |     |     |
| Glu | Glu  | Pro | Gln | Gly | Pro | Val  | Asp | Arg | Val | Arg | Arg  | Ala | Tyr | His |
|     | 8270 |     |     |     |     | 8275 |     |     |     |     | 8280 |     |     |     |
| Arg | Leu  | Gly | Pro | Gly | Arg | Pro  | His | Leu | Pro | Arg | Ala  | Pro | Ala | Ala |
|     | 8285 |     |     |     |     | 8290 |     |     |     |     | 8295 |     |     |     |

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Asp Ala Ala Gln Arg Ala Ala Arg Leu Tyr Glu Pro Lys His Val  
 8300 8305 8310  
  
 Ala Lys Leu Ser Leu Phe His Pro Arg Thr Leu Arg Asp Pro Ala  
 8315 8320 8325  
  
 Arg His Leu Leu Arg Ala Ala Leu Gly Leu Arg Ala Ala Asp Leu  
 8330 8335 8340  
  
 Pro Arg Val Pro Pro Ala Ala Leu Glu Pro Leu Leu Leu Ala Ala  
 8345 8350 8355  
  
 Pro Gly Gln Leu Pro Gly Leu Pro Leu Gly Arg Asp Arg Gly Arg  
 8360 8365 8370  
  
 Gln Arg Arg Gly Ser Ala Gly Val Pro Leu Pro Leu Gln Pro Leu  
 8375 8380 8385  
  
 His Ala Ala Pro Leu Pro Gly Leu Gln Pro Pro Ala Ala Glu Arg  
 8390 8395 8400  
  
 Asp Pro Asp His Arg His Leu Arg Val Ala Arg Pro Arg Arg Arg  
 8405 8410 8415  
  
 Arg Gly Gln Gly Gly Ser Glu Thr His Pro Gly Ala Val Asp Leu  
 8420 8425 8430  
  
 Gly Leu Leu Ala Gln Val Arg Ala Arg Gly Leu Pro Ser Leu Arg  
 8435 8440 8445  
  
 Asp Gln Val Leu Arg Gly Pro Ile Pro Ala Ala Gln Gly Arg Ala  
 8450 8455 8460  
  
 Val Gly Leu Arg His His Pro Gly Gly His Pro Gly Pro Ile Ala  
 8465 8470 8475  
  
 Ser His Pro Glu Ile Pro Pro Arg Ile Ser Ala Glu Lys Gly Pro  
 8480 8485 8490  
  
 Arg Gly Leu Leu Gly Pro Pro Asp Arg Arg Gly Ala Gln Pro Gln  
 8495 8500 8505  
  
 Leu Pro Pro Gly Cys Pro Glu Glu Ala Ala Arg Ser Lys Trp Ser  
 8510 8515 8520  
  
 Cys Arg Arg Arg Arg Ile Trp Arg Lys Thr Gly Arg Ala Val Arg  
 8525 8530 8535

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Gln Arg Arg Arg Arg Trp Lys Thr Gly Thr Ala Leu Arg Gln Arg  
 8540 8545 8550  
 Arg Thr Ala Cys Lys Thr Val Trp Arg Arg Lys Thr Arg Trp Arg  
 8555 8560 8565  
 Arg Gln Arg Lys Lys Gln Pro Pro Pro Asp Arg Arg Pro Arg Arg  
 8570 8575 8580  
 Arg Lys Gln Ala Ala Arg Ile Pro Ser Pro Leu Arg Val Gly Val  
 8585 8590 8595  
 Ala Ala Ala Gly Pro Thr Val Gly Gly Thr Arg Pro Gly Ala Ser  
 8600 8605 8610  
 Arg Thr Pro Pro Pro Arg Pro Val Arg Arg Ser Gly Arg Asp Thr  
 8615 8620 8625  
 Ser Pro Gly Gly Gly Thr Lys Thr Pro Ser Ser Pro Ala Cys Lys  
 8630 8635 8640  
 Pro Ala Gly Ala Thr Ser Pro Ser Pro Gly Ala Thr Cys Ser Ser  
 8645 8650 8655  
 Thr Ala Gly Thr Ser Pro Ala Thr Ser Cys Ile Thr Thr Val Thr  
 8660 8665 8670  
 Ser Thr Ala Pro Thr Thr Val Ser Lys Lys Arg Gln Lys Pro Ser  
 8675 8680 8685  
 Ser Ser Arg Lys Pro Ala Ala Ala Ala Ala Arg Lys Ser Thr Ala  
 8690 8695 8700  
 Ala Ala Gly Gly Leu Arg Ile Ala Ala Asn Glu Pro Ala Gln Thr  
 8705 8710 8715  
 Arg Glu Leu Arg Asn Arg Ile Phe Pro Thr Leu Tyr Ala Ile Phe  
 8720 8725 8730  
 Gln Gln Ser Arg Gly Gln Glu Gln Glu Leu Lys Val Lys Asn Arg  
 8735 8740 8745  
 Ser Leu Arg Ser Leu Thr Arg Ser Cys Leu Tyr His Lys Ser Glu  
 8750 8755 8760  
 Asp Gln Leu Gln Arg Thr Leu Glu Asp Ala Glu Ala Leu Phe Asn  
 8765 8770 8775

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Lys Tyr Cys Ala Leu Thr Leu Lys Glu Pro Ala Pro Ala His Thr  
 8780 8785 8790  
 Arg Lys Lys Ala Gly Ile Thr Ser Pro Pro Ala Pro Phe Ala Arg  
 8795 8800 8805  
 Pro Ser Ala Lys Arg Phe Pro Arg Leu Thr Cys Gly Ala Thr Ser  
 8810 8815 8820  
 Pro Arg Trp Ala Trp Pro Pro Ala Pro Pro Arg Thr Thr Pro Pro  
 8825 8830 8835  
 Ala Thr Gly Ser Val Pro Gly Pro Arg Ser His Gly Met Thr Ser  
 8840 8845 8850  
 Ala Pro Thr Glu Thr Arg Tyr Ser Asn Ser Gln Arg Ser Pro Pro  
 8855 8860 8865  
 Arg Pro Ala Ile Thr Leu Ile Arg Val Ile Gly Pro Pro Pro Trp  
 8870 8875 8880  
 Cys Thr Arg Lys Phe Pro Ser Pro Arg Pro Tyr Tyr Phe Arg Glu  
 8885 8890 8895  
 Thr Pro Arg Pro Lys Ser Ser Leu Thr Gln Val Ser Ser Trp Pro  
 8900 8905 8910  
 Ala Ala Pro Pro Cys Val Val Thr Ala Pro Leu Arg Val Ser Gly  
 8915 8920 8925  
 Trp Ser Glu Ala Glu Ala His Ser Ser Thr Thr Arg Trp Ala Leu  
 8930 8935 8940  
 Arg Trp Val Cys Asp Leu Thr Glu Ser Ser Asn Ser Pro Asp Arg  
 8945 8950 8955  
 Gly Asp Leu Pro Ser Arg Leu Val Arg Pro Ser Leu Trp Arg Val  
 8960 8965 8970  
 Arg Pro Arg Ser Pro Ala Arg Ala Ala Ser Ala Leu Ser Ser Ser  
 8975 8980 8985  
 Trp Arg Ser Ser Leu Pro Arg Ser Thr Ser Thr Pro Ser Pro Ala  
 8990 8995 9000  
 Pro Pro Ala Thr Thr Arg Thr Ser Ser Ser Arg Thr Ser Thr Pro

9005

9010

9015

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser  | Ala | Ser | Arg | Trp | Thr | Ala  | Thr | Ile | Glu | Cys | Pro  | Met | Val | Ala |
| 9020 |     |     |     |     |     | 9025 |     |     |     |     | 9030 |     |     |     |
| Gln  | Leu | Thr | Leu | Gly | Phe | Asp  | Thr | Trp | Thr | Thr | Ala  | Ala | Ala | Ser |
| 9035 |     |     |     |     |     | 9040 |     |     |     |     | 9045 |     |     |     |
| Ala  | Ala | Ser | Leu | Gly | Ile | Ser  | Pro | Ser | Leu | Pro | Thr  | Leu | Ser | Cys |
| 9050 |     |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Pro  | Arg | Ser | Thr | Leu | Arg | Ala  | Gln | Pro | Thr | Glu | Cys  | Gly | Ser | Ser |
| 9065 |     |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Ser  | Lys | Gly | Ala | Ser | Thr | Pro  | Thr | Cys | Phe | Gly | Ser  | Ser | Ala | Ser |
| 9080 |     |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Asp  | Arg | Ser | Trp | Ser | Ser | Ala  | Asn | Lys | Asp | Arg | Pro  | Phe | Leu | Leu |
| 9095 |     |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Cys  | Thr | Ala | Ser | Ala | Thr | Thr  | Pro | Ala | Cys | Met | Lys  | Val | Phe | Val |
| 9110 |     |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Val  | Cys | Cys | Val | Leu | Ser | Ile  | Ile | Lys | Ala | Glu | Ile  | Ser | Asp | Tyr |
| 9125 |     |     |     |     |     | 9130 |     |     |     |     | 9135 |     |     |     |
| Ser  | Gly | Leu | Asp | Cys | Gly | Val  | Pro | Ala | Ile | Asn | Arg  | Ser | Leu | Phe |
| 9140 |     |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Phe  | Thr | Gly | Asn | Glu | Thr | Glu  | Leu | Gln | Leu | Gln | Cys  | Lys | Pro | His |
| 9155 |     |     |     |     |     | 9160 |     |     |     |     | 9165 |     |     |     |
| Lys  | Lys | Tyr | Leu | Thr | Trp | Leu  | Phe | Gln | Gly | Ser | Pro  | Ile | Ala | Val |
| 9170 |     |     |     |     |     | 9175 |     |     |     |     | 9180 |     |     |     |
| Val  | Asn | His | Cys | Asp | Asn | Asp  | Gly | Val | Leu | Leu | Ser  | Gly | Pro | Ala |
| 9185 |     |     |     |     |     | 9190 |     |     |     |     | 9195 |     |     |     |
| Asn  | Leu | Thr | Phe | Ser | Thr | Arg  | Arg | Ser | Lys | Leu | Gln  | Leu | Phe | Gln |
| 9200 |     |     |     |     |     | 9205 |     |     |     |     | 9210 |     |     |     |
| Pro  | Phe | Leu | Pro | Gly | Thr | Tyr  | Gln | Cys | Val | Ser | Gly  | Pro | Cys | His |
| 9215 |     |     |     |     |     | 9220 |     |     |     |     | 9225 |     |     |     |
| His  | Thr | Phe | His | Leu | Ile | Pro  | Asn | Thr | Thr | Ala | Pro  | Leu | Pro | Ala |
| 9230 |     |     |     |     |     | 9235 |     |     |     |     | 9240 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Asn  | Asn | Gln | Thr | Thr | His  | Gln | Arg | His | Arg | Arg  | Asp | Leu | Ser |
|     | 9245 |     |     |     |     | 9250 |     |     |     |     | 9255 |     |     |     |
| Ser | Glu  | Ser | Asn | Thr | Thr | Thr  | Gly | Gly | Glu | Leu | Arg  | Gly | Arg | Pro |
|     | 9260 |     |     |     |     | 9265 |     |     |     |     | 9270 |     |     |     |
| Thr | Ser  | Gly | Ile | Tyr | Tyr | Gly  | Pro | Trp | Glu | Val | Val  | Gly | Leu | Ile |
|     | 9275 |     |     |     |     | 9280 |     |     |     |     | 9285 |     |     |     |
| Ala | Asn  | Lys | Lys | Asn | Asn | His  | Leu | Ile | Asn | Lys | Asp  | Thr | Ile | Ile |
|     | 9290 |     |     |     |     | 9295 |     |     |     |     | 9300 |     |     |     |
| Leu | Met  | Ile | Val | Gln | Lys | Arg  | Ile | Thr | Tyr | Leu | Lys  | Ser | Asp | Thr |
|     | 9305 |     |     |     |     | 9310 |     |     |     |     | 9315 |     |     |     |
| Arg | Ser  | Leu | Ser | Met | Phe | Ser  | Ala | Asn | Thr | Thr | Ser  | Leu | Pro | Ser |
|     | 9320 |     |     |     |     | 9325 |     |     |     |     | 9330 |     |     |     |
| Ser | Gln  | Leu | Trp | Tyr | Cys | Arg  | Pro | Arg | Arg | Ala | Ala  | Asn | Phe | Leu |
|     | 9335 |     |     |     |     | 9340 |     |     |     |     | 9345 |     |     |     |
| His | Thr  | Leu | Lys | Gly | Met | Ser  | Asn | Ser | Ser | Cys | Pro  | Ser | Ile | Phe |
|     | 9350 |     |     |     |     | 9355 |     |     |     |     | 9360 |     |     |     |
| Ile | Leu  | Ser | Ser | Ile | Arg | Cys  | Pro | Lys | Ser | Ala | Ser  | Gly | Trp | Met |
|     | 9365 |     |     |     |     | 9370 |     |     |     |     | 9375 |     |     |     |
| Met | Thr  | Ser | Thr | Pro | Ser | Thr  | Pro | Thr | Met | Gln | Thr  | Thr | His | Arg |
|     | 9380 |     |     |     |     | 9385 |     |     |     |     | 9390 |     |     |     |
| Pro | Cys  | Pro | Ser | Ser | Thr | Pro  | Pro | Ser | Ser | Leu | Gln  | Met | Asp | Ser |
|     | 9395 |     |     |     |     | 9400 |     |     |     |     | 9405 |     |     |     |
| Lys | Arg  | Ser | Pro | Trp | Gly | Cys  | Cys | Pro | Cys | Asp | Trp  | Leu | Thr | Pro |
|     | 9410 |     |     |     |     | 9415 |     |     |     |     | 9420 |     |     |     |
| Ser | Pro  | Pro | Arg | Thr | Gly | Lys  | Ser | Pro | Ser | Ser | Trp  | Glu | Arg | Gly |
|     | 9425 |     |     |     |     | 9430 |     |     |     |     | 9435 |     |     |     |
| Trp | Thr  | Ser | Thr | Arg | Arg | Glu  | Asn | Ser | Ser | Pro | Thr  | Arg | Pro | Pro |
|     | 9440 |     |     |     |     | 9445 |     |     |     |     | 9450 |     |     |     |
| Arg | Pro  | Pro | Pro | Leu | Ser | Val  | Phe | Gln | Thr | Thr | Pro  | Phe | Pro | Leu |
|     | 9455 |     |     |     |     | 9460 |     |     |     |     | 9465 |     |     |     |
| Lys | Leu  | Leu | Pro | Leu | Ser | Thr  | Thr | Thr | Met | Glu | Leu  | Ala | Ser | Met |
|     | 9470 |     |     |     |     | 9475 |     |     |     |     | 9480 |     |     |     |

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Ser Pro His His Gln Tyr Phe Pro His Leu Thr Leu Ala Val Leu  
 9485 9490 9495  
  
 Glu Thr Val Phe Arg Leu Gln Ile Ser Cys Leu Tyr Asn Leu Ile  
 9500 9505 9510  
  
 Leu Leu His Ser Ala Gln Ile Ala Ser Gln Lys Gln Thr Lys Gly  
 9515 9520 9525  
  
 Tyr Ile Leu Thr Pro Val Glu Thr Glu Asp Leu Arg Leu Ile Ala  
 9530 9535 9540  
  
 Lys Glu Asp Phe Leu Thr Val Met Leu Leu Gln His Ile Leu Glu  
 9545 9550 9555  
  
 Met Ala Thr Met Asp Leu Met Ile Val Met Glu Lys Gln Asp Pro  
 9560 9565 9570  
  
 Leu Pro Lys Leu Glu Gln Asp Ile Leu Met Leu Thr Lys Gln Leu  
 9575 9580 9585  
  
 Ser Asn Ala Gln Val Val Leu Thr Pro Leu Val Pro Gln Leu Glu  
 9590 9595 9600  
  
 Thr Asn Arg Met Thr Ser His Phe Gly Leu Pro Leu Thr Gln Ala  
 9605 9610 9615  
  
 Leu Ile Val Asn Tyr Phe Gln Thr Glu Met Pro Asn Leu Leu Ser  
 9620 9625 9630  
  
 Val Leu Gln Asn Ala Val Val Lys Tyr Ala Leu Trp Gln Trp Arg  
 9635 9640 9645  
  
 Leu Leu Leu Asp Gln His Ile Gln Leu Met Thr Gln Ser Lys Ala  
 9650 9655 9660  
  
 Pro Phe Ser Leu Asp Leu Ile Pro Met Val Tyr Ser Cys Gln Thr  
 9665 9670 9675  
  
 His Gln Trp Val Ile Thr Gly Thr Leu Gly Arg Asp Arg Pro Leu  
 9680 9685 9690  
  
 Lys Val Pro Ile Gln Met Leu Trp Asp Ser Cys Gln Ile Val His  
 9695 9700 9705  
  
 Ile Gln Lys Pro Lys Val Lys His Leu Lys Ile Ala Ser Val Arg  
 9710 9715 9720



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Tyr  | Ile | Leu | Glu | Lys | Leu | Leu  | Cys | Gln | His | Pro | Leu  | Ser | Met | Ala |
| 9725 |     |     |     |     |     | 9730 |     |     |     |     | 9735 |     |     |     |
| Leu  | Met | Lys | Lys | Thr | Gln | Pro  | Gln | Leu | Ala | Pro | Thr  | Leu | Leu | Leu |
| 9740 |     |     |     |     |     | 9745 |     |     |     |     | 9750 |     |     |     |
| His  | Gly | Ser | Gly | Leu | Glu | Thr  | Ile | Arg | Thr | Lys | Ile  | Leu | Pro | Leu |
| 9755 |     |     |     |     |     | 9760 |     |     |     |     | 9765 |     |     |     |
| Leu  | Pro | Thr | His | Ser | Leu | Phe  | Pro | Thr | Ser | Pro | Arg  | Asn | Asn | Pro |
| 9770 |     |     |     |     |     | 9775 |     |     |     |     | 9780 |     |     |     |
| Thr  | Gln | Gln | Ala | Asn | Pro | Phe  | Ser | His | His | Leu | Cys  | Leu | Tyr | Gly |
| 9785 |     |     |     |     |     | 9790 |     |     |     |     | 9795 |     |     |     |
| Asn  | Ser | Glu | Thr | Glu | Lys | Ser  | Ser | Ser | Val | Leu | Leu  | Asn | Gln | Gln |
| 9800 |     |     |     |     |     | 9805 |     |     |     |     | 9810 |     |     |     |
| Phe  | Tyr | Arg | Thr | Arg | Ala | Val  | Ile | Phe | Pro | Pro | Pro  | Ser | Gln | Asp |
| 9815 |     |     |     |     |     | 9820 |     |     |     |     | 9825 |     |     |     |
| Met  | Glu | Tyr | Thr | Thr | Leu | Ser  | Pro | Arg | Thr | Ala | Leu  | Asn | Ile | Met |
| 9830 |     |     |     |     |     | 9835 |     |     |     |     | 9840 |     |     |     |
| Pro  | Leu | Val | Met | Asp | Met | Leu  | Leu | Val | Ser | Thr | Phe  | His | Thr | Val |
| 9845 |     |     |     |     |     | 9850 |     |     |     |     | 9855 |     |     |     |
| Ser  | Glu | Arg | Ala | Ser | Leu | Gly  | Ser | Val | Arg | Glu | Met  | Lys | Pro | Ser |
| 9860 |     |     |     |     |     | 9865 |     |     |     |     | 9870 |     |     |     |
| Gly  | His | Ser | Arg | Ile | Cys | Thr  | Ser | Gln | Leu | Asn | Ser  | Gly | Leu | Ser |
| 9875 |     |     |     |     |     | 9880 |     |     |     |     | 9885 |     |     |     |
| Ser  | Val | Val | Gly | Ile | Thr | Val  | Ile | Trp | Lys | Lys | Gln  | Lys | Ser | Gly |
| 9890 |     |     |     |     |     | 9895 |     |     |     |     | 9900 |     |     |     |
| Gly  | Gly | Asn | His | Ser | Pro | Arg  | Thr | Gly | Ser | Ala | Gly  | Gly | Val | Ala |
| 9905 |     |     |     |     |     | 9910 |     |     |     |     | 9915 |     |     |     |
| Ser  | Gly | Pro | Ala | Ala | Val | Ala  | Ala | Ala | Ala | Ala | Pro  | Ser | Ser | Cys |
| 9920 |     |     |     |     |     | 9925 |     |     |     |     | 9930 |     |     |     |
| Cys  | Ser | Gly | Gly | Ser | Gly | Pro  | Gly | Thr | Pro | Ser | Ala  | Cys | Pro | Arg |
| 9935 |     |     |     |     |     | 9940 |     |     |     |     | 9945 |     |     |     |
| Pro  | Ser | Ala | Ser | Val | Val | Trp  | Cys | Gly | Gly | Arg | Ser  | Ser | Ala | Cys |

9950

9955

9960

Glu Ser Arg Ser Gly His Cys Ser Thr Cys Asn Thr Gly Pro Pro  
 9965 9970 9975

Gly Cys Ser Thr Val His Ser Ser Thr Arg Ser Ser Arg Asn Ser  
 9980 9985 9990

Ser Arg Glu Gly Cys Tyr Pro Arg Gly Arg Arg Thr Arg Ser Ser  
 9995 10000 10005

Gly Lys Ser Ser Gly Ala Pro Ser Arg Arg Arg Cys Pro Cys Thr  
 10010 10015 10020

Ser Pro Trp Ala Cys Gly Gly Ser Pro Pro Pro Gly Thr Thr Ser  
 10025 10030 10035

Pro Ser Gly Thr Cys Ser Pro Gly Ser Cys Gly Thr Thr Gly Pro  
 10040 10045 10050

Ala Pro Pro Arg Pro Pro Cys Ser Glu Glu Thr Pro Asp Pro Gly  
 10055 10060 10065

Asn Asp Asn Gly Gly Pro Thr Ala Arg Thr Arg Gly Ser Ser Gly  
 10070 10075 10080

Ser Thr Ser Leu Cys Trp His Ser Thr Gly Ile Cys Ser Cys Ile  
 10085 10090 10095

Ser Ser Ala Leu Ser Ala Pro Arg Gly Ser Lys Pro Tyr Pro Arg  
 10100 10105 10110

Ala Arg Gly Thr Leu Ala Gly Gln Arg Thr Pro Gln Asn Arg Ala  
 10115 10120 10125

Ile Leu Ala His Asn Leu His Cys Ala Trp Thr Gly Tyr Arg Asn  
 10130 10135 10140

Gln Ala Ala Pro Gly Asp Pro Pro Pro Glu Lys Arg Gly Ser Arg  
 10145 10150 10155

Ser Pro His Ser Val Val Arg Gly Pro Ala Asp Thr Gly Asp Gly  
 10160 10165 10170

Gly Thr Arg Leu Ile Val Phe Ser Thr Val Ser Cys Ser Cys Phe  
 10175 10180 10185

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Arg | Thr   | Phe | Ser | Tyr | Leu | Leu   | Gln | Asn | Leu | Val | Arg   | Ala | Leu | His |
|     | 10190 |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| Thr | Asp   | Arg | Arg | Arg | Arg | Ser   | Arg | Arg | Leu | Glu | Arg   | Ser | Val | Leu |
|     | 10205 |     |     |     |     | 10210 |     |     |     |     | 10215 |     |     |     |
| Lys | Leu   | Asn | Ser | His | Ser | Leu   | Arg | Pro | Cys | Ser | Arg   | Ser | Arg | Ala |
|     | 10220 |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |
| Ser | Gly   | Val | Met | Lys | Ile | Pro   | Ser | Cys | Leu | Ile | Ala   | Leu | Ile | Thr |
|     | 10235 |     |     |     |     | 10240 |     |     |     |     | 10245 |     |     |     |
| Ser | Thr   | Thr | Val | Glu | Trp | Ala   | Arg | Pro | Ser | Gln | Met   | Met | Gln | Phe |
|     | 10250 |     |     |     |     | 10255 |     |     |     |     | 10260 |     |     |     |
| Cys | Trp   | Val | Ser | Val | Thr | Ala   | Gly | Glu | Gly | Arg | Thr   | Gly | Arg | Thr |
|     | 10265 |     |     |     |     | 10270 |     |     |     |     | 10275 |     |     |     |
| Met | Ile   | Asn | Phe | Ser | Lys | Arg   | Ser | Arg | Ser | Thr | Ser   | Lys | Arg | Ser |
|     | 10280 |     |     |     |     | 10285 |     |     |     |     | 10290 |     |     |     |
| Arg | Arg   | Trp | His | Leu | Ser | Pro   | Pro | Leu | Cys | Trp | Trp   | Lys | Ile | Thr |
|     | 10295 |     |     |     |     | 10300 |     |     |     |     | 10305 |     |     |     |
| Ala | Arg   | Ser | Lys | Val | Ile | Arg   | Phe | Ser | Arg | Cys | Ser   | Thr | Val | Ala |
|     | 10310 |     |     |     |     | 10315 |     |     |     |     | 10320 |     |     |     |
| Ser | Ser   | Lys | Ala | Ser | Thr | Arg   | Thr | Ser | Arg | Asn | Lys   | Thr | Ile | Ala |
|     | 10325 |     |     |     |     | 10330 |     |     |     |     | 10335 |     |     |     |
| Lys | Ala   | Gly | Gly | Phe | Ser | Asn   | Ser | Ser | Thr | Ile | Met   | Leu | His | Ser |
|     | 10340 |     |     |     |     | 10345 |     |     |     |     | 10350 |     |     |     |
| Cys | Thr   | Ile | Pro | Arg | Phe | Ser   | Phe | Phe | Gln | Pro | Met   | Ile | Arg | Thr |
|     | 10355 |     |     |     |     | 10360 |     |     |     |     | 10365 |     |     |     |
| Ser | Ser   | Gly | Lys | Ser | Lys | Pro   | Ala | Met | Ile | Lys | Ser   | Ser | Arg | Arg |
|     | 10370 |     |     |     |     | 10375 |     |     |     |     | 10380 |     |     |     |
| Ala | Pro   | Ser | Thr | Gly | Ile | Leu   | Lys | His | Thr | Leu | Ile   | Ile | Pro | Arg |
|     | 10385 |     |     |     |     | 10390 |     |     |     |     | 10395 |     |     |     |
| Tyr | Ser   | Ala | Pro | Gly | Ser | Pro   | Ala | Ala | Asp | Gln | Ala   | Glu | Tyr | Gln |
|     | 10400 |     |     |     |     | 10405 |     |     |     |     | 10410 |     |     |     |
| Asn | Leu   | Cys | Arg | Asp | Pro | Ala   | Pro | Pro | Ser | Ala | Ile   | Thr | Val | Ser |
|     | 10415 |     |     |     |     | 10420 |     |     |     |     | 10425 |     |     |     |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Thr | Leu   | Ser | Tyr | Arg | Leu | Arg   | Asn | Phe | Pro | Asp | Pro   | Gln | Glu | Glu |
|     | 10430 |     |     |     |     | 10435 |     |     |     |     | 10440 |     |     |     |
| Lys | Gly   | Lys | Pro | His | Tyr | Arg   | Thr | Glu | Val | Pro | Pro   | Ser | Glu | His |
|     | 10445 |     |     |     |     | 10450 |     |     |     |     | 10455 |     |     |     |
| Cys | Gln   | Met | Asp | Asn | Lys | His   | Ala | Gly | Thr | Arg | Tyr   | Leu | Pro | Asp |
|     | 10460 |     |     |     |     | 10465 |     |     |     |     | 10470 |     |     |     |
| Asn | Trp   | Thr | Glu | Asn | Arg | Val   | Ser | Asn | Phe | Glu | Asn   | Gln | Gln | Lys |
|     | 10475 |     |     |     |     | 10480 |     |     |     |     | 10485 |     |     |     |
| Lys | Asn   | Leu | Pro | Gly | Ala | Arg   | Leu | Gly | Pro | Arg | Glu   | Gln | Arg | Trp |
|     | 10490 |     |     |     |     | 10495 |     |     |     |     | 10500 |     |     |     |
| Ser | Lys   | Cys | Lys | Gly | Cys | Val   | Pro | Ala | Trp | Leu | Val   | Ser | Ser | Val |
|     | 10505 |     |     |     |     | 10510 |     |     |     |     | 10515 |     |     |     |
| Lys | Lys   | Gln | Lys | Ile | Lys | His   | Thr | Met | Leu | Ala | Trp   | Arg | Thr | Gly |
|     | 10520 |     |     |     |     | 10525 |     |     |     |     | 10530 |     |     |     |
| Gly | Ile   | Val | Leu | Ser | Ser | Thr   | Arg | Gln | Ala | Thr | Gly   | Ser | Pro | Ala |
|     | 10535 |     |     |     |     | 10540 |     |     |     |     | 10545 |     |     |     |
| Arg | Pro   | Ser | Lys | Leu | Ser | Leu   | Leu | Lys | Thr | Ile | Thr   | Glu | Arg | Arg |
|     | 10550 |     |     |     |     | 10555 |     |     |     |     | 10560 |     |     |     |
| Ser | Arg   | Trp | Pro | Ala | Met | Ile   | Arg | Glu | Glu | Ala | Tyr   | Thr | Pro | Gly |
|     | 10565 |     |     |     |     | 10570 |     |     |     |     | 10575 |     |     |     |
| Thr | Leu   | Glu | Ser | Val | Ser | Glu   | Lys | Lys | Arg | Pro | Arg   | Lys | Gln | Gly |
|     | 10580 |     |     |     |     | 10585 |     |     |     |     | 10590 |     |     |     |
| Thr | Thr   | Thr | Leu | Thr | Leu | Lys   | Ser | Ser | Lys | Ala | Met   | Pro | Cys | Gly |
|     | 10595 |     |     |     |     | 10600 |     |     |     |     | 10605 |     |     |     |
| Ser | Thr   | Lys | Phe | Ser | Gly | Ala   | Lys | Met | Leu | Leu | Pro   | Ser | Cys | Thr |
|     | 10610 |     |     |     |     | 10615 |     |     |     |     | 10620 |     |     |     |
| Gly | Ser   | Glu | Ala | Pro | Asp | Pro   | Ser | Arg | Tyr | Thr | Tyr   | Lys | Ala | Ser |
|     | 10625 |     |     |     |     | 10630 |     |     |     |     | 10635 |     |     |     |
| Ala | Ser   | Ile | Ala | Tyr | Arg | Ala   | Ala | Ala | Ala | Ala | Ala   | His | Asn | Arg |
|     | 10640 |     |     |     |     | 10645 |     |     |     |     | 10650 |     |     |     |
| Arg | Lys   | Ser | Gln | Arg | Lys | Asp   | Ala | Leu | Thr | Cys | Pro   | Pro | Ala | Leu |
|     | 10655 |     |     |     |     | 10660 |     |     |     |     | 10665 |     |     |     |

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Cys Ser Ile Tyr Ser Pro Arg Ser Thr Leu Thr Arg Pro Lys Ser  
 10670 10675 10680

Lys Asn Thr Arg Gln Ile Ile Thr His Ala Gln His Thr Pro Arg  
 10685 10690 10695

Asn Arg His Thr Gln Lys Asn Thr Arg Thr Ser Ser Asn Gly Gln  
 10700 10705 10710

Thr Ala Val Ile Ser Gly Phe Pro Arg Tyr Val Ile Lys Thr Arg  
 10715 10720 10725

Leu Ser Asn Ser Val Asp Arg Lys His His Pro Pro Arg Pro Arg  
 10730 10735 10740

Ser Pro Leu Pro Gln Pro Ile Thr Phe Leu Pro Pro Gln Ile Gln  
 10745 10750 10755

Thr Ala His Leu His Ile Asn Ala His Gln Lys Phe Glu Val Tyr  
 10760 10765 10770

Tyr

<210> 11  
 <211> 10925  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Artificially Synthesized

<220>  
 <221> misc\_feature  
 <222> (1794)..(1794)  
 <223> Xaa can be any naturally occurring amino acid

<400> 11

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
 1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Arg Glu Thr Gly Asp Arg  
 20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Val Arg Arg Ser Arg Phe  
 35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg

50

55

60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
 65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
 85 90 95

Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
 100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
 115 120 125

Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
 130 135 140

Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
 145 150 155 160

Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
 165 170 175

Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
 180 185 190

Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
 195 200 205

Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
 210 215 220

Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
 225 230 235 240

Ser Met Pro Ser Thr Pro Pro Ile Asp Val Asn Asp Gly Lys Trp Pro  
 245 250 255

Ala Trp His Tyr Ala Gln Tyr Met Thr Leu Trp Asp Phe Pro Thr Trp  
 260 265 270

Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile Thr Met Val Met Arg Phe  
 275 280 285

Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe Asp Ser Arg Gly Phe Pro  
 290 295 300

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

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Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Thr Asp Lys Lys Lys Lys  
                   565                                  570                                  575  
  
 Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Ala Leu Asp Gly Lys  
                   580                                  585                                  590  
  
 Glu Thr Asn Ser Thr Asn Ser Ser Glu Tyr Arg Leu Ile Asn Cys Asn  
                   595                                  600                                  605  
  
 Thr Ser Ala Val Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile  
                   610                                  615                                  620  
  
 Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn  
                   625                                  630                                  635                                  640  
  
 Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val  
                   645                                  650                                  655  
  
 Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu  
                   660                                  665                                  670  
  
 Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Phe Glu Asn Leu  
                   675                                  680                                  685  
  
 Thr Asn Asn Ala Lys Ile Ile Ile Val His Leu Asn Glu Ser Val Glu  
                   690                                  695                                  700  
  
 Ile Asn Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Val Arg Ile  
                   705                                  710                                  715                                  720  
  
 Gly Pro Gly Gln Thr Phe Phe Ala Thr Gly Asp Ile Ile Gly Asp Ile  
                   725                                  730                                  735  
  
 Arg Gln Ala His Cys Asn Ile Ser Arg Lys Lys Trp Asn Thr Thr Leu  
                   740                                  745                                  750  
  
 Gln Arg Val Lys Glu Lys Leu Lys Glu Lys Phe Pro Asn Lys Thr Ile  
                   755                                  760                                  765  
  
 Gln Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser  
                   770                                  775                                  780  
  
 Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Tyr Thr Ser Asp Leu Phe  
                   785                                  790                                  795                                  800  
  
 Asn Ser Thr Tyr Met Ser Asn Asn Thr Gly Gly Ala Asn Ile Thr Leu  
                   805                                  810                                  815



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Gln Cys Arg Ile Lys Gln Ile Ile Arg Met Trp Gln Gly Val Gly Gln  
820 825 830

Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn  
835 840 845

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Glu Lys Asn Asp  
850 855 860

Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg  
865 870 875 880

Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile  
885 890 895

Ala Pro Asp Lys Ala Lys Leu Thr Val Gln Ala Arg Gln Leu Leu Ser  
900 905 910

Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln  
915 920 925

Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr  
930 935 940

Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly  
945 950 955 960

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp  
965 970 975

Asn Ala Ser Trp Ser Asn Lys Ser Tyr Glu Glu Ile Trp Gly Asn Met  
980 985 990

Thr Trp Met Gln Trp Asp Arg Glu Ile Asn Asn Tyr Thr Asn Thr Ile  
995 1000 1005

Tyr Ser Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu  
1010 1015 1020

Lys Asp Leu Leu Ala Leu Asp Ser Trp Glu Ser Leu Trp Ser Trp  
1025 1030 1035

Phe Asn Ile Thr Asn Trp Leu Trp Gly Thr Ser Arg Val Asp Pro  
1040 1045 1050

Gly Gly Gln Thr Ala Asp Gln Pro Arg Leu Cys Leu Leu Val Ala

1055

1060

1065

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser | His  | Leu | Leu | Phe | Ala | Pro  | Pro | Pro | Cys | Leu | Pro  | Pro | Trp | Lys |
|     | 1070 |     |     |     |     | 1075 |     |     |     |     | 1080 |     |     |     |
| Val | Pro  | Leu | Pro | Leu | Ser | Phe  | Pro | Asn | Lys | Met | Arg  | Lys | Leu | His |
|     | 1085 |     |     |     |     | 1090 |     |     |     |     | 1095 |     |     |     |
| Arg | Ile  | Val | Val | Gly | Val | Ile  | Leu | Phe | Trp | Gly | Val  | Gly | Trp | Gly |
|     | 1100 |     |     |     |     | 1105 |     |     |     |     | 1110 |     |     |     |
| Arg | Thr  | Ala | Arg | Gly | Arg | Ile  | Gly | Lys | Thr | Ile | Ala  | Gly | Met | Leu |
|     | 1115 |     |     |     |     | 1120 |     |     |     |     | 1125 |     |     |     |
| Gly | Met  | Arg | Trp | Ala | Leu | Trp  | Leu | Leu | Arg | Arg | Lys  | Glu | Pro | Ala |
|     | 1130 |     |     |     |     | 1135 |     |     |     |     | 1140 |     |     |     |
| Asp | Leu  | Gln | Ile | Ile | His | Leu  | Cys | Arg | Val | Arg | Arg  | Lys | Arg | Asn |
|     | 1145 |     |     |     |     | 1150 |     |     |     |     | 1155 |     |     |     |
| Gly | Ile  | Met | Gly | Ile | Met | Gly  | Leu | His | Ile | Gly | Gln  | Ile | Ser | Ile |
|     | 1160 |     |     |     |     | 1165 |     |     |     |     | 1170 |     |     |     |
| Cys | Trp  | Pro | Pro | Cys | Met | Pro  | Arg | Thr | Pro | Ala | Arg  | His | Gly | Pro |
|     | 1175 |     |     |     |     | 1180 |     |     |     |     | 1185 |     |     |     |
| Ser | Ser  | Ser | Thr | Thr | Ser | Pro  | Asp | Ala | Met | Cys | Thr  | Trp | Gly | Pro |
|     | 1190 |     |     |     |     | 1195 |     |     |     |     | 1200 |     |     |     |
| Ala | Glu  | Ala | Cys | Ser | Cys | Pro  | Thr | Ser | Ala | Thr | Cys  | Asn | Leu | Arg |
|     | 1205 |     |     |     |     | 1210 |     |     |     |     | 1215 |     |     |     |
| Cys | Cys  | Trp | Ser | Pro | Met | Pro  | Cys | Pro | Glu | Ala | Arg  | Gly | Cys | Leu |
|     | 1220 |     |     |     |     | 1225 |     |     |     |     | 1230 |     |     |     |
| Thr | Met  | Trp | Ser | Cys | Gly | Lys  | Phe | Asp | Met | Met | Asn  | Pro | Arg | Pro |
|     | 1235 |     |     |     |     | 1240 |     |     |     |     | 1245 |     |     |     |
| Gly | Ala  | Gly | Pro | Ala | Asn | Ala  | Glu | Ala | Ser | Thr | Pro  | Gly | Phe | Ser |
|     | 1250 |     |     |     |     | 1255 |     |     |     |     | 1260 |     |     |     |
| Pro | Cys  | Val | Trp | Arg | Arg | Arg  | Thr | Cys | Asp | Pro | Ile  | Ile | Trp | Cys |
|     | 1265 |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |
| Cys | Pro  | Ala | Thr | Gly | Arg | Ser  | Ser | Ala | Pro | Ala | Gly  | Lys | Asn | Leu |
|     | 1280 |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|------|-----|-----|
| Thr | Arg  | Val | Ser | Ser | Val | Trp  | Gly | Arg | Trp | Arg | Ala  | Cys  | Met | Arg |
|     | 1295 |     |     |     |     | 1300 |     |     |     |     |      | 1305 |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Gly | Arg  | Met | Thr | Lys | Ile | Cys  | Val | Phe | Leu | Cys | Val  | Ala  | Ala | Ala |
|     | 1310 |     |     |     |     | 1315 |     |     |     |     | 1320 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Ala | Glu  | Ala | Pro | Pro | Leu | Arg  | Glu | Gly | Tyr | Ser | Ala  | Leu  | Ile | Arg |
|     | 1325 |     |     |     |     | 1330 |     |     |     |     | 1335 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Gly | Val  | Ser | Pro | Pro | Gly | Arg  | Glu | Cys | Val | Arg | Met  | Trp  | Asp | Pro |
|     | 1340 |     |     |     |     | 1345 |     |     |     |     | 1350 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Arg | Trp  | Thr | Ala | Gly | Pro | Cys  | Ser | Pro | Arg | Thr | Leu  | Gln  | Pro | Pro |
|     | 1355 |     |     |     |     | 1360 |     |     |     |     | 1365 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Thr | Arg  | Pro | Ala | Pro | Arg | Pro  | Trp | Thr | Gln | Leu | Pro  | Pro  | Gln | Leu |
|     | 1370 |     |     |     |     | 1375 |     |     |     |     | 1380 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Leu | Leu  | Pro | Pro | Pro | Ala | Pro  | Cys | Ala | Glu | Trp | Pro  | Trp  | Ala | Pro |
|     | 1385 |     |     |     |     | 1390 |     |     |     |     | 1395 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Ala | Thr  | Thr | Ala | Leu | Trp | Trp  | Pro | Thr | Arg | Leu | Pro  | Pro  | Ile | Ile |
|     | 1400 |     |     |     |     | 1405 |     |     |     |     | 1410 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Pro | Pro  | Ala | Thr | Arg | Arg | Ser  | Cys | Cys | Cys | Trp | Pro  | Ser  | Ser | Arg |
|     | 1415 |     |     |     |     | 1420 |     |     |     |     | 1425 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Pro | Pro  | Ser | Ala | Trp | Ala | Ser  | Pro | Ser | Arg | Trp | Leu  | Ser  | Cys | Arg |
|     | 1430 |     |     |     |     | 1435 |     |     |     |     | 1440 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Arg | Arg  | Arg | Gly | Pro | Arg | Leu  | Pro | Arg | Lys | Pro | Asn  | Lys  | Lys | Ile |
|     | 1445 |     |     |     |     | 1450 |     |     |     |     | 1455 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Asn | Lys  | Thr | Glu | Thr | Val | Val  | Asp | Phe | Asn | Thr | Glu  | Ser  | Ile | Phe |
|     | 1460 |     |     |     |     | 1465 |     |     |     |     | 1470 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Ile | Phe  | Phe | Ala | Arg | Gly | Arg  | Pro | Trp | Thr | Thr | Gly  | Leu  | Asp | His |
|     | 1475 |     |     |     |     | 1480 |     |     |     |     | 1485 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Ala | Pro  | Gly | Gly | Phe | Phe | Pro  | Gly | Pro | Gly | Arg | Gly  | Gly  | Leu | Gly |
|     | 1490 |     |     |     |     | 1495 |     |     |     |     | 1500 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Cys | Gly  | Thr | Trp | Ala | Ala | Arg  | Pro | Gly | Gly | Gly | Gly  | Ser  | Ser | Ile |
|     | 1505 |     |     |     |     | 1510 |     |     |     |     | 1515 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Ala | Gly  | Pro | Arg | Ala | Arg | Gly  | Trp | Cys | Cys | Lys | Ser  | Pro  | Ser | His |
|     | 1520 |     |     |     |     | 1525 |     |     |     |     | 1530 |      |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser | Arg  | Gly | Ala | Gly | Arg | Gly  | Ala | Ala | Arg | Cys | Pro  | Gly | Gly | Asp |
|     | 1535 |     |     |     |     | 1540 |     |     |     |     | 1545 |     |     |     |
| Trp | Pro  | Arg | Ala | Ala | Pro | Trp  | Cys | Arg | Cys | Arg | Thr  | Cys | Ala | Gly |
|     | 1550 |     |     |     |     | 1555 |     |     |     |     | 1560 |     |     |     |
| Arg | Asp  | Ala | Cys | Gly | Gly | Arg  | Asp | Ala | Ser | Trp | Pro  | Gly | Ser | Asp |
|     | 1565 |     |     |     |     | 1570 |     |     |     |     | 1575 |     |     |     |
| Trp | Arg  | Cys | Ser | Arg | Pro | Asp  | Pro | Ala | Gly | Gly | Ser  | Cys | Cys | Ala |
|     | 1580 |     |     |     |     | 1585 |     |     |     |     | 1590 |     |     |     |
| Gly | Pro  | Pro | Ala | Arg | Cys | Ile  | Arg | Arg | Thr | Trp | Gly  | Ile | Cys | His |
|     | 1595 |     |     |     |     | 1600 |     |     |     |     | 1605 |     |     |     |
| Ala | Thr  | Trp | Lys | Gly | Arg | Arg  | Glu | Arg | Ile | Trp | Arg  | Arg | Pro | Cys |
|     | 1610 |     |     |     |     | 1615 |     |     |     |     | 1620 |     |     |     |
| Asp | Arg  | Pro | Gly | Phe | Pro | Cys  | Thr | His | Pro | Trp | Arg  | Trp | Ala | Arg |
|     | 1625 |     |     |     |     | 1630 |     |     |     |     | 1635 |     |     |     |
| Gly | Arg  | Arg | Pro | Gly | Gln | Arg  | Arg | Phe | Gly | Gly | Arg  | Thr | His | Arg |
|     | 1640 |     |     |     |     | 1645 |     |     |     |     | 1650 |     |     |     |
| Ser | Cys  | Gly | Pro | Gly | Ala | Arg  | His | Arg | Pro | Phe | Ile  | Trp | Gly | Gly |
|     | 1655 |     |     |     |     | 1660 |     |     |     |     | 1665 |     |     |     |
| Gly | Cys  | Pro | Thr | Gly | Gly | Arg  | Arg | Cys | Pro | Arg | Ser  | Arg | Gly | Arg |
|     | 1670 |     |     |     |     | 1675 |     |     |     |     | 1680 |     |     |     |
| Ser | Cys  | Pro | Arg | Arg | Ser | Ala  | Ser | Pro | Arg | Pro | Ala  | Arg | Arg | Gly |
|     | 1685 |     |     |     |     | 1690 |     |     |     |     | 1695 |     |     |     |
| Gly | Ser  | Cys | Pro | Pro | Ala | Gly  | Arg | Lys | Lys | Arg | Phe  | Pro | Gly | Arg |
|     | 1700 |     |     |     |     | 1705 |     |     |     |     | 1710 |     |     |     |
| Gly | Arg  | Ala | Gly | Pro | Lys | Ala  | Gly | Ser | Gly | Ala | Ala  | Gly | Thr | Cys |
|     | 1715 |     |     |     |     | 1720 |     |     |     |     | 1725 |     |     |     |
| Arg | Ser  | Arg | Trp | Gly | Arg | Arg  | Pro | Arg | Pro | Ala | Ala  | Gly | Gly | Ser |
|     | 1730 |     |     |     |     | 1735 |     |     |     |     | 1740 |     |     |     |
| Gly | Arg  | Asp | Ser | Cys | Arg | Pro  | Arg | Gly | Gly | Gly | Gly  | Pro | Pro | Arg |
|     | 1745 |     |     |     |     | 1750 |     |     |     |     | 1755 |     |     |     |
| Ser | Ser  | Ser | Arg | Ala | His | Ala  | Cys | Ser | Arg | Ala | Arg  | Val | Pro | Pro |
|     | 1760 |     |     |     |     | 1765 |     |     |     |     | 1770 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly | Gly  | Ala | Arg | Pro | Pro | Ala  | Arg | Gly | Ala | Leu | Ala  | Ala | Arg | Arg |
|     | 1775 |     |     |     |     | 1780 |     |     |     |     | 1785 |     |     |     |
| Ser | Phe  | Ser | Ala | Ala | Xaa | Arg  | Arg | Pro | Trp | Ala | Phe  | Trp | Arg | Gly |
|     | 1790 |     |     |     |     | 1795 |     |     |     |     | 1800 |     |     |     |
| Ser | Val  | Ala | Arg | Val | Pro | Asp  | Gly | Pro | Arg | Ala | Arg  | Cys | Ala | Leu |
|     | 1805 |     |     |     |     | 1810 |     |     |     |     | 1815 |     |     |     |
| Gly | His  | Leu | Asp | Pro | Ala | Asp  | Leu | Leu | Val | Ser | Arg  | Val | Gly | Ala |
|     | 1820 |     |     |     |     | 1825 |     |     |     |     | 1830 |     |     |     |
| Thr | Ala  | Gly | Val | Gly | His | Gln  | Ala | Met | Gly | Val | Gln  | Arg | Gly | Gln |
|     | 1835 |     |     |     |     | 1840 |     |     |     |     | 1845 |     |     |     |
| Gly | Pro  | Val | Leu | Pro | Gly | Ser  | Gln | Gly | Pro | Arg | Gln  | Arg | Gly | Leu |
|     | 1850 |     |     |     |     | 1855 |     |     |     |     | 1860 |     |     |     |
| Arg | His  | Gly | Glu | Gly | Val | Arg  | Ala | Gly | Leu | Gly | Ala  | Cys | Glu | Gly |
|     | 1865 |     |     |     |     | 1870 |     |     |     |     | 1875 |     |     |     |
| Ala | Leu  | Gln | Ala | His | Pro | Ala  | Gly | Arg | Glu | Pro | Leu  | Pro | Val | Gly |
|     | 1880 |     |     |     |     | 1885 |     |     |     |     | 1890 |     |     |     |
| Ala | Leu  | Arg | Val | Gly | Gln | Val  | Ala | Ile | Glu | His | Glu  | Phe | Val | Val |
|     | 1895 |     |     |     |     | 1900 |     |     |     |     | 1905 |     |     |     |
| Glu | Arg  | Leu | Gly | Arg | Val | Ala  | Leu | Gly | Ala | Glu | Leu  | Thr | Phe | Gly |
|     | 1910 |     |     |     |     | 1915 |     |     |     |     | 1920 |     |     |     |
| Ser | Val  | Ser | Ala | Asp | Gly | Thr  | Glu | Glu | Gly | Leu | Glu  | Gly | Val | Glu |
|     | 1925 |     |     |     |     | 1930 |     |     |     |     | 1935 |     |     |     |
| Leu | Gly  | Gly | Glu | Glu | Asp | Gly  | Leu | Gly | Gly | Val | Gly  | Val | Arg | Ala |
|     | 1940 |     |     |     |     | 1945 |     |     |     |     | 1950 |     |     |     |
| Ala | Ala  | Gly | Ala | Asp | Gly | Leu  | Ala | Leu | His | Glu | Pro  | Gly | Glu | Val |
|     | 1955 |     |     |     |     | 1960 |     |     |     |     | 1965 |     |     |     |
| Gly | Pro  | Val | Gly | Val | Lys | Asn  | Glu | Val | Ser | Ser | Val  | Leu | Phe | Asp |
|     | 1970 |     |     |     |     | 1975 |     |     |     |     | 1980 |     |     |     |
| Ala | Phe  | Leu | Thr | Ser | Gly | Leu  | His | Glu | Leu | Val | Ser  | Pro | Leu | Gly |
|     | 1985 |     |     |     |     | 1990 |     |     |     |     | 1995 |     |     |     |
| Asp | Lys  | Glu | Ala | Val | Arg | Val  | Pro | Val | Asp | Arg | Leu  | Tyr | Gly | Pro |

2000

2005

2010

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | Leu | Glu | Arg | Gly | Ala | Ala  | Val | Leu | Val | Val | Glu  | Glu | Pro | Arg |
| 2015 |     |     |     |     |     | 2020 |     |     |     |     | 2025 |     |     |     |
| Pro  | Leu | Arg | Asp | Glu | Gly | Pro  | Gly | Pro | Gly | Gln | His  | Glu | Gly | Gly |
| 2030 |     |     |     |     |     | 2035 |     |     |     |     | 2040 |     |     |     |
| His  | Val | Gly | Gly | Val | Ala | Val  | Val | Val | His | Gln | Arg  | Val | His | Leu |
| 2045 |     |     |     |     |     | 2050 |     |     |     |     | 2055 |     |     |     |
| Leu  | Gln | Gly | Met | Gln | Ala | His  | Val | Pro | Leu | Val | His  | Ile | Gln | Glu |
| 2060 |     |     |     |     |     | 2065 |     |     |     |     | 2070 |     |     |     |
| Gly  | Asp | Trp | Leu | Val | Ser | Val  | Gly | His | Val | Thr | Gly  | Gly | Pro | Gly |
| 2075 |     |     |     |     |     | 2080 |     |     |     |     | 2085 |     |     |     |
| Arg  | Gly | Gly | Ile | Lys | Gly | Gly  | Gly | Pro | Leu | Leu | Val  | Leu | Thr | Val |
| 2090 |     |     |     |     |     | 2095 |     |     |     |     | 2100 |     |     |     |
| Phe  | Arg | Ile | Ala | Val | Gln | Glu  | Arg | Gln | Leu | Leu | Gly  | Val | Phe | Pro |
| 2105 |     |     |     |     |     | 2110 |     |     |     |     | 2115 |     |     |     |
| Leu  | Glu | Gly | Trp | His | Asn | Leu  | Gly | Thr | Gln | Val | Val  | Ser | Phe | Lys |
| 2120 |     |     |     |     |     | 2125 |     |     |     |     | 2130 |     |     |     |
| Arg  | Gly | Gly | Phe | Asp | Ile | Asp  | Gly | Ala | Val | Gly | Asp  | Ala | Phe | His |
| 2135 |     |     |     |     |     | 2140 |     |     |     |     | 2145 |     |     |     |
| Glu  | Pro | Leu | Val | His | Leu | Val  | Arg | Lys | Asp | Asp | Leu  | Phe | Val | Val |
| 2150 |     |     |     |     |     | 2155 |     |     |     |     | 2160 |     |     |     |
| Glu  | Leu | Gly | Gly | Glu | Gly | Ala  | Val | Glu | Gly | Val | Gly  | Glu | Glu | Leu |
| 2165 |     |     |     |     |     | 2170 |     |     |     |     | 2175 |     |     |     |
| Gly  | Asp | Gly | Ala | His | Gly | Leu  | Val | Leu | Phe | Leu | Val  | Gly | Ala | Leu |
| 2180 |     |     |     |     |     | 2185 |     |     |     |     | 2190 |     |     |     |
| Leu  | Gly | Gly | Asp | Val | Glu | Leu  | His | Val | Leu | Ala | Arg  | His | Ala | Leu |
| 2195 |     |     |     |     |     | 2200 |     |     |     |     | 2205 |     |     |     |
| Pro  | Phe | Gly | Glu | Asp | Gly | Gly  | Glu | Leu | Val | Gly | His  | Asp | Ser | Asp |
| 2210 |     |     |     |     |     | 2215 |     |     |     |     | 2220 |     |     |     |
| Pro  | Pro | Ala | Ala | Val | Val | Gln  | Gly | Asp | Glu | Val | His  | Ala | Gly | Gly |
| 2225 |     |     |     |     |     | 2230 |     |     |     |     | 2235 |     |     |     |

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His Leu Ala Ala Gln Gly Leu Val Gly Pro Ala Glu Ala Pro Ala  
 2240 2245 2250  
  
 Leu Ala Arg Ala Glu Gly Gly Gln Arg Val Gln His Glu Leu Val  
 2255 2260 2265  
  
 Gly Gly Val Gly Val His Gly Glu Asp Ala Gly Gln Lys Leu Gly  
 2270 2275 2280  
  
 Val Glu Val Ala Asp Ala Gly Val Gln Ile Val Gln Arg Arg Leu  
 2285 2290 2295  
  
 Pro Val Ala His Gly Gln Arg Ala Leu Val Gly Ala Glu Gly Arg  
 2300 2305 2310  
  
 Ala Pro Gly His Gly Val Arg Glu Arg Gly Gly Val His Ala Ala  
 2315 2320 2325  
  
 Asp Val Val Asp Val Glu Gly Leu Leu Glu Asp Ala Asp Val Gly  
 2330 2335 2340  
  
 Gly Val Ala Ala Pro Pro Ala Asp Ala Gly Ala His Val Val Val  
 2345 2350 2355  
  
 Gln Leu Val Arg Gly Arg Glu Glu Pro Arg Ala Glu Val Gly Ala  
 2360 2365 2370  
  
 Leu Arg Leu Phe Gly Ala Val Asp Asp Leu Ala Glu Asp Gly Val  
 2375 2380 2385  
  
 Gly Val Gly Gly Asp Gly Gly Pro Leu Glu Asp Val Glu Val Gly  
 2390 2395 2400  
  
 Val Gly Gln Ala Asp Arg Val Pro Asp Glu Val Gly Val Gly Val  
 2405 2410 2415  
  
 Leu Gln Leu Gly Asp Glu Leu Gly Gly Asp Glu Asp Val Gln Gly  
 2420 2425 2430  
  
 Ala Val Val Glu Gly Leu Leu Asp Asp Val Val Leu Glu Leu Ala  
 2435 2440 2445  
  
 Leu Leu Leu Pro Gln Leu Ala Val Glu Lys Glu Leu Phe Ala Val  
 2450 2455 2460  
  
 Leu Pro Val Leu Phe Glu Gly Glu Pro Val Leu Ile Gly Thr Val  
 2465 2470 2475

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Ala  | His | His | Val | Glu | Leu  | Val | Asp | Gly | Leu | Val  | Gly | Ala | Ala |
|     | 2480 |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Ala | Leu  | Leu | His | Gly | Glu | Gly  | Val | Ser | Leu | Cys | Gly  | Leu | Ala | Gln |
|     | 2495 |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Gly | Gly  | Val | Gly | Glu | Gly | Glu  | Gly | Val | Ala | His | His  | Asp | Leu | Glu |
|     | 2510 |     |     |     |     | 2515 |     |     |     |     | 2520 |     |     |     |
| Glu | Leu  | Val | Leu | Glu | Val | Glu  | Val | Val | Ala | Ala | Ala  | Leu | Leu | Pro |
|     | 2525 |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Glu | Leu  | Glu | Val | Arg | Ala | Leu  | Leu | Val | Gly | Gly | Val  | Gly | Gln | Ser |
|     | 2540 |     |     |     |     | 2545 |     |     |     |     | 2550 |     |     |     |
| Glu | Ser  | Asn | Ile | Val | Glu | Glu  | Asp | Leu | Ala | Arg | Ala  | Gly | His | Glu |
|     | 2555 |     |     |     |     | 2560 |     |     |     |     | 2565 |     |     |     |
| Val | Ala  | Ser | Asp | Ala | Glu | Arg  | Leu | Gly | His | Leu | Gly  | Pro | Val | Val |
|     | 2570 |     |     |     |     | 2575 |     |     |     |     | 2580 |     |     |     |
| Asp | Asp  | Leu | Gly | Gly | Glu | Asp  | Asp | Leu | Val | Glu | Ala  | Val | Asp | Val |
|     | 2585 |     |     |     |     | 2590 |     |     |     |     | 2595 |     |     |     |
| Val | Pro  | Asp | Asp | Val | Glu | Phe  | His | Glu | Ser | Arg | Ala  | Ala | Leu | Asn |
|     | 2600 |     |     |     |     | 2605 |     |     |     |     | 2610 |     |     |     |
| Val | Gly  | Gln | Leu | Leu | Glu | Leu  | Val | Val | Gly | Glu | Leu  | Gly | Gly | Val |
|     | 2615 |     |     |     |     | 2620 |     |     |     |     | 2625 |     |     |     |
| Ala | Glu  | Pro | Val | Leu | Leu | Glu  | Gly | Pro | Val | Gly | Asp  | Val | Gly | Val |
|     | 2630 |     |     |     |     | 2635 |     |     |     |     | 2640 |     |     |     |
| Gly | Ala  | Glu | Glu | Gly | Ser | Pro  | Glu | Ile | His | Gly | Gln  | Gly | Gly | Leu |
|     | 2645 |     |     |     |     | 2650 |     |     |     |     | 2655 |     |     |     |
| Gln | Ala  | Val | Pro | Val | Leu | Thr  | Glu | Leu | Leu | Ala | His  | Gly | His | Phe |
|     | 2660 |     |     |     |     | 2665 |     |     |     |     | 2670 |     |     |     |
| Phe | Gly  | Gly | Asp | Ala | Val | Glu  | Gly | Ala | Gly | Val | Ala  | Val | Pro | Ala |
|     | 2675 |     |     |     |     | 2680 |     |     |     |     | 2685 |     |     |     |
| Val | Pro  | Leu | Glu | Leu | Glu | Gly  | Glu | Val | Val | Gly | Glu  | Leu | Asp | Glu |
|     | 2690 |     |     |     |     | 2695 |     |     |     |     | 2700 |     |     |     |
| Arg | Arg  | Val | Pro | Gly | Glu | Phe  | His | Asp | Gln | His | Glu  | Gly | Asp | Glu |
|     | 2705 |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu  | Leu | Ala | Glu | Gly | Pro | His  | Pro | Gly | Val | Gly | Phe  | His | Ile | Val |
| 2720 |     |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |
| Gly  | Glu | Glu | Glu | Pro | Phe | Gly  | Ala | Arg | Met | Arg | Ala  | Asp | Gly | Glu |
| 2735 |     |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |
| Glu  | Leu | Asp | Leu | Leu | Pro | Pro  | Val | Gly | Gly | Met | Ala  | Val | Asp | Val |
| 2750 |     |     |     |     |     | 2755 |     |     |     |     | 2760 |     |     |     |
| Met  | Glu | Val | Glu | Met | Pro | Thr  | Ala | Arg | Arg | Ala | Leu  | Val | Leu | Val |
| 2765 |     |     |     |     |     | 2770 |     |     |     |     | 2775 |     |     |     |
| Phe  | Ile | Gln | Ala | Ser | Ala | Val  | Leu | Ala | Thr | Leu | His  | Gly | Met | His |
| 2780 |     |     |     |     |     | 2785 |     |     |     |     | 2790 |     |     |     |
| Val  | Leu | His | Glu | Leu | Tyr | Leu  | Gly | Ser | Phe | Asp | Glu  | Glu | Phe | Gln |
| 2795 |     |     |     |     |     | 2800 |     |     |     |     | 2805 |     |     |     |
| Trp  | Ala | Val | Glu | Arg | Trp | Arg  | Leu | His | Leu | Val | Leu  | Tyr | Tyr | Val |
| 2810 |     |     |     |     |     | 2815 |     |     |     |     | 2820 |     |     |     |
| Leu  | Ala | Ile | Gly | Val | Ala | Ile  | Val | Cys | Leu | Asp | Gly  | Gly | His | Ala |
| 2825 |     |     |     |     |     | 2830 |     |     |     |     | 2835 |     |     |     |
| Asp  | Glu | Pro | Ala | Arg | Glu | Ala  | Gly | Pro | Asp | Phe | Gly  | Ser | Asp | Gly |
| 2840 |     |     |     |     |     | 2845 |     |     |     |     | 2850 |     |     |     |
| Ser  | Glu | Ser | Glu | Asp | Glu | Gly  | Ala | Gln | Ala | Gly | Ala  | Val | Gln | Gly |
| 2855 |     |     |     |     |     | 2860 |     |     |     |     | 2865 |     |     |     |
| Pro  | Glu | Thr | Leu | Arg | Ser | Gln  | Val | Ser | Gly | Gln | Arg  | Arg | Arg | Ala |
| 2870 |     |     |     |     |     | 2875 |     |     |     |     | 2880 |     |     |     |
| Val  | Asp | Leu | Gln | Glu | Leu | Phe  | Gln | Gly | Ala | Arg | Glu  | Val | Gln | Met |
| 2885 |     |     |     |     |     | 2890 |     |     |     |     | 2895 |     |     |     |
| Val  | Leu | Asp | Leu | His | Gly | Ala  | Val | Gly | Gly | Asp | Val  | His | Gly | Leu |
| 2900 |     |     |     |     |     | 2905 |     |     |     |     | 2910 |     |     |     |
| Gln  | Gly | Pro | Val | Pro | Leu | Gly  | Arg | His | His | Arg | Ala  | Pro | Phe | Leu |
| 2915 |     |     |     |     |     | 2920 |     |     |     |     | 2925 |     |     |     |
| Leu  | Gly | Arg | Cys | Phe | His | Ala  | Gly | Gln | Lys | Arg | Arg  | Arg | Gly | Arg |
| 2930 |     |     |     |     |     | 2935 |     |     |     |     | 2940 |     |     |     |
| Ala  | Pro | Gly | Gly | Arg | Gly | Gly  | Ser | Gly | Pro | Gly | Gly  | Arg | Gly | Gly |

2945

2950

2955

Arg Gly Thr Ser Ala Pro Arg Ala Gly Arg Phe Trp Tyr Cys Ala  
 2960 2965 2970

Arg Arg Arg Leu Ala Ala Thr Thr Arg Arg Leu Thr Ser Trp Ile  
 2975 2980 2985

Arg Leu Trp Val Lys Ala Thr Gly Pro Val Ser Leu Asn Leu Lys  
 2990 3000

Glu Ser Ser Thr Glu Ser Ile Ser Val Ser Leu Thr Ala Ala Cys  
 3005 3010 3015

Arg Arg Ile Ser Cys Thr Ser Pro Glu Leu Ser Trp Ala Ile Ser  
 3020 3025 3030

Val Met Asn Cys Ser Ile Ser Ser Ser Arg Ser Pro Arg Pro Ala  
 3035 3040 3045

Arg Ser Thr Val Ala Ala Arg Ser Leu Glu Met Arg Pro Met Ser  
 3050 3055 3060

Cys Glu Lys Ala Phe Met Pro Ala Ser Phe Gln Thr Arg Leu Thr  
 3065 3070 3075

Thr Ala Pro Ser Gly Ser Arg Ala Arg Met Thr Thr Trp Ala Arg  
 3080 3085 3090

Leu Ser Ser Thr Trp Arg Val Lys Thr Ala Leu Gln Arg Arg Trp  
 3095 3100 3105

Arg Leu Ser Val Val Ala Met Cys Ser Val Thr Lys Lys Tyr Met  
 3110 3115 3120

Ile Gln Arg Arg Ser Gly Ile Ser Leu Thr Ser Pro Arg Ala Ser  
 3125 3130 3135

Lys Arg Ser Met Ala Ser Lys Ser Thr Ala Lys Leu Lys Asn Trp  
 3140 3145 3150

Glu Leu Arg Ala Glu Thr Val Asn Ser Ser Ser Arg Arg Arg Met  
 3155 3160 3165

Ser Ser Ala Met Val Ala Arg Thr Ser Arg Ser Lys Ala Pro Gly  
 3170 3175 3180

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Gly Ser Ser Ser Ser Ile Ser Ser Ser Ser Thr Asn Ile Ser Ser  
 3185 3190 3195  
 Thr Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Ala Leu Arg Arg  
 3200 3205 3210  
 Arg Arg Arg Thr Gly Arg Arg Ser Met Lys Arg Ser Met Val Ser  
 3215 3220 3225  
 Pro Arg Arg Arg Arg Met Val Ser Val Thr Ala Arg Pro Ser Ser  
 3230 3235 3240  
 Arg Gly Arg Ser Val Lys Thr Pro Pro Arg Ile Ser Arg Trp Pro  
 3245 3250 3255  
 Pro Gly Gly Ser Pro Leu Gly Arg Glu Arg Ala Leu Thr Met His  
 3260 3265 3270  
 Leu Ile Asn Trp Pro Val Gly Thr Pro Arg Lys Asp Leu Ser Val  
 3275 3280 3285  
 Ser Arg Ser Thr Gly Ser Glu Asn Arg Thr Lys Ala Ser Ser Gln  
 3290 3295 3300  
 Ser Gln Ser Gln Gly Arg Leu Ser Pro Val Ser Cys Ser Ser Gly  
 3305 3310 3315  
 Ile Ser Gly Gly Gly Arg Ala Met Leu Leu Val Met Lys Leu Lys  
 3320 3325 3330  
 Ala Val Leu Arg Arg Arg Met Val Ala Arg Ser Thr Arg Ser Leu  
 3335 3340 3345  
 Gly Pro Ala Cys Trp Met Arg Arg Arg Ser Ala Met Pro Gln Ala  
 3350 3355 3360  
 Trp Ser His Leu Ala Arg Ser Leu Ser Cys Met Ser Arg Ser Thr  
 3365 3370 3375  
 Gly Thr Ser Ser Ser Pro Ala Arg Pro Cys Met Arg Val Ser Pro  
 3380 3385 3390  
 Asn Pro Arg Trp Gly Trp Thr Ser Ala Arg Ser Ala Thr Thr Arg  
 3395 3400 3405  
 Ser Ala Arg Met Ala Cys Cys Ile Trp Val Arg Val Val Trp Lys  
 3410 3415 3420

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Ser Ser Lys Ser Thr Lys Arg Trp Ala Pro Val Leu Met Val Glu  
 3425 3430 3435  
  
 Gln Leu Ala Met Thr Asp Gln Leu Thr Val Trp Trp Pro Gly Arg  
 3440 3445 3450  
  
 Thr Ser Ser Trp Tyr Leu Arg Arg Glu Ala Arg Val Ser Lys Met  
 3455 3460 3465  
  
 Ser Leu Gln Val Arg Thr Arg Tyr Trp Tyr Pro Thr Arg Lys Cys  
 3470 3475 3480  
  
 Gly Gly Gly Trp Arg Ser Gly His Arg Ser Val Ala Gly Ala Pro  
 3485 3490 3495  
  
 Gly Ala Arg Ser Ser Ser Met Arg Arg Trp Pro Met Tyr Leu Asp  
 3500 3505 3510  
  
 Ile Gln Val Met Pro Ala Ala Val Val Glu Ala Arg Gly Asn Ser  
 3515 3520 3525  
  
 Arg Thr Arg Phe Gln Met Leu Arg Ser Gly Arg Lys Phe Met Val  
 3530 3535 3540  
  
 Ala Ala Val Trp Pro Val Arg Arg Ala Gln Ser Trp Met Leu Thr  
 3545 3550 3555  
  
 Tyr Gly Gln Lys Arg Lys Arg Ser Ala Ala Arg Leu Arg Gly Leu  
 3560 3565 3570  
  
 Glu Ala Lys Arg Thr Gly Trp Ala Ala Arg Val Pro Arg Phe Glu  
 3575 3580 3585  
  
 Ser Arg Ile Arg Leu Glu Pro Gln Leu Thr Trp Tyr Trp His Ser  
 3590 3595 3600  
  
 Arg Leu Asp Pro Ser Leu Leu Thr Lys Pro Pro Gly Tyr Gly Gly  
 3605 3610 3615  
  
 Gly Ser Phe Phe Gly Leu Gly Arg Trp Ser Lys Thr Ser Lys Arg  
 3620 3625 3630  
  
 Gly Lys Arg Pro Pro Ala Met Ala Arg Cys Arg Ser Leu Glu Lys  
 3635 3640 3645  
  
 Glu Ser Pro Gly Leu Arg Cys Gly Val Pro Arg Phe Glu Pro Gln  
 3650 3655 3660

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Arg Ser Ala Pro Ala Gly Phe Arg Gly Arg Gly Arg Gly Cys Pro  
3665 3670 3675

Val Val Ser Lys Thr Pro Pro Ala Asp Phe Ser Ser Tyr Gly Ala  
3680 3685 3690

Ser Pro Ser Phe Ser Cys Val Phe Ala Arg Cys Ile Pro Tyr Cys  
3695 3700 3705

Gly Arg Cys Ala Pro Thr Leu His Leu Asn Arg Pro Tyr Arg Arg  
3710 3715 3720

Ser Ser Ser Asn Ser Arg Arg Phe Cys Pro Arg Pro Ser Ser Ser  
3725 3730 3735

Gln Pro Leu Pro Arg Arg Pro Pro Ala Glu Pro Ala Phe Ser Met  
3740 3745 3750

Thr Trp Pro Trp Lys Arg Ala Arg Gly Trp Arg Gly Trp Gly Arg  
3755 3760 3765

Arg Arg Arg Ser Gly Thr Arg Ala Cys Arg Lys Gly Thr Leu Ala  
3770 3775 3780

Arg Pro Thr Cys Pro Ser Arg Thr Cys Ser Glu Thr Gly Ala Ala  
3785 3790 3795

Arg Ser Pro Arg Arg Cys Ala Pro Pro Ala Ser Thr Arg Gly Gly  
3800 3805 3810

Ser Cys Gly Ala Ala Trp Thr Glu Ser Gly Cys Gly Thr Arg Ile  
3815 3820 3825

Ser Arg Arg Thr Ser Arg Gly Ser Ala Pro Arg Ala Arg Thr Trp  
3830 3835 3840

Pro Arg Pro Thr Trp Ser Arg Arg Thr Ser Arg Pro Arg Arg Arg  
3845 3850 3855

Ala Thr Ser Lys Asn Pro Ser Thr Thr Thr Cys Ala Arg Ser Arg  
3860 3865 3870

Ala Arg Arg Pro Trp Ala Cys Thr Cys Gly Thr Cys Trp Arg Pro  
3875 3880 3885

Ser Cys Arg Thr Pro Arg Ala Ser Arg Arg Arg Ser Cys Phe Trp

3890

3895

3900

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Trp | Cys  | Ser | Thr | Val | Gly | Thr  | Thr | Arg | Arg | Ser | Gly  | Arg | Arg | Cys |
|     | 3905 |     |     |     |     | 3910 |     |     |     |     | 3915 |     |     |     |
| Ile | Ser  | Pro | Ser | Pro | Arg | Ala  | Ala | Gly | Ser | Trp | Thr  | Trp | Thr | Phe |
|     | 3920 |     |     |     |     | 3925 |     |     |     |     | 3930 |     |     |     |
| Cys | Arg  | Ala | Ser | Trp | Cys | Arg  | Ser | Ala | Gly | Cys | Arg  | Cys | Pro | Arg |
|     | 3935 |     |     |     |     | 3940 |     |     |     |     | 3945 |     |     |     |
| Ser | Trp  | Arg | Leu | Ser | Thr | Ser  | Arg | Cys | Ala | Trp | Ala  | Ser | Thr | Thr |
|     | 3950 |     |     |     |     | 3955 |     |     |     |     | 3960 |     |     |     |
| Leu | Gly  | Arg | Ser | Thr | Arg | Pro  | Arg | Thr | Cys | Pro | Thr  | Arg | Arg | Arg |
|     | 3965 |     |     |     |     | 3970 |     |     |     |     | 3975 |     |     |     |
| Ser | Thr  | Gly | Phe | Thr | Cys | Ala  | Pro | Lys | Cys | Pro | Ala  | Thr | Ile | Trp |
|     | 3980 |     |     |     |     | 3985 |     |     |     |     | 3990 |     |     |     |
| Gly | Cys  | Thr | Ala | Thr | Thr | Gly  | Cys | Thr | Ala | Arg | Ala  | Pro | Ala | Ala |
|     | 3995 |     |     |     |     | 4000 |     |     |     |     | 4005 |     |     |     |
| Gly | Ala  | Ser | Ala | Thr | Arg | Ser  | Cys | Thr | Ala | Cys | Ser  | Gly | Pro | Pro |
|     | 4010 |     |     |     |     | 4015 |     |     |     |     | 4020 |     |     |     |
| Gly | Pro  | Gly | Pro | Arg | Gly | Arg  | Ala | Thr | Leu | Thr | Trp  | Ala | Arg | Thr |
|     | 4025 |     |     |     |     | 4030 |     |     |     |     | 4035 |     |     |     |
| Cys | Ala  | Gly | Ser | Pro | Ala | Ala  | Gly | Pro | Trp | Lys | Leu  | Pro | Ala | Val |
|     | 4040 |     |     |     |     | 4045 |     |     |     |     | 4050 |     |     |     |
| Pro | Pro  | Thr | Trp | Arg | Arg | Trp  | Thr | Met | Arg | Arg | Arg  | Arg | Ala | Ser |
|     | 4055 |     |     |     |     | 4060 |     |     |     |     | 4065 |     |     |     |
| Thr | Trp  | Lys | Thr | Asp | Gly | Ala  | Thr | Val | Phe | Leu | Leu  | Asp | Ala | Ala |
|     | 4070 |     |     |     |     | 4075 |     |     |     |     | 4080 |     |     |     |
| Thr | Ala  | Thr | Ala | Ser | Ser | Arg  | Asp | Ala | Gly | Gly | Ala  | Ala | Glu | Pro |
|     | 4085 |     |     |     |     | 4090 |     |     |     |     | 4095 |     |     |     |
| Ala | Val  | Arg | His | Leu | Leu | Gly  | Arg | Leu | Asp | Pro | Gly  | His | Ala | Thr |
|     | 4100 |     |     |     |     | 4105 |     |     |     |     | 4110 |     |     |     |
| His | His  | Gly | Ala | Asp | Asp | Pro  | Gln | Ser | Arg | Ser | Leu  | Thr | Ala | Ala |
|     | 4115 |     |     |     |     | 4120 |     |     |     |     | 4125 |     |     |     |

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Ser Gly Gln Pro Ala Leu Gly His Pro Gly Gly Arg Gly Ala Leu  
 4130 4135 4140  
 Ala Leu Glu Pro His Ala Arg Glu Gly Ala Gly His Arg Glu Arg  
 4145 4150 4155  
 Ala Gly Gly Glu Gln Gly His Pro Arg Arg Arg Gly Arg Ala Gly  
 4160 4165 4170  
 Val Gln Arg Ala Ala Gly Ala Arg Gly Pro Leu Gln Gln His Gln  
 4175 4180 4185  
 Arg Ala Asp Glu Pro Gly Pro His Gly Asp Arg Arg Ala Arg Gly  
 4190 4195 4200  
 Gly Val Ala Ala Arg Ala Val Pro Pro Arg Val Glu Pro Gly Leu  
 4205 4210 4215  
 His Gly Gly Ala Glu Arg Leu Pro Glu His Ala Ala Arg Gln Arg  
 4220 4225 4230  
 Ala Pro Gly Pro Gly Gly Leu His Gln Leu His Gln Arg Ala Ala  
 4235 4240 4245  
 Ala Asp Gly Gly Arg Gly Ala Pro Glu Arg Gly Val Pro Val Gly  
 4250 4255 4260  
 Ala Gly Leu Leu Leu Pro Asp Gln Ser Pro Gly Leu Ala Asp Arg  
 4265 4270 4275  
 Glu Pro Glu Pro Gly Phe Gln Glu Leu Ala Gly Thr Val Gly Arg  
 4280 4285 4290  
 Ala Gly Pro Gly Arg Gly Pro Arg Asp Gly Val Glu Pro Ala Asp  
 4295 4300 4305  
 Ala Glu Leu Ala Pro Ala Ala Ala Ala Gly Gly Ala Leu His Gly  
 4310 4315 4320  
 Gln Arg Gln Arg Glu Pro Arg Leu Val Pro Gly Leu Pro Ala Pro  
 4325 4330 4335  
 Val Pro Arg Gly His Arg Ala Gly Ala Arg Gly Arg Ala Asp Leu  
 4340 4345 4350  
 Pro Gly Asp His Pro Arg Glu Pro Arg Ala Gly Pro Gly Gly Pro  
 4355 4360 4365

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Gly Gln Pro Gly Gly His Pro Glu Leu Pro Ala Asp Gln Pro Val  
 4370 4375 4380  
 Ala Glu Asp Pro Ala Pro Val Arg Ala Glu His Arg Gly Gly Ala  
 4385 4390 4395  
 His Pro Ala Leu Arg Ala Ala Glu Arg Gly Ala Val Pro Asp Ala  
 4400 4405 4410  
 Gly Gly Gly His Ala Gln Arg Arg Ala Arg His Asp Arg Ala Gln  
 4415 4420 4425  
 His Gly Ala Gln His Val Arg Ser Gln Pro Pro Val His Gln Ala  
 4430 4435 4440  
 Asp Gly Leu Leu Ala Ser Gly Gly Arg His Glu Leu Gly Leu Leu  
 4445 4450 4455  
 Tyr Gln Arg His Leu Glu Pro Ala Leu Ala Pro Ala Ala Arg Val  
 4460 4465 4470  
 Leu His Gly Arg Val Arg His Ala Arg Pro Gln Arg Arg Val Pro  
 4475 4480 4485  
 Val Gly Arg Arg Gly Gln Gln Arg Val Leu Ala Ala Pro Arg His  
 4490 4495 4500  
 His Arg Val Glu Glu Arg Gly Arg Gly Pro Ala Ala Val Leu Gly  
 4505 4510 4515  
 Ala Val Arg Ser Arg Gly Cys Cys Arg Gly Gly Ala Gly Arg Gln  
 4520 4525 4530  
 Pro Leu Pro Glu Pro Ala Leu Phe Ala Glu Gln Arg Ala Gln Gln  
 4535 4540 4545  
 Arg Ala Gly Ser Ala Asp Ala Ala Ala Pro Ala Gly Arg Gly Gly  
 4550 4555 4560  
 Val Pro Glu Arg Leu Leu Val Glu Ala Arg Ala Arg Glu Glu Leu  
 4565 4570 4575  
 Pro Gln Arg Asp Arg Glu Pro Gly Gly Gln Asp Glu Pro Leu Glu  
 4580 4585 4590  
 Asp Val Arg Ala Arg Ala Gln Gly Arg Ala Pro Ser Gln Gln Arg  
 4595 4600 4605



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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | His  | Pro | Thr | Pro | Ala | Thr  | Arg | Gln | Ala | Ala | Gly  | Ser | Gly | Val |
|     | 4610 |     |     |     |     | 4615 |     |     |     |     | 4620 |     |     |     |
| Gly | Arg  | Gly | Phe | Arg | Arg | Arg  | Gln | Gln | Arg | Val | Gly  | Leu | Gly | Trp |
|     | 4625 |     |     |     |     | 4630 |     |     |     |     | 4635 |     |     |     |
| Glu | Trp  | Trp | Trp | Pro | Val | Arg  | Ser | Leu | Ala | Pro | Pro  | Tyr | Arg | Ala |
|     | 4640 |     |     |     |     | 4645 |     |     |     |     | 4650 |     |     |     |
| Pro | Asp  | Val | Arg | Ile | Lys | Asn  | Lys | Lys | Arg | Tyr | Ser  | Pro | Arg | Pro |
|     | 4655 |     |     |     |     | 4660 |     |     |     |     | 4665 |     |     |     |
| Trp | Arg  | Pro | Ala | Cys | Val | Leu  | Leu | Cys | Cys | Leu | Tyr  | Asp | Glu | Ala |
|     | 4670 |     |     |     |     | 4675 |     |     |     |     | 4680 |     |     |     |
| Arg | Val  | Pro | Gly | Gly | Ser | Ser  | Ser | Leu | Val | Arg | Glu  | Arg | Asp | Ala |
|     | 4685 |     |     |     |     | 4690 |     |     |     |     | 4695 |     |     |     |
| Ala | Gly  | Gly | Gly | Gly | Gly | Asp  | Ala | Ala | Pro | Ala | Gly  | Gly | Ala | Leu |
|     | 4700 |     |     |     |     | 4705 |     |     |     |     | 4710 |     |     |     |
| Arg | Ala  | Pro | Ala | Val | Pro | Gly  | Ala | Tyr | Gly | Gly | Ala  | Glu | Gln | His |
|     | 4715 |     |     |     |     | 4720 |     |     |     |     | 4725 |     |     |     |
| Ser | Leu  | Leu | Gly | Ala | Gly | Thr  | Leu | Val | Arg | Tyr | His  | Pro | Val | Val |
|     | 4730 |     |     |     |     | 4735 |     |     |     |     | 4740 |     |     |     |
| Pro | Gly  | Gly | Gln | Gln | Val | Gly  | Gly | His | Arg | Leu | Ala  | Glu | Leu | Pro |
|     | 4745 |     |     |     |     | 4750 |     |     |     |     | 4755 |     |     |     |
| Glu | Arg  | Pro | Gln | Gln | Leu | Pro  | Asp | His | Arg | Gly | Ala  | Glu | Gln | Arg |
|     | 4760 |     |     |     |     | 4765 |     |     |     |     | 4770 |     |     |     |
| Phe | His  | Pro | His | Gly | Gly | Gln  | His | Pro | Asp | His | Gln  | Leu | Arg | Ala |
|     | 4775 |     |     |     |     | 4780 |     |     |     |     | 4785 |     |     |     |
| Leu | Ala  | Val | Gly | Arg | Pro | Ala  | Glu | Asn | His | His | Ala  | His | Gln | His |
|     | 4790 |     |     |     |     | 4795 |     |     |     |     | 4800 |     |     |     |
| Ala | Gln  | Arg | Glu | Arg | Val | His  | Val | Gln | Gln | Gln | Val  | Gln | Gly | Ala |
|     | 4805 |     |     |     |     | 4810 |     |     |     |     | 4815 |     |     |     |
| Gly | Asp  | Gly | Leu | Ala | Gln | Asp  | Pro | Gln | Trp | Gly | Arg  | Gly | Gly | Glu |
|     | 4820 |     |     |     |     | 4825 |     |     |     |     | 4830 |     |     |     |
| Leu | Trp  | Ser | Gly | Arg | Ala | Asp  | Leu | Arg | Val | Gly | Gly  | Val | Ala | Ala |

4835

4840

4845

Arg Gly Gln Leu Leu Gly Asp His Asp His Arg Ser Asp Glu Gln  
4850 4855 4860

Arg His His Arg Gln Leu Leu Gly Gly Gly Ala Ser Glu Arg Gly  
4865 4870 4875

Ala Gly Glu Arg His Arg Arg Glu Val Arg His Ala Gln Leu Pro  
4880 4885 4890

Ala Gly Leu Gly Pro Arg Asp Arg Ala Gly Asp Ala Gly Arg Val  
4895 4900 4905

His Gln Arg Gly Leu Pro Pro Arg His Arg Pro Ala Ala Arg Leu  
4910 4915 4920

Arg Arg Gly Leu His Arg Glu Pro Pro Gln Gln Pro Ala Gly His  
4925 4930 4935

Pro Gln Ala Ala Ala Leu Pro Gly Gly Leu Pro Asp Pro Val Arg  
4940 4945 4950

Gly Pro Gly Gly Gly Gln His Pro Arg Ala Leu Gly Cys Arg Ser  
4955 4960 4965

Leu Glu Lys Gln Gly Gly Gly Arg Arg Ser Gly Asp Arg Ser Arg  
4970 4975 4980

Gly His Arg Leu Tyr Arg Gly Ala Gly Arg Phe Cys Arg Arg Gly  
4985 4990 4995

Ser Gly Arg Gly Gly Asn Arg Lys Asp Ser His Pro Ala Gly Gly  
5000 5005 5010

Glu Gly Gln Gln Gly Gln Glu Leu Gln Arg Ala Arg Gly Gln Glu  
5015 5020 5025

Lys His Arg Leu Pro Gln Leu Val Pro Gly Leu Gln Leu Arg Arg  
5030 5035 5040

Pro Arg Glu Gly Arg Ala Leu Leu Asp Ala Ala His His Leu Gly  
5045 5050 5055

Arg His Leu Arg Arg Gly Ala Ser Leu Leu Val Ala Ala Arg His  
5060 5065 5070

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Asp Ala Arg Pro Gly His Leu Pro Leu His Ala Ser Ser Gln Leu  
 5075 5080 5085  
  
 Pro Gly Gly Gly Arg Arg Ala Pro Ala Arg Leu Leu Gln Glu Leu  
 5090 5095 5100  
  
 Leu Gln Arg Ala Gly Arg Leu Leu Ala Ala Ala Ala Arg Leu His  
 5105 5110 5115  
  
 Leu Ala His Ala Arg Leu Gln Pro Leu Pro Arg Glu Pro Asp Pro  
 5120 5125 5130  
  
 Arg Pro Pro Ala Arg Ala His His Tyr His Arg Gln Lys Arg Ser  
 5135 5140 5145  
  
 Cys Ser His Arg Ser Arg Asp Pro Ala Ala Ala Gln Gln Tyr Pro  
 5150 5155 5160  
  
 Gly Ser Pro Ala Arg Asp Arg His Arg Gln Thr Pro His Leu Pro  
 5165 5170 5175  
  
 Leu Arg Leu Gln Gly Pro Gly Arg Ser Arg Ala Ala Arg Pro Leu  
 5180 5185 5190  
  
 Glu Pro His Leu Leu Lys Asn Val His Ser His Leu Ala Gln His  
 5195 5200 5205  
  
 Arg Leu Gly Pro Ala Arg Ala Gln Gln Asp Val Arg Arg Arg Ser  
 5210 5215 5220  
  
 Pro Thr Leu His Ala Thr Pro Arg Ala Arg Ala Arg Ala Leu Pro  
 5225 5230 5235  
  
 Arg Ser Leu Gly Arg Pro Gln Gly Pro Arg Ala Leu Ala His His  
 5240 5245 5250  
  
 Arg Arg Arg Arg Asp Arg Pro Gly Gly Gly Arg Arg Ala Gln Leu  
 5255 5260 5265  
  
 His Ala Arg Arg Arg Ala Arg Leu His Arg Gly Arg Arg His Arg  
 5270 5275 5280  
  
 Gln Arg Gly Gly Arg Cys Ala Pro Val Arg Pro Arg Gln Glu Pro  
 5285 5290 5295  
  
 Ala Ala Ala His Arg Pro Ala Ala Pro Glu His Pro Arg His Ala  
 5300 5305 5310

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Arg Gly Ala Ser Leu Ala Ala Gln Gly Gln Ala His Gly Thr Gln  
5315 5320 5325

Gly His Ala Gln Gly Gly Gln Thr Arg Gly Leu Arg Gln Gln Gln  
5330 5335 5340

Arg Arg Gln Asp Pro Gln Thr Arg Gly His Gly Gly Gly Gly Gly  
5345 5350 5355

His Arg Gln His Val Pro Pro Ala Ala Arg Gln Arg Val Leu Gly  
5360 5365 5370

Ala Arg Arg Arg His Arg Cys Ala Arg Ala Arg Ala His Pro Pro  
5375 5380 5385

Pro Ser His Leu Lys Met Leu Thr Ser Arg Cys Cys Val Pro Ala  
5390 5395 5400

Ala Arg Arg Met Ser Lys Arg Lys Tyr Lys Glu Glu Met Leu Gln  
5405 5410 5415

Val Ile Ala Pro Glu Ile Tyr Gly Pro Ala Val Lys Glu Glu Arg  
5420 5425 5430

Lys Pro Arg Lys Leu Lys Arg Val Lys Lys Asp Lys Lys Glu Glu  
5435 5440 5445

Glu Asp Val Asp Gly Leu Val Glu Phe Val Arg Glu Phe Ala Pro  
5450 5455 5460

Arg Arg Arg Val Gln Trp Arg Gly Arg Lys Val Lys Pro Val Leu  
5465 5470 5475

Arg Pro Gly Thr Thr Val Val Phe Thr Pro Gly Glu Arg Ser Gly  
5480 5485 5490

Ser Ala Ser Lys Arg Ser Tyr Asp Glu Val Tyr Gly Asp Glu Asp  
5495 5500 5505

Ile Leu Glu Gln Ala Val Glu Arg Leu Gly Glu Phe Ala Tyr Gly  
5510 5515 5520

Lys Arg Ser Arg Pro Ala Pro Leu Lys Glu Glu Ala Val Ser Ile  
5525 5530 5535

Pro Leu Asp His Gly Asn Pro Thr Pro Ser Leu Lys Pro Val Thr  
5540 5545 5550

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Leu Gln Gln Val Leu Pro Ser Ala Ala Pro Arg Arg Gly Phe Lys  
 5555 5560 5565  
 Arg Glu Gly Gly Glu Asp Leu Tyr Pro Thr Met Gln Leu Met Val  
 5570 5575 5580  
 Pro Lys Arg Gln Lys Leu Glu Asp Val Leu Glu His Met Lys Val  
 5585 5590 5595  
 Asp Pro Glu Val Gln Pro Glu Val Lys Val Arg Pro Ile Lys Gln  
 5600 5605 5610  
 Val Ala Pro Gly Leu Gly Val Gln Thr Val Asp Ile Lys Ile Pro  
 5615 5620 5625  
 Thr Glu Pro Met Glu Thr Gln Thr Glu Pro Val Lys Pro Ser Thr  
 5630 5635 5640  
 Ser Thr Met Glu Val Gln Thr Asp Pro Trp Met Pro Ala Pro Ala  
 5645 5650 5655  
 Ser Thr Thr Arg Arg Arg Arg Lys Tyr Gly Ala Ala Ser Leu Leu  
 5660 5665 5670  
 Met Pro Asn Tyr Ala Leu His Pro Ser Ile Ile Pro Thr Pro Gly  
 5675 5680 5685  
 Tyr Arg Gly Thr Arg Phe Tyr Arg Gly Tyr Thr Ser Ser Arg Arg  
 5690 5695 5700  
 Lys Thr Thr Thr Arg Arg Arg Arg Arg Arg Thr Arg Arg Ser Ser  
 5705 5710 5715  
 Thr Ala Thr Ser Ala Ala Ala Leu Val Arg Arg Val Tyr Arg Ser  
 5720 5725 5730  
 Gly Arg Glu Pro Leu Thr Leu Pro Arg Ala Arg Tyr His Pro Ser  
 5735 5740 5745  
 Ile Ala Ile Leu Cys Arg Arg Leu Leu Leu Ala Asp Met Ala Leu  
 5750 5755 5760  
 Thr Cys Arg Leu Arg Val Pro Ile Thr Gly Tyr Arg Gly Arg Lys  
 5765 5770 5775  
 Pro Arg Arg Arg Arg Leu Thr Gly Asn Gly Leu Arg Arg His His

5780

5785

5790

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| His  | Arg | Arg | Arg | Arg | Ala | Ile  | Ser | Lys | Arg | Leu | Gly  | Gly | Gly | Phe |
| 5795 |     |     |     |     |     | 5800 |     |     |     |     | 5805 |     |     |     |
| Leu  | Pro | Ala | Leu | Ile | Pro | Ile  | Ile | Ala | Ala | Ala | Ile  | Gly | Ala | Ile |
| 5810 |     |     |     |     |     | 5815 |     |     |     |     | 5820 |     |     |     |
| Pro  | Gly | Ile | Ala | Ser | Val | Ala  | Val | Gln | Ala | Ser | Gln  | Arg | His | Asp |
| 5825 |     |     |     |     |     | 5830 |     |     |     |     | 5835 |     |     |     |
| Thr  | Ala | Trp | Lys | Ile | Cys | Asn  | Lys | Lys | Met | Asp | Arg  | Ser | Trp | Ser |
| 5840 |     |     |     |     |     | 5845 |     |     |     |     | 5850 |     |     |     |
| Cys  | Asp | Val | Cys | Phe | Met | Glu  | Asp | Ile | Asn | Phe | Ser  | Ser | Leu | Ala |
| 5855 |     |     |     |     |     | 5860 |     |     |     |     | 5865 |     |     |     |
| Pro  | Arg | His | Gly | Thr | Arg | Pro  | Phe | Met | Gly | Thr | Trp  | Ser | Asp | Ile |
| 5870 |     |     |     |     |     | 5875 |     |     |     |     | 5880 |     |     |     |
| Gly  | Asn | Ser | Gln | Leu | Asn | Gly  | Gly | Ala | Phe | Asn | Trp  | Ser | Ser | Leu |
| 5885 |     |     |     |     |     | 5890 |     |     |     |     | 5895 |     |     |     |
| Trp  | Ser | Gly | Leu | Lys | Asn | Phe  | Gly | Ser | Thr | Leu | Lys  | Thr | Tyr | Gly |
| 5900 |     |     |     |     |     | 5905 |     |     |     |     | 5910 |     |     |     |
| Asn  | Lys | Ala | Trp | Asn | Ser | Ser  | Thr | Gly | Gln | Ala | Leu  | Arg | Glu | Lys |
| 5915 |     |     |     |     |     | 5920 |     |     |     |     | 5925 |     |     |     |
| Leu  | Lys | Glu | Gln | Asn | Phe | Gln  | Gln | Lys | Val | Val | Asp  | Gly | Leu | Ala |
| 5930 |     |     |     |     |     | 5935 |     |     |     |     | 5940 |     |     |     |
| Ser  | Gly | Ile | Asn | Gly | Val | Val  | Asp | Leu | Ala | Asn | Gln  | Ala | Val | Gln |
| 5945 |     |     |     |     |     | 5950 |     |     |     |     | 5955 |     |     |     |
| Lys  | Gln | Ile | Asn | Ser | Arg | Leu  | Asp | Ala | Val | Pro | Pro  | Ala | Gly | Ser |
| 5960 |     |     |     |     |     | 5965 |     |     |     |     | 5970 |     |     |     |
| Val  | Glu | Met | Pro | Gln | Val | Glu  | Glu | Glu | Leu | Pro | Pro  | Leu | Asp | Lys |
| 5975 |     |     |     |     |     | 5980 |     |     |     |     | 5985 |     |     |     |
| Arg  | Gly | Asp | Lys | Arg | Pro | Arg  | Pro | Asp | Ala | Glu | Glu  | Thr | Leu | Leu |
| 5990 |     |     |     |     |     | 5995 |     |     |     |     | 6000 |     |     |     |
| Thr  | His | Thr | Asp | Glu | Pro | Pro  | Pro | Tyr | Glu | Glu | Ala  | Val | Lys | Leu |
| 6005 |     |     |     |     |     | 6010 |     |     |     |     | 6015 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly  | Leu | Pro | Thr | Thr | Arg | Pro  | Val | Ala | Pro | Leu | Ala  | Thr | Gly | Val |
| 6020 |     |     |     |     |     | 6025 |     |     |     |     | 6030 |     |     |     |
| Leu  | Lys | Pro | Ser | Ser | Ser | Ser  | Gln | Pro | Ala | Thr | Leu  | Asp | Leu | Pro |
| 6035 |     |     |     |     |     | 6040 |     |     |     |     | 6045 |     |     |     |
| Pro  | Pro | Ala | Ser | Arg | Pro | Ser  | Thr | Val | Ala | Lys | Pro  | Leu | Pro | Pro |
| 6050 |     |     |     |     |     | 6055 |     |     |     |     | 6060 |     |     |     |
| Val  | Ala | Val | Ala | Ser | Arg | Ala  | Pro | Arg | Gly | Arg | Pro  | Gln | Ala | Asn |
| 6065 |     |     |     |     |     | 6070 |     |     |     |     | 6075 |     |     |     |
| Trp  | Gln | Ser | Thr | Leu | Asn | Ser  | Ile | Val | Gly | Leu | Gly  | Val | Gln | Ser |
| 6080 |     |     |     |     |     | 6085 |     |     |     |     | 6090 |     |     |     |
| Val  | Lys | Arg | Arg | Arg | Cys | Tyr  | Lys | Thr | Leu | Arg | Leu  | Thr | Cys | Leu |
| 6095 |     |     |     |     |     | 6100 |     |     |     |     | 6105 |     |     |     |
| Ser  | Val | Cys | Ile | Cys | Met | Ser  | Ala | Asp | Gln | Lys | Glu  | Glu | Glu | Ala |
| 6110 |     |     |     |     |     | 6115 |     |     |     |     | 6120 |     |     |     |
| Arg  | Arg | Arg | Val | Ala | Arg | Trp  | Pro | Pro | His | Arg | Cys  | Cys | Pro | Ser |
| 6125 |     |     |     |     |     | 6130 |     |     |     |     | 6135 |     |     |     |
| Gly  | Arg | Thr | Cys | Thr | Ser | Pro  | Asp | Arg | Thr | Leu | Arg  | Ser | Thr | Val |
| 6140 |     |     |     |     |     | 6145 |     |     |     |     | 6150 |     |     |     |
| Arg  | Val | Trp | Cys | Ser | Ser | Pro  | Ala | Pro | Gln | Thr | Pro  | Thr | Ser | Val |
| 6155 |     |     |     |     |     | 6160 |     |     |     |     | 6165 |     |     |     |
| Trp  | Gly | Thr | Ser | Leu | Gly | Thr  | Pro | Arg | Trp | Arg | Pro  | Arg | Thr | Met |
| 6170 |     |     |     |     |     | 6175 |     |     |     |     | 6180 |     |     |     |
| Pro  | Pro | Thr | Ala | Ala | Ser | Gly  | Arg | Cys | Ala | Ser | Cys  | Pro | Trp | Thr |
| 6185 |     |     |     |     |     | 6190 |     |     |     |     | 6195 |     |     |     |
| Ala  | Arg | Thr | Thr | Pro | Thr | Arg  | Thr | Lys | Cys | Ala | Thr  | Arg | Trp | Pro |
| 6200 |     |     |     |     |     | 6205 |     |     |     |     | 6210 |     |     |     |
| Trp  | Ala | Thr | Thr | Ala | Cys | Trp  | Thr | Trp | Pro | Ala | Pro  | Thr | Leu | Thr |
| 6215 |     |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Ser  | Ala | Ala | Cys | Trp | Ile | Gly  | Gly | Pro | Ala | Ser | Asn  | Pro | Thr | Pro |
| 6230 |     |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Ala  | Pro | Pro | Thr | Thr | Ala | Trp  | Leu | Pro | Arg | Glu | Arg  | Pro | Thr | Leu |
| 6245 |     |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |

## 368530-7006W01\_SequenceListing\_ST25.txt

Ala Ser Gly His Ile Lys Leu Val Ile Leu Ile Gln Lys Lys Pro  
 6260 6265 6270  
 Ile His Met Glu Met His Leu Cys Lys Ala Leu Ala Leu Gln Arg  
 6275 6280 6285  
 Met Val Phe Asn Leu Glu Leu Thr Ala Met Val Arg Gln Ser Met  
 6290 6295 6300  
 Gln Thr Lys Leu Ile Asn Gln Ser Leu Lys Trp Val Met Leu Asn  
 6305 6310 6315  
 Gly Met Thr Ser Leu Val Leu Met Lys Asn Met Glu Ala Glu Leu  
 6320 6325 6330  
 Leu Ser Leu Thr Pro Lys Ser Leu Ala Met Val Leu Leu Pro Ser  
 6335 6340 6345  
 Leu Pro Ile Lys Lys Glu Ala Arg Gln Met Lys Pro Lys Gln Ala  
 6350 6355 6360  
 Val Pro Lys Asn Met Thr Leu Thr Trp His Ser Ser Ile Ile Glu  
 6365 6370 6375  
 Val Gln Leu Pro Pro Ala Pro Gln Lys Leu Phe Cys Ile Leu Arg  
 6380 6385 6390  
 Met Trp Ile Trp Lys Leu Gln Ile Pro Ile Leu Tyr Thr Arg Gln  
 6395 6400 6405  
 Val Gln Met Thr Val Ala Leu Leu Ser Ile Trp Val Ser Ser Pro  
 6410 6415 6420  
 Cys Pro Thr Asp Pro Thr Thr Leu Ala Ser Glu Thr Thr Leu Ser  
 6425 6430 6435  
 Val Cys Thr Thr Thr Ala Leu Ala Ile Trp Val Tyr Trp Leu Asp  
 6440 6445 6450  
 Arg Pro Pro Ser Met Leu Trp Trp Thr Cys Arg Thr Glu Thr Pro  
 6455 6460 6465  
 Asn Cys Pro Thr Ser Ser Cys Leu Thr Leu Trp Val Thr Glu Pro  
 6470 6475 6480  
 Gly Ile Ser Val Cys Gly Ile Arg Arg Trp Thr Val Met Thr Pro  
 6485 6490 6495



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Met  | Cys | Ala | Leu | Leu | Lys | Ile  | Thr | Val | Trp | Arg | Met  | Asn | Phe | Leu |
| 6500 |     |     |     |     |     | 6505 |     |     |     |     | 6510 |     |     |     |
| Thr  | Ile | Ala | Ser | Pro | Trp | Met  | Leu | Trp | Val | Glu | Leu  | Ile | Leu | Thr |
| 6515 |     |     |     |     |     | 6520 |     |     |     |     | 6525 |     |     |     |
| Arg  | Glu | Leu | Arg | Pro | Met | Val  | Ile | Ile | Lys | Pro | Pro  | Gly | Pro | Lys |
| 6530 |     |     |     |     |     | 6535 |     |     |     |     | 6540 |     |     |     |
| Met  | Ile | Leu | Leu | Met | Met | Leu  | Met | Asn | Trp | Ala | Arg  | Ala | Ile | Leu |
| 6545 |     |     |     |     |     | 6550 |     |     |     |     | 6555 |     |     |     |
| Ser  | Pro | Trp | Arg | Ser | Thr | Ser  | Arg | Pro | Thr | Cys | Gly  | Gly | Thr | Ser |
| 6560 |     |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Ser  | Thr | Arg | Thr | Trp | Arg | Cys  | Thr | Cys | Pro | Thr | Pro  | Thr | Ser | Thr |
| 6575 |     |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Arg  | Arg | Pro | Thr | Ser | Arg | Cys  | Pro | Pro | Thr | Pro | Thr  | Pro | Thr | Ile |
| 6590 |     |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Thr  | Thr | Ala | Ala | Trp | Trp | Arg  | Pro | Arg | Trp | Trp | Thr  | Pro | Thr | Ser |
| 6605 |     |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Thr  | Ser | Gly | Arg | Ala | Gly | Arg  | Trp | Thr | Pro | Trp | Thr  | Thr | Ser | Thr |
| 6620 |     |     |     |     |     | 6625 |     |     |     |     | 6630 |     |     |     |
| Pro  | Ser | Thr | Thr | Thr | Ala | Thr  | Arg | Ala | Cys | Asp | Thr  | Ala | Pro | Cys |
| 6635 |     |     |     |     |     | 6640 |     |     |     |     | 6645 |     |     |     |
| Ser  | Trp | Ala | Thr | Gly | Ala | Thr  | Cys | Pro | Ser | Thr | Ser  | Arg | Cys | Pro |
| 6650 |     |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |
| Lys  | Ser | Phe | Ser | Pro | Ser | Arg  | Ala | Ser | Cys | Ser | Cys  | Pro | Gly | Pro |
| 6665 |     |     |     |     |     | 6670 |     |     |     |     | 6675 |     |     |     |
| Thr  | Pro | Thr | Ser | Gly | Thr | Ser  | Ala | Arg | Thr | Ser | Thr  | Ser | Cys | Arg |
| 6680 |     |     |     |     |     | 6685 |     |     |     |     | 6690 |     |     |     |
| Ala  | Pro | Ser | Ala | Thr | Thr | Cys  | Ala | Arg | Thr | Gly | Pro  | Pro | Ser | Pro |
| 6695 |     |     |     |     |     | 6700 |     |     |     |     | 6705 |     |     |     |
| Ser  | Pro | Ala | Ser | Thr | Ser | Thr  | Pro | Pro | Ser | Ser | Pro  | Trp | Arg | Thr |
| 6710 |     |     |     |     |     | 6715 |     |     |     |     | 6720 |     |     |     |
| Thr  | Pro | Pro | Pro | Arg | Ser | Arg  | Pro | Cys | Cys | Ala | Thr  | Thr | Pro | Thr |

6725

6730

6735

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr  | Ser | Pro | Ser | Thr | Thr | Thr  | Ser | Arg | Arg | Pro | Thr  | Cys | Ser | Thr |
| 6740 |     |     |     |     |     | 6745 |     |     |     |     | 6750 |     |     |     |
| Pro  | Ser | Arg | Pro | Thr | Pro | Pro  | Thr | Cys | Pro | Ser | Pro  | Ser | Pro | Arg |
| 6755 |     |     |     |     |     | 6760 |     |     |     |     | 6765 |     |     |     |
| Ala  | Thr | Gly | Pro | Pro | Ser | Ala  | Ala | Gly | Pro | Ser | Arg  | Ala | Ser | Arg |
| 6770 |     |     |     |     |     | 6775 |     |     |     |     | 6780 |     |     |     |
| Pro  | Ala | Arg | Arg | Pro | Arg | Ser  | Ala | Pro | Gly | Ser | Thr  | Pro | Thr | Ser |
| 6785 |     |     |     |     |     | 6790 |     |     |     |     | 6795 |     |     |     |
| Ser  | Thr | Arg | Ala | Pro | Ser | Pro  | Thr | Ser | Thr | Ala | Pro  | Ser | Thr | Ser |
| 6800 |     |     |     |     |     | 6805 |     |     |     |     | 6810 |     |     |     |
| Thr  | Thr | Pro | Ser | Arg | Arg | Ser  | Pro | Ser | Pro | Ser | Thr  | Pro | Pro | Ser |
| 6815 |     |     |     |     |     | 6820 |     |     |     |     | 6825 |     |     |     |
| Ala  | Gly | Pro | Ala | Thr | Thr | Ala  | Ser | Arg | Pro | Thr | Ser  | Ser | Lys | Ser |
| 6830 |     |     |     |     |     | 6835 |     |     |     |     | 6840 |     |     |     |
| Ser  | Ala | Pro | Ser | Thr | Glu | Arg  | Gly | Thr | Thr | Trp | Pro  | Ser | Ala | Thr |
| 6845 |     |     |     |     |     | 6850 |     |     |     |     | 6855 |     |     |     |
| Pro  | Arg | Thr | Gly | Ser | Trp | Ser  | Arg | Cys | Trp | Pro | Thr  | Thr | Thr | Ser |
| 6860 |     |     |     |     |     | 6865 |     |     |     |     | 6870 |     |     |     |
| Ala  | Thr | Arg | Ala | Ser | Thr | Cys  | Pro | Arg | Ala | Thr | Arg  | Thr | Ala | Cys |
| 6875 |     |     |     |     |     | 6880 |     |     |     |     | 6885 |     |     |     |
| Thr  | Pro | Ser | Ser | Ala | Thr | Ser  | Ser | Pro | Ala | Ala | Arg  | Ser | Trp | Thr |
| 6890 |     |     |     |     |     | 6895 |     |     |     |     | 6900 |     |     |     |
| Arg  | Ser | Thr | Thr | Arg | Thr | Thr  | Arg | Pro | Ser | Pro | Trp  | Pro | Thr | Ser |
| 6905 |     |     |     |     |     | 6910 |     |     |     |     | 6915 |     |     |     |
| Thr  | Thr | Thr | Arg | Ala | Ser | Ser  | Ala | Thr | Ser | Arg | Pro  | Pro | Cys | Ala |
| 6920 |     |     |     |     |     | 6925 |     |     |     |     | 6930 |     |     |     |
| Arg  | Ala | Ser | Pro | Thr | Pro | Pro  | Thr | Thr | Pro | Thr | Arg  | Ser | Ser | Ala |
| 6935 |     |     |     |     |     | 6940 |     |     |     |     | 6945 |     |     |     |
| Arg  | Ala | Pro | Ser | Pro | Ala | Ser  | Pro | Arg | Lys | Ser | Ser  | Ser | Ala | Thr |
| 6950 |     |     |     |     |     | 6955 |     |     |     |     | 6960 |     |     |     |

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Gly Ser Cys Gly Ala Ser Pro Ser Pro Ala Thr Ser Cys Pro Trp  
 6965 6970 6975  
  
 Ala Arg Ser Pro Thr Ser Ala Arg Thr Cys Ser Thr Pro Thr Pro  
 6980 6985 6990  
  
 Pro Thr Arg Thr Ile Ser Lys Ser Thr Pro Trp Met Ser Pro Pro  
 6995 7000 7005  
  
 Phe Ser Met Leu Ser Ser Lys Ser Ser Thr Ser Ser Glu Cys Thr  
 7010 7015 7020  
  
 Ser Pro Thr Ala Ala Ser Ser Arg Pro Ser Thr Cys Ala Arg Pro  
 7025 7030 7035  
  
 Ser Arg Pro Ala Thr Pro Pro Pro Lys Pro Leu Ala Ser Cys Lys  
 7040 7045 7050  
  
 Met Thr Ala Cys Ala Gly Ser Gly Glu Gln Glu Leu Arg Ala Ile  
 7055 7060 7065  
  
 Leu Arg Asp Leu Gly Cys Gly Pro Cys Phe Leu Gly Thr Phe Asp  
 7070 7075 7080  
  
 Lys Arg Phe Pro Gly Phe Met Ala Pro His Lys Leu Ala Cys Ala  
 7085 7090 7095  
  
 Ile Val Asn Thr Ala Gly Arg Glu Thr Gly Gly Glu His Trp Leu  
 7100 7105 7110  
  
 Ala Phe Ala Trp Asn Pro Arg Ser His Thr Cys Tyr Leu Phe Asp  
 7115 7120 7125  
  
 Pro Phe Gly Phe Ser Asp Glu Arg Leu Lys Gln Ile Tyr Gln Phe  
 7130 7135 7140  
  
 Glu Tyr Glu Gly Leu Leu Arg Arg Ser Ala Leu Ala Thr Glu Asp  
 7145 7150 7155  
  
 Arg Cys Val Thr Leu Glu Lys Ser Thr Gln Thr Val Gln Gly Pro  
 7160 7165 7170  
  
 Arg Ser Ala Ala Cys Gly Leu Phe Cys Cys Met Phe Leu His Ala  
 7175 7180 7185  
  
 Phe Val His Trp Pro Asp Arg Pro Met Asp Lys Asn Pro Thr Met  
 7190 7195 7200

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asn | Leu  | Leu | Thr | Gly | Val | Pro  | Asn | Gly | Met | Leu | Gln  | Ser | Pro | Gln |
|     | 7205 |     |     |     |     | 7210 |     |     |     |     | 7215 |     |     |     |
| Val | Glu  | Pro | Thr | Leu | Arg | Arg  | Asn | Gln | Glu | Ala | Leu  | Tyr | Arg | Phe |
|     | 7220 |     |     |     |     | 7225 |     |     |     |     | 7230 |     |     |     |
| Leu | Asn  | Ala | His | Ser | Ala | Tyr  | Phe | Arg | Ser | His | Arg  | Ala | Arg | Ile |
|     | 7235 |     |     |     |     | 7240 |     |     |     |     | 7245 |     |     |     |
| Glu | Lys  | Ala | Thr | Ala | Phe | Asp  | Arg | Met | Asn | Gln | Asp  | Met | Ser | Gly |
|     | 7250 |     |     |     |     | 7255 |     |     |     |     | 7260 |     |     |     |
| Val | Cys  | Met | Met | Leu | Tyr | Ser  | Ser | Thr | Ala | His | Val  | Tyr | Ala | Thr |
|     | 7265 |     |     |     |     | 7270 |     |     |     |     | 7275 |     |     |     |
| Phe | Ser  | Glu | Ala | Leu | Thr | Leu  | Phe | Arg | Asn | Arg | Arg  | Gly | Ser | Ala |
|     | 7280 |     |     |     |     | 7285 |     |     |     |     | 7290 |     |     |     |
| Gly | Ser  | Arg | His | Gly | Pro | Arg  | Ala | Gly | Ile | Arg | Cys  | Gly | Thr | Gly |
|     | 7295 |     |     |     |     | 7300 |     |     |     |     | 7305 |     |     |     |
| Thr | Trp  | Ala | Ala | Thr | Thr | Arg  | Gly | Ser | Ala | Ala | Ser  | Ala | Arg | Gly |
|     | 7310 |     |     |     |     | 7315 |     |     |     |     | 7320 |     |     |     |
| Gly | Arg  | Gly | Thr | Ser | Arg | Ser  | Thr | Ala | Cys | Ala | Val  | Ala | Gly | Arg |
|     | 7325 |     |     |     |     | 7330 |     |     |     |     | 7335 |     |     |     |
| Pro | Ala  | Gly | Arg | Ala | Arg | Arg  | Ser | Asn | Arg | Ser | Trp  | Asp | Pro | Arg |
|     | 7340 |     |     |     |     | 7345 |     |     |     |     | 7350 |     |     |     |
| Ser | Ala  | Arg | Glu | Ser | Tyr | Gly  | Thr | Arg | Gly | Cys | Ser  | Thr | Gly | Thr |
|     | 7355 |     |     |     |     | 7360 |     |     |     |     | 7365 |     |     |     |
| Pro | Ser  | Gly | Pro | Gly | Ala | Ser  | Arg | Ser | Pro | Ala | Pro  | Ser | Arg | Arg |
|     | 7370 |     |     |     |     | 7375 |     |     |     |     | 7380 |     |     |     |
| Cys | Pro  | Pro | Arg | Pro | Asp | Pro  | Arg | Arg | Trp | Pro | Ser  | Arg | Arg | Gly |
|     | 7385 |     |     |     |     | 7390 |     |     |     |     | 7395 |     |     |     |
| Ser | Ser  | Cys | Arg | Ser | Ala | Ala  | Pro | Cys | Trp | Ala | Arg  | Ser | Arg | Ala |
|     | 7400 |     |     |     |     | 7405 |     |     |     |     | 7410 |     |     |     |
| Cys | Gly  | Cys | Asn | Arg | Ser | Ala  | Gly | Gly | Ser | Ala | Ser  | Ser | Gly | Pro |
|     | 7415 |     |     |     |     | 7420 |     |     |     |     | 7425 |     |     |     |
| Ala | Arg  | Ser | Ser | Cys | Pro | Gly  | Thr | Trp | Pro | Ser | Lys  | Pro | Pro | Ala |
|     | 7430 |     |     |     |     | 7435 |     |     |     |     | 7440 |     |     |     |

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Gly Gly Arg Pro Ala Ala Pro Cys Arg Pro Arg Arg Arg Pro Arg  
7445 7450 7455

Arg Thr Cys Arg Thr Gly Trp Trp Arg Ser Gln Arg Arg Ala Arg  
7460 7465 7470

Ser Ser Ala Arg Arg Cys Trp Pro Ala Ala Pro Arg Cys Ala Pro  
7475 7480 7485

Ser Gly Ser Gly Ser Trp Pro Gly Arg Gly Ser Pro Ser Ala Arg  
7490 7495 7500

Ala Ala Arg Ser Arg Ser Pro His Pro Ser Arg Ser Cys Ala Pro  
7505 7510 7515

Ser Gly Ser Ser Arg Ser Arg Ala Gly Thr Ala Ala Cys Pro Arg  
7520 7525 7530

Pro Arg Cys Thr Arg Ala Ala Thr Ala Arg Ser Arg Cys Ser Pro  
7535 7540 7545

Ser Ser Cys Gly Arg Ser Gly Ser Ala Ser Ala Arg Ser Pro Ala  
7550 7555 7560

Gly Ser Gly Pro Ser Ser Trp Ser Gly Ser Cys Cys Trp Arg Ser  
7565 7570 7575

Ala Glu Cys Arg Gly Ala Pro Arg Ser His Thr Gly Gly Arg Tyr  
7580 7585 7590

Gly Gly Thr Pro Arg Pro Ala Arg Ala Ser Ala Gly Arg Arg Thr  
7595 7600 7605

Ser Gly Arg Ser Pro Arg Gly Thr Gly Pro Ser Ala Ala Ser Ser  
7610 7615 7620

Leu Pro Cys Pro Ser Pro Arg Pro Lys Arg Ser Ala Gly Ser Gly  
7625 7630 7635

Gly Ser Ser Pro Leu Ser Ser Ser Pro Pro Pro Lys Ser Gly Gly  
7640 7645 7650

Arg Ser Arg Pro Gly Ser Gln Thr Leu Ala Cys Arg Pro Ser Arg  
7655 7660 7665

Cys Ala Arg Gly Glu Ser Ser Pro Arg Pro Pro Ala Pro Pro Arg

|      |     |     |     |     |     |      |     |     |     |     |      |     |         |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|---------|
| 7670 |     |     |     |     |     |      |     |     |     |     |      |     |         |
|      |     |     |     |     |     |      |     |     |     |     |      |     |         |
| Pro  | Ala | Phe | Arg | Pro | Arg | Cys  | Pro | Gly | Cys | Leu | Ala  | Lys | Ala His |
| 7685 |     |     |     |     |     | 7690 |     |     |     |     | 7695 |     |         |
| Ala  | Trp | Ser | Cys | Gly | Val | Ser  | Phe | Trp | Ala | Ala | Glu  | Ala | Ala Ala |
| 7700 |     |     |     |     |     | 7705 |     |     |     |     | 7710 |     |         |
| Glu  | Thr | Cys | Trp | Ala | Ser | Ala  | Ser | Ser | Arg | Ser | Pro  | Arg | Leu Phe |
| 7715 |     |     |     |     |     | 7720 |     |     |     |     | 7725 |     |         |
| Leu  | Leu | Leu | Gly | Arg | Arg | Pro  | Arg | Pro | Arg | Gly | Gly  | Arg | His Ala |
| 7730 |     |     |     |     |     | 7735 |     |     |     |     | 7740 |     |         |
| Ser  | Ser | Gly | Ala | Glu | Ala | Glu  | Ala | Thr | Gly | Ser | Arg  | Gly | Ser Ala |
| 7745 |     |     |     |     |     | 7750 |     |     |     |     | 7755 |     |         |
| Gly  | Gly | Trp | Gln | Ser | Pro | Phe  | Arg | Val | Arg | Gly | Cys  | Ala | Pro Gly |
| 7760 |     |     |     |     |     | 7765 |     |     |     |     | 7770 |     |         |
| Gly  | Ala | Ala | Leu | Thr | Asp | Phe  | Leu | Arg | Gly | Arg | Pro  | Leu | Cys Ser |
| 7775 |     |     |     |     |     | 7780 |     |     |     |     | 7785 |     |         |
| Pro  | Arg | Glu | Gln | Ala | Trp | Arg  | Leu | Ser | His | Arg | Arg  | Gln | His Arg |
| 7790 |     |     |     |     |     | 7795 |     |     |     |     | 7800 |     |         |
| His  | Leu | Pro | Pro | Pro | Pro | Pro  | Thr | Arg | Thr | Ser | Ser  | Ser | Arg Met |
| 7805 |     |     |     |     |     | 7810 |     |     |     |     | 7815 |     |         |
| Lys  | Ala | Pro | Pro | Arg | Arg | Pro  | Ala | Pro | Pro | Pro | Thr  | Pro | Gln Pro |
| 7820 |     |     |     |     |     | 7825 |     |     |     |     | 7830 |     |         |
| Gln  | Thr | Cys | Lys | Arg | Trp | Arg  | Asn | Pro | Ser | Arg | Leu  | Thr | Trp Ala |
| 7835 |     |     |     |     |     | 7840 |     |     |     |     | 7845 |     |         |
| Thr  | Arg | Pro | Arg | Ser | Thr | Arg  | Arg | Ser | Trp | Gln | Arg  | Ala | Phe Gln |
| 7850 |     |     |     |     |     | 7855 |     |     |     |     | 7860 |     |         |
| Pro  | Arg | Lys | Arg | Thr | Thr | Lys  | Ser | Ser | Gln | Ser | Arg  | Lys | Gln Arg |
| 7865 |     |     |     |     |     | 7870 |     |     |     |     | 7875 |     |         |
| Ala  | Ser | Arg | Thr | Arg | Leu | Gly  | Ser | Ser | Met | Ala | Thr  | Thr | Ala Gly |
| 7880 |     |     |     |     |     | 7885 |     |     |     |     | 7890 |     |         |
| Gln  | Arg | Thr | Cys | Ser | Ser | Ser  | Ile | Trp | Pro | Ala | Asn  | Ala | Ser Ser |
| 7895 |     |     |     |     |     | 7900 |     |     |     |     | 7905 |     |         |

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Ser Arg Thr Arg Cys Ser Thr Ala Pro Arg Cys Pro Ser Ala Trp  
 7910 7915 7920  
 Arg Ser Ser Ala Ala Pro Thr Ser Ala Thr Ser Ser Arg Arg Ala  
 7925 7930 7935  
 Cys Pro Pro Ser Ala Ser Pro Thr Ala Pro Ala Ser Pro Thr Arg  
 7940 7945 7950  
 Ala Ser Thr Ser Thr Arg Ser Ser Arg Cys Pro Arg Pro Trp Pro  
 7955 7960 7965  
 Pro Thr Thr Ser Phe Ser Arg Thr Lys Gly Ser Pro Ser Pro Ala  
 7970 7975 7980  
 Ala Pro Thr Ala Pro Ala Pro Thr Pro Cys Ser Thr Trp Ala Pro  
 7985 7990 7995  
 Ala Pro Ala Tyr Leu Ile Ser Pro Pro Trp Lys Arg Phe Pro Arg  
 8000 8005 8010  
 Ser Ser Arg Val Trp Ala Ala Thr Arg Leu Gly Pro Arg Thr Leu  
 8015 8020 8025  
 Cys Lys Glu Ala Glu Arg Ser Met Ser Thr Thr Ala Pro Trp Trp  
 8030 8035 8040  
 Ser Trp Lys Ala Thr Thr Arg Ala Trp Arg Ser Ser Ser Ala Arg  
 8045 8050 8055  
 Ser Ser Pro Thr Ser Pro Thr Arg Arg Ser Thr Cys Pro Pro Arg  
 8060 8065 8070  
 Ser Ala Pro Ser Trp Thr Arg Cys Ser Ser Ser Ala Pro Arg Pro  
 8075 8080 8085  
 Ser Arg Arg Arg Arg Cys Arg Thr Pro Arg Ala Arg Thr Arg Ala  
 8090 8095 8100  
 Ser Pro Trp Ser Ala Thr Ser Ser Trp Arg Ala Gly Trp Glu Arg  
 8105 8110 8115  
 Val Ala Pro Pro Arg Ala Trp Lys Ser Gly Ala Ser Ser Trp Pro  
 8120 8125 8130  
 Trp Ser Trp Pro Trp Ser Trp Ser Val Cys Ala Ala Ser Ser Pro  
 8135 8140 8145

## 368530-7006W01\_SequenceListing\_ST25.txt

Thr Arg Arg Pro Cys Ala Arg Ser Arg Arg Thr Cys Thr Thr Ser  
 8150 8155 8160  
 Ser Asp Thr Gly Ser Cys Ala Arg Pro Ala Arg Ser Pro Thr Trp  
 8165 8170 8175  
 Ser Pro Thr Trp Ser Pro Thr Trp Ala Ser Cys Thr Arg Thr Ala  
 8180 8185 8190  
 Trp Gly Arg Thr Cys Cys Thr Pro Pro Cys Ala Gly Arg Pro Ala  
 8195 8200 8205  
 Ala Thr Thr Ser Ala Thr Ala Ser Thr Cys Thr Ser Ala Thr Pro  
 8210 8215 8220  
 Gly Arg Arg Ala Trp Ala Cys Gly Ser Ser Ala Trp Arg Ser Arg  
 8225 8230 8235  
 Thr Lys Ser Ser Ala Ser Ser Cys Arg Arg Thr Ser Arg Pro Cys  
 8240 8245 8250  
 Gly Pro Gly Ser Thr Ser Ala Pro Pro Pro Arg Thr Trp Pro Thr  
 8255 8260 8265  
 Ser Ser Ser Pro Ser Ala Cys Gly Arg Cys Ala Thr Gly Cys Pro  
 8270 8275 8280  
 Thr Leu Ala Lys Ala Cys Cys Lys Thr Phe Ala Leu Ser Ser Ser  
 8285 8290 8295  
 Asn Ala Pro Gly Ser Cys Pro Pro Pro Ala Pro Arg Cys Pro Arg  
 8300 8305 8310  
 Thr Ser Cys Arg Pro Ser Ala Ser Ala Pro Arg Arg Ser Gly Ala  
 8315 8320 8325  
 Thr Ala Thr Cys Cys Ala Trp Pro Thr Thr Trp Pro Thr Thr Arg  
 8330 8335 8340  
 Thr Ser Arg Thr Ser Ala Ala Arg Ala Cys Ser Ser Ala Thr Ala  
 8345 8350 8355  
 Ala Ala Thr Ser Ala Arg Arg Thr Ala Pro Trp Pro Ala Thr Pro  
 8360 8365 8370  
 Ser Cys Ala Arg Pro Arg Ser Ser Ala Pro Ser Ser Cys Lys Ala  
 8375 8380 8385



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro  | Ala | Arg | Ala | Arg | Gly | Val  | Asn | Ser | Pro | Arg | Gly  | Cys | Gly | Pro |
| 8390 |     |     |     |     |     | 8395 |     |     |     |     | 8400 |     |     |     |
| Arg  | Pro | Thr | Cys | Ala | Ser | Ser  | Cys | Pro | Arg | Thr | Thr  | Ile | Pro | Ser |
| 8405 |     |     |     |     |     | 8410 |     |     |     |     | 8415 |     |     |     |
| Arg  | Ser | Gly | Ser | Thr | Arg | Thr  | Asn | Pro | Ser | Arg | Pro  | Arg | Pro | Ser |
| 8420 |     |     |     |     |     | 8425 |     |     |     |     | 8430 |     |     |     |
| Cys  | Arg | Pro | Ala | Ser | Ser | Pro  | Arg | Gly | Pro | Ser | Trp  | Pro | Asn | Cys |
| 8435 |     |     |     |     |     | 8440 |     |     |     |     | 8445 |     |     |     |
| Lys  | Pro | Ser | Arg | Asn | Pro | Ala  | Lys | Asn | Phe | Cys | Lys  | Arg | Ala | Thr |
| 8450 |     |     |     |     |     | 8455 |     |     |     |     | 8460 |     |     |     |
| Gly  | Ser | Thr | Trp | Thr | Pro | Arg  | Pro | Glu | Arg | Ser | Ser  | Thr | Pro | Ala |
| 8465 |     |     |     |     |     | 8470 |     |     |     |     | 8475 |     |     |     |
| Ser  | Pro | Arg | Met | Pro | Arg | Gly  | Ser | Ser | Lys | Lys | Leu  | Lys | Val | Glu |
| 8480 |     |     |     |     |     | 8485 |     |     |     |     | 8490 |     |     |     |
| Leu  | Pro | Pro | Pro | Pro | Glu | Asp  | Leu | Glu | Glu | Asp | Trp  | Glu | Ser | Ser |
| 8495 |     |     |     |     |     | 8500 |     |     |     |     | 8505 |     |     |     |
| Gln  | Ala | Glu | Glu | Glu | Glu | Met  | Glu | Asp | Trp | Asp | Ser  | Thr | Gln | Ala |
| 8510 |     |     |     |     |     | 8515 |     |     |     |     | 8520 |     |     |     |
| Glu  | Glu | Asp | Ser | Leu | Gln | Asp  | Ser | Leu | Glu | Glu | Glu  | Asp | Glu | Val |
| 8525 |     |     |     |     |     | 8530 |     |     |     |     | 8535 |     |     |     |
| Glu  | Glu | Ala | Glu | Glu | Glu | Ala  | Ala | Ala | Ala | Arg | Pro  | Ser | Ser | Ser |
| 8540 |     |     |     |     |     | 8545 |     |     |     |     | 8550 |     |     |     |
| Ala  | Glu | Glu | Glu | Lys | Ala | Ser  | Ser | Thr | Asp | Thr | Ile  | Ser | Ala | Pro |
| 8555 |     |     |     |     |     | 8560 |     |     |     |     | 8565 |     |     |     |
| Gly  | Arg | Gly | Arg | Gly | Gly | Arg  | Ala | His | Ser | Arg | Trp  | Asp | Glu | Thr |
| 8570 |     |     |     |     |     | 8575 |     |     |     |     | 8580 |     |     |     |
| Gly  | Arg | Phe | Pro | Asn | Pro | Thr  | Thr | Gln | Thr | Gly | Lys  | Lys | Glu | Arg |
| 8585 |     |     |     |     |     | 8590 |     |     |     |     | 8595 |     |     |     |
| Gln  | Gly | Tyr | Lys | Ser | Trp | Arg  | Gly | His | Lys | Asn | Ala  | Ile | Val | Ser |
| 8600 |     |     |     |     |     | 8605 |     |     |     |     | 8610 |     |     |     |
| Cys  | Leu | Gln | Ala | Cys | Gly | Gly  | Asn | Ile | Ser | Phe | Thr  | Arg | Arg | Tyr |

|             |     |     |     |     |             |     |     |     |     |             |     |     |     |
|-------------|-----|-----|-----|-----|-------------|-----|-----|-----|-----|-------------|-----|-----|-----|
| Leu<br>8630 | Phe | His | Arg | Gly | Val<br>8635 | Asn | Phe | Pro | Arg | Asn<br>8640 | Ile | Leu | His |
| Tyr<br>8645 | Arg | His | Leu | His | Ser<br>8650 | Pro | Tyr | Tyr | Cys | Phe<br>8655 | Gln | Glu | Glu |
| Ala<br>8660 | Glu | Thr | Gln | Gln | Gln<br>8665 | Gln | Gln | Gln | Lys | Thr<br>8670 | Ser | Gly | Ser |
| Ser<br>8675 | Lys | Ile | His | Ser | Gly<br>8680 | Arg | Trp | Thr | Glu | Asp<br>8685 | Arg | Gly | Glu |
| Arg<br>8690 | Ala | Gly | Ala | Asp | Pro<br>8695 | Ala | Glu | Glu | Pro | Asp<br>8700 | Leu | Ser | His |
| Pro<br>8705 | Leu | Cys | His | Leu | Pro<br>8710 | Glu | Ser | Gly | Ala | Arg<br>8715 | Ala | Gly | Thr |
| Glu<br>8720 | Ser | Gln | Glu | Pro | Phe<br>8725 | Ala | Leu | Ala | His | Pro<br>8730 | Gln | Leu | Ser |
| Val<br>8735 | Ser | Gln | Glu | Arg | Arg<br>8740 | Thr | Ser | Ala | His | Ser<br>8745 | Arg | Gly | Arg |
| Arg<br>8750 | Gly | Ser | Leu | Gln | Gln<br>8755 | Leu | Arg | Ala | His | Ser<br>8760 | Arg | Val | Ala |
| Arg<br>8765 | Ala | Arg | Pro | His | Thr<br>8770 | Lys | Gly | Gly | Asn | Tyr<br>8775 | Val | Thr | Thr |
| Cys<br>8780 | Ala | Leu | Arg | Pro | Thr<br>8785 | Ile | Ile | Met | Ser | Lys<br>8790 | Ile | Pro | Thr |
| Pro<br>8795 | Tyr | Met | Trp | Ser | Tyr<br>8800 | Gln | Pro | Gln | Met | Gly<br>8805 | Ala | Ala | Gly |
| Ala<br>8810 | Ala | Gln | Asp | Tyr | Ser<br>8815 | Thr | Arg | Met | Asn | Trp<br>8820 | Ser | Ala | Gly |
| Pro<br>8825 | Ala | Met | Ile | Ser | Arg<br>8830 | Val | Asn | Asp | Ile | Arg<br>8835 | His | Arg | Asn |
| Gln<br>8840 | Ile | Leu | Leu | Glu | Gln<br>8845 | Ser | Ala | Ile | Thr | Ala<br>8850 | Pro | Arg | His |

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His Leu Asn Pro Arg Asn Trp Pro Ala Ala Leu Val Tyr Gln Glu  
 8855 8860 8865  
  
 Ile Pro Gln Pro Thr Thr Val Leu Leu Pro Arg Asp Ala Gln Ala  
 8870 8875 8880  
  
 Glu Val Gln Leu Thr Asn Ser Gly Val Gln Leu Ala Gly Gly Ala  
 8885 8890 8895  
  
 Ala Leu Cys Arg His Arg Pro Ala Gln Gly Ile Lys Arg Leu Val  
 8900 8905 8910  
  
 Ile Arg Gly Arg Gly Thr Gln Leu Asn Asp Glu Val Val Ser Ser  
 8915 8920 8925  
  
 Ser Leu Gly Leu Arg Pro Asp Gly Val Phe Gln Leu Ala Gly Ser  
 8930 8935 8940  
  
 Gly Arg Ser Ser Phe Thr Pro Arg Gln Ala Val Leu Thr Leu Glu  
 8945 8950 8955  
  
 Ser Ser Ser Ser Gln Pro Arg Ser Gly Gly Ile Gly Thr Leu Gln  
 8960 8965 8970  
  
 Phe Val Glu Glu Phe Thr Pro Ser Val Tyr Phe Asn Pro Phe Ser  
 8975 8980 8985  
  
 Gly Ser Pro Gly His Tyr Pro Asp Glu Phe Ile Pro Asn Phe Asp  
 8990 8995 9000  
  
 Ala Ile Ser Glu Ser Val Asp Gly Tyr Asp Met Ser His Gly Gly  
 9005 9010 9015  
  
 Ala Ala Asp Leu Ala Arg Leu Arg His Leu Asp His Cys Arg Arg  
 9020 9025 9030  
  
 Phe Arg Cys Phe Ala Arg Asp Leu Ala Glu Phe Ala Tyr Phe Glu  
 9035 9040 9045  
  
 Leu Pro Glu Glu His Pro Gln Gly Pro Ala His Gly Val Arg Ile  
 9050 9055 9060  
  
 Val Val Glu Gly Gly Leu Asp Ser His Leu Leu Arg Ile Phe Ser  
 9065 9070 9075  
  
 Gln Arg Pro Ile Leu Ala Glu Arg Glu Gln Gly Gln Thr Leu Leu  
 9080 9085 9090

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Thr Leu Tyr Cys Ile Cys Asn His Pro Gly Leu His Glu Ser Leu  
 9095 9100 9105  
 Cys Cys Leu Leu Cys Thr Glu Tyr Asn Lys Ser Asp Gln Arg Leu  
 9110 9115 9120  
 Leu Arg Thr Ser Val Cys Ser Cys Tyr Gln Pro Val Pro Val Leu  
 9125 9130 9135  
 His Arg Glu Arg Asp Arg Ala Pro Ala Pro Val Ala Pro Gln Glu  
 9140 9145 9150  
 Val Pro His Leu Ala Val Pro Gly Leu Ser Asp Arg Arg Cys Gln  
 9155 9160 9165  
 Pro Leu Arg Gln Arg Arg Ser Pro Ala Glu Arg Pro Cys Gln Pro  
 9170 9175 9180  
 Tyr Phe Phe His Pro Gln Lys Gln Ala Pro Ala Leu Pro Thr Leu  
 9185 9190 9195  
 Pro Pro Arg Asp Leu Ser Val Arg Leu Gly Thr Leu Pro Ser His  
 9200 9205 9210  
 Leu Pro Pro Asp Pro Glu Tyr His Ser Val Ala Pro Arg Tyr Gln  
 9215 9220 9225  
 Pro Asn Tyr Pro Pro Thr Pro Pro Ser Arg Pro Arg Thr Cys Thr  
 9230 9235 9240  
 Glu Leu Glu Lys Tyr Ala Thr Ile His Ala His Ile Arg Leu Gly  
 9245 9250 9255  
 Arg Ala Thr Ala Thr His Ala Pro Arg Tyr Leu Leu Gln Ser Asn  
 9260 9265 9270  
 Arg Arg Arg Leu Thr His Trp Pro Thr Thr Thr Ser Thr Thr Phe  
 9275 9280 9285  
 Ser Trp Thr Trp Thr Ala Ala Pro Arg Ser Ser Asp Ser Pro Asn  
 9290 9295 9300  
 Phe Ala Phe Ala Ser Ser Arg Arg Glu Pro Ser Arg Ser Cys Arg  
 9305 9310 9315  
 Thr Ala Pro Ser Thr Ser Ala Arg Lys Ala Ser Ser Ala Trp Asn  
 9320 9325 9330

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Pro  | Arg | Ser | Pro | Thr | Arg  | Ser | Pro | Arg | Pro | Thr  | Ile | Ala | Ser |
|     | 9335 |     |     |     |     | 9340 |     |     |     |     | 9345 |     |     |     |
| Pro | Thr  | Ser | Ser | Cys | Ser | Ser  | Ala | Arg | Ser | Ser | Pro  | Ala | Trp | Ser |
|     | 9350 |     |     |     |     | 9355 |     |     |     |     | 9360 |     |     |     |
| Glu | Ser  | Thr | Pro | Ser | Ser | Ser  | Pro | Ser | Ser | Arg | Ala  | Ile | Pro | Arg |
|     | 9365 |     |     |     |     | 9370 |     |     |     |     | 9375 |     |     |     |
| Gly | Ala  | Ser | Thr | Ala | Pro | Ala  | Thr | Pro | Pro | Thr | Ala  | Ser | Thr | Leu |
|     | 9380 |     |     |     |     | 9385 |     |     |     |     | 9390 |     |     |     |
| Ser | Arg  | Pro | Ser | Ala | Ala | Ser  | Ala | Thr | Ser | Ser | Pro  | Thr | Asn | His |
|     | 9395 |     |     |     |     | 9400 |     |     |     |     | 9405 |     |     |     |
| Pro | Leu  | Ile | Gln | Asn | Lys | Tyr  | His | Ile | Asp | Asp | Asp  | Leu | Asn | Lys |
|     | 9410 |     |     |     |     | 9415 |     |     |     |     | 9420 |     |     |     |
| Lys | Ser  | Phe | Asp | Leu | Lys | Arg  | Tyr | Asn | His | Ile | Asp  | Asp | Leu | Ser |
|     | 9425 |     |     |     |     | 9430 |     |     |     |     | 9435 |     |     |     |
| Phe | Lys  | Lys | Arg | Ile | Thr | Tyr  | Leu | Lys | Ser | Asp | Thr  | Arg | Ser | Leu |
|     | 9440 |     |     |     |     | 9445 |     |     |     |     | 9450 |     |     |     |
| Ser | Met  | Phe | Ser | Ala | Asn | Thr  | Thr | Ser | Leu | Pro | Ser  | Ser | Gln | Leu |
|     | 9455 |     |     |     |     | 9460 |     |     |     |     | 9465 |     |     |     |
| Trp | Tyr  | Cys | Arg | Pro | Arg | Arg  | Ala | Ala | Asn | Phe | Leu  | His | Thr | Leu |
|     | 9470 |     |     |     |     | 9475 |     |     |     |     | 9480 |     |     |     |
| Lys | Gly  | Met | Ser | Asn | Ser | Ser  | Cys | Pro | Ser | Ile | Phe  | Ile | Leu | Ser |
|     | 9485 |     |     |     |     | 9490 |     |     |     |     | 9495 |     |     |     |
| Ser | Ile  | Arg | Cys | Pro | Lys | Ser  | Ala | Ser | Gly | Trp | Met  | Met | Thr | Ser |
|     | 9500 |     |     |     |     | 9505 |     |     |     |     | 9510 |     |     |     |
| Thr | Pro  | Ser | Thr | Pro | Thr | Met  | Gln | Thr | Thr | His | Arg  | Pro | Cys | Pro |
|     | 9515 |     |     |     |     | 9520 |     |     |     |     | 9525 |     |     |     |
| Ser | Ser  | Thr | Pro | Pro | Ser | Ser  | Leu | Gln | Met | Asp | Ser  | Lys | Arg | Ser |
|     | 9530 |     |     |     |     | 9535 |     |     |     |     | 9540 |     |     |     |
| Pro | Trp  | Gly | Cys | Cys | Pro | Cys  | Asp | Trp | Leu | Thr | Pro  | Ser | Pro | Pro |
|     | 9545 |     |     |     |     | 9550 |     |     |     |     | 9555 |     |     |     |
| Arg | Thr  | Gly | Lys | Ser | Pro | Ser  | Ser | Trp | Glu | Arg | Gly  | Trp | Thr | Ser |

9560

9565

9570

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Pro  | Arg | Glu | Asn | Ser | Ser  | Pro | Thr | Arg | Pro | Pro  | Arg | Pro | Pro |
|     | 9575 |     |     |     |     | 9580 |     |     |     |     | 9585 |     |     |     |
| Pro | Leu  | Ser | Val | Phe | Pro | Thr  | Thr | Pro | Phe | Pro | Leu  | Thr | Trp | Ile |
|     | 9590 |     |     |     |     | 9595 |     |     |     |     | 9600 |     |     |     |
| Pro | Leu  | Phe | Ile | Pro | Lys | Met  | Glu | Asn | Tyr | Pro | Tyr  | Lys | Phe | Leu |
|     | 9605 |     |     |     |     | 9610 |     |     |     |     | 9615 |     |     |     |
| His | Arg  | Thr | Tyr | Asn | Gln | Pro  | Phe | Thr | His | Leu | Leu  | Met | Asp | Gln |
|     | 9620 |     |     |     |     | 9625 |     |     |     |     | 9630 |     |     |     |
| Val | Asp  | Val | Val | Ala | Leu | Leu  | Leu | Gln | Tyr | Ser | Trp  | Pro | Leu | His |
|     | 9635 |     |     |     |     | 9640 |     |     |     |     | 9645 |     |     |     |
| Ser | Leu  | Leu | Met | Lys | Lys | Glu  | Ile | Leu | Lys | Leu | Thr  | Pro | Val | Val |
|     | 9650 |     |     |     |     | 9655 |     |     |     |     | 9660 |     |     |     |
| His | Gln  | Leu | Met | Gln | Val | Asp  | Leu | Val | Ser | Thr | Ala  | Lys | Glu | Gly |
|     | 9665 |     |     |     |     | 9670 |     |     |     |     | 9675 |     |     |     |
| Ser | Leu  | Ser | Leu | Pro | Gln | Glu  | Met | Gln | Leu | Lys | Ala  | Thr | Ala | Gly |
|     | 9680 |     |     |     |     | 9685 |     |     |     |     | 9690 |     |     |     |
| Leu | Lys  | Val | Asp | Leu | Lys | Val  | Met | Ala | Leu | Gln | Thr  | Leu | Ala | Glu |
|     | 9695 |     |     |     |     | 9700 |     |     |     |     | 9705 |     |     |     |
| Asp | Trp  | Asn | Leu | Glu | Pro | Leu  | Val | Gln | Arg | Leu | Met  | Ser | Gln | Met |
|     | 9710 |     |     |     |     | 9715 |     |     |     |     | 9720 |     |     |     |
| His | Thr  | Gln | Phe | Lys | Leu | Asn  | Trp | Val | Leu | Ala | Leu  | Pro | Leu | Thr |
|     | 9725 |     |     |     |     | 9730 |     |     |     |     | 9735 |     |     |     |
| Val | Gln  | Ala | Pro | Leu | Leu | Leu  | Gly | Thr | Lys | Arg | Met  | Ile | Asn | Leu |
|     | 9740 |     |     |     |     | 9745 |     |     |     |     | 9750 |     |     |     |
| His | Tyr  | Gly | Pro | Gln | Pro | Thr  | Pro | Arg | Gln | Ile | Ala  | Lys | Tyr | Thr |
|     | 9755 |     |     |     |     | 9760 |     |     |     |     | 9765 |     |     |     |
| Leu | Lys  | Lys | Met | Pro | Asn | Ser  | His | Phe | Ala | Gln | Ser  | Val | Glu | Val |
|     | 9770 |     |     |     |     | 9775 |     |     |     |     | 9780 |     |     |     |
| Lys | Phe  | Trp | Val | Leu | Leu | Tyr  | Trp | Gln | Ile | Met | Glu  | Val | Ser | Thr |
|     | 9785 |     |     |     |     | 9790 |     |     |     |     | 9795 |     |     |     |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Gln | Ser   | Gln | Thr | Gln | Ala | Leu   | His | Ser | Ser | Pro | Ser   | Ser | Leu | Met |
|     | 9800  |     |     |     |     | 9805  |     |     |     |     | 9810  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Gln | Val   | Glu | Phe | Cys | Ala | Ala   | Pro | His | Thr | Lys | Asn   | Ile | Gly | Thr |
|     | 9815  |     |     |     |     | 9820  |     |     |     |     | 9825  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Ser | Glu   | Arg | Glu | Met | Leu | His   | Leu | Leu | Ser | Pro | Ile   | Leu | Met | Leu |
|     | 9830  |     |     |     |     | 9835  |     |     |     |     | 9840  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Val | Leu   | Cys | Leu | Thr | Arg | Pro   | Ile | Leu | Lys | Thr | His   | Leu | Gln | Leu |
|     | 9845  |     |     |     |     | 9850  |     |     |     |     | 9855  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Gln | Lys   | Ala | Ile | Leu | Ser | Val   | Lys | Phe | Ile | Ser | Met   | Gly | Met | Arg |
|     | 9860  |     |     |     |     | 9865  |     |     |     |     | 9870  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Pro | Asn   | His | Cys | Leu | Leu | Leu   | Leu | Met | Lys | Leu | Arg   | Met | Gln | Leu |
|     | 9875  |     |     |     |     | 9880  |     |     |     |     | 9885  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Ala | Pro   | Thr | Val | Ser | Leu | Phe   | Asn | Gly | Asn | Gly | Ile   | Val | Leu | Ser |
|     | 9890  |     |     |     |     | 9895  |     |     |     |     | 9900  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Thr | Gln   | Val | Lys | His | Leu | Leu   | Pro | Ala | Pro | Ser | Pro   | Ser | Pro | Thr |
|     | 9905  |     |     |     |     | 9910  |     |     |     |     | 9915  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Ser | Pro   | Lys | Asn | Glu | His | Cys   | Ile | Pro | Pro | Cys | Met   | Pro | Thr | Leu |
|     | 9920  |     |     |     |     | 9925  |     |     |     |     | 9930  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Pro | Thr   | Pro | Leu | Cys | Leu | Trp   | Lys | Lys | Leu | Ser | Thr   | Lys | Asn | Lys |
|     | 9935  |     |     |     |     | 9940  |     |     |     |     | 9945  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Val | Gln   | Val | Phe | Tyr | Phe | Asn   | Ser | Phe | Thr | Gly | Phe   | Glu | Gln | Leu |
|     | 9950  |     |     |     |     | 9955  |     |     |     |     | 9960  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Phe | Phe   | Leu | His | Pro | Pro | Arg   | Thr | Trp | Asn | Thr | Pro   | Pro | Ser | Pro |
|     | 9965  |     |     |     |     | 9970  |     |     |     |     | 9975  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Pro | Ala   | Gln | Pro | Thr | Ser | Glu   | Cys | His | Trp | Trp | Thr   | Cys | Phe | Trp |
|     | 9980  |     |     |     |     | 9985  |     |     |     |     | 9990  |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Ser | Pro   | Arg | Ser | Thr | Gln | Phe   | Gln | Ser | Glu | Pro | Val   | Ser | Gly | Arg |
|     | 9995  |     |     |     |     | 10000 |     |     |     |     | 10005 |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Ser | Gly   | Arg | Asn | Pro | Pro | Gly   | Thr | Pro | Ala | Ser | Ala   | Pro | His | Ser |
|     | 10010 |     |     |     |     | 10015 |     |     |     |     | 10020 |     |     |     |
|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Ser | Thr   | Ala | Glu | Asp | Cys | Pro   | Arg | Trp | Ser | Gly | Ser   | Arg | Leu | Ser |
|     | 10025 |     |     |     |     | 10030 |     |     |     |     | 10035 |     |     |     |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Gly | Arg   | Ser | Arg | Arg | Ala | Ala   | Val | Gly | Ile | Ile | Val   | Arg | Glu | Arg |
|     | 10040 |     |     |     |     | 10045 |     |     |     |     | 10050 |     |     |     |
| Asp | Arg   | Pro | Val | Val | Ser | His   | Gln | Ala | Pro | Gln | Gln   | Ser | Leu | Pro |
|     | 10055 |     |     |     |     | 10060 |     |     |     |     | 10065 |     |     |     |
| Pro | Pro   | Leu | Arg | Gln | Ala | Ala   | Ala | Gln | Gly | Val | Arg   | Val | Gln | Gly |
|     | 10070 |     |     |     |     | 10075 |     |     |     |     | 10080 |     |     |     |
| Leu | Pro   | Gln | His | Asp | Ala | His   | Gly | Pro | Gln | His | Gln   | Ser | Ser | Gly |
|     | 10085 |     |     |     |     | 10090 |     |     |     |     | 10095 |     |     |     |
| Ala | Ala   | Gly | Ala | Ala | Ala | His   | Ala | Asp | Leu | Ala | Gln   | Val | Ala | Ala |
|     | 10100 |     |     |     |     | 10105 |     |     |     |     | 10110 |     |     |     |
| Val | Arg   | Ala | Thr | Gln | Asp | His   | Gln | Val | Val | Gln | Gln   | Ser | Ile | Val |
|     | 10115 |     |     |     |     | 10120 |     |     |     |     | 10125 |     |     |     |
| Gln | His   | Ala | Pro | Ala | Glu | Thr   | His | Arg | Gly | Lys | Asp   | Ala | Thr | His |
|     | 10130 |     |     |     |     | 10135 |     |     |     |     | 10140 |     |     |     |
| Val | Ala   | Val | Val | Pro | Asp | Pro   | Gln | Val | Asn | Gln | Val   | Ala | Leu | Pro |
|     | 10145 |     |     |     |     | 10150 |     |     |     |     | 10155 |     |     |     |
| Pro | Glu   | His | Ala | Ala | His | Val   | His | Asp | Leu | Leu | Gly   | His | Val | Ala |
|     | 10160 |     |     |     |     | 10165 |     |     |     |     | 10170 |     |     |     |
| Val | His   | His | Leu | Pro | Val | Pro   | His | His | Pro | Leu | Val   | Glu | His | Ala |
|     | 10175 |     |     |     |     | 10180 |     |     |     |     | 10185 |     |     |     |
| Ala | Pro   | Asp | Asp | Pro | Ala | Glu   | Pro | Gln | Gly | Gln | His   | Arg | Pro | Ala |
|     | 10190 |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| Arg | His   | Ala | Ala | Lys | Arg | Pro   | Arg | Val | Pro | Ala | Met   | Ala | Met | Glu |
|     | 10205 |     |     |     |     | 10210 |     |     |     |     | 10215 |     |     |     |
| Asp | Pro   | Pro | Leu | Val | Pro | Val   | Asp | His | Leu | Gly | Ala   | Glu | Gln | Val |
|     | 10220 |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |
| Tyr | Val   | Gly | Thr | Ala | Gln | Ala   | Tyr | Ala | His | Ala | Ser   | Leu | Gln | His |
|     | 10235 |     |     |     |     | 10240 |     |     |     |     | 10245 |     |     |     |
| Ser | Gln   | Leu | Leu | Gly | Gly | Gln   | Asn | His | Ile | Pro | Gly   | His | Gly | Glu |
|     | 10250 |     |     |     |     | 10255 |     |     |     |     | 10260 |     |     |     |
| Leu | Leu   | Gln | Asp | Ser | Glu | Pro   | Arg | Arg | Thr | Gly | Gln   | Ser | Ser | His |
|     | 10265 |     |     |     |     | 10270 |     |     |     |     | 10275 |     |     |     |



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|                  |                              |                              |             |
|------------------|------------------------------|------------------------------|-------------|
| Ile Thr<br>10280 | Tyr Ile Val His Gly<br>10285 | Gln Gly Ile Ala Ile<br>10290 | Arg Gln His |
| Arg Val<br>10295 | Ile Leu His Gln Arg<br>10300 | Ser Ala Gly Leu Gly<br>10305 | Leu Leu Thr |
| Ala Trp<br>10310 | Gly Gly Arg Pro Ile<br>10315 | Arg Val Met Ala Gly<br>10320 | Arg Gly Ser |
| Cys Ser<br>10325 | Arg Pro Cys His Asp<br>10330 | Ala Val Ala Phe Gly<br>10335 | His Phe Arg |
| Thr Cys<br>10340 | Cys Ser Arg Thr Trp<br>10345 | Ser Gly Arg Cys Thr<br>10350 | Pro Ile Ala |
| Gly Gly<br>10355 | Gly Pro Gly Ala Trp<br>10360 | Asn Ala Arg Cys Asn<br>10365 | Cys Lys Thr |
| Ala Thr<br>10370 | Leu Ser Asp Arg Ala<br>10375 | Ala Asp Leu Gly Pro<br>10380 | Gln Glu Arg |
| Ser His<br>10385 | His Ala Leu Ser His<br>10390 | Arg Pro Pro Trp Asn<br>10395 | Gly Pro Asp |
| Pro Ala<br>10400 | Arg Cys Asn Phe Val<br>10405 | Gly Phe Arg Arg Arg<br>10410 | Gly Arg Glu |
| Glu Gln<br>10415 | Glu Glu Pro Leu Thr<br>10420 | Phe Asn Pro Asn Gly<br>10425 | Leu Gly Ala |
| Leu Gln<br>10430 | Asn Glu Gly Arg Gly<br>10435 | Asp Gly Thr Ser Arg<br>10440 | Pro Arg Cys |
| Val Gly<br>10445 | Gly Lys Gln Pro Gly<br>10450 | Gln Arg Tyr Gly Ser<br>10455 | Arg Asp Val |
| Pro Arg<br>10460 | Trp Leu Pro Ala Lys<br>10465 | Pro Pro Arg Ala His<br>10470 | Pro Glu Thr |
| Arg Gln<br>10475 | Arg Lys Arg Glu Gly<br>10480 | Ser Leu Ile Pro Gln<br>10485 | Ser Ser Cys |
| Tyr Thr<br>10490 | Pro Ala Pro Ser Pro<br>10495 | Asp Asn Phe His Phe<br>10500 | Ser Ser Leu |
| Glu Phe          | Glu Leu Val Pro Glu          | Val Asn Pro Ser Gln          | Pro Arg Ala |

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10505

10510

10515

|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Arg   | Ala | Glu | Arg | Pro | Pro | Pro   | Ala | Phe | Leu | Ser | Thr   | Pro | Ser | Phe |
| 10520 |     |     |     |     |     | 10525 |     |     |     |     | 10530 |     |     |     |
| Gln   | Asp | Ile | Leu | Leu | Leu | Val   | His | Leu | Gln | Gln | Ile   | Asp | Lys | Arg |
| 10535 |     |     |     |     |     | 10540 |     |     |     |     | 10545 |     |     |     |
| Asn   | Ile | Lys | Ile | Ser | Ala | Ala   | Ile | Pro | Lys | Leu | Leu   | Pro | Gln | Gln |
| 10550 |     |     |     |     |     | 10555 |     |     |     |     | 10560 |     |     |     |
| Leu   | Val | Leu | Phe | His | Ile | Leu   | Ser | Glu | Ile | Phe | Ser   | His | Arg | Thr |
| 10565 |     |     |     |     |     | 10570 |     |     |     |     | 10575 |     |     |     |
| Thr   | Arg | Asn | Lys | Ile | Arg | Ala   | Ser | His | Ser | Thr | Asp   | Lys | Pro | Lys |
| 10580 |     |     |     |     |     | 10585 |     |     |     |     | 10590 |     |     |     |
| Ser   | Ser | Pro | Val | Ser | Ile | Ala   | Lys | Cys | Lys | Thr | Ala   | Ile | Ser | Met |
| 10595 |     |     |     |     |     | 10600 |     |     |     |     | 10605 |     |     |     |
| Leu   | Ala | Arg | Pro | Gly | Asp | Ile   | Phe | Gln | Ile | Thr | Gly   | Gln | Lys | Ile |
| 10610 |     |     |     |     |     | 10615 |     |     |     |     | 10620 |     |     |     |
| Thr   | Gln | Ala | Ile | Phe | Lys | Lys   | Ile | Asn | Lys | Arg | Lys   | Ile | Leu | Gln |
| 10625 |     |     |     |     |     | 10630 |     |     |     |     | 10635 |     |     |     |
| Val   | His | Val | Ser | Leu | Gly | Asn   | Asn | Asp | Glu | Val | Asn   | Ala | Ser | Gly |
| 10640 |     |     |     |     |     | 10645 |     |     |     |     | 10650 |     |     |     |
| Ala   | Phe | Gln | His | Gly | Leu | Ala   | Asp | Leu | Lys | Thr | Lys   | Asn | Lys | Thr |
| 10655 |     |     |     |     |     | 10660 |     |     |     |     | 10665 |     |     |     |
| Leu   | Asn | His | Ala | Ser | Leu | Ala   | Asn | Arg | Trp | Val | Asn   | Arg | Ser | Leu |
| 10670 |     |     |     |     |     | 10675 |     |     |     |     | 10680 |     |     |     |
| Gln   | His | Gln | Ala | Gly | His | Gly   | Val | Ser | Gly | Ala | Thr   | Leu | Val | Lys |
| 10685 |     |     |     |     |     | 10690 |     |     |     |     | 10695 |     |     |     |
| Ile   | Val | Ala | Met | Ile | Glu | Asn   | His | His | Arg | Glu | Thr   | Phe | Pro | Val |
| 10700 |     |     |     |     |     | 10705 |     |     |     |     | 10710 |     |     |     |
| Ala   | Gly | Val | Asn | Asp | Ser | Thr   | Arg | Ile | His | Pro | Arg   | Asn | Ile | Gly |
| 10715 |     |     |     |     |     | 10720 |     |     |     |     | 10725 |     |     |     |
| Val   | Arg | Glu | Lys | Lys | Ala | Pro   | Glu | Glu | Ala | Ile | Arg   | His | Tyr | Asn |
| 10730 |     |     |     |     |     | 10735 |     |     |     |     | 10740 |     |     |     |

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Ala Gln Ser Gln Val Gln Gln Ser Asp Ala Met Arg Met Lys His  
 10745 10750 10755

Lys Ile Leu Arg Cys Val Gln Asn Val Ile Thr Pro Leu Leu His  
 10760 10765 10770

Arg Gln Arg Ser Pro Arg Ser Leu Gln Ile His Ile Gln Ser Leu  
 10775 10780 10785

Ser Val His Ser Leu Pro Ser Ser Ser Thr Gln Gln Ala Gln Glu  
 10790 10795 10800

Ser Glu Lys Gly Ala Leu Thr Cys Pro Pro Ala Leu Cys Ser Ile  
 10805 10810 10815

Tyr Ser Pro Asp Leu His Arg Lys Gly Gln Ser Leu Lys Ile Pro  
 10820 10825 10830

Ala Lys Ser His Thr Pro Ser Thr Arg Pro Glu Thr Gly Asp Thr  
 10835 10840 10845

Leu Lys Lys Ile Arg Ala Leu Pro Gln Thr Pro Lys Leu Pro Ser  
 10850 10855 10860

Phe Pro Gly Ser His Ala Thr Ser Ser Glu Phe Asp Phe Gln Ile  
 10865 10870 10875

Pro Ser Thr Val Lys Asn Val Thr Arg Pro Ala Pro Asn Gly Arg  
 10880 10885 10890

Pro Ser Leu Gly Gln Ser Pro Ser Ser Leu Pro Lys Phe Lys Gln  
 10895 10900 10905

Leu Ile Cys Ile Leu Thr Arg Thr Lys Ser Leu Arg Tyr Ile Ile  
 10910 10915 10920

Asp Asp  
 10925

<210> 12  
 <211> 10908  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Artificially Synthesized

<400> 12

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala

```

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

```

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Arg Val Thr Leu Thr Val Asn Gly Pro Pro Gly Pro Pro Asn Asp Pro  
 260 265 270

Arg Pro Leu Thr Ser Ile Met Thr Tyr Val Pro Ile Val Thr Pro Ile  
 275 280 285

Gly Thr Phe His Arg Gln Trp Val Glu Tyr Leu Arg Thr Ala His Leu  
 290 295 300

Ala Val His Gln Val Tyr His Met Pro Ser Thr Pro Pro Ile Asp Val  
 305 310 315 320

Asn Asp Gly Lys Trp Pro Ala Trp His Tyr Ala Gln Tyr Met Thr Leu  
 325 330 335

Trp Asp Phe Pro Thr Trp Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile  
 340 345 350

Thr Met Val Met Arg Phe Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe  
 355 360 365

Asp Ser Arg Gly Phe Pro Ser Leu His Pro Ile Asp Val Asn Gly Ser  
 370 375 380

Leu Phe Trp His Gln Asn Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn  
 385 390 395 400

Ser Ala Pro Leu Thr Gln Met Gly Gly Arg Arg Val Arg Trp Glu Val  
 405 410 415

Tyr Ile Ser Arg Ala Arg Leu Val Asn Arg Gln Ile Thr Arg Ser Phe  
 420 425 430

Ile Ala Val Val Tyr His Ser Ile Ala Asn Ala Val Ser Ala Ser Asp  
 435 440 445

Thr Thr Val Ser Asn Leu Ser Cys Arg Ser Trp Ser Gly Thr Gly Gln  
 450 455 460

Val Ser Ile Lys Val Thr Arg Gln Val Gly Asp Gln Lys Leu Gly Leu  
 465 470 475 480

Ser Arg Gln Arg Arg Leu Leu Arg Phe Ala Pro Ile Gly Leu Thr Asp  
 485 490 495

Ile His Phe Ala Phe Leu Ser Thr Gly Val His Ser Gln Phe Asn Tyr  
 500 505 510

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Ser Ser Gly Ser Thr Tyr Asp Ser Leu Ala Ser Ala Thr Met Gly Ala  
515 520 525

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile  
530 535 540

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val  
545 550 555 560

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu  
565 570 575

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser  
580 585 590

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala  
595 600 605

Thr Leu Tyr Cys Val His Gln Arg Ile Glu Val Lys Asp Thr Lys Glu  
610 615 620

Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala  
625 630 635 640

Gln Gln Ala Ala Ala Asp Thr Gly Asn Ser Ser Gln Val Ser Gln Asn  
645 650 655

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile  
660 665 670

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala  
675 680 685

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala  
690 695 700

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln  
705 710 715 720

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu  
725 730 735

Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln  
740 745 750

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu  
755 760 765

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Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly  
770 775 780

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg  
785 790 795 800

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu  
805 810 815

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
820 825 830

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
835 840 845

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
850 855 860

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
865 870 875 880

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr  
885 890 895

Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg  
900 905 910

Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys  
915 920 925

Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu  
930 935 940

Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly  
945 950 955 960

Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser  
965 970 975

Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg Phe Gly Glu  
980 985 990

Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp Lys Glu Leu  
995 1000 1005

Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Asn Asp Pro Ser

|     |             |     |     |     |     |             |     |     |     |     |             |     |     |     |
|-----|-------------|-----|-----|-----|-----|-------------|-----|-----|-----|-----|-------------|-----|-----|-----|
| Ser | Gln<br>1025 | Ser | Ser | Val | Thr | Gly<br>1030 | Pro | Leu | Glu | Ser | Thr<br>1035 | Arg | Ala | Ala |
| Lys | Pro<br>1040 | Leu | Ile | Ser | Leu | Asp<br>1045 | Cys | Ala | Phe | Leu | Pro<br>1050 | Ala | Ile | Cys |
| Cys | Leu<br>1055 | Pro | Leu | Pro | Arg | Ala<br>1060 | Phe | Leu | Asp | Pro | Gly<br>1065 | Arg | Cys | His |
| Ser | His<br>1070 | Cys | Pro | Phe | Leu | Ile<br>1075 | Lys | Gly | Asn | Cys | Ile<br>1080 | Ala | Leu | Ser |
| Glu | Val<br>1085 | Ser | Phe | Tyr | Ser | Gly<br>1090 | Gly | Trp | Gly | Gly | Ala<br>1095 | Gly | Gln | Gln |
| Gly | Gly<br>1100 | Gly | Leu | Gly | Arg | Gln<br>1105 | Gln | Ala | Cys | Trp | Gly<br>1110 | Cys | Gly | Gly |
| Leu | Tyr<br>1115 | Gly | Phe | Gly | Gly | Lys<br>1120 | Asn | Gln | Gln | Ile | Cys<br>1125 | Arg | Ser | Glu |
| Phe | Ile<br>1130 | Tyr | Val | Gly | Cys | Gly<br>1135 | Glu | Arg | Gly | Asn | Glu<br>1140 | Met | Ala | Leu |
| Trp | Val<br>1145 | Leu | Trp | Val | Cys | Ile<br>1150 | Asn | Glu | Ser | Ala | Arg<br>1155 | Tyr | Ala | Gly |
| His | Arg<br>1160 | Ala | Cys | Asp | Leu | Ala<br>1165 | Pro | Pro | Gln | Asp | Met<br>1170 | Ala | Arg | Val |
| Arg | Ala<br>1175 | Gln | Arg | His | Asp | Pro<br>1180 | Met | Gln | Cys | Ala | Pro<br>1185 | Gly | Val | Pro |
| Pro | Arg<br>1190 | His | Val | His | Ala | Leu<br>1195 | Pro | Val | Gln | His | Ala<br>1200 | Ile | Cys | Glu |
| Gly | Ala<br>1205 | Ala | Gly | Ala | Arg | Cys<br>1210 | His | Val | Gln | Ser | Glu<br>1215 | Pro | Asp | Gly |
| Gly | Val<br>1220 | His | Glu | Cys | Gly | Ala<br>1225 | Val | Glu | Asn | Ser | Glu<br>1230 | Ile | Ile | Gln |
| Asp | Gln<br>1235 | Val | Pro | Gly | Leu | Arg<br>1240 | Met | Arg | Arg | Gln | Ala<br>1245 | Arg | Gln | Ala |



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Ser Ala Arg Val Cys Gly Gly Asp Gly Gly Pro Ala Thr Arg Ser  
 1250 1255 1260  
  
 Phe Gly Val Val Leu Gln Arg Asp Gly Val Arg Leu Gln Arg Gly  
 1265 1270 1275  
  
 Arg Ile Leu Glu Val Val Phe Gly Gly Gly Gly Gly Leu Val Gly  
 1280 1285 1290  
  
 Ala Glu Leu Lys Ser Val Phe Phe Cys Val Leu Gln Gln His Glu  
 1295 1300 1305  
  
 Arg Lys Arg Leu Leu Gly Arg Gly Ile Gln Pro Leu Ser Asp Gly  
 1310 1315 1320  
  
 Ala Ser Pro Leu Leu Gly Gly Ser Ala Ser Glu Cys Asp Gly Ile  
 1325 1330 1335  
  
 His Gly Gly Arg Pro Ala Arg Ala Ala Arg Glu Leu Phe Asn Pro  
 1340 1345 1350  
  
 Asp Leu Arg Asp Pro Glu Leu Leu Val Arg Gly Arg Ser Cys Arg  
 1355 1360 1365  
  
 Arg Ser Cys Cys Phe Arg Arg Gln Arg Arg Ala Arg Asn Gly Pro  
 1370 1375 1380  
  
 Gly Arg Arg Leu Leu Gln Leu Ser Gly Gly Gln Leu Asp Phe His  
 1385 1390 1395  
  
 Gln Ser Arg Gln Pro Glu Arg Gly Glu Ala Ala Ala Ala Asp Gly  
 1400 1405 1410  
  
 Pro Ala Arg Gly Pro Asp Pro Ala Pro Gly Arg Ala Asp Pro Ala  
 1415 1420 1425  
  
 Gly Gly Ser Ala Ala Gly Gly Asp Ala Gly Arg Gly Cys His Gly  
 1430 1435 1440  
  
 Glu Asn Gln Ile Lys Asn Glu Ser Ile Asn Lys Arg Arg Arg Leu  
 1445 1450 1455  
  
 Leu Ile Leu Thr Gln Ser Leu Glu Ser Leu Phe Asp Phe Ser Arg  
 1460 1465 1470  
  
 Ala Val Gly Pro Gly Pro Pro Val Ser Ile Ile Glu His Pro Val  
 1475 1480 1485

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp | Phe  | Phe | Gln | Asp | Pro | Val  | Glu | Val | Gly | Leu | Asp  | Val | Glu | Val |
|     | 1490 |     |     |     |     | 1495 |     |     |     |     | 1500 |     |     |     |
| His | Gly  | His | Glu | Pro | Val | Pro  | Gly | Val | Glu | Val | Ala  | Pro | Leu | Gln |
|     | 1505 |     |     |     |     | 1510 |     |     |     |     | 1515 |     |     |     |
| Gly | Leu  | Val | Leu | Gly | Gly | Gly  | Val | Val | Asn | His | Pro  | Val | Ile | Ala |
|     | 1520 |     |     |     |     | 1525 |     |     |     |     | 1530 |     |     |     |
| Gly | Ala  | Gln | Gly | Val | Val | Leu  | His | Asp | Val | Leu | Glu  | Glu | Glu | Thr |
|     | 1535 |     |     |     |     | 1540 |     |     |     |     | 1545 |     |     |     |
| Asp | Gly  | His | Gly | Gln | Pro | Leu  | Gly | Val | Gly | Val | Asp  | Glu | Pro | Val |
|     | 1550 |     |     |     |     | 1555 |     |     |     |     | 1560 |     |     |     |
| Glu | Leu  | Gly | Gly | Met | His | Ala  | Gly | Gly | Asp | Glu | Met  | His | Leu | Gly |
|     | 1565 |     |     |     |     | 1570 |     |     |     |     | 1575 |     |     |     |
| Leu | Asp  | Leu | Glu | Ile | Gly | Asp  | Val | Pro | Ala | Gln | Ile  | Pro | Pro | Gly |
|     | 1580 |     |     |     |     | 1585 |     |     |     |     | 1590 |     |     |     |
| Val | His  | Val | Val | Gln | Asp | His  | Gln | His | Gly | Val | Ser  | Gly | Ala | Leu |
|     | 1595 |     |     |     |     | 1600 |     |     |     |     | 1605 |     |     |     |
| Gly | Glu  | Phe | Val | Met | Gln | Leu  | Gly | Arg | Glu | Gly | Val  | Lys | Glu | Phe |
|     | 1610 |     |     |     |     | 1615 |     |     |     |     | 1620 |     |     |     |
| Gly | Asp  | Ala | Leu | Val | Thr | Ala  | Gln | Val | Phe | His | Ala  | Leu | Ile | His |
|     | 1625 |     |     |     |     | 1630 |     |     |     |     | 1635 |     |     |     |
| Asp | Asp  | Gly | Asp | Gly | Pro | Val  | Gly | Gly | Gly | Leu | Gly  | Lys | Asp | Val |
|     | 1640 |     |     |     |     | 1645 |     |     |     |     | 1650 |     |     |     |
| Ser | Gly  | Val | Gly | His | Ile | Val  | Val | Val | Val | Leu | Gly  | Glu | Leu | Val |
|     | 1655 |     |     |     |     | 1660 |     |     |     |     | 1665 |     |     |     |
| Ile | Gly  | His | Phe | Asn | Glu | Phe  | Gly | Ala | Glu | Gly | Ala  | Arg | Leu | Gly |
|     | 1670 |     |     |     |     | 1675 |     |     |     |     | 1680 |     |     |     |
| Asp | Glu  | Gly | Ala | Leu | Asp | Pro  | Gly | Gly | Val | Val | Ala  | Leu | Ala | Asp |
|     | 1685 |     |     |     |     | 1690 |     |     |     |     | 1695 |     |     |     |
| Leu | His  | Leu | Pro | Gly | Leu | Glu  | Leu | Gly | Gly | Gly | Asp  | His | Val | His |
|     | 1700 |     |     |     |     | 1705 |     |     |     |     | 1710 |     |     |     |
| Leu | Arg  | Gly | Asp | Glu | Lys | Asn  | Gly | Phe | Arg | Gly | Gly  | Gly | Asp | Glu |
|     | 1715 |     |     |     |     | 1720 |     |     |     |     | 1725 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu | Gly  | Arg | Lys | Gln | Val | Pro  | Glu | Gln | Leu | Gly | Leu  | Ala | Ala | Ala |
|     | 1730 |     |     |     |     | 1735 |     |     |     |     | 1740 |     |     |     |
| Gly | Gly  | Ala | Val | Asp | Asp | Pro  | Asp | Asp | Arg | Leu | Gln  | Val | Val | Val |
|     | 1745 |     |     |     |     | 1750 |     |     |     |     | 1755 |     |     |     |
| Glu | Gly  | Glu | Thr | Ala | Ala | Val  | Leu | Ala | Glu | Glu | Gly  | Gly | His | Leu |
|     | 1760 |     |     |     |     | 1765 |     |     |     |     | 1770 |     |     |     |
| Val | His  | His | Leu | Ala | His | Met  | His | Val | Leu | Ala | His  | Glu | Phe | Arg |
|     | 1775 |     |     |     |     | 1780 |     |     |     |     | 1785 |     |     |     |
| Gln | Glu  | Ala | Leu | Ala | Pro | Gln  | Arg | Glu | Glu | Leu | Leu  | Gln | Arg | Gly |
|     | 1790 |     |     |     |     | 1795 |     |     |     |     | 1800 |     |     |     |
| Glu | Val  | Phe | Gln | Arg | Leu | Glu  | Pro | Val | Gly | His | Gly  | His | Phe | Gly |
|     | 1805 |     |     |     |     | 1810 |     |     |     |     | 1815 |     |     |     |
| Glu | Gly  | Leu | Leu | Gln | Glu | Phe  | Gln | Thr | Val | Pro | Glu  | Leu | Gly | Asp |
|     | 1820 |     |     |     |     | 1825 |     |     |     |     | 1830 |     |     |     |
| Val | Leu  | Gly | Ile | Ser | Ile | Gln  | Gln | Thr | Ser | Ser | Phe  | Arg | Gly | Leu |
|     | 1835 |     |     |     |     | 1840 |     |     |     |     | 1845 |     |     |     |
| Gly | Arg  | Leu | Arg | Glu | Gly | Thr  | Arg | Arg | Trp | Ala | Ser  | Ser | Glu | Ala |
|     | 1850 |     |     |     |     | 1855 |     |     |     |     | 1860 |     |     |     |
| Arg | Val  | Arg | Ser | Phe | Gln | Gly  | Arg | Arg | Val | Arg | Val  | Ser | Val | Val |
|     | 1865 |     |     |     |     | 1870 |     |     |     |     | 1875 |     |     |     |
| Ser | Val  | Thr | Val | Lys | Gly | Cys  | Ala | Pro | Gly | Trp | Ala  | Leu | Ala | Arg |
|     | 1880 |     |     |     |     | 1885 |     |     |     |     | 1890 |     |     |     |
| Val | Arg  | Phe | Arg | Leu | Ile | Arg  | Leu | Val | Glu | Asn | Arg  | Ser | Arg | Ser |
|     | 1895 |     |     |     |     | 1900 |     |     |     |     | 1905 |     |     |     |
| Ala | Pro  | Cys | Ala | Ser | Ala | Arg  | Gln | Leu | Ser | Met | Ser  | Ser | Leu | Ser |
|     | 1910 |     |     |     |     | 1915 |     |     |     |     | 1920 |     |     |     |
| Ala | Ser  | Ala | Ala | Trp | Pro | Leu  | Ala | Arg | Ser | Leu | Pro  | Leu | Glu | Val |
|     | 1925 |     |     |     |     | 1930 |     |     |     |     | 1935 |     |     |     |
| Cys | Pro  | Gln | Thr | Gly | Gln | Arg  | Arg | Asp | Leu | Arg | Ala  | Ser | Leu | Gly |
|     | 1940 |     |     |     |     | 1945 |     |     |     |     | 1950 |     |     |     |
| Ala | Arg  | Lys | Thr | Asp | Ser | Gly  | Ala | Ala | Ser | Ala | Pro  | Gln | Leu | Ala |

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gln  | Thr | Val | Ser | His | Ser | Thr  | Ser | Gln | Val | Arg | Ser  | Gly | Arg | Leu |
| 1970 |     |     |     |     |     | 1975 |     |     |     |     | 1980 |     |     |     |
| Gly  | Ser | Lys | Thr | Arg | Phe | Pro  | Pro | Cys | Phe | Leu | Met  | Arg | Phe | Leu |
| 1985 |     |     |     |     |     | 1990 |     |     |     |     | 1995 |     |     |     |
| Pro  | Leu | Val | Ser | Met | Ser | Ser  | Cys | Pro | Arg | Trp | Val  | Thr | Lys | Arg |
| 2000 |     |     |     |     |     | 2005 |     |     |     |     | 2010 |     |     |     |
| Leu  | Ser | Val | Ser | Pro | Thr | Asp  | Phe | Met | Gly | Arg | Ser  | Ser | Ser | Gly |
| 2015 |     |     |     |     |     | 2020 |     |     |     |     | 2025 |     |     |     |
| Val  | Pro | Arg | Ser | Ser | Ser | Arg  | Asn | Pro | Ala | His | Ser  | Glu | Thr | Lys |
| 2030 |     |     |     |     |     | 2035 |     |     |     |     | 2040 |     |     |     |
| Ala  | Arg | Val | Gln | Ala | Ser | Thr  | Lys | Glu | Ala | Thr | Trp  | Glu | Gly | Arg |
| 2045 |     |     |     |     |     | 2050 |     |     |     |     | 2055 |     |     |     |
| Ser  | Leu | Ser | Thr | Ser | Gly | Ser  | Thr | Phe | Ser | Arg | Val  | Cys | Lys | His |
| 2060 |     |     |     |     |     | 2065 |     |     |     |     | 2070 |     |     |     |
| Met  | Ser | Pro | Ser | Ser | Thr | Ser  | Arg | Lys | Val | Ile | Gly  | Leu | Val | Ala |
| 2075 |     |     |     |     |     | 2080 |     |     |     |     | 2085 |     |     |     |
| Thr  | Pro | Gly | Val | Pro | Ala | Gly  | Gly | Val | Lys | Gly | Ala  | Gly | Pro | Cys |
| 2090 |     |     |     |     |     | 2095 |     |     |     |     | 2100 |     |     |     |
| Ser  | Ser | Ser | Leu | Ser | Ser | Gly  | Ser | Leu | Ser | Arg | Ser  | Ala | Ser | Cys |
| 2105 |     |     |     |     |     | 2110 |     |     |     |     | 2115 |     |     |     |
| Trp  | Gly | Arg | Tyr | Ser | Leu | Ser  | Lys | Ala | Gly | Ile | Thr  | Ser | Ala | Leu |
| 2120 |     |     |     |     |     | 2125 |     |     |     |     | 2130 |     |     |     |
| Arg  | Leu | Ser | Val | Ser | Arg | Asn  | Glu | Glu | Asp | Leu | Ile  | Leu | Thr | Val |
| 2135 |     |     |     |     |     | 2140 |     |     |     |     | 2145 |     |     |     |
| Pro  | Leu | Glu | Thr | Pro | Phe | Met  | Ser | Pro | Ser | Ser | Ile  | Trp | Ser | Glu |
| 2150 |     |     |     |     |     | 2155 |     |     |     |     | 2160 |     |     |     |
| Lys  | Thr | Ile | Phe | Leu | Leu | Ser  | Ser | Leu | Val | Ala | Lys  | Glu | Pro | Arg |
| 2165 |     |     |     |     |     | 2170 |     |     |     |     | 2175 |     |     |     |
| Ala  | Leu | Glu | Arg | Ser | Leu | Ala  | Met | Glu | Arg | Met | Val  | Trp | Phe | Phe |
| 2180 |     |     |     |     |     | 2185 |     |     |     |     | 2190 |     |     |     |

## 368530-7006W01\_SequenceListing\_ST25.txt

Ser Leu Ser Ala Arg Ser Leu Ala Ala Met Leu Ser Cys Thr Tyr  
 2195 2200 2205  
  
 Ser Arg Ala Thr His Phe His Ser Gly Lys Thr Val Val Ser Ser  
 2210 2215 2220  
  
 Ser Gly Thr Ile Leu Thr Arg Gln Pro Arg Leu Cys Arg Val Met  
 2225 2230 2235  
  
 Arg Ser Thr Leu Val Ala Thr Ser Pro Arg Arg Gly Ser Leu Val  
 2240 2245 2250  
  
 Gln Gln Arg Arg Pro Pro Leu Arg Glu Gln Lys Gly Gly Ser Gly  
 2255 2260 2265  
  
 Ser Ser Met Ser Ser Ser Gly Gly Ser Ala Ser Thr Val Lys Met  
 2270 2275 2280  
  
 Pro Gly Arg Ser Ser Gly Ser Lys Leu Met Gln Val Ser Arg Ser  
 2285 2290 2295  
  
 Ser Ser Ala Ala Cys Gln Ser Arg Thr Ala Ser Ala Arg Ser Gly  
 2300 2305 2310  
  
 Leu Arg Gly Val Pro Gln Gly Met Gly Cys Val Ser Ala Glu Ala  
 2315 2320 2325  
  
 Tyr Met Pro Gln Met Ser Thr Arg Gly Ser Ser Arg Thr Pro Met  
 2330 2335 2340  
  
 Val Gly Gln Arg Pro Pro Arg Met Leu Ala Arg Thr Ser Tyr Ser  
 2345 2350 2355  
  
 Ser Cys Glu Gly Ala Arg Ser Pro Val Pro Arg Leu Glu Arg Cys  
 2360 2365 2370  
  
 Gly Phe Ser Ala Arg Thr Ile Trp Arg Lys Met Ala Trp Glu Leu  
 2375 2380 2385  
  
 Glu Glu Met Val Gly Leu Trp Lys Met Leu Lys Trp Ala Trp Gly  
 2390 2395 2400  
  
 Arg Pro Thr Glu Ser Leu Met Lys Trp Ala Glu Ser Cys Ser Leu  
 2405 2410 2415  
  
 Ala Thr Ser Ser Ala Val Thr Arg Thr Ser Arg Ala Gln Ser Arg  
 2420 2425 2430

368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val | Ser  | Trp | Met | Met | Ser | Tyr  | Leu | Ser | Trp | Pro | Phe  | Cys | Phe | His |
|     | 2435 |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |
| Ser | Ser  | Arg | Leu | Arg | Arg | Asn  | Ser | Ser | Arg | Ser | Phe  | Gln | Tyr | Ser |
|     | 2450 |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |
| Ser | Arg  | Gly | Asn | Pro | Ser | Ser  | Ala | Arg | Glu | Pro | Thr  | Met | Asn | Trp |
|     | 2465 |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |
| Leu | Thr  | Ala | Leu | Ala | Gln | Gln  | Pro | Phe | Ser | Thr | Gly  | Arg | Ala | Ala |
|     | 2480 |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Cys | Ala  | Ala | Leu | Arg | Arg | Glu  | Val | Trp | Val | Arg | Ala  | Lys | Val | Ser |
|     | 2495 |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Arg | Thr  | Met | Thr | Leu | Arg | Asn  | Trp | Cys | Leu | Lys | Ser  | Arg | Ser | Ser |
|     | 2510 |     |     |     |     | 2515 |     |     |     |     | 2520 |     |     |     |
| Gln | Pro  | Pro | Cys | Ser | Gln | Ser  | Trp | Lys | Ser | Val | Arg  | Phe | Leu | Ala |
|     | 2525 |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Gly | Leu  | Gly | Lys | Ala | Lys | Val  | Thr | Ser | Leu | Lys | Arg  | Ile | Leu | Pro |
|     | 2540 |     |     |     |     | 2545 |     |     |     |     | 2550 |     |     |     |
| Ala | Arg  | Gly | Met | Lys | Leu | Arg  | Val | Met | Arg | Lys | Gly  | Trp | Gly | Thr |
|     | 2555 |     |     |     |     | 2560 |     |     |     |     | 2565 |     |     |     |
| Ser | Ala  | Arg | Leu | Leu | Met | Thr  | Trp | Ala | Ala | Arg | Thr  | Ile | Ser | Ser |
|     | 2570 |     |     |     |     | 2575 |     |     |     |     | 2580 |     |     |     |
| Lys | Pro  | Leu | Met | Leu | Cys | Pro  | Thr | Met | Ser | Ser | Thr  | Asn | Arg | Gly |
|     | 2585 |     |     |     |     | 2590 |     |     |     |     | 2595 |     |     |     |
| Arg | Pro  | Leu | Thr | Trp | Gly | Ser  | Phe | Leu | Ser | Ser | Ser  | Val | Ser | Ser |
|     | 2600 |     |     |     |     | 2605 |     |     |     |     | 2610 |     |     |     |
| Ala | Gly  | Ser | Leu | Ser | Pro | Cys  | Cys | Ser | Arg | Ala | Gln  | Ser | Ala | Thr |
|     | 2615 |     |     |     |     | 2620 |     |     |     |     | 2625 |     |     |     |
| Trp | Gly  | Leu | Ala | Leu | Arg | Lys  | Glu | Val | Gln | Arg | Ser  | Thr | Ala | Arg |
|     | 2630 |     |     |     |     | 2635 |     |     |     |     | 2640 |     |     |     |
| Ala | Val  | Cys | Lys | Arg | Ser | Arg  | Tyr | Arg | Asn | Cys | Trp  | Pro | Thr | Ala |
|     | 2645 |     |     |     |     | 2650 |     |     |     |     | 2655 |     |     |     |
| Ile | Phe  | Ser | Gly | Val | Thr | Gln  | Lys | Val | Arg | Gly | Ser  | Pro | Cys | Gln |
|     | 2660 |     |     |     |     | 2665 |     |     |     |     | 2670 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Ser | His | Leu | Ser | Trp | Arg  | Ala | Arg | Ser | Trp | Ala  | Ser | Ser | Thr |
| 2675 |     |     |     |     |     | 2680 |     |     |     |     | 2685 |     |     |     |
| Ser  | Gly | Gly | Ser | Pro | Glu | Ser  | Phe | Met | Thr | Ser | Met  | Lys | Gly | Thr |
| 2690 |     |     |     |     |     | 2695 |     |     |     |     | 2700 |     |     |     |
| Ser  | Cys | Leu | Pro | Lys | Asp | Pro  | Ile | Gln | Val | Val | Ser  | Thr | Ser | Val |
| 2705 |     |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |
| Arg  | Lys | Ser | Leu | Ser | Val | Arg  | Gly | Cys | Glu | Pro | Met  | Gly | Lys | Asn |
| 2720 |     |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |
| Trp  | Ile | Ser | Cys | His | Gln | Leu  | Glu | Glu | Trp | Leu | Leu  | Met | Trp | Lys |
| 2735 |     |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |
| Lys  | Cys | Arg | Arg | Arg | Ala | Glu  | His | Ser | Cys | Leu | Cys  | Leu | Tyr | Lys |
| 2750 |     |     |     |     |     | 2755 |     |     |     |     | 2760 |     |     |     |
| Arg  | Pro | Gln | Cys | Ser | Gln | Arg  | Cys | Thr | Gly | Cys | Thr  | Cys | Cys | Thr |
| 2765 |     |     |     |     |     | 2770 |     |     |     |     | 2775 |     |     |     |
| Ser  | Cys | Thr | Trp | Val | Pro | Leu  | Thr | Arg | Asn | Phe | Ser  | Gly | Gln | Trp |
| 2780 |     |     |     |     |     | 2785 |     |     |     |     | 2790 |     |     |     |
| Ser  | Ala | Gly | Gly | Cys | Ile | Trp  | Cys | Cys | Thr | Thr | Ser  | Trp | Pro | Ser |
| 2795 |     |     |     |     |     | 2800 |     |     |     |     | 2805 |     |     |     |
| Ala  | Trp | Pro | Ser | Ser | Ala | Ser  | Met | Val | Val | Met | Leu  | Thr | Ser | Pro |
| 2810 |     |     |     |     |     | 2815 |     |     |     |     | 2820 |     |     |     |
| Arg  | Gly | Arg | Gln | Val | Gln | Thr  | Ser | Ala | Arg | Thr | Gly  | Arg | Arg | Ala |
| 2825 |     |     |     |     |     | 2830 |     |     |     |     | 2835 |     |     |     |
| Arg  | Thr | Arg | Ala | Arg | Arg | Pro  | Glu | Leu | Ser | Arg | Val  | Leu | Arg | Arg |
| 2840 |     |     |     |     |     | 2845 |     |     |     |     | 2850 |     |     |     |
| Cys  | Gly | Val | Arg | Ser | Val | Gly  | Ser | Gly | Gly | Ala | Arg  | Leu | Thr | Cys |
| 2855 |     |     |     |     |     | 2860 |     |     |     |     | 2865 |     |     |     |
| Arg  | Ser | Phe | Ser | Arg | Ala | Arg  | Gly | Arg | Ser | Arg | Trp  | Tyr | Leu | Ile |
| 2870 |     |     |     |     |     | 2875 |     |     |     |     | 2880 |     |     |     |
| Ser  | Thr | Ala | Pro | Leu | Val | Ala  | Thr | Ser | Thr | Ala | Cys  | Arg | Val | Pro |
| 2885 |     |     |     |     |     | 2890 |     |     |     |     | 2895 |     |     |     |
| Cys  | Pro | Trp | Gly | Ala | Thr | Thr  | Val | Pro | Arg | Phe | Phe  | Leu | Gly | Ala |

2900

2905

2910

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Ser | Met | Pro | Val | Arg | Ser  | Gly | Gly | Glu | Asp | Ala  | Arg | Arg | Ala |
| 2915 |     |     |     |     |     | 2920 |     |     |     |     | 2925 |     |     |     |
| Ala  | Gly | Ala | Ala | Arg | Asp | Pro  | Glu | Ala | Gly | Ala | Ala  | Gly | Ala | Arg |
| 2930 |     |     |     |     |     | 2935 |     |     |     |     | 2940 |     |     |     |
| Arg  | Arg | Arg | Ala | Arg | Ala | Gly  | Ser | Gly | Thr | Ala | Pro  | Gly | Glu | Asp |
| 2945 |     |     |     |     |     | 2950 |     |     |     |     | 2955 |     |     |     |
| Trp  | Arg | Glu | Arg | Arg | Arg | Asp  | Gly | Arg | Pro | Gly | Ser  | Asp | Ala | Ser |
| 2960 |     |     |     |     |     | 2965 |     |     |     |     | 2970 |     |     |     |
| Gly  | Arg | Pro | Arg | Asp | Pro | Val  | Thr | Lys | Arg | Val | Arg  | Gln | Asn | Gln |
| 2975 |     |     |     |     |     | 2980 |     |     |     |     | 2985 |     |     |     |
| Ser  | Arg | Tyr | Arg | Arg | Arg | Pro  | Ala | Ala | Gly | Ser | Leu  | Ala | Arg | Arg |
| 2990 |     |     |     |     |     | 2995 |     |     |     |     | 3000 |     |     |     |
| Pro  | Ser | Cys | Pro | Gly | Arg | Arg  | Ser | Arg | Ser | Thr | Ala  | Arg | Ser | Pro |
| 3005 |     |     |     |     |     | 3010 |     |     |     |     | 3015 |     |     |     |
| Pro  | Pro | Glu | Gly | Leu | Arg | Gly  | Arg | Arg | Ala | Arg | Arg  | Trp | Pro | Arg |
| 3020 |     |     |     |     |     | 3025 |     |     |     |     | 3030 |     |     |     |
| Gly  | Arg | Trp | Arg | Cys | Gly | Pro  | Ala | Ala | Arg | Arg | Arg  | Ser | Cys | Arg |
| 3035 |     |     |     |     |     | 3040 |     |     |     |     | 3045 |     |     |     |
| Pro  | Arg | Ser | Arg | Arg | Gly | Cys  | Arg | Pro | Arg | Leu | Arg  | Arg | Gly | Arg |
| 3050 |     |     |     |     |     | 3055 |     |     |     |     | 3060 |     |     |     |
| Ala  | Arg | Ala | Pro | Pro | Gly | Arg  | Gly | Ala | Arg | Arg | Gly  | Ala | Arg | Pro |
| 3065 |     |     |     |     |     | 3070 |     |     |     |     | 3075 |     |     |     |
| Arg  | Ser | Cys | Arg | Gly | Ala | Gly  | Arg | Gly | Ser | Ala | Trp  | Trp | Arg | Cys |
| 3080 |     |     |     |     |     | 3085 |     |     |     |     | 3090 |     |     |     |
| Ala  | Arg | Arg | Arg | Ser | Thr | Ser  | Ser | Gly | Gly | Ala | Ala  | Ser | Arg | Arg |
| 3095 |     |     |     |     |     | 3100 |     |     |     |     | 3105 |     |     |     |
| Arg  | Pro | Gly | Leu | Pro | Ser | Ala  | Pro | Trp | Pro | Arg | Arg  | Ser | Pro | Arg |
| 3110 |     |     |     |     |     | 3115 |     |     |     |     | 3120 |     |     |     |
| Arg  | Ser | Lys | Thr | Gly | Ser | Cys  | Ala | Pro | Arg | Arg | Ser  | Thr | Pro | Pro |
| 3125 |     |     |     |     |     | 3130 |     |     |     |     | 3135 |     |     |     |



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Pro Glu Asp Gly Ala Gln Arg Trp Trp Arg Ala Pro Arg Ala Arg  
 3140 3145 3150  
 Arg Pro Arg Gly Ala Pro Leu Leu Pro Ser Leu Pro Pro Pro Leu  
 3155 3160 3165  
 Thr Ser Leu Leu Leu Pro Pro Gln Glu Ala Ala Ala Gly Glu Gly  
 3170 3175 3180  
 Pro Cys Val Ala Gly Gly Ala Arg Ala Asp Gly Arg Ser Ala Arg  
 3185 3190 3195  
 Trp Ser Pro Arg Ala Gly Asp Ala Trp Ser Arg Arg Arg Ala Arg  
 3200 3205 3210  
 Pro Arg Gly Ala Ala Ala Arg Arg Arg Arg Ala Ser Pro Gly Gly  
 3215 3220 3225  
 Arg Arg Gly Gly Leu Arg Trp Ala Gly Arg Gly Arg Arg Cys Ile  
 3230 3235 3240  
 Leu Ser Ile Gly Pro Gly Leu Arg Ala Arg Thr Ala Ser Arg Asp  
 3245 3250 3255  
 Pro Arg Asp Pro Lys Thr Ala Glu Arg Arg Leu Arg Ala Ser Arg  
 3260 3265 3270  
 Ser Arg Lys Val Gly Ala Arg Phe Leu Val Leu Arg Gly Phe Arg  
 3275 3280 3285  
 Glu Ala Gly Gly Arg Cys Cys Trp Ser Ser Arg Arg Ser Asp Gly  
 3290 3295 3300  
 Gly Trp Trp Arg Gly Ala Pro Gly Pro Trp Ala Arg Leu Ala Gly  
 3305 3310 3315  
 Cys Ala Asp Gly Arg Pro Cys Pro Arg Arg Gly Pro Asp Thr Trp  
 3320 3325 3330  
 Arg Gly Pro Cys Ser Ser Pro Ala Ala Ala Pro Arg Ala Pro Pro  
 3335 3340 3345  
 Pro Arg Pro Arg Gly Arg Ala Cys Ala Ala Arg Thr Arg Ala Gly  
 3350 3355 3360  
 Ala Gly Arg Ala Pro Gly Arg Arg Arg Arg Ala Arg Arg Gly Trp  
 3365 3370 3375

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Ala  | Val | Ser | Gly | Gly | Trp  | Ser | Gly | Ser | Arg | Arg  | Ser | Arg | Arg |
|     | 3380 |     |     |     |     | 3385 |     |     |     |     | 3390 |     |     |     |
| Ser | Gly  | Gly | Arg | Leu | Arg | Cys  | Trp | Tyr | Arg | Ser | Ser  | Trp | Pro | Arg |
|     | 3395 |     |     |     |     | 3400 |     |     |     |     | 3405 |     |     |     |
| Thr | Ser  | Arg | Ser | Gly | Gly | Arg  | Val | Ala | Arg | Ala | Arg  | Gly | Thr | Gly |
|     | 3410 |     |     |     |     | 3415 |     |     |     |     | 3420 |     |     |     |
| Ala | Ser  | Arg | Arg | Ala | Cys | Arg  | Arg | Cys | Ser | Arg | Cys  | Arg | Cys | Ala |
|     | 3425 |     |     |     |     | 3430 |     |     |     |     | 3435 |     |     |     |
| Arg | Gly  | Thr | Gly | Ile | Arg | Arg  | Gly | Ser | Ala | Ala | Ala  | Ala | Gly | Gly |
|     | 3440 |     |     |     |     | 3445 |     |     |     |     | 3450 |     |     |     |
| Arg | Ala  | Ala | Ile | Ala | Arg | Trp  | Arg | Gly | Arg | Arg | Ala  | Arg | Gly | Pro |
|     | 3455 |     |     |     |     | 3460 |     |     |     |     | 3465 |     |     |     |
| Arg | Ala  | Gly | Gly | Gly | Ser | Arg  | Arg | Cys | Thr | Trp | Thr  | Ser | Arg | Cys |
|     | 3470 |     |     |     |     | 3475 |     |     |     |     | 3480 |     |     |     |
| Arg | Arg  | Arg | Trp | Trp | Arg | Arg  | Ala | Gly | Thr | Arg | Gly  | Arg | Gly | Ser |
|     | 3485 |     |     |     |     | 3490 |     |     |     |     | 3495 |     |     |     |
| Arg | Cys  | Cys | Ala | Ala | Ala | Gly  | Ser | Ser | Ser | Trp | Trp  | Pro | Arg | Ser |
|     | 3500 |     |     |     |     | 3505 |     |     |     |     | 3510 |     |     |     |
| Gly | Pro  | Gly | Ala | Arg | Ser | Arg  | Gly | Cys | Ser | Arg | His  | Thr | Gly | Lys |
|     | 3515 |     |     |     |     | 3520 |     |     |     |     | 3525 |     |     |     |
| Asn | Glu  | Ser | Gly | Gln | Arg | Leu  | Asp | Ser | Val | Ala | Trp  | Arg | Leu | Ser |
|     | 3530 |     |     |     |     | 3535 |     |     |     |     | 3540 |     |     |     |
| Glu | Arg  | Val | Gly | Leu | Arg | Val  | Tyr | Pro | Gly | Ser | Asn  | Leu | Glu | Ser |
|     | 3545 |     |     |     |     | 3550 |     |     |     |     | 3555 |     |     |     |
| Gly | Trp  | Ser | Arg | Ser | Arg | Gly  | Thr | Gly | Thr | Pro | Val  | Ser | Thr | Gln |
|     | 3560 |     |     |     |     | 3565 |     |     |     |     | 3570 |     |     |     |
| Ala | Cys  | Arg | Asn | Leu | Gln | Asp  | Thr | Glu | Ala | Gly | Arg  | Phe | Leu | Ala |
|     | 3575 |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
| Leu | Val  | Ala | Gly | His | Glu | Lys  | Leu | Val | Ser | Ala | Glu  | Ser | Asp | Arg |
|     | 3590 |     |     |     |     | 3595 |     |     |     |     | 3600 |     |     |     |
| Pro | Arg  | Trp | Leu | Ala | Ala | Val  | Val | Trp | Arg | Lys | Asn  | Arg | Gln | Gly |
|     | 3605 |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Cys  | Val | Ala | Val | Cys | Pro | Gly  | Ser | Ser | Leu | Ser | Ala  | Arg | Arg | Arg |
| 3620 |     |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
| Pro  | Asp | Ser | Ala | Ala | Asn | Val  | Gly | Val | Ala | Ala | Pro  | Ser | Phe | Pro |
| 3635 |     |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
| Arg  | Pro | Leu | Ser | Gln | Pro | Thr  | Ser | Pro | Val | Thr | Glu  | Arg | Ala | Pro |
| 3650 |     |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
| Leu  | Phe | Leu | Val | Phe | Leu | Pro  | Asp | Ala | Ser | Arg | Thr  | Ala | Ala | Asp |
| 3665 |     |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
| Ala  | Pro | Pro | Pro | Ser | Thr | Ser  | Thr | Ala | Pro | Thr | Ala  | Ala | Ala | Ala |
| 3680 |     |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |
| Ala  | Thr | Ala | Gly | Ala | Ser | Ala  | Pro | Ala | Pro | Ala | Ala  | Ala | Ser | His |
| 3695 |     |     |     |     |     | 3700 |     |     |     |     | 3705 |     |     |     |
| Tyr  | Arg | Gly | Gly | Arg | Arg | Glu  | Arg | Ser | Arg | Arg | Ser  | Val | Pro | Gly |
| 3710 |     |     |     |     |     | 3715 |     |     |     |     | 3720 |     |     |     |
| Leu  | Gly | Arg | Gly | Arg | Gly | Ala  | Gly | Ala | Ala | Gly | Gly  | Val | Val | Ala |
| 3725 |     |     |     |     |     | 3730 |     |     |     |     | 3735 |     |     |     |
| Gly  | Ala | Ala | Pro | Ala | Arg | Ala  | Asp | Glu | Lys | Gly | Arg  | Ser | Arg | Gly |
| 3740 |     |     |     |     |     | 3745 |     |     |     |     | 3750 |     |     |     |
| Leu  | Arg | Ala | Gln | Ala | Glu | Pro  | Val | Gln | Arg | Gln | Glu  | Arg | Arg | Gly |
| 3755 |     |     |     |     |     | 3760 |     |     |     |     | 3765 |     |     |     |
| Ala  | Arg | Gly | Asp | Ala | Arg | Leu  | Pro | Leu | Pro | Arg | Gly  | Ala | Gly | Ala |
| 3770 |     |     |     |     |     | 3775 |     |     |     |     | 3780 |     |     |     |
| Ala  | Ala | Arg | Pro | Gly | Pro | Lys  | Ala | Gly | Ala | Glu | Gly  | Arg | Gly | Phe |
| 3785 |     |     |     |     |     | 3790 |     |     |     |     | 3795 |     |     |     |
| Arg  | Gly | Gly | Arg | Ala | Asp | Gly  | Asp | Gln | Pro | Arg | Ala  | Arg | Ala | Arg |
| 3800 |     |     |     |     |     | 3805 |     |     |     |     | 3810 |     |     |     |
| Gly  | Arg | Gly | Gln | Pro | Gly | His  | Gly | Val | Arg | Ala | Asp  | Arg | Glu | Gly |
| 3815 |     |     |     |     |     | 3820 |     |     |     |     | 3825 |     |     |     |
| Gly  | Glu | Gln | Leu | Pro | Lys | Ile  | Leu | Gln | Gln | Pro | Arg  | Ala | His | Ala |
| 3830 |     |     |     |     |     | 3835 |     |     |     |     | 3840 |     |     |     |
| Asp  | Arg | Ala | Arg | Gly | Gly | Asp  | Pro | Gly | Pro | Asp | Ala  | Pro | Val | Gly |

3845

3850

3855

Pro Ala Gly Gly His Arg Ala Glu Pro His Glu Gln Ala Ala Asp  
 3860 3865 3870  
 Gly Ala Ala Val Ser Gly Gly Ala Ala Gln Ser Gly Gln Arg Asp  
 3875 3880 3885  
 Val Gln Gly Gly Ala Ala Glu Tyr His Arg Ala Arg Gly Pro Leu  
 3890 3895 3900  
 Ala Pro Gly Pro Gly Glu His Ser Ala Glu His Arg Gly Ala Gly  
 3905 3910 3915  
 Ala Arg Ala Ala Ala Val Arg Glu Ala Gly Gly Tyr Gln Leu Leu  
 3920 3925 3930  
 Gly Ala Glu Pro Gly Gln Val Leu Arg Glu Asp Leu Gln Asp Pro  
 3935 3940 3945  
 Val Arg Ala His Arg Gln Gly Gly Glu Asp Arg Arg Val Leu His  
 3950 3955 3960  
 Ala His Asp Pro Glu Ser Ala Asp Pro Glu Arg Arg Ser Gly Gly  
 3965 3970 3975  
 Val Pro Gln Arg Gln Asp Ala Pro Arg Gly Glu Arg Gln Pro Pro  
 3980 3985 3990  
 Ala Arg Ala Glu Arg Pro Gly Ala Asp Ala Gln Pro Ala Ala Gly  
 3995 4000 4005  
 Pro Asp Arg Gly Arg Asp Arg Gly Gly Glu Leu Leu His Gly Arg  
 4010 4015 4020  
 Gly Pro Ala Leu Ala Ala Gln Pro Pro Gly Leu Gly Ser Cys Arg  
 4025 4030 4035  
 Arg Phe Pro Leu Arg Gly Gly Gly Gly Arg Gly Gly Gly Gly Arg  
 4040 4045 4050  
 Val Pro Gly Arg Leu Met Ala Arg Pro Tyr Phe Cys Met Gln Gln  
 4055 4060 4065  
 Gln Pro Pro Pro Pro Asp Pro Ala Met Arg Ala Ala Leu Gln Ser  
 4070 4075 4080

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Gln Pro Ser Gly Ile Asn Ser Ser Asp Asp Trp Thr Gln Ala Met  
 4085 4090 4095  
  
 Gln Arg Ile Met Ala Leu Thr Thr Arg Asn Pro Glu Ala Phe Arg  
 4100 4105 4110  
  
 Gln Gln Pro Gln Ala Asn Arg Leu Ser Ala Ile Leu Glu Ala Val  
 4115 4120 4125  
  
 Val Pro Ser Arg Ser Asn Pro Thr His Glu Lys Val Leu Ala Ile  
 4130 4135 4140  
  
 Val Asn Ala Leu Val Glu Asn Lys Ala Ile Arg Gly Asp Glu Ala  
 4145 4150 4155  
  
 Gly Leu Val Tyr Asn Ala Leu Leu Glu Arg Val Ala Arg Tyr Asn  
 4160 4165 4170  
  
 Ser Thr Asn Val Gln Thr Asn Leu Asp Arg Met Val Thr Asp Val  
 4175 4180 4185  
  
 Arg Glu Ala Val Ser Gln Arg Glu Arg Phe His Arg Glu Ser Asn  
 4190 4195 4200  
  
 Leu Gly Ser Met Val Ala Leu Asn Ala Phe Leu Ser Thr Gln Pro  
 4205 4210 4215  
  
 Ala Asn Val Pro Arg Gly Gln Glu Asp Tyr Thr Asn Phe Ile Ser  
 4220 4225 4230  
  
 Ala Leu Arg Leu Met Val Ala Glu Val Pro Gln Ser Glu Val Tyr  
 4235 4240 4245  
  
 Gln Ser Gly Pro Asp Tyr Phe Phe Gln Thr Ser Arg Gln Gly Leu  
 4250 4255 4260  
  
 Gln Thr Val Asn Leu Ser Gln Ala Phe Lys Asn Leu Gln Gly Leu  
 4265 4270 4275  
  
 Trp Gly Val Gln Ala Pro Val Gly Asp Arg Ala Thr Val Ser Ser  
 4280 4285 4290  
  
 Leu Leu Thr Pro Asn Ser Arg Leu Leu Leu Leu Leu Val Ala Pro  
 4295 4300 4305  
  
 Phe Thr Asp Ser Gly Ser Val Ser Arg Asp Ser Tyr Leu Gly Tyr  
 4310 4315 4320

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Leu Leu Asn Leu Tyr Arg Glu Ala Ile Gly Gln Ala His Val Asp  
 4325 4330 4335  
 Glu Gln Thr Tyr Gln Glu Ile Thr His Val Ser Arg Ala Leu Gly  
 4340 4345 4350  
 Gln Glu Asp Pro Gly Asn Leu Glu Ala Thr Leu Asn Phe Leu Leu  
 4355 4360 4365  
 Thr Asn Arg Ser Gln Lys Ile Pro Pro Gln Tyr Ala Leu Ser Thr  
 4370 4375 4380  
 Glu Glu Glu Arg Ile Leu Arg Tyr Val Gln Gln Ser Val Gly Leu  
 4385 4390 4395  
 Phe Leu Met Gln Glu Gly Ala Thr Pro Ser Ala Ala Leu Asp Met  
 4400 4405 4410  
 Thr Ala Arg Asn Met Glu Pro Ser Met Tyr Ala Arg Asn Arg Pro  
 4415 4420 4425  
 Phe Ile Asn Lys Leu Met Asp Tyr Leu His Arg Ala Ala Ala Met  
 4430 4435 4440  
 Asn Ser Asp Tyr Phe Thr Asn Ala Ile Leu Asn Pro His Trp Leu  
 4445 4450 4455  
 Pro Pro Pro Gly Phe Tyr Thr Gly Glu Tyr Asp Met Pro Asp Pro  
 4460 4465 4470  
 Asn Asp Gly Phe Leu Trp Asp Asp Val Asp Ser Ser Val Phe Ser  
 4475 4480 4485  
 Pro Arg Pro Ala Thr Thr Val Trp Lys Lys Glu Gly Gly Asp Arg  
 4490 4495 4500  
 Arg Pro Ser Ser Ala Leu Ser Gly Arg Ala Gly Ala Ala Ala Ala  
 4505 4510 4515  
 Val Pro Glu Ala Ala Ser Pro Phe Pro Ser Leu Pro Phe Ser Leu  
 4520 4525 4530  
 Asn Ser Val Arg Ser Ser Glu Leu Gly Arg Leu Thr Arg Pro Arg  
 4535 4540 4545  
 Leu Leu Gly Glu Glu Glu Tyr Leu Asn Asp Ser Leu Leu Arg Pro  
 4550 4555 4560

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Glu Arg Glu Lys Asn Phe Pro Asn Asn Gly Ile Glu Ser Leu Val  
4565 4570 4575

Asp Lys Met Ser Arg Trp Lys Thr Tyr Ala His Glu His Arg Asp  
4580 4585 4590

Glu Pro Arg Ala Ser Ser Ser Ala Gly Thr Arg Arg Arg Gln Arg  
4595 4600 4605

His Asp Arg Gln Arg Gly Leu Val Trp Asp Asp Glu Asp Ser Ala  
4610 4615 4620

Asp Asp Ser Ser Val Leu Asp Leu Gly Gly Ser Gly Gly Gly Asn  
4625 4630 4635

Pro Phe Ala His Leu Arg Pro Arg Ile Gly Arg Leu Met Glu Ser  
4640 4645 4650

Glu Lys Ile Lys Asn Gly Thr His Gln Gly His Gly Asp Gln Arg  
4655 4660 4665

Ala Phe Phe Ser Val Val Cys Ser Ser Met Met Arg Arg Val Tyr  
4670 4675 4680

Pro Glu Gly Pro Pro Pro Ser Tyr Glu Ser Val Met Gln Gln Ala  
4685 4690 4695

Val Ala Ala Ala Met Gln Pro Pro Leu Glu Ala Pro Tyr Val Pro  
4700 4705 4710

Pro Arg Tyr Leu Ala Pro Thr Glu Gly Arg Asn Ser Ile Arg Tyr  
4715 4720 4725

Ser Glu Leu Ala Pro Leu Tyr Asp Thr Thr Arg Leu Tyr Leu Val  
4730 4735 4740

Asp Asn Lys Ser Ala Asp Ile Ala Ser Leu Asn Tyr Gln Asn Asp  
4745 4750 4755

His Ser Asn Phe Leu Thr Thr Val Val Gln Asn Asn Asp Phe Thr  
4760 4765 4770

Pro Thr Glu Ala Ser Thr Gln Thr Ile Asn Phe Asp Glu Arg Ser  
4775 4780 4785

Arg Trp Gly Gly Gln Leu Lys Thr Ile Met His Thr Asn Met Pro

4790

4795

4800

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asn | Val  | Asn | Glu | Phe | Met | Tyr  | Ser | Asn | Lys | Phe | Lys  | Ala | Arg | Val |
|     | 4805 |     |     |     |     | 4810 |     |     |     |     | 4815 |     |     |     |
| Met | Val  | Ser | Arg | Lys | Thr | Pro  | Asn | Gly | Val | Ala | Val  | Asp | Glu | Asn |
|     | 4820 |     |     |     |     | 4825 |     |     |     |     | 4830 |     |     |     |
| Tyr | Asp  | Gly | Ser | Gln | Asp | Glu  | Leu | Thr | Tyr | Glu | Trp  | Val | Glu | Phe |
|     | 4835 |     |     |     |     | 4840 |     |     |     |     | 4845 |     |     |     |
| Glu | Leu  | Pro | Glu | Gly | Asn | Phe  | Ser | Val | Thr | Met | Thr  | Ile | Asp | Leu |
|     | 4850 |     |     |     |     | 4855 |     |     |     |     | 4860 |     |     |     |
| Met | Asn  | Asn | Ala | Ile | Ile | Asp  | Asn | Tyr | Leu | Ala | Val  | Gly | Arg | Gln |
|     | 4865 |     |     |     |     | 4870 |     |     |     |     | 4875 |     |     |     |
| Asn | Gly  | Val | Leu | Glu | Ser | Asp  | Ile | Gly | Val | Lys | Phe  | Asp | Thr | Arg |
|     | 4880 |     |     |     |     | 4885 |     |     |     |     | 4890 |     |     |     |
| Asn | Phe  | Arg | Leu | Gly | Trp | Asp  | Pro | Val | Thr | Glu | Leu  | Val | Met | Pro |
|     | 4895 |     |     |     |     | 4900 |     |     |     |     | 4905 |     |     |     |
| Gly | Val  | Tyr | Thr | Asn | Glu | Ala  | Phe | His | Pro | Asp | Ile  | Val | Leu | Leu |
|     | 4910 |     |     |     |     | 4915 |     |     |     |     | 4920 |     |     |     |
| Pro | Gly  | Cys | Gly | Val | Asp | Phe  | Thr | Glu | Ser | Arg | Leu  | Ser | Asn | Leu |
|     | 4925 |     |     |     |     | 4930 |     |     |     |     | 4935 |     |     |     |
| Leu | Gly  | Ile | Arg | Lys | Arg | Gln  | Pro | Phe | Gln | Glu | Gly  | Phe | Gln | Ile |
|     | 4940 |     |     |     |     | 4945 |     |     |     |     | 4950 |     |     |     |
| Leu | Tyr  | Glu | Asp | Leu | Glu | Gly  | Gly | Asn | Ile | Pro | Ala  | Leu | Leu | Asp |
|     | 4955 |     |     |     |     | 4960 |     |     |     |     | 4965 |     |     |     |
| Val | Glu  | Ala | Tyr | Glu | Lys | Ser  | Lys | Glu | Glu | Ala | Ala  | Ala | Ala | Ala |
|     | 4970 |     |     |     |     | 4975 |     |     |     |     | 4980 |     |     |     |
| Thr | Ala  | Ala | Val | Ala | Thr | Ala  | Ser | Thr | Glu | Val | Arg  | Gly | Asp | Asn |
|     | 4985 |     |     |     |     | 4990 |     |     |     |     | 4995 |     |     |     |
| Phe | Ala  | Ser | Ala | Ala | Ala | Val  | Ala | Glu | Ala | Ala | Glu  | Thr | Glu | Ser |
|     | 5000 |     |     |     |     | 5005 |     |     |     |     | 5010 |     |     |     |
| Lys | Ile  | Val | Ile | Gln | Pro | Val  | Glu | Lys | Asp | Ser | Lys  | Asp | Arg | Ser |
|     | 5015 |     |     |     |     | 5020 |     |     |     |     | 5025 |     |     |     |



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Tyr Asn Val Leu Ala Asp Lys Lys Asn Thr Ala Tyr Arg Ser Trp  
 5030 5035 5040  
 Tyr Leu Ala Tyr Asn Tyr Gly Asp Pro Glu Lys Gly Val Arg Ser  
 5045 5050 5055  
 Trp Thr Leu Leu Thr Thr Ser Asp Val Thr Cys Gly Val Glu Gln  
 5060 5065 5070  
 Val Tyr Trp Ser Leu Pro Asp Met Met Gln Asp Pro Val Thr Phe  
 5075 5080 5085  
 Arg Ser Thr Arg Gln Val Ser Asn Tyr Pro Val Val Gly Ala Glu  
 5090 5095 5100  
 Leu Leu Pro Val Tyr Ser Lys Ser Phe Phe Asn Glu Gln Ala Val  
 5105 5110 5115  
 Tyr Ser Gln Gln Leu Arg Ala Phe Thr Ser Leu Thr His Val Phe  
 5120 5125 5130  
 Asn Arg Phe Pro Glu Asn Gln Ile Leu Val Arg Pro Pro Ala Pro  
 5135 5140 5145  
 Thr Ile Thr Thr Val Ser Glu Asn Val Pro Ala Leu Thr Asp His  
 5150 5155 5160  
 Gly Thr Leu Pro Leu Arg Ser Ser Ile Arg Gly Val Gln Arg Val  
 5165 5170 5175  
 Thr Val Thr Asp Ala Arg Arg Arg Thr Cys Pro Tyr Val Tyr Lys  
 5180 5185 5190  
 Ala Leu Gly Val Val Ala Pro Arg Val Leu Ser Ser Arg Thr Phe  
 5195 5200 5205  
 Lys Met Ser Ile Leu Ile Ser Pro Ser Asn Asn Thr Gly Trp Gly  
 5210 5215 5220  
 Leu Arg Ala Pro Ser Lys Met Tyr Gly Gly Ala Arg Gln Arg Ser  
 5225 5230 5235  
 Thr Gln His Pro Val Arg Val Arg Gly His Phe Arg Ala Pro Trp  
 5240 5245 5250  
 Gly Ala Leu Lys Gly Arg Val Arg Ser Arg Thr Thr Val Asp Asp  
 5255 5260 5265

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val | Ile  | Asp | Gln | Val | Val | Ala  | Asp | Ala | Arg | Asn | Tyr  | Thr | Pro | Ala |
|     | 5270 |     |     |     |     | 5275 |     |     |     |     | 5280 |     |     |     |
| Ala | Ala  | Pro | Ala | Ser | Thr | Val  | Asp | Ala | Val | Ile | Asp  | Ser | Val | Val |
|     | 5285 |     |     |     |     | 5290 |     |     |     |     | 5295 |     |     |     |
| Ala | Asp  | Ala | Arg | Arg | Tyr | Ala  | Arg | Ala | Lys | Ser | Arg  | Arg | Arg | Arg |
|     | 5300 |     |     |     |     | 5305 |     |     |     |     | 5310 |     |     |     |
| Ile | Ala  | Arg | Arg | His | Arg | Ser  | Thr | Pro | Ala | Met | Arg  | Ala | Ala | Arg |
|     | 5315 |     |     |     |     | 5320 |     |     |     |     | 5325 |     |     |     |
| Ala | Leu  | Leu | Arg | Arg | Ala | Arg  | Arg | Thr | Gly | Arg | Arg  | Ala | Met | Leu |
|     | 5330 |     |     |     |     | 5335 |     |     |     |     | 5340 |     |     |     |
| Arg | Ala  | Ala | Arg | Arg | Ala | Ala  | Ser | Gly | Ser | Ser | Ser  | Ala | Gly | Arg |
|     | 5345 |     |     |     |     | 5350 |     |     |     |     | 5355 |     |     |     |
| Thr | Arg  | Arg | Arg | Ala | Ala | Thr  | Ala | Ala | Ala | Ala | Ala  | Ile | Ala | Ser |
|     | 5360 |     |     |     |     | 5365 |     |     |     |     | 5370 |     |     |     |
| Met | Ser  | Arg | Pro | Arg | Arg | Gly  | Asn | Val | Tyr | Trp | Val  | Arg | Asp | Ala |
|     | 5375 |     |     |     |     | 5380 |     |     |     |     | 5385 |     |     |     |
| Ala | Thr  | Gly | Val | Arg | Val | Pro  | Val | Arg | Thr | Arg | Pro  | Pro | Arg | Thr |
|     | 5390 |     |     |     |     | 5395 |     |     |     |     | 5400 |     |     |     |
| Arg | Cys  | Leu | Arg | Asp | Val | Asp  | Val | Ser | Gln | Arg | Arg  | Gly | Gly | Cys |
|     | 5405 |     |     |     |     | 5410 |     |     |     |     | 5415 |     |     |     |
| Pro | Ser  | Ala | Asn | Thr | Arg | Lys  | Arg | Cys | Ser | Arg | Ser  | Ser | Arg | Leu |
|     | 5420 |     |     |     |     | 5425 |     |     |     |     | 5430 |     |     |     |
| Arg | Ser  | Thr | Ala | Pro | Arg | Arg  | Arg | Lys | Glu | Ser | Pro  | Ala | Asn | Ser |
|     | 5435 |     |     |     |     | 5440 |     |     |     |     | 5445 |     |     |     |
| Gly | Ser  | Lys | Arg | Thr | Lys | Arg  | Arg | Arg | Lys | Met | Trp  | Thr | Asp | Trp |
|     | 5450 |     |     |     |     | 5455 |     |     |     |     | 5460 |     |     |     |
| Trp | Ser  | Leu | Cys | Ala | Ser | Ser  | Pro | Pro | Gly | Gly | Ala  | Cys | Ser | Gly |
|     | 5465 |     |     |     |     | 5470 |     |     |     |     | 5475 |     |     |     |
| Ala | Gly  | Gly | Lys | Asn | Arg | Cys  | Cys | Gly | Pro | Ala | Pro  | Arg | Trp | Ser |
|     | 5480 |     |     |     |     | 5485 |     |     |     |     | 5490 |     |     |     |
| Ser | Arg  | Pro | Ala | Ser | Val | Pro  | Ala | Pro | Pro | Pro | Ser  | Ala | Pro | Thr |
|     | 5495 |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr  | Arg | Cys | Thr | Gly | Thr | Arg  | Thr | Ser | Ser | Ser | Arg  | Arg | Ser | Ser |
| 5510 |     |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
| Val  | Trp | Ala | Ser | Leu | Leu | Thr  | Ala | Ser | Ala | Ala | Ala  | Pro | Arg | Pro |
| 5525 |     |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
| Lys  | Arg | Arg | Arg | Cys | Pro | Ser  | Arg | Trp | Thr | Thr | Ala  | Thr | Pro | Arg |
| 5540 |     |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
| Arg  | Ala | Ser | Arg | Pro | Cys | Ser  | Arg | Cys | Cys | Arg | Ala  | Arg | Arg | Arg |
| 5555 |     |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
| Ala  | Gly | Ala | Ser | Ser | Ala | Arg  | Ala | Ala | Arg | Ile | Cys  | Thr | Arg | Pro |
| 5570 |     |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |
| Cys  | Ser | Trp | Cys | Pro | Ser | Ala  | Arg | Ser | Trp | Arg | Thr  | Cys | Trp | Ser |
| 5585 |     |     |     |     |     | 5590 |     |     |     |     | 5595 |     |     |     |
| Thr  | Arg | Trp | Thr | Pro | Arg | Cys  | Ser | Pro | Arg | Ser | Arg  | Cys | Gly | Pro |
| 5600 |     |     |     |     |     | 5605 |     |     |     |     | 5610 |     |     |     |
| Ser  | Ser | Arg | Trp | Pro | Arg | Ala  | Trp | Ala | Cys | Arg | Pro  | Trp | Thr | Ser |
| 5615 |     |     |     |     |     | 5620 |     |     |     |     | 5625 |     |     |     |
| Arg  | Ser | Pro | Arg | Ser | Pro | Trp  | Lys | Arg | Arg | Pro | Ser  | Pro | Ser | Pro |
| 5630 |     |     |     |     |     | 5635 |     |     |     |     | 5640 |     |     |     |
| Ala  | Pro | Ala | Pro | Trp | Arg | Cys  | Arg | Arg | Ile | Pro | Gly  | Cys | Arg | Arg |
| 5645 |     |     |     |     |     | 5650 |     |     |     |     | 5655 |     |     |     |
| Arg  | Leu | Pro | Pro | Leu | Ala | Glu  | Asp | Ala | Ser | Thr | Ala  | Arg | Pro | Ala |
| 5660 |     |     |     |     |     | 5665 |     |     |     |     | 5670 |     |     |     |
| Cys  | Cys | Pro | Thr | Thr | Arg | Cys  | Ile | Leu | Pro | Ser | Ser  | Pro | Arg | Arg |
| 5675 |     |     |     |     |     | 5680 |     |     |     |     | 5685 |     |     |     |
| Ala  | Thr | Ala | Ala | Arg | Ala | Ser  | Thr | Ala | Ala | Thr | Pro  | Ala | Ala | Ala |
| 5690 |     |     |     |     |     | 5695 |     |     |     |     | 5700 |     |     |     |
| Ala  | Arg | Pro | Pro | Pro | Ala | Ala  | Ala | Val | Val | Ala | Pro  | Ala | Ala | Ala |
| 5705 |     |     |     |     |     | 5710 |     |     |     |     | 5715 |     |     |     |
| Ala  | Pro | Arg | Leu | Pro | Pro | Pro  | Pro | Trp | Cys | Gly | Glu  | Cys | Thr | Ala |
| 5720 |     |     |     |     |     | 5725 |     |     |     |     | 5730 |     |     |     |
| Ala  | Gly | Ala | Ser | Leu | Pro | Cys  | Arg | Ala | Arg | Ala | Thr  | Thr | Arg | Ala |

5735

5740

5745

Ser Pro Phe Asn Ser Ala Val Ala Ser Tyr Leu Gln Ile Trp Pro  
 5750 5755 5760

Ser His Ala Ala Ser Ala Ser Pro Leu Arg Ala Thr Glu Glu Glu  
 5765 5770 5775

Ser Arg Ala Val Glu Gly Arg Gly Thr Gly Cys Val Ala Ile Thr  
 5780 5785 5790

Thr Gly Gly Gly Ala Pro Ser Ala Ser Gly Trp Gly Glu Ala Ser  
 5795 5800 5805

Cys Pro Arg Ser Pro Ser Ser Pro Arg Arg Ser Gly Arg Ser Pro  
 5810 5815 5820

Ala Leu Pro Trp Arg Cys Arg Pro Leu Ser Ala Thr Glu Thr Gln  
 5825 5830 5835

Leu Gly Lys Phe Val Ile Lys Lys Trp Thr Asp Ala Pro Gly Pro  
 5840 5845 5850

Val Met Cys Val Phe Arg Trp Lys Thr Ser Ile Phe Arg Pro Trp  
 5855 5860 5865

His Arg Asp Thr Ala Arg Gly Arg Leu Trp Ala Pro Gly Ala Thr  
 5870 5875 5880

Ser Ala Thr Ala Asn Thr Gly Ala Pro Ser Ile Gly Ala Val Ser  
 5885 5890 5895

Gly Ala Gly Leu Arg Ile Ser Gly Pro Arg Ser Lys Pro Met Ala  
 5900 5905 5910

Thr Arg Arg Gly Thr Ala Ala Gln Gly Arg Arg Gly Lys Ser Lys  
 5915 5920 5925

Ser Arg Thr Ser Ser Arg Arg Trp Ser Met Ala Trp Pro Arg Ala  
 5930 5935 5940

Ser Thr Gly Trp Trp Thr Trp Pro Thr Arg Pro Cys Arg Asn Arg  
 5945 5950 5955

Ser Thr Ala Ala Trp Thr Arg Ser Arg Pro Arg Gly Pro Trp Arg  
 5960 5965 5970

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Cys Pro Arg Trp Arg Arg Ser Cys Leu Pro Trp Thr Ser Ala Ala  
 5975 5980 5985  
  
 Thr Ser Asp Arg Val Pro Thr Arg Arg Arg Arg Cys Arg Thr Arg  
 5990 5995 6000  
  
 Thr Ser Arg Pro Arg Thr Arg Arg Arg Asn Trp Val Cys Pro Pro  
 6005 6010 6015  
  
 Arg Gly Pro Trp Arg Leu Trp Pro Pro Gly Cys Asn Pro Ala Ala  
 6020 6025 6030  
  
 Ala Ala Ser Pro Arg Pro Trp Thr Cys Leu Arg Leu Leu Pro Ala  
 6035 6040 6045  
  
 Pro Pro Gln Trp Leu Ser Pro Cys Arg Arg Trp Pro Ser Arg Arg  
 6050 6055 6060  
  
 Ala Pro Pro Glu Ala Ala Pro Arg Arg Thr Gly Arg Ala Leu Thr  
 6065 6070 6075  
  
 Ala Ser Trp Val Trp Glu Cys Arg Val Ser Ala Ala Ala Ala Ile  
 6080 6085 6090  
  
 Lys Arg His Cys Ser Ala Leu Ala Cys Leu Cys Val Tyr Val Cys  
 6095 6100 6105  
  
 Pro Pro Thr Arg Arg Arg Lys Arg Arg Val Ala Glu Leu Gln Asp  
 6110 6115 6120  
  
 Gly His Pro Ile Asp Ala Ala Pro Val Gly Val His Ala His Arg  
 6125 6130 6135  
  
 Arg Thr Gly Arg Phe Gly Val Pro Glu Ser Gly Ser Gly Ala Val  
 6140 6145 6150  
  
 Arg Pro Arg His Arg His Leu Leu Gln Ser Gly Glu Gln Val Glu  
 6155 6160 6165  
  
 Pro His Gly Gly Ala His Ala Arg Cys Asp His Arg Pro Gln Pro  
 6170 6175 6180  
  
 Ala Ala Asp Ala Ala Leu Arg Ala Arg Gly Pro Arg Gly Gln His  
 6185 6190 6195  
  
 Leu Leu Val Gln Ser Ala Leu His Ala Gly Arg Gly Arg Gln Pro  
 6200 6205 6210

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Ala  | Gly | His | Gly | Gln | His  | Leu | Leu | His | Pro | Arg  | Arg | Ala | Gly |
|     | 6215 |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Ser | Gly  | Ala | Gln | Leu | Gln | Thr  | Leu | Leu | Arg | His | Arg  | Leu | Gln | Gln |
|     | 6230 |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Pro | Gly  | Ser | Gln | Gly | Ser | Ala  | Gln | His | Leu | Pro | Val  | Asp | Ile | Ser |
|     | 6245 |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |
| Trp | Tyr  | Tyr | Arg | Lys | Asn | Leu  | Tyr | Ile | Trp | Lys | Cys  | Thr | Cys | Ala |
|     | 6260 |     |     |     |     | 6265 |     |     |     |     | 6270 |     |     |     |
| Arg | His  | His | Tyr | Lys | Gly | Trp  | Tyr | Ser | Thr | Trp | Asn  | Gln | Arg | Trp |
|     | 6275 |     |     |     |     | 6280 |     |     |     |     | 6285 |     |     |     |
| Ser | Gly  | Asn | Leu | Cys | Arg | Arg  | Asn | Leu | Ser | Thr | Arg  | Ala | Ser | Ser |
|     | 6290 |     |     |     |     | 6295 |     |     |     |     | 6300 |     |     |     |
| Gly | Cys  | Met | Ala | His | His | Trp  | Tyr | Lys | Ile | Trp | Arg  | Gln | Ser | Ser |
|     | 6305 |     |     |     |     | 6310 |     |     |     |     | 6315 |     |     |     |
| Ala | His  | Gln | Asn | Glu | Ala | Leu  | Leu | Trp | Phe | Phe | Cys  | Gln | Ala | Tyr |
|     | 6320 |     |     |     |     | 6325 |     |     |     |     | 6330 |     |     |     |
| Gln | Arg  | Arg | Arg | Pro | Gly | Lys  | Cys | Glu | Asn | Arg | Asn  | Arg | Arg | Tyr |
|     | 6335 |     |     |     |     | 6340 |     |     |     |     | 6345 |     |     |     |
| Gln | Arg  | Ile | His | His | Gly | Ile  | Leu | Arg | Ser | Lys | Cys  | Ser | Cys | Arg |
|     | 6350 |     |     |     |     | 6355 |     |     |     |     | 6360 |     |     |     |
| Arg | Pro  | Ser | Pro | Arg | Asn | Cys  | Phe | Val | Tyr | Glu | Cys  | Gly | Ser | Gly |
|     | 6365 |     |     |     |     | 6370 |     |     |     |     | 6375 |     |     |     |
| Asn | Ser  | Arg | Tyr | Pro | Tyr | Cys  | Ile | Gln | Gly | Arg | Tyr  | Arg | Gln | Leu |
|     | 6380 |     |     |     |     | 6385 |     |     |     |     | 6390 |     |     |     |
| Phe | Tyr  | Gln | Phe | Gly | Ser | Ala  | Val | His | Ala | Gln | Gln  | Thr | Gln | Leu |
|     | 6395 |     |     |     |     | 6400 |     |     |     |     | 6405 |     |     |     |
| His | Trp  | Leu | Gln | Arg | Gln | Leu  | Tyr | Arg | Ser | Asp | Val  | Leu | Gln | Gln |
|     | 6410 |     |     |     |     | 6415 |     |     |     |     | 6420 |     |     |     |
| His | Trp  | Gln | Tyr | Gly | Cys | Thr  | Gly | Trp | Thr | Gly | Leu  | Pro | Ala | Glu |
|     | 6425 |     |     |     |     | 6430 |     |     |     |     | 6435 |     |     |     |
| Cys | Cys  | Gly | Gly | Leu | Ala | Gly  | Gln | Lys | His | Arg | Thr  | Val | Leu | Pro |
|     | 6440 |     |     |     |     | 6445 |     |     |     |     | 6450 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Leu | Ala | Leu | Ser | Gly | Gln  | Asn | Gln | Val | Phe | Gln  | Tyr | Val | Glu |
| 6455 |     |     |     |     |     | 6460 |     |     |     |     | 6465 |     |     |     |
| Ser  | Gly | Gly | Gly | Gln | Leu | Pro  | Arg | Cys | Ala | His | Tyr  | Lys | Ser | Arg |
| 6470 |     |     |     |     |     | 6475 |     |     |     |     | 6480 |     |     |     |
| Cys  | Gly | Gly | Thr | Ser | Leu | Leu  | Leu | Pro | Pro | Gly | Cys  | Cys | Gly | Asn |
| 6485 |     |     |     |     |     | 6490 |     |     |     |     | 6495 |     |     |     |
| Tyr  | Leu | Pro | Gly | Asn | Gly | Gln  | Trp | Ser | Asn | His | Leu  | Asp | Gln | Arg |
| 6500 |     |     |     |     |     | 6505 |     |     |     |     | 6510 |     |     |     |
| Tyr  | Cys | Cys | Ile | Gly | Gln | Gly  | Gln | Ser | Phe | Arg | His  | Gly | Asp | Gln |
| 6515 |     |     |     |     |     | 6520 |     |     |     |     | 6525 |     |     |     |
| His  | Pro | Gly | Gln | Pro | Val | Ala  | Glu | Leu | Pro | Leu | Arg  | Glu | Arg | Gly |
| 6530 |     |     |     |     |     | 6535 |     |     |     |     | 6540 |     |     |     |
| Ala  | Val | Pro | Ala | Arg | Leu | Leu  | Gln | Val | His | Ala | Gly  | Gln | His | His |
| 6545 |     |     |     |     |     | 6550 |     |     |     |     | 6555 |     |     |     |
| Ala  | Ala | His | Gln | His | Gln | His  | Leu | Arg | Leu | His | Glu  | Arg | Pro | Arg |
| 6560 |     |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Gly  | Gly | Ala | Leu | Ala | Gly | Gly  | Arg | Leu | His | Gln | His  | Arg | Gly | Ala |
| 6575 |     |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Leu  | Val | Ala | Gly | Pro | His | Gly  | Gln | Arg | Gln | Pro | Leu  | Gln | Pro | Pro |
| 6590 |     |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Pro  | Gln | Arg | Gly | Pro | Ala | Ile  | Pro | Leu | His | Ala | Pro  | Gly | Gln | Arg |
| 6605 |     |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Ala  | Leu | Arg | Ala | Leu | Pro | His  | Pro | Gly | Ala | Pro | Lys  | Val | Phe | Arg |
| 6620 |     |     |     |     |     | 6625 |     |     |     |     | 6630 |     |     |     |
| His  | Gln | Glu | Pro | Pro | Ala | Pro  | Ala | Arg | Val | Leu | His  | Leu | Arg | Val |
| 6635 |     |     |     |     |     | 6640 |     |     |     |     | 6645 |     |     |     |
| Glu  | Leu | Pro | Gln | Gly | Arg | Gln  | His | Asp | Pro | Ala | Glu  | Leu | Pro | Arg |
| 6650 |     |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |
| Gln  | Arg | Pro | Ala | His | Gly | Arg  | Gly | Leu | His | Arg | Leu  | His | Gln | His |
| 6665 |     |     |     |     |     | 6670 |     |     |     |     | 6675 |     |     |     |
| Gln  | Pro | Leu | Arg | His | Leu | Leu  | Pro | His | Gly | Ala | Gln  | His | Arg | Leu |

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6680

6685

6690

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| His  | Ala | Arg | Gly | His | Ala | Ala  | Gln | Arg | His | Gln | Arg  | Pro | Val | Leu |
| 6695 |     |     |     |     |     | 6700 |     |     |     |     | 6705 |     |     |     |
| Gln  | Arg | Leu | Pro | Leu | Gly | Gly  | Gln | His | Ala | Leu | Pro  | His | Pro | Gly |
| 6710 |     |     |     |     |     | 6715 |     |     |     |     | 6720 |     |     |     |
| Gln  | Arg | His | Gln | Arg | Ala | His  | Leu | His | Pro | Leu | Ala  | Gln | Leu | Gly |
| 6725 |     |     |     |     |     | 6730 |     |     |     |     | 6735 |     |     |     |
| Arg  | Leu | Pro | Arg | Leu | Val | Leu  | His | Ala | Pro | Gln | Asp  | Pro | Arg | Asp |
| 6740 |     |     |     |     |     | 6745 |     |     |     |     | 6750 |     |     |     |
| Ala  | Leu | Ala | Arg | Leu | Arg | Val  | Arg | Pro | Leu | Leu | Arg  | Leu | Leu | Gly |
| 6755 |     |     |     |     |     | 6760 |     |     |     |     | 6765 |     |     |     |
| Leu  | His | Pro | Leu | Pro | Arg | Arg  | His | Leu | Leu | Pro | Gln  | Pro | His | Leu |
| 6770 |     |     |     |     |     | 6775 |     |     |     |     | 6780 |     |     |     |
| Gln  | Glu | Gly | Leu | His | His | Leu  | Arg | Leu | Leu | Arg | Gln  | Leu | Ala | Arg |
| 6785 |     |     |     |     |     | 6790 |     |     |     |     | 6795 |     |     |     |
| Gln  | Arg | Pro | Pro | Pro | Asp | Ala  | Gln | Arg | Val | Arg | Asn  | Gln | Ala | His |
| 6800 |     |     |     |     |     | 6805 |     |     |     |     | 6810 |     |     |     |
| Arg  | Arg | Arg | Arg | Gly | Val | Gln  | Arg | Gly | Pro | Val | Gln  | His | Asp | Gln |
| 6815 |     |     |     |     |     | 6820 |     |     |     |     | 6825 |     |     |     |
| Gly  | Leu | Val | Pro | Gly | Pro | Asp  | Ala | Gly | Pro | Leu | Gln  | His | Arg | Leu |
| 6830 |     |     |     |     |     | 6835 |     |     |     |     | 6840 |     |     |     |
| Pro  | Gly | Leu | Leu | Arg | Ala | Arg  | Gly | Leu | Gln | Gly | Pro  | His | Val | Leu |
| 6845 |     |     |     |     |     | 6850 |     |     |     |     | 6855 |     |     |     |
| Leu  | Leu | Pro | Gln | Leu | Pro | Ala  | His | Glu | Pro | Pro | Gly  | Arg | Gly | Arg |
| 6860 |     |     |     |     |     | 6865 |     |     |     |     | 6870 |     |     |     |
| Gly  | Gln | Leu | Gln | Gly | Leu | Pro  | Gly | Arg | His | Pro | Gly  | Leu | Pro | Ala |
| 6875 |     |     |     |     |     | 6880 |     |     |     |     | 6885 |     |     |     |
| Gln  | Gln | Leu | Gly | Leu | Arg | Arg  | Leu | Pro | Arg | Ala | His  | His | Ala | Pro |
| 6890 |     |     |     |     |     | 6895 |     |     |     |     | 6900 |     |     |     |
| Gly  | Pro | Ala | Leu | Pro | Arg | Gln  | Leu | Pro | Leu | Pro | Ala  | His | Arg | Gln |
| 6905 |     |     |     |     |     | 6910 |     |     |     |     | 6915 |     |     |     |



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Glu Arg Arg Arg Gln Arg His Pro Glu Lys Val Pro Leu Arg Pro  
 6920 6925 6930  
  
 Gly His Val Ala His Pro Leu Leu Gln Gln Leu His Val His Gly  
 6935 6940 6945  
  
 Arg Ala His Arg Pro Arg Pro Glu His Ala Leu Arg Gln Leu Arg  
 6950 6955 6960  
  
 Pro Arg Ala Arg His Glu Phe Arg Ser Arg Pro His Gly Val His  
 6965 6970 6975  
  
 Pro Ser Leu Cys Cys Leu Arg Ser Leu Arg Arg Arg Pro Ser Ala  
 6980 6985 6990  
  
 Pro Ala Pro Pro Arg Arg His Arg Gly Arg Leu Pro Ala His Ala  
 6995 7000 7005  
  
 Leu Leu Gly Arg Gln Arg His His Leu Ser Leu Leu Leu Ala  
 7010 7015 7020  
  
 Arg Arg Pro Ala Arg Ala Pro Ala Ser Arg Ser Ser Gly Pro Ser  
 7025 7030 7035  
  
 Ser Ala Thr Trp Ala Ala Gly Pro Ala Ser Trp Ala Pro Ser Thr  
 7040 7045 7050  
  
 Ser Ala Ser Arg Asp Ser Trp Pro Arg Thr Ser Trp Pro Ala Pro  
 7055 7060 7065  
  
 Ser Ser Thr Arg Pro Ala Ala Arg Pro Gly Ala Ser Thr Gly Trp  
 7070 7075 7080  
  
 Pro Ser Pro Gly Thr Arg Ala Pro Thr Pro Ala Thr Ser Ser Thr  
 7085 7090 7095  
  
 Pro Ser Gly Ser Arg Thr Ser Ala Ser Ser Arg Ser Thr Ser Ser  
 7100 7105 7110  
  
 Ser Thr Arg Ala Cys Cys Val Ala Ala Pro Trp Pro Pro Arg Thr  
 7115 7120 7125  
  
 Ala Ala Ser Pro Trp Lys Ser Pro Pro Arg Pro Cys Arg Val Arg  
 7130 7135 7140  
  
 Ala Arg Pro Pro Ala Gly Ser Ser Ala Ala Cys Ser Cys Thr Pro  
 7145 7150 7155

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Ser Cys Thr Gly Pro Thr Ala Pro Trp Thr Arg Thr Pro Pro Thr  
 7160 7165 7170  
  
 Cys Arg Gly Cys Pro Thr Ala Cys Ser Ser Arg Pro Arg Trp Asn  
 7175 7180 7185  
  
 Pro Pro Cys Ala Ala Thr Arg Arg Arg Ser Thr Ala Ser Ser Thr  
 7190 7195 7200  
  
 Pro Thr Pro Pro Thr Phe Ala Pro Thr Ala Arg Ala Ser Arg Arg  
 7205 7210 7215  
  
 Pro Pro Pro Ser Thr Ala Ile Lys Thr Cys Asn Pro Val Cys Val  
 7220 7225 7230  
  
 Cys Glu Cys Phe Ile His His Asn Lys Gln His Met Phe Met Pro  
 7235 7240 7245  
  
 Pro Ser Leu Arg Leu Leu Tyr Leu Glu Ile Glu Gly Val Leu Pro  
 7250 7255 7260  
  
 Ala Leu Gly Met Ala Arg Gly Gln Gly Tyr Val Ala Glu Leu Val  
 7265 7270 7275  
  
 Leu Gly Gln Pro Leu Glu Leu Gly Asp Gln Gln Leu Arg His Gly  
 7280 7285 7290  
  
 Glu Val Gly Glu Arg Val Ala Pro Gln Leu Ala Arg Glu Leu Gln  
 7295 7300 7305  
  
 Gly Ala Gln Gln Val Gly Arg Gly Asp Leu Glu Ile Ala Val Gly  
 7310 7315 7320  
  
 Thr Arg Val Leu Arg Ala Arg Val Thr Val His Gly Val Ala Ala  
 7325 7330 7335  
  
 Leu Glu His His Gln Gly Arg Val Leu His Ala Arg Gln His Arg  
 7340 7345 7350  
  
 Arg Val Gly Asp Ala Leu His Val Gln Ile Leu Gly Val Gly His  
 7355 7360 7365  
  
 Pro Glu Gly Gly His Leu Ala Gly Leu Pro Pro His Ala Gly His  
 7370 7375 7380  
  
 Ala Ala Gly Leu Val Val Ala Ile Ala Val Gln Gly Asp Gln His  
 7385 7390 7395

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| His  | Leu | Gly | Leu | Leu | Gly | Ala  | His | Ala | Arg | Val | His  | Gly | Leu | His |
| 7400 |     |     |     |     |     | 7405 |     |     |     |     | 7410 |     |     |     |
| Glu  | Ser | Leu | Gln | Leu | Ala | Glu  | Gly | Leu | Leu | Arg | Leu  | Ala | Ala | Leu |
| 7415 |     |     |     |     |     | 7420 |     |     |     |     | 7425 |     |     |     |
| Gly  | Glu | Glu | Asp | Pro | Ala | Gly  | Leu | Ala | Arg | Glu | Leu  | Val | Gly | Gly |
| 7430 |     |     |     |     |     | 7435 |     |     |     |     | 7440 |     |     |     |
| Ala  | Ala | Ser | Val | Val | His | Ala  | Ala | Ala | Arg | Val | Val  | Val | Gly | Gln |
| 7445 |     |     |     |     |     | 7450 |     |     |     |     | 7455 |     |     |     |
| Leu  | His | His | Ala | Ala | Pro | Pro  | Ala | Val | Leu | Gly | Asp  | Leu | Gly | Pro |
| 7460 |     |     |     |     |     | 7465 |     |     |     |     | 7470 |     |     |     |
| Val  | Gly | Val | Leu | Leu | Gln | Arg  | Ala | Leu | Pro | Val | Leu  | Ala | Arg | His |
| 7475 |     |     |     |     |     | 7480 |     |     |     |     | 7485 |     |     |     |
| Ile  | His | Leu | Asp | Arg | Val | Leu  | Leu | Leu | Asp | His | His  | Gly | Pro | Val |
| 7490 |     |     |     |     |     | 7495 |     |     |     |     | 7500 |     |     |     |
| Gln  | Ala | Pro | Gln | Leu | Ala | Leu  | Gly | Leu | Gly | Ala | Pro  | Val | Gln | Pro |
| 7505 |     |     |     |     |     | 7510 |     |     |     |     | 7515 |     |     |     |
| Gln  | Arg | Ala | Ala | Gly | Ala | Leu  | Pro | Val | Leu | Val | Gly  | Asp | Leu | Gly |
| 7520 |     |     |     |     |     | 7525 |     |     |     |     | 7530 |     |     |     |
| Val  | Arg | Val | His | Glu | Ala | Leu  | Gln | Glu | Ala | Ala | His  | His | Arg | Gly |
| 7535 |     |     |     |     |     | 7540 |     |     |     |     | 7545 |     |     |     |
| Gln  | Gly | Leu | Val | Ala | Gly | Glu  | Gly | Gln | Arg | Asn | Ala  | Ala | Val | Leu |
| 7550 |     |     |     |     |     | 7555 |     |     |     |     | 7560 |     |     |     |
| Leu  | Val | His | Ile | Gln | Val | Ala  | Asp | Thr | Ala | Val | His  | Leu | Ala | Leu |
| 7565 |     |     |     |     |     | 7570 |     |     |     |     | 7575 |     |     |     |
| Leu  | Gly | His | Gln | Leu | Glu | Gly  | Gly | Leu | Gln | Val | Ala  | Leu | His | Ala |
| 7580 |     |     |     |     |     | 7585 |     |     |     |     | 7590 |     |     |     |
| Val  | Pro | Val | His | Gln | Gln | Arg  | His | His | Phe | His | Ala  | Leu | Leu | Pro |
| 7595 |     |     |     |     |     | 7600 |     |     |     |     | 7605 |     |     |     |
| Gly  | Arg | Asn | Asp | Arg | Gln | Ala  | Gln | Gly | Val | Leu | His  | Arg | Cys | His |
| 7610 |     |     |     |     |     | 7615 |     |     |     |     | 7620 |     |     |     |
| Leu  | Ser | Arg | Arg | Arg | Arg | Ser  | Gln | Gly | Val | Val | Leu  | Val | Gln | Gly |

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu | Lys  | His | Ser | Leu | Ala | Val  | Leu | Leu | Gly | Asp | Ala  | His | Gly | Gly |
|     | 7640 |     |     |     |     | 7645 |     |     |     |     | 7650 |     |     |     |
| Lys | Ala  | Glu | Ala | His | Gly | Arg  | Gln | Leu | Leu | Leu | Gly  | Leu | Pro | Phe |
|     | 7655 |     |     |     |     | 7660 |     |     |     |     | 7665 |     |     |     |
| Val | Leu  | Ala | Val | Leu | Ala | Asp  | Val | Leu | Gln | Arg | His  | Met | Leu | Gly |
|     | 7670 |     |     |     |     | 7675 |     |     |     |     | 7680 |     |     |     |
| Leu | Ala  | Gly | Phe | Leu | Phe | Gly  | Arg | Gln | Arg | Arg | Arg  | Arg | Arg | Arg |
|     | 7685 |     |     |     |     | 7690 |     |     |     |     | 7695 |     |     |     |
| Ala | Gly  | Arg | Ala | Arg | Val | Leu  | Ala | His | His | Asp | Tyr  | Phe | Phe | Ser |
|     | 7700 |     |     |     |     | 7705 |     |     |     |     | 7710 |     |     |     |
| Leu | Ala  | Val | Val | Arg | Asp | His  | Ala | Ala | Val | Gly | Met  | Pro | Leu | Leu |
|     | 7715 |     |     |     |     | 7720 |     |     |     |     | 7725 |     |     |     |
| Gly | Gln  | Arg | Arg | Arg | Arg | Arg  | Ala | Leu | Ala | Val | Arg  | Arg | Ala | Ala |
|     | 7730 |     |     |     |     | 7735 |     |     |     |     | 7740 |     |     |     |
| Gly | Arg  | Ala | Pro | Ser | Ala | Phe  | Gly | Gly | Ala | Leu | Leu  | Ala | Ala | Leu |
|     | 7745 |     |     |     |     | 7750 |     |     |     |     | 7755 |     |     |     |
| Leu | Leu  | Thr | Ser | Ser | Ala | Ala  | Gly | His | Cys | Val | Leu  | Leu | Gly | Ser |
|     | 7760 |     |     |     |     | 7765 |     |     |     |     | 7770 |     |     |     |
| Lys | His  | Gly | Asp | Ser | Ala | Ile  | Val | Ala | Asn | Ile | Ala  | Ile | Cys | Pro |
|     | 7775 |     |     |     |     | 7780 |     |     |     |     | 7785 |     |     |     |
| Arg | Arg  | Arg | Arg | Arg | Glu | Pro  | Ala | Ala | Ala | Glu | Lys  | Leu | Asn | Arg |
|     | 7790 |     |     |     |     | 7795 |     |     |     |     | 7800 |     |     |     |
| Pro | Ala  | Ala | Gln | Pro | His | Leu  | Arg | Arg | Arg | Ser | Pro  | Arg | His | Ala |
|     | 7805 |     |     |     |     | 7810 |     |     |     |     | 7815 |     |     |     |
| Arg | Asp  | Gly | Gly | Ile | His | Arg  | Asp | Pro | Gly | Leu | Arg  | Asp | Ala | Arg |
|     | 7820 |     |     |     |     | 7825 |     |     |     |     | 7830 |     |     |     |
| Gly | Ala  | Arg | Gly | Gly | Ala | Gly  | Ser | Ala | Leu | Phe | Ser  | Pro | Gly | Arg |
|     | 7835 |     |     |     |     | 7840 |     |     |     |     | 7845 |     |     |     |
| Glu | Pro  | Pro | Arg | Ala | Ala | Arg  | Ala | Gly | Ser | Arg | Glu  | Arg | Ala | Glu |
|     | 7850 |     |     |     |     | 7855 |     |     |     |     | 7860 |     |     |     |

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Pro Gly Trp Ala Arg Ala Trp Arg Leu Pro Glu Arg Gly Arg Gly  
 7865 7870 7875  
  
 Arg Ala His Gln Ala Ser Gly Pro Pro Met His His Arg Gln Gly  
 7880 7885 7890  
  
 Arg Ala Ala Arg Pro Arg Arg Gly Ala Pro Gln Arg Gly Gly Ala  
 7895 7900 7905  
  
 Gln Pro Arg Leu Arg Ala Gln Pro Leu Leu Ala Ala Arg Ala Pro  
 7910 7915 7920  
  
 Gln Ala Pro Ala Gln Arg His Leu Arg Ala Gln Pro Ala Pro Gln  
 7925 7930 7935  
  
 Leu Leu Pro Gly Leu Arg Gly Ala Arg Gly Pro Gly His Leu Pro  
 7940 7945 7950  
  
 Pro Leu Phe Gln Glu Pro Lys Asp Pro Arg Leu Leu Pro Arg Gln  
 7955 7960 7965  
  
 Pro His Pro Arg Arg Arg Pro Ala Gln Pro Gly Pro Arg Arg Pro  
 7970 7975 7980  
  
 Pro Thr Tyr Arg Leu Leu Gly Arg Gly Ser Gln Asp Leu Arg Gly  
 7985 7990 7995  
  
 Ser Gly Gln Arg Arg Asp Ser Gly Arg Glu Arg Ser Ala Arg Lys  
 8000 8005 8010  
  
 Arg Arg Gly Ala Ala Pro Gln Arg Pro Gly Gly Val Gly Arg Arg  
 8015 8020 8025  
  
 Gln Arg Ala Pro Gly Gly Pro Gln Ala His Gly Arg Ala Asp Pro  
 8030 8035 8040  
  
 Leu Arg Leu Pro Gly Ala Gln Pro Ala Pro Gln Gly His Glu Arg  
 8045 8050 8055  
  
 Arg His Gly Pro Gly Ala His Gln Ala Arg Leu Ala Pro Leu Gly  
 8060 8065 8070  
  
 Gly Gly Asp Ala Gly Pro Arg Glu Leu Gly Arg Gly Gln Ala Arg  
 8075 8080 8085  
  
 Gly Gln Arg Arg Ala Ala Gly Ala Leu Ala Gly Ser Glu His Pro  
 8090 8095 8100

## 368530-7006W01\_SequenceListing\_ST25.txt

Pro Glu    Pro Gly Arg Ala Ala    Gln Ala His Asp Gly    Arg Gly Pro  
           8105                               8110                               8115  
  
 Gly Asp    Arg Gly Ala Gly Val    Ser Ala Pro Leu Leu    Arg Arg Arg  
           8120                               8125                               8130  
  
 Gly Asp    Pro Ala Gln Gly Arg    Gly Glu Pro Ala Leu    Pro Leu Gln  
           8135                               8140                               8145  
  
 Thr Arg    Val Arg Ala Pro Gly    Leu Gln Asp Leu Gln    Arg Gly Ala  
           8150                               8155                               8160  
  
 Asp Gln    Pro Gly Leu Leu His    Gly His Pro Ala Arg    Glu Pro Pro  
           8165                               8170                               8175  
  
 Gly Ala    Glu Arg Ala Ala His    His Pro Ala Arg Gly    Gly Pro Pro  
           8180                               8185                               8190  
  
 Arg Leu    His Pro Arg Leu Arg    Leu Pro Val Pro Leu    Pro His Leu  
           8195                               8200                               8205  
  
 Ala Asp    Gly His Gly Arg Val    Ala Ala Val Pro Gly    Gly Ala Glu  
           8210                               8215                               8220  
  
 Pro Glu    Arg Ala Leu Gln Ala    Pro Ala Glu Glu Pro    Gln Gly Pro  
           8225                               8230                               8235  
  
 Val Asp    Arg Val Arg Arg Ala    His His Arg Arg Gly    Pro Gly Arg  
           8240                               8245                               8250  
  
 Pro His    Leu Pro Arg Ala Pro    Ala Ala Asp Ala Ala    Gln Arg Ala  
           8255                               8260                               8265  
  
 Ala Arg    Leu Tyr Glu Pro Lys    His Val Ala Lys Leu    Ser Leu Phe  
           8270                               8275                               8280  
  
 His Pro    Arg Thr Leu Arg Asp    Pro Ala Arg His Leu    Leu Arg Ala  
           8285                               8290                               8295  
  
 Ala Leu    Gly Leu Arg Ala Ala    Asp Leu Pro Arg Val    Pro Pro Ala  
           8300                               8305                               8310  
  
 Ala Leu    Glu Pro Leu Leu Pro    Ala Ala Pro Gly Gln    Leu Pro Gly  
           8315                               8320                               8325  
  
 Leu Pro    Leu Gly Arg Asp Arg    Gly Arg Gln Arg Arg    Gly Pro Ala  
           8330                               8335                               8340

## 368530-7006W01\_SequenceListing\_ST25.txt

Arg Val Pro Leu Pro Leu Gln Pro Leu His Ala Ala Pro Leu Pro  
 8345 8350 8355  
 Gly Leu Gln Pro Pro Ala Ala Glu Arg Asp Pro Asp His Arg His  
 8360 8365 8370  
 Leu Arg Val Ala Arg Pro Arg Arg Gly Gln Gly Gly Ser Glu Thr  
 8375 8380 8385  
 His Pro Gly Ala Val Asp Leu Gly Leu Leu Ala Gln Val Arg Ala  
 8390 8395 8400  
 Arg Gly Leu Pro Ser Leu Arg Asp Gln Val Leu Arg Gly Pro Ile  
 8405 8410 8415  
 Pro Ala Ala Gln Gly Arg Ala Val Gly Leu Arg His His Pro Gly  
 8420 8425 8430  
 Gly His Pro Gly Pro Ile Ala Ser His Pro Glu Ile Pro Pro Arg  
 8435 8440 8445  
 Ile Ser Ala Glu Lys Gly Pro Arg Gly Leu Leu Gly Pro Pro Asp  
 8450 8455 8460  
 Arg Arg Gly Ala Gln Pro Gln Leu Pro Pro Gly Cys Pro Glu Glu  
 8465 8470 8475  
 Ala Ala Arg Ser Lys Trp Ser Cys Arg Arg Arg Arg Arg Ile Trp  
 8480 8485 8490  
 Arg Lys Thr Gly Arg Ala Val Arg Gln Arg Arg Arg Arg Trp Lys  
 8495 8500 8505  
 Thr Gly Thr Ala Leu Arg Gln Arg Arg Thr Ala Cys Lys Thr Val  
 8510 8515 8520  
 Trp Arg Arg Lys Thr Arg Trp Arg Arg Gln Arg Lys Lys Gln Pro  
 8525 8530 8535  
 Pro Pro Asp Arg Arg Pro Arg Arg Arg Arg Arg Lys Gln Ala Ala  
 8540 8545 8550  
 Arg Ile Pro Ser Pro Leu Arg Val Gly Val Ala Ala Ala Gly Pro  
 8555 8560 8565  
 Thr Val Asp Gly Thr Arg Pro Gly Ala Ser Arg Thr Pro Pro Pro

8570

8575

8580

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Pro | Val | Arg | Arg | Ser | Gly  | Arg | Asp | Thr | Ser | Pro  | Gly | Gly | Gly |
| 8585 |     |     |     |     |     | 8590 |     |     |     |     | 8595 |     |     |     |
| Thr  | Lys | Thr | Pro | Ser | Ser | Pro  | Ala | Cys | Lys | Pro | Ala  | Gly | Ala | Thr |
| 8600 |     |     |     |     |     | 8605 |     |     |     |     | 8610 |     |     |     |
| Ser  | Pro | Ser | Pro | Gly | Ala | Thr  | Cys | Ser | Ser | Thr | Ala  | Gly | Thr | Ser |
| 8615 |     |     |     |     |     | 8620 |     |     |     |     | 8625 |     |     |     |
| Pro  | Ala | Thr | Ser | Cys | Ile | Thr  | Thr | Val | Thr | Ser | Thr  | Ala | Pro | Thr |
| 8630 |     |     |     |     |     | 8635 |     |     |     |     | 8640 |     |     |     |
| Thr  | Val | Ser | Lys | Lys | Arg | Gln  | Lys | Pro | Ser | Ser | Ser  | Ser | Ser | Ser |
| 8645 |     |     |     |     |     | 8650 |     |     |     |     | 8655 |     |     |     |
| Arg  | Lys | Pro | Ala | Ala | Ala | Ala  | Arg | Lys | Ser | Thr | Ala  | Ala | Ala | Gly |
| 8660 |     |     |     |     |     | 8665 |     |     |     |     | 8670 |     |     |     |
| Gly  | Leu | Arg | Ile | Ala | Ala | Asn  | Glu | Pro | Ala | Gln | Thr  | Arg | Glu | Leu |
| 8675 |     |     |     |     |     | 8680 |     |     |     |     | 8685 |     |     |     |
| Arg  | Asn | Arg | Ile | Phe | Pro | Thr  | Leu | Tyr | Ala | Ile | Phe  | Gln | Gln | Ser |
| 8690 |     |     |     |     |     | 8695 |     |     |     |     | 8700 |     |     |     |
| Arg  | Gly | Gln | Glu | Gln | Glu | Leu  | Lys | Val | Lys | Asn | Arg  | Ser | Leu | Arg |
| 8705 |     |     |     |     |     | 8710 |     |     |     |     | 8715 |     |     |     |
| Ser  | Leu | Thr | Arg | Ser | Cys | Leu  | Tyr | His | Lys | Ser | Glu  | Asp | Gln | Leu |
| 8720 |     |     |     |     |     | 8725 |     |     |     |     | 8730 |     |     |     |
| Gln  | Arg | Thr | Leu | Glu | Asp | Ala  | Glu | Ala | Leu | Phe | Asn  | Lys | Tyr | Cys |
| 8735 |     |     |     |     |     | 8740 |     |     |     |     | 8745 |     |     |     |
| Ala  | Leu | Thr | Leu | Lys | Glu | Pro  | Ala | Pro | Ala | His | Thr  | Arg | Lys | Lys |
| 8750 |     |     |     |     |     | 8755 |     |     |     |     | 8760 |     |     |     |
| Ala  | Gly | Ile | Thr | Ser | Pro | Pro  | Ala | Pro | Phe | Ala | Arg  | Pro | Ser | Ser |
| 8765 |     |     |     |     |     | 8770 |     |     |     |     | 8775 |     |     |     |
| Ala  | Lys | Arg | Phe | Pro | Arg | Leu  | Thr | Cys | Gly | Ala | Thr  | Ser | Pro | Arg |
| 8780 |     |     |     |     |     | 8785 |     |     |     |     | 8790 |     |     |     |
| Trp  | Ala | Trp | Pro | Pro | Ala | Pro  | Pro | Arg | Thr | Thr | Pro  | Pro | Ala | Thr |
| 8795 |     |     |     |     |     | 8800 |     |     |     |     | 8805 |     |     |     |



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Gly Ser Val Pro Gly Pro Arg Ser His Gly Met Thr Ser Ala Pro  
 8810 8815 8820  
 Thr Glu Thr Arg Tyr Ser Asn Ser Gln Arg Ser Pro Pro Arg Pro  
 8825 8830 8835  
 Ala Ile Thr Leu Ile Arg Val Ile Gly Pro Pro Pro Trp Cys Thr  
 8840 8845 8850  
 Arg Lys Phe Pro Ser Pro Arg Pro Tyr Tyr Phe Arg Glu Thr Pro  
 8855 8860 8865  
 Arg Pro Lys Ser Ser Leu Thr Gln Val Ser Ser Trp Pro Ala Ala  
 8870 8875 8880  
 Pro Pro Cys Val Val Thr Ala Pro Leu Arg Val Ser Gly Trp Ser  
 8885 8890 8895  
 Glu Ala Glu Ala His Ser Ser Thr Thr Arg Trp Ala Leu Arg Trp  
 8900 8905 8910  
 Val Cys Asp Leu Thr Glu Ser Ser Asn Ser Pro Asp Arg Gly Asp  
 8915 8920 8925  
 Leu Pro Ser Arg Leu Val Arg Pro Ser Leu Trp Arg Val Arg Pro  
 8930 8935 8940  
 Arg Ser Pro Ala Arg Val Ala Ser Ala Leu Ser Ser Ser Trp Arg  
 8945 8950 8955  
 Ser Ser Leu Pro Arg Ser Thr Ser Thr Pro Ser Pro Ala Pro Pro  
 8960 8965 8970  
 Ala Thr Thr Arg Thr Ser Ser Ser Arg Thr Ser Thr Pro Ser Ala  
 8975 8980 8985  
 Ser Arg Trp Thr Ala Thr Ile Glu Cys Pro Met Val Ala Arg Leu  
 8990 8995 9000  
 Thr Leu Gly Phe Asp Thr Trp Thr Thr Ala Ala Ala Ser Ala Ala  
 9005 9010 9015  
 Ser Leu Gly Ile Ser Pro Ser Leu Pro Thr Leu Ser Cys Pro Arg  
 9020 9025 9030  
 Ser Thr Leu Arg Ala Arg Pro Thr Glu Cys Gly Ser Ser Ser Lys  
 9035 9040 9045

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly | Val  | Ser | Thr | Pro | Thr | Cys  | Phe | Gly | Ser | Ser | Ala  | Ser | Val | Arg |
|     | 9050 |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Ser | Trp  | Pro | Ser | Ala | Ser | Lys  | Asp | Arg | Pro | Phe | Pro  | Cys | Thr | Ala |
|     | 9065 |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Ser | Ala  | Thr | Thr | Pro | Ala | Cys  | Met | Lys | Val | Phe | Val  | Val | Cys | Cys |
|     | 9080 |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Val | Leu  | Ser | Ile | Ile | Lys | Ala  | Glu | Ile | Ser | Asp | Tyr  | Ser | Gly | Leu |
|     | 9095 |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Pro | Cys  | Val | Pro | Ala | Ile | Asn  | Gln | Ser | Leu | Phe | Phe  | Thr | Gly | Asn |
|     | 9110 |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Glu | Thr  | Glu | Leu | Gln | Leu | Gln  | Cys | Lys | Pro | His | Lys  | Lys | Tyr | Leu |
|     | 9125 |     |     |     |     | 9130 |     |     |     |     | 9135 |     |     |     |
| Thr | Trp  | Leu | Phe | Gln | Gly | Ser  | Pro | Ile | Ala | Val | Val  | Asn | His | Cys |
|     | 9140 |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Asp | Asn  | Asp | Gly | Val | Leu | Leu  | Ser | Gly | Pro | Ala | Asn  | Leu | Thr | Phe |
|     | 9155 |     |     |     |     | 9160 |     |     |     |     | 9165 |     |     |     |
| Ser | Thr  | Arg | Arg | Ser | Lys | Leu  | Gln | Leu | Phe | Gln | Pro  | Phe | Leu | Pro |
|     | 9170 |     |     |     |     | 9175 |     |     |     |     | 9180 |     |     |     |
| Gly | Thr  | Tyr | Gln | Cys | Val | Ser  | Gly | Pro | Cys | His | His  | Thr | Phe | His |
|     | 9185 |     |     |     |     | 9190 |     |     |     |     | 9195 |     |     |     |
| Leu | Ile  | Pro | Asn | Thr | Thr | Ala  | Ser | Leu | Pro | Ala | Thr  | Asn | Asn | Gln |
|     | 9200 |     |     |     |     | 9205 |     |     |     |     | 9210 |     |     |     |
| Thr | Thr  | His | Gln | Arg | His | Arg  | Arg | Asp | Arg | Gly | His  | Val | Gln | Ser |
|     | 9215 |     |     |     |     | 9220 |     |     |     |     | 9225 |     |     |     |
| Ser | Arg  | Ser | Thr | Arg | Pro | Gln  | Tyr | Met | Pro | Ile | Leu  | Asp | Tyr | Glu |
|     | 9230 |     |     |     |     | 9235 |     |     |     |     | 9240 |     |     |     |
| Ala | Glu  | Pro | Gln | Arg | Pro | Met  | Leu | Pro | Ala | Ile | Ser  | Tyr | Phe | Asn |
|     | 9245 |     |     |     |     | 9250 |     |     |     |     | 9255 |     |     |     |
| Leu | Thr  | Gly | Gly | Asp | Asp | Pro  | Thr | Gly | Gln | Gln | Gln  | Arg | Gln | Arg |
|     | 9260 |     |     |     |     | 9265 |     |     |     |     | 9270 |     |     |     |
| Pro | Ser  | Pro | Gly | His | Gly | Arg  | Pro | Arg | Leu | Gly | Ala  | Ala | Thr | Arg |
|     | 9275 |     |     |     |     | 9280 |     |     |     |     | 9285 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro  | Thr | Ser | His | Ser | Pro | Ala  | Ala | Gly | Glu | Ser | Arg  | Gln | Gly | Ala |
| 9290 |     |     |     |     |     | 9295 |     |     |     |     | 9300 |     |     |     |
| Ala  | Gly | Arg | His | Ser | His | Pro  | Pro | Val | Gln | Glu | Arg  | His | Leu | Leu |
| 9305 |     |     |     |     |     | 9310 |     |     |     |     | 9315 |     |     |     |
| Pro  | Gly | Glu | Thr | Gly | Gln | Asp  | Leu | Leu | Arg | Gly | His  | Pro | Asp | Arg |
| 9320 |     |     |     |     |     | 9325 |     |     |     |     | 9330 |     |     |     |
| Pro  | Ser | Pro | Leu | Leu | Arg | Ala  | Pro | Ala | Ala | Ala | Pro  | Glu | Val | His |
| 9335 |     |     |     |     |     | 9340 |     |     |     |     | 9345 |     |     |     |
| Leu  | Pro | Gly | Arg | Ser | Gln | Pro  | His | Arg | His | His | Pro  | Ala | Val | Gly |
| 9350 |     |     |     |     |     | 9355 |     |     |     |     | 9360 |     |     |     |
| Arg  | Tyr | Gln | Gly | Val | His | Pro  | Leu | Leu | Leu | Arg | Leu  | Pro | Arg | Leu |
| 9365 |     |     |     |     |     | 9370 |     |     |     |     | 9375 |     |     |     |
| Arg  | Pro | His | Ser | Asp | Gln | Asp  | Pro | Leu | Arg | Pro | Pro  | Arg | Pro | Pro |
| 9380 |     |     |     |     |     | 9385 |     |     |     |     | 9390 |     |     |     |
| Pro  | His | Glu | Leu | Ile | Thr | Pro  | Leu | Ser | Ser | Glu | Ile  | Asn | Ile | Ile |
| 9395 |     |     |     |     |     | 9400 |     |     |     |     | 9405 |     |     |     |
| Leu  | Met | Met | Ile | Ile | Lys | Asn  | Asn | His | Leu | Ile | Asn  | Lys | Asp | Thr |
| 9410 |     |     |     |     |     | 9415 |     |     |     |     | 9420 |     |     |     |
| Ile  | Ile | Leu | Met | Ile | Val | Leu  | Lys | Asn | Lys | Glu | Ser  | Leu | Thr | Asn |
| 9425 |     |     |     |     |     | 9430 |     |     |     |     | 9435 |     |     |     |
| Leu  | Ile | Pro | Gly | Leu | Cys | Pro  | Cys | Phe | Leu | Pro | Thr  | Pro | Pro | His |
| 9440 |     |     |     |     |     | 9445 |     |     |     |     | 9450 |     |     |     |
| Ser  | Pro | Leu | Pro | Ser | Ser | Gly  | Thr | Ala | Asp | Pro | Gly  | Gly | Leu | Gln |
| 9455 |     |     |     |     |     | 9460 |     |     |     |     | 9465 |     |     |     |
| Thr  | Ser | Ser | Thr | Arg | Arg | Gly  | Cys | Gln | Ile | Pro | Pro  | Val | Pro | Gln |
| 9470 |     |     |     |     |     | 9475 |     |     |     |     | 9480 |     |     |     |
| Ser  | Ser | Phe | Tyr | Leu | Leu | Ser  | Asp | Val | Gln | Lys | Ala  | Arg | Pro | Gly |
| 9485 |     |     |     |     |     | 9490 |     |     |     |     | 9495 |     |     |     |
| Gly  | Leu | Arg | Pro | Arg | Leu | Pro  | Leu | Arg | Cys | Arg | Gln  | Arg | Thr | Asp |
| 9500 |     |     |     |     |     | 9505 |     |     |     |     | 9510 |     |     |     |
| Arg  | Ala | Leu | His | Gln | Pro | Pro  | Leu | Arg | Leu | Phe | Arg  | Trp | Ile | Pro |

9515

9520

9525

Arg Glu Ala Pro Gly Gly Ala Val Pro Ala Thr Gly Pro Arg His  
 9530 9535 9540

His Gln Glu Arg Gly Asn His Pro Gln Ala Gly Arg Gly Gly Gly  
 9545 9550 9555

Pro Arg Leu Leu Gly Lys Thr His Leu Gln His Gly His Gln Gly  
 9560 9565 9570

Arg Arg Pro Ser Gln Phe Phe Gln Gln His His Phe Pro His Gly  
 9575 9580 9585

Tyr Pro Ser Leu Tyr Gln Arg Trp Lys Ile Ile Leu Thr Ser Phe  
 9590 9595 9600

Ser Thr Val Lys His Ile Lys Ile Asn His Ser Glu His Ile Ser  
 9605 9610 9615

Cys Ser Leu Trp Ile Arg Phe Arg Thr Glu Trp Trp His Cys Ser  
 9620 9625 9630

Cys Ser Thr Val Gly Leu Ser Thr His Phe Lys Arg Lys Tyr Asn  
 9635 9640 9645

Pro Ser Gln Trp Ser Ile Asn Ser Cys Lys Ser Thr Tyr Gln Leu  
 9650 9655 9660

Gln Lys Arg Gly His Cys His Tyr Leu Arg Arg Cys Asn Lys Gln  
 9665 9670 9675

His Lys Leu Ala Arg Tyr Lys Ile Arg Trp His Ser Cys Lys His  
 9680 9685 9690

Trp Gln Arg Ile Gly Ile Trp Asn His Tyr Arg Asp Cys His Arg  
 9695 9700 9705

Cys Ile Pro Asn Ser Ser Ile Gly Tyr Trp Pro Tyr Leu Gln Tyr  
 9710 9715 9720

Arg Arg His Cys Cys Leu Glu Gln Arg Gly Thr Tyr Ile Met Asp  
 9725 9730 9735

His Ser Arg Pro Leu Ala Lys Leu Gln Asn Ile Leu Lys Arg Cys  
 9740 9745 9750

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Gln Thr His Thr Leu Leu Asp Lys Val Trp Lys Ser Asn Ser Gly  
 9755 9760 9765  
  
 Tyr Cys Asp Cys Ile Gly Ser Glu Trp Lys Ser Gln Pro Asn His  
 9770 9775 9780  
  
 Lys His Ser Lys His Cys Thr Arg Leu Pro Gln Val Cys Lys Trp  
 9785 9790 9795  
  
 Ser Phe Ala Lys Gln Leu His Ile Arg Gln Arg Ile Leu Glu Leu  
 9800 9805 9810  
  
 Gln Lys Gly Arg Cys Tyr Thr Cys Ala Leu Tyr Cys Tyr Arg Phe  
 9815 9820 9825  
  
 Tyr Ala His Lys Gly Leu Ser Lys His Ile Cys Ser Phe Lys Lys  
 9830 9835 9840  
  
 Pro Tyr Cys Gln Ser Ser Leu Ser Gln Trp Gly Gly Gln Thr Thr  
 9845 9850 9855  
  
 Asp Ala Asp Tyr Tyr Phe Asn Gly Cys Asn Leu His Leu Gln Tyr  
 9860 9865 9870  
  
 His Phe Ser Met Glu Met Gly Tyr Val His Arg Asn Thr Cys Tyr  
 9875 9880 9885  
  
 Gln Leu Leu His Leu Leu Leu His Arg Pro Arg Met Asn Thr Val  
 9890 9895 9900  
  
 Ser His Pro Ala Cys Gln Pro Phe Pro Pro His Ser Val Tyr Gly  
 9905 9910 9915  
  
 Lys Asn Ser Glu Ala Gln Asn Lys Ile Lys Phe Lys Cys Phe Ile  
 9920 9925 9930  
  
 Asp Ser Thr Val Leu Gln Asp Ser Ser Ser Tyr Phe Ser Ser Thr  
 9935 9940 9945  
  
 Leu Pro Gly His Gly Ile His His Pro Leu Pro Pro His Ser Leu  
 9950 9955 9960  
  
 Glu His Leu Asn Ala Ile Gly Asp Gly His Ala Phe Gly Leu His  
 9965 9970 9975  
  
 Val Pro His Ser Phe Arg Ala Ser Gln Ser Arg Val Gly Gln Gly  
 9980 9985 9990

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|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Asp   | Glu | Thr | Leu | Arg | Ala | Leu   | Pro | His | Leu | His | Leu   | Thr | Ala | Gln |
| 9995  |     |     |     |     |     | 10000 |     |     |     |     | 10005 |     |     |     |
| Gln   | Leu | Arg | Ile | Val | Leu | Gly   | Gly | Arg | Asp | His | Gly   | Tyr | Leu | Glu |
| 10010 |     |     |     |     |     | 10015 |     |     |     |     | 10020 |     |     |     |
| Glu   | Ala | Glu | Glu | Arg | Arg | Trp   | Glu | Ser | Ser | Ala | Asn   | Gly | Ile | Gly |
| 10025 |     |     |     |     |     | 10030 |     |     |     |     | 10035 |     |     |     |
| Arg   | Trp | Cys | Arg | Ile | Arg | Pro   | Arg | Ser | Ser | Arg | Cys   | Arg | Arg | Arg |
| 10040 |     |     |     |     |     | 10045 |     |     |     |     | 10050 |     |     |     |
| Ser   | Val | Lys | Leu | Leu | Leu | Arg   | Gly | Ser | Gly | Ser | Arg   | Asp | Ser | Leu |
| 10055 |     |     |     |     |     | 10060 |     |     |     |     | 10065 |     |     |     |
| Ser   | Met | Met | Pro | Thr | Ala | Leu   | Ser | Ile | Ser | Arg | Leu   | Val | Arg | Arg |
| 10070 |     |     |     |     |     | 10075 |     |     |     |     | 10080 |     |     |     |
| Ala   | Gln | Gln | Arg | Met | Arg | Ile   | Ser | Leu | Arg | Ser | Leu   | Gln | Tyr | Val |
| 10085 |     |     |     |     |     | 10090 |     |     |     |     | 10095 |     |     |     |
| Gln   | His | Arg | Thr | Thr | Arg | Leu   | Phe | Asn | Ser | Pro | Phe   | Asn | Thr | Leu |
| 10100 |     |     |     |     |     | 10105 |     |     |     |     | 10110 |     |     |     |
| Gln   | Pro | Lys | Leu | Ile | Ala | Gly   | Arg | Met | Leu | Pro | Thr   | Trp | Pro | Ser |
| 10115 |     |     |     |     |     | 10120 |     |     |     |     | 10125 |     |     |     |
| Tyr   | Gln | Ile | Leu | Arg | Ile | Lys   | Trp | Arg | Ser | Leu | Gln   | Asn | Thr | Leu |
| 10130 |     |     |     |     |     | 10135 |     |     |     |     | 10140 |     |     |     |
| Pro   | Thr | Tyr | Met | Ile | Ser | Leu   | Gly | Met | Trp | Arg | Phe   | Thr | Thr | Ser |
| 10145 |     |     |     |     |     | 10150 |     |     |     |     | 10155 |     |     |     |
| Arg   | Tyr | His | Ile | Thr | Leu | Trp   | Leu | Asn | Met | Gln | Pro   | Arg | Met | Ile |
| 10160 |     |     |     |     |     | 10165 |     |     |     |     | 10170 |     |     |     |
| Leu   | Arg | Asn | His | Arg | Ala | Ser   | Thr | Ala | Pro | Pro | Ala   | Met | Gln | Arg |
| 10175 |     |     |     |     |     | 10180 |     |     |     |     | 10185 |     |     |     |
| Arg   | Asp | Pro | Gly | Ser | Arg | Gln   | Trp | Gln | Trp | Arg | Thr   | His | Arg | Ser |
| 10190 |     |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| Tyr   | Pro | Trp | Ile | Ile | Trp | Glu   | Leu | Asn | Lys | Ser | Met   | Leu | Ala | Gln |
| 10205 |     |     |     |     |     | 10210 |     |     |     |     | 10215 |     |     |     |
| His   | Arg | His | Met | Leu | Met | His   | Leu | Phe | Ser | Thr | Leu   | Ser | Ser | Ser |
| 10220 |     |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |

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|                  |                     |              |                              |             |
|------------------|---------------------|--------------|------------------------------|-------------|
| Gly Val<br>10235 | Lys Thr Ile Ser     | Gln<br>10240 | Gly Thr Gly Asn Ser<br>10245 | Cys Arg Thr |
| Ala Asn<br>10250 | Pro Ala Glu Gln     | Gly<br>10255 | Asn Pro Arg Thr Leu<br>10260 | Thr Leu Cys |
| Met Asp<br>10265 | Arg Val Ser Gln     | Ser<br>10270 | Gly Ser Thr Gly Ser<br>10275 | Ser Thr Arg |
| Glu Ala<br>10280 | Arg Val Ser Val     | Ser<br>10285 | Ser Gln Arg Gly Lys<br>10290 | Gly Ala Gly |
| Arg Tyr<br>10295 | Gly Trp Arg Asp     | Ala<br>10300 | Ala Asp Arg Val Arg<br>10305 | Asp Arg Val |
| Met Met<br>10310 | Gln Leu Leu Ser     | Asp<br>10315 | Ile Phe Val Leu Ala<br>10320 | Val Ala Glu |
| Pro Gly<br>10325 | Pro Gly Ala Ala     | His<br>10330 | Arg Ser Pro Ala Ala<br>10335 | Val Pro Ala |
| Leu Gly<br>10340 | Thr Leu Gly Val     | Glu<br>10345 | Ile Val Lys Gln Pro<br>10350 | Leu Ser Gln |
| Thr Val<br>10355 | Gln Gln Ile Gly     | Leu<br>10360 | Arg Ser Asp Glu Asp<br>10365 | Pro Ile Met |
| Pro Asp<br>10370 | Ser Ser Asp His     | Ile<br>10375 | Asp His Arg Gly Met<br>10380 | Gly Gln Thr |
| Gln Pro<br>10385 | Asp Asp Ala Ile     | Leu<br>10390 | Leu Gly Phe Gly Asp<br>10395 | Gly Gly Gly |
| Gly Lys<br>10400 | Asn Arg Lys Asn     | His<br>10405 | Asp Leu Leu Ile Gln<br>10410 | Thr Val Ser |
| Glu His<br>10415 | Phe Lys Met Lys     | Val<br>10420 | Ala Glu Met Ala Pro<br>10425 | Leu Ala Pro |
| Ala Val<br>10430 | Leu Val Glu Asn     | Asn<br>10435 | Ser Gln Val Lys Gly<br>10440 | Asp Thr Val |
| Leu Glu<br>10445 | Met Phe His Gly     | Gly<br>10450 | Phe Gln Gln Ser Leu<br>10455 | His Ala His |
| Ile Gln          | Lys Gln Asp Asn Ser |              | Glu Ser Gly Arg Val          | Leu Phe Leu |

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|       |       |     |     |     |     |       |     |     |     |     |       |             |
|-------|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-------------|
| 10460 |       |     |     |     |     |       |     |     |     |     |       |             |
|       |       |     |     |     |     |       |     |     |     |     |       |             |
| Asn   | His   | His | Val | Thr | Leu | Leu   | His | His | Pro | Gln | Ile   | Ile Phe Ile |
|       | 10475 |     |     |     |     | 10480 |     |     |     |     | 10485 |             |
| Phe   | Pro   | Ala | Leu | Asn | Asp | Ser   | Asn | Phe | Leu | Arg | Ile   | Gln Ala Ser |
|       | 10490 |     |     |     |     | 10495 |     |     |     |     | 10500 |             |
| His   | Asp   | Lys | Glu | Leu | Ala | Gln   | Ser | Ala | Leu | His | Arg   | His Ser Ala |
|       | 10505 |     |     |     |     | 10510 |     |     |     |     | 10515 |             |
| His   | Pro   | His | Asn | Ser | Lys | Ile   | Phe | Cys | Ser | Trp | Phe   | Thr Cys Ser |
|       | 10520 |     |     |     |     | 10525 |     |     |     |     | 10530 |             |
| Arg   | Leu   | Thr | Ser | Gly | Ile | Ser   | Lys | Ser | Leu | Pro | Arg   | Ser Leu Ser |
|       | 10535 |     |     |     |     | 10540 |     |     |     |     | 10545 |             |
| Ser   | Ser   | Leu | Ser | Asn | Asn | Cys   | Lys | Tyr | Ser | Phe | Ile   | Ser Ser Pro |
|       | 10550 |     |     |     |     | 10555 |     |     |     |     | 10560 |             |
| Lys   | Phe   | Leu | Ala | Ile | Gly | Pro   | Pro | Gly | Ile | Arg | Leu   | Gly Gln Ala |
|       | 10565 |     |     |     |     | 10570 |     |     |     |     | 10575 |             |
| Thr   | Val   | Gln | Ile | Asn | Arg | Ser   | Pro | Pro | Gln | Ala | Leu   | Pro Asn Ala |
|       | 10580 |     |     |     |     | 10585 |     |     |     |     | 10590 |             |
| Arg   | Leu   | Leu | Ala | Cys | Trp | Leu   | Asp | Pro | Val | Ile | Ser   | Ser Arg Leu |
|       | 10595 |     |     |     |     | 10600 |     |     |     |     | 10605 |             |
| Asp   | Arg   | Lys | Ser | Pro | Arg | Gln   | Phe | Leu | Arg | Lys | Ser   | Thr Lys Glu |
|       | 10610 |     |     |     |     | 10615 |     |     |     |     | 10620 |             |
| Lys   | Ser   | Ser | Arg | Cys | Thr | Phe   | Arg | Ala | Ser | Gly | Thr   | Thr Met Lys |
|       | 10625 |     |     |     |     | 10630 |     |     |     |     | 10635 |             |
| Met   | Gln   | Ala | Val | Arg | Ser | Ser   | Met | Val | Ser | Leu | Ile   | Cys Lys Lys |
|       | 10640 |     |     |     |     | 10645 |     |     |     |     | 10650 |             |
| Gln   | Lys   | Ile | Lys | His | Thr | Met   | Leu | Ala | Trp | Arg | Thr   | Gly Gly Ile |
|       | 10655 |     |     |     |     | 10660 |     |     |     |     | 10665 |             |
| Val   | Leu   | Ser | Ser | Thr | Arg | Gln   | Ala | Thr | Gly | Ser | Pro   | Ala Arg Pro |
|       | 10670 |     |     |     |     | 10675 |     |     |     |     | 10680 |             |
| Ser   | Lys   | Leu | Ser | Leu | Leu | Lys   | Thr | Ile | Thr | Glu | Arg   | Arg Ser Arg |
|       | 10685 |     |     |     |     | 10690 |     |     |     |     | 10695 |             |



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Trp Pro Ala Met Ile Arg Gln Asp Glu Tyr Thr Pro Gly Thr Leu  
 10700 10705 10710  
 Ala Ser Ala Ser Glu Lys Lys Arg Pro Arg Lys Gln Gly Thr Thr  
 10715 10720 10725  
 Met Leu Ser Leu Lys Ser Ser Lys Ala Met Pro Cys Gly Ser Thr  
 10730 10735 10740  
 Lys Ser Ser Gly Ala Tyr Lys Met Leu Leu Pro Ser Cys Thr Gly  
 10745 10750 10755  
 Ser Glu Ala Pro Asp Pro Ser Arg Tyr Thr Tyr Lys Ala Ser Ala  
 10760 10765 10770  
 Ser Ile Ala Tyr Arg Ala Ala Ala His Asn Arg Arg Lys Ser Gln  
 10775 10780 10785  
 Arg Lys Ala Glu Leu Pro Val His Pro Leu Ser Ala Gln Tyr Ile  
 10790 10795 10800  
 Ala Gln Ile Tyr Thr Asp Val Lys Ala Lys Val Lys Tyr Pro Pro  
 10805 10810 10815  
 Asn Asn His Thr Arg Pro Ala His Ala Gln Lys Pro Val Thr His  
 10820 10825 10830  
 Ser Lys Lys Tyr Ala His Phe Leu Lys Arg Pro Asn Cys Arg His  
 10835 10840 10845  
 Phe Arg Val Pro Thr Leu Arg His Arg Asn Ser Thr Phe Lys Phe  
 10850 10855 10860  
 Arg Arg Pro Leu Lys Thr Ser Pro Ala Pro Pro Leu Thr Val Ala  
 10865 10870 10875  
 Arg Leu Ser Ala Asn His Leu Pro Pro Ser Pro Asn Ser Asn Ser  
 10880 10885 10890  
 Ser Phe Ala Tyr Arg Ala Pro Lys Val Gly Ile Leu Leu Met Met  
 10895 10900 10905

<210> 13  
 <211> 11238  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Artificially Synthesized

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&lt;400&gt; 13

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
 1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Cys Gly Ser Gly Asp Arg  
 20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Met Arg Arg Ser Arg Phe  
 35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg  
 50 55 60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
 65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
 85 90 95

Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
 100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
 115 120 125

Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
 130 135 140

Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
 145 150 155 160

Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
 165 170 175

Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
 180 185 190

Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
 195 200 205

Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
 210 215 220

Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
 225 230 235 240

## 368530-7006W01\_SequenceListing\_ST25.txt

Ser Met Pro Ser Thr Pro Pro Ile Asp Val Asn Asp Gly Lys Trp Pro  
 245 250 255  
 Ala Trp His Tyr Ala Gln Tyr Met Thr Leu Trp Asp Phe Pro Thr Trp  
 260 265 270  
 Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile Thr Met Val Met Arg Phe  
 275 280 285  
 Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe Asp Ser Arg Gly Phe Pro  
 290 295 300  
 Ser Leu His Pro Ile Asp Val Asn Gly Ser Leu Phe Trp His Gln Asn  
 305 310 315 320  
 Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn Ser Ala Pro Leu Thr Gln  
 325 330 335  
 Met Gly Gly Arg Arg Val Arg Trp Glu Val Tyr Ile Ser Arg Ala Arg  
 340 345 350  
 Leu Val Asn Arg Gln Ile Thr Arg Ser Phe Ile Ala Val Val Tyr His  
 355 360 365  
 Ser Ile Ala Asn Ala Val Ser Ala Ser Asp Thr Thr Val Ser Asn Leu  
 370 375 380  
 Arg Leu Glu Tyr Leu Ile Arg Leu Thr Ile Gly Leu Arg Leu Glu Phe  
 385 390 395 400  
 Asp Ala Thr Met Arg Val Met Gly Ile Leu Arg Ser Tyr Gln Gln Trp  
 405 410 415  
 Trp Ile Trp Gly Ile Leu Gly Phe Trp Met Leu Met Ile Cys Asn Val  
 420 425 430  
 Trp Gly Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys  
 435 440 445  
 Glu Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala His Lys  
 450 455 460  
 Glu Glu Val His Asn Ile Trp Ala Thr His Ala Cys Val Pro Thr Asp  
 465 470 475 480  
 Pro Asn Pro Gln Glu Ile Val Leu Lys Asn Val Thr Glu Asn Phe Asn  
 485 490 495

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Met Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser  
500 505 510

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys  
515 520 525

Val Thr Leu Asn Cys Ser Asp Val Lys Ile Lys Gly Thr Asn Ala Thr  
530 535 540

Tyr Asn Asn Ala Thr Tyr Asn Asn Asn Asn Thr Ile Ser Asp Met Lys  
545 550 555 560

Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Thr Asp Lys Lys Lys Lys  
565 570 575

Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Ala Leu Asp Gly Lys  
580 585 590

Glu Thr Asn Ser Thr Asn Ser Ser Glu Tyr Arg Leu Ile Asn Cys Asn  
595 600 605

Thr Ser Ala Val Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile  
610 615 620

Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn  
625 630 635 640

Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val  
645 650 655

Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu  
660 665 670

Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Phe Glu Asn Leu  
675 680 685

Thr Asn Asn Ala Lys Ile Ile Ile Val His Leu Asn Glu Ser Val Glu  
690 695 700

Ile Asn Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Val Arg Ile  
705 710 715 720

Gly Pro Gly Gln Thr Phe Phe Ala Thr Gly Asp Ile Ile Gly Asp Ile  
725 730 735

Arg Gln Ala His Cys Asn Ile Ser Arg Lys Lys Trp Asn Thr Thr Leu  
740 745 750

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Gln Arg Val Lys Glu Lys Leu Lys Glu Lys Phe Pro Asn Lys Thr Ile  
755 760 765

Gln Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser  
770 775 780

Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Tyr Thr Ser Asp Leu Phe  
785 790 795 800

Asn Ser Thr Tyr Met Ser Asn Asn Thr Gly Gly Ala Asn Ile Thr Leu  
805 810 815

Gln Cys Arg Ile Lys Gln Ile Ile Arg Met Trp Gln Gly Val Gly Gln  
820 825 830

Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn  
835 840 845

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Glu Lys Asn Asp  
850 855 860

Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg  
865 870 875 880

Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile  
885 890 895

Ala Pro Asp Lys Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala  
900 905 910

Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser  
915 920 925

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu  
930 935 940

Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu  
945 950 955 960

Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu  
965 970 975

Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu  
980 985 990

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val

995

1000

1005

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro  | Trp | Asn | Ala | Ser | Trp | Ser  | Asn | Lys | Ser | Tyr | Glu  | Glu | Ile | Trp |
| 1010 |     |     |     |     |     | 1015 |     |     |     |     | 1020 |     |     |     |
| Gly  | Asn | Met | Thr | Trp | Met | Gln  | Trp | Asp | Arg | Glu | Ile  | Asn | Asn | Tyr |
| 1025 |     |     |     |     |     | 1030 |     |     |     |     | 1035 |     |     |     |
| Thr  | Asn | Thr | Ile | Tyr | Ser | Leu  | Leu | Glu | Glu | Ser | Gln  | Asn | Gln | Gln |
| 1040 |     |     |     |     |     | 1045 |     |     |     |     | 1050 |     |     |     |
| Glu  | Lys | Asn | Glu | Lys | Asp | Leu  | Leu | Ala | Leu | Asp | Ser  | Trp | Glu | Ser |
| 1055 |     |     |     |     |     | 1060 |     |     |     |     | 1065 |     |     |     |
| Leu  | Trp | Ser | Trp | Phe | Asn | Ile  | Thr | Asn | Trp | Leu | Trp  | Tyr | Ile | Arg |
| 1070 |     |     |     |     |     | 1075 |     |     |     |     | 1080 |     |     |     |
| Ile  | Phe | Ile | Ile | Ile | Val | Gly  | Gly | Leu | Ile | Gly | Leu  | Arg | Ile | Ile |
| 1085 |     |     |     |     |     | 1090 |     |     |     |     | 1095 |     |     |     |
| Phe  | Ala | Val | Leu | Ser | Ile | Val  | Asn | Arg | Val | Arg | Gln  | Gly | Tyr | Ser |
| 1100 |     |     |     |     |     | 1105 |     |     |     |     | 1110 |     |     |     |
| Pro  | Leu | Ser | Phe | Gln | Thr | Leu  | Thr | Pro | Ser | Pro | Arg  | Glu | Pro | Asp |
| 1115 |     |     |     |     |     | 1120 |     |     |     |     | 1125 |     |     |     |
| Arg  | Leu | Gly | Arg | Ile | Glu | Glu  | Glu | Gly | Gly | Glu | Gln  | Asp | Arg | Ala |
| 1130 |     |     |     |     |     | 1135 |     |     |     |     | 1140 |     |     |     |
| Arg  | Ser | Val | Arg | Leu | Val | Asn  | Gly | Phe | Leu | Ala | Leu  | Ala | Trp | Glu |
| 1145 |     |     |     |     |     | 1150 |     |     |     |     | 1155 |     |     |     |
| Asp  | Leu | Arg | Ser | Leu | Cys | Leu  | Phe | Ser | Tyr | His | Arg  | Leu | Arg | Asp |
| 1160 |     |     |     |     |     | 1165 |     |     |     |     | 1170 |     |     |     |
| Leu  | Ile | Leu | Ile | Ala | Ala | Arg  | Ala | Ala | Ala | Leu | Leu  | Gly | Arg | Ser |
| 1175 |     |     |     |     |     | 1180 |     |     |     |     | 1185 |     |     |     |
| Ser  | Leu | Trp | Gly | Leu | Gln | Lys  | Gly | Trp | Glu | Ala | Leu  | Lys | Tyr | Leu |
| 1190 |     |     |     |     |     | 1195 |     |     |     |     | 1200 |     |     |     |
| Gly  | Ser | Leu | Val | Gln | Tyr | Trp  | Gly | Leu | Glu | Leu | Lys  | Lys | Ser | Ala |
| 1205 |     |     |     |     |     | 1210 |     |     |     |     | 1215 |     |     |     |
| Ile  | Ser | Leu | Phe | Asp | Ala | Ile  | Ala | Ile | Thr | Val | Ala  | Glu | Gly | Thr |
| 1220 |     |     |     |     |     | 1225 |     |     |     |     | 1230 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp  | Arg | Ile | Ile | Asn | Ile | Val  | Gln | Arg | Ile | Ser | Arg  | Ala | Phe | Tyr |
| 1235 |     |     |     |     |     | 1240 |     |     |     |     | 1245 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asn  | Ile | Pro | Arg | Arg | Ile | Arg  | Gln | Gly | Phe | Glu | Ala  | Thr | Leu | Gln |
| 1250 |     |     |     |     |     | 1255 |     |     |     |     | 1260 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly  | Thr | Ser | Arg | Val | Asp | Pro  | Gly | Gly | Gln | Thr | Ala  | Asp | Gln | Pro |
| 1265 |     |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Leu | Cys | Leu | Leu | Val | Ala  | Ser | His | Leu | Leu | Phe  | Ala | Pro | Pro |
| 1280 |     |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Cys | Leu | Pro | Pro | Trp | Lys  | Val | Pro | Leu | Pro | Leu  | Ser | Phe | Pro |
| 1295 |     |     |     |     |     | 1300 |     |     |     |     | 1305 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asn  | Lys | Met | Arg | Lys | Leu | His  | Arg | Ile | Val | Val | Gly  | Val | Ile | Leu |
| 1310 |     |     |     |     |     | 1315 |     |     |     |     | 1320 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Phe  | Trp | Gly | Val | Gly | Trp | Gly  | Arg | Thr | Ala | Arg | Gly  | Arg | Ile | Gly |
| 1325 |     |     |     |     |     | 1330 |     |     |     |     | 1335 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Lys  | Thr | Ile | Ala | Gly | Met | Leu  | Gly | Met | Arg | Trp | Ala  | Leu | Trp | Leu |
| 1340 |     |     |     |     |     | 1345 |     |     |     |     | 1350 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Leu  | Arg | Arg | Lys | Glu | Pro | Ala  | Asp | Leu | Gln | Ile | Ile  | His | Leu | Cys |
| 1355 |     |     |     |     |     | 1360 |     |     |     |     | 1365 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Val | Arg | Arg | Lys | Arg | Asn  | Gly | Ile | Met | Gly | Ile  | Met | Gly | Leu |
| 1370 |     |     |     |     |     | 1375 |     |     |     |     | 1380 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| His  | Ile | Gly | Gln | Ile | Ser | Thr  | Tyr | Ala | Gly | His | Arg  | Ala | Cys | Gly |
| 1385 |     |     |     |     |     | 1390 |     |     |     |     | 1395 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Leu  | Ala | Pro | Pro | Gln | Asp | Met  | Ala | Arg | Val | Arg | Ala  | Gln | Arg | His |
| 1400 |     |     |     |     |     | 1405 |     |     |     |     | 1410 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asp  | Pro | Leu | Gln | Cys | Ala | Pro  | Gly | Leu | Pro | Pro | Arg  | His | Val | His |
| 1415 |     |     |     |     |     | 1420 |     |     |     |     | 1425 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Leu | Pro | Val | Gln | His | Ala  | Ile | Cys | Glu | Gly | Ala  | Ala | Gly | Ala |
| 1430 |     |     |     |     |     | 1435 |     |     |     |     | 1440 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Cys | His | Val | Gln | Ser | Glu  | Pro | Asp | Gly | Gly | Val  | His | Glu | Cys |
| 1445 |     |     |     |     |     | 1450 |     |     |     |     | 1455 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly  | Ala | Val | Glu | Asn | Ser | Glu  | Ile | Ile | Gln | Asp | Gln  | Val | Pro | Gly |
| 1460 |     |     |     |     |     | 1465 |     |     |     |     | 1470 |     |     |     |

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Leu Arg Met Arg Arg Gln Ala Arg Gln Ala Ser Ala Arg Val Cys  
 1475 1480 1485  
 Gly Gly Asp Gly Gly Pro Ala Thr Arg Ser Phe Gly Val Val Leu  
 1490 1495 1500  
 Gln Arg Asp Gly Val Arg Leu Gln Arg Gly Arg Ile Leu Glu Val  
 1505 1510 1515  
 Val Phe Gly Ala Gly Cys Glu Pro Ala Gly Ala Glu Leu Lys Ser  
 1520 1525 1530  
 Val Val Phe Cys Val Leu Gln Gln His Glu Arg Lys Arg Leu Leu  
 1535 1540 1545  
 Gly Arg Gly Ile Gln Pro Leu Ser Asp Gly Ala Ser Pro Leu Leu  
 1550 1555 1560  
 Gly Gly Ser Ala Ser Glu Cys Asp Gly Ile His Gly Gly Arg Pro  
 1565 1570 1575  
 Ala Arg Ala Ala Arg Glu Leu Phe Asn Pro Asp Leu Arg Asp Pro  
 1580 1585 1590  
 Glu Leu Leu Val Arg Gly Arg Ser Cys Arg Arg Ser Cys Cys Phe  
 1595 1600 1605  
 Arg Arg Gln Arg Arg Ala Arg Asn Gly Pro Gly Arg Arg Leu Leu  
 1610 1615 1620  
 Gln Leu Ser Gly Gly Gln Leu Glu Phe His Gln Ser Arg Gln Pro  
 1625 1630 1635  
 Glu Arg Gly Glu Ala Ala Ala Ala Asp Gly Pro Ala Arg Gly Pro  
 1640 1645 1650  
 Asp Pro Ala Pro Gly Arg Ala Asp Pro Ala Gly Gly Ser Ala Ala  
 1655 1660 1665  
 Gly Gly Asp Ala Gly Arg Gly Cys His Gly Glu Asn Gln Ile Lys  
 1670 1675 1680  
 Asn Glu Ser Ile Asn Lys Arg Arg Arg Leu Leu Ile Leu Thr Gln  
 1685 1690 1695  
 Ser Leu Glu Ser Leu Phe Asp Phe Ser Arg Ala Val Gly Pro Gly  
 1700 1705 1710



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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Pro  | Val | Ser | Ile | Ile | Glu  | His | Pro | Val | Asp | Leu  | Phe | Gln | Asp |
|     | 1715 |     |     |     |     | 1720 |     |     |     |     | 1725 |     |     |     |
| Pro | Val  | Glu | Val | Gly | Leu | Asp  | Val | Glu | Val | His | Gly  | His | Glu | Pro |
|     | 1730 |     |     |     |     | 1735 |     |     |     |     | 1740 |     |     |     |
| Val | Pro  | Gly | Val | Glu | Val | Ala  | Pro | Leu | Gln | Gly | Leu  | Val | Leu | Gly |
|     | 1745 |     |     |     |     | 1750 |     |     |     |     | 1755 |     |     |     |
| Asp | Gly  | Val | Val | Asn | His | Pro  | Val | Ile | Ala | Gly | Ala  | Gln | Gly | Val |
|     | 1760 |     |     |     |     | 1765 |     |     |     |     | 1770 |     |     |     |
| Val | Leu  | His | Asp | Val | Leu | Glu  | Glu | Glu | Thr | Asp | Gly  | His | Gly | Gln |
|     | 1775 |     |     |     |     | 1780 |     |     |     |     | 1785 |     |     |     |
| Pro | Leu  | Gly | Val | Gly | Val | Asp  | Glu | Pro | Val | Glu | Leu  | Gly | Gly | Met |
|     | 1790 |     |     |     |     | 1795 |     |     |     |     | 1800 |     |     |     |
| His | Ala  | Gly | Gly | Asp | Glu | Met  | His | Leu | Gly | Leu | Asp  | Leu | Glu | Ile |
|     | 1805 |     |     |     |     | 1810 |     |     |     |     | 1815 |     |     |     |
| Gly | Asp  | Val | Pro | Ala | Gln | Ile  | Pro | Pro | Gly | Val | His  | Val | Val | Gln |
|     | 1820 |     |     |     |     | 1825 |     |     |     |     | 1830 |     |     |     |
| Asp | His  | Gln | His | Gly | Val | Ser  | Gly | Ala | Leu | Gly | Glu  | Phe | Val | Met |
|     | 1835 |     |     |     |     | 1840 |     |     |     |     | 1845 |     |     |     |
| Gln | Leu  | Gly | Arg | Glu | Gly | Val  | Lys | Glu | Phe | Gly | Asp  | Ala | Leu | Val |
|     | 1850 |     |     |     |     | 1855 |     |     |     |     | 1860 |     |     |     |
| Thr | Ala  | Gln | Val | Phe | His | Ala  | Leu | Ile | His | Asp | Asp  | Gly | Asp | Gly |
|     | 1865 |     |     |     |     | 1870 |     |     |     |     | 1875 |     |     |     |
| Pro | Val  | Gly | Gly | Gly | Leu | Gly  | Lys | Asp | Val | Ser | Gly  | Val | Gly | His |
|     | 1880 |     |     |     |     | 1885 |     |     |     |     | 1890 |     |     |     |
| Ile | Val  | Val | Val | Val | Leu | Gly  | Glu | Leu | Val | Ile | Gly  | His | Phe | Asn |
|     | 1895 |     |     |     |     | 1900 |     |     |     |     | 1905 |     |     |     |
| Glu | Phe  | Gly | Ala | Glu | Gly | Ala  | Arg | Leu | Gly | Asp | Glu  | Gly | Ala | Leu |
|     | 1910 |     |     |     |     | 1915 |     |     |     |     | 1920 |     |     |     |
| Asp | Pro  | Gly | Gly | Val | Val | Ala  | Leu | Ala | Asp | Leu | His  | Leu | Pro | Gly |
|     | 1925 |     |     |     |     | 1930 |     |     |     |     | 1935 |     |     |     |
| Leu | Glu  | Leu | Gly | Gly | Gly | Asp  | His | Val | His | Leu | Arg  | Gly | Asp | Glu |

| 1940 | 1945 | 1950 |     |     |     |      |     |     |     |     |      |     |     |     |
|------|------|------|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Lys  | Asn  | Gly  | Phe | Arg | Gly | Gly  | Gly | Asp | Glu | Leu | Gly  | Arg | Lys | Gln |
|      | 1955 |      |     |     |     | 1960 |     |     |     |     | 1965 |     |     |     |
| Val  | Pro  | Glu  | Gln | Leu | Gly | Leu  | Ala | Ala | Thr | Gly | Gly  | Ala | Val | Asp |
|      | 1970 |      |     |     |     | 1975 |     |     |     |     | 1980 |     |     |     |
| Asp  | Pro  | Asp  | Asp | Arg | Leu | Gln  | Val | Val | Val | Glu | Gly  | Glu | Thr | Ala |
|      | 1985 |      |     |     |     | 1990 |     |     |     |     | 1995 |     |     |     |
| Ala  | Val  | Leu  | Ala | Glu | Glu | Gly  | Gly | His | Leu | Val | His  | His | Leu | Ala |
|      | 2000 |      |     |     |     | 2005 |     |     |     |     | 2010 |     |     |     |
| His  | Met  | His  | Val | Leu | Ala | His  | Glu | Phe | Arg | Gln | Glu  | Ala | Leu | Ala |
|      | 2015 |      |     |     |     | 2020 |     |     |     |     | 2025 |     |     |     |
| Pro  | Gln  | Arg  | Glu | Glu | Leu | Leu  | Gln | Arg | Gly | Glu | Val  | Phe | Gln | Arg |
|      | 2030 |      |     |     |     | 2035 |     |     |     |     | 2040 |     |     |     |
| Leu  | Glu  | Ser  | Val | Gly | His | Gly  | His | Phe | Gly | Glu | Gly  | Leu | Leu | Gln |
|      | 2045 |      |     |     |     | 2050 |     |     |     |     | 2055 |     |     |     |
| Glu  | Phe  | Gln  | Thr | Val | Pro | Glu  | Leu | Gly | Asp | Val | Leu  | Gly | Ile | Ser |
|      | 2060 |      |     |     |     | 2065 |     |     |     |     | 2070 |     |     |     |
| Ile  | Gln  | Gln  | Thr | Ser | Ser | Phe  | Arg | Gly | Leu | Gly | Arg  | Leu | Arg | Glu |
|      | 2075 |      |     |     |     | 2080 |     |     |     |     | 2085 |     |     |     |
| Gly  | Thr  | Arg  | Arg | Trp | Ala | Ser  | Ser | Glu | Ala | Arg | Val  | Arg | Ser | Phe |
|      | 2090 |      |     |     |     | 2095 |     |     |     |     | 2100 |     |     |     |
| Gln  | Gly  | Arg  | Arg | Val | Arg | Val  | Ser | Val | Val | Ser | Val  | Thr | Val | Lys |
|      | 2105 |      |     |     |     | 2110 |     |     |     |     | 2115 |     |     |     |
| Gly  | Cys  | Ala  | Pro | Gly | Trp | Ala  | Leu | Ala | Arg | Val | Arg  | Phe | Arg | Leu |
|      | 2120 |      |     |     |     | 2125 |     |     |     |     | 2130 |     |     |     |
| Ile  | Arg  | Leu  | Val | Glu | Asn | Arg  | Ser | Arg | Ser | Ala | Pro  | Cys | Ala | Ser |
|      | 2135 |      |     |     |     | 2140 |     |     |     |     | 2145 |     |     |     |
| Ala  | Arg  | Gln  | Leu | Ser | Met | Ser  | Ser | Leu | Ser | Ala | Ser  | Ala | Ala | Trp |
|      | 2150 |      |     |     |     | 2155 |     |     |     |     | 2160 |     |     |     |
| Pro  | Leu  | Ala  | Arg | Ser | Leu | Pro  | Leu | Glu | Val | Cys | Pro  | Gln | Thr | Gly |
|      | 2165 |      |     |     |     | 2170 |     |     |     |     | 2175 |     |     |     |

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Gln Arg Arg Asp Leu Arg Ala Ser Leu Gly Ala Arg Lys Thr Asp  
 2180 2185 2190  
  
 Ser Gly Ala Ala Ser Ala Pro Gln Leu Ala Gln Thr Val Ser His  
 2195 2200 2205  
  
 Ser Thr Ser Gln Val Arg Ser Gly Arg Leu Gly Ser Lys Thr Arg  
 2210 2215 2220  
  
 Phe Pro Pro Cys Phe Leu Met Arg Phe Leu Pro Leu Val Ser Met  
 2225 2230 2235  
  
 Ser Ser Cys Pro Arg Trp Val Thr Lys Arg Leu Ser Val Ser Pro  
 2240 2245 2250  
  
 Thr Asp Phe Met Gly Arg Ser Ser Ser Gly Val Pro Arg Ser Ser  
 2255 2260 2265  
  
 Ser Arg Asn Pro Ala His Ser Glu Thr Lys Ala Arg Val Gln Ala  
 2270 2275 2280  
  
 Ser Thr Lys Glu Ala Thr Trp Glu Gly Arg Ser Leu Ser Thr Ser  
 2285 2290 2295  
  
 Gly Ser Thr Phe Ser Arg Val Cys Lys His Met Ser Pro Ser Ser  
 2300 2305 2310  
  
 Thr Ser Arg Lys Val Ile Gly Leu Val Ala Thr Pro Gly Val Pro  
 2315 2320 2325  
  
 Ala Gly Gly Val Lys Gly Ala Gly Pro Cys Ser Ser Ser Leu Ser  
 2330 2335 2340  
  
 Ser Gly Ser Leu Ser Arg Ser Ala Ser Cys Trp Gly Arg Tyr Ser  
 2345 2350 2355  
  
 Leu Ser Lys Ala Gly Met Thr Ser Ala Leu Arg Leu Ser Val Ser  
 2360 2365 2370  
  
 Arg Asn Glu Glu Asp Leu Ile Leu Thr Val Pro Leu Glu Thr Pro  
 2375 2380 2385  
  
 Phe Met Ser Pro Ser Ser Ile Trp Ser Glu Lys Thr Ile Phe Leu  
 2390 2395 2400  
  
 Leu Ser Ser Leu Val Ala Lys Glu Pro Arg Ala Leu Glu Ser Ser  
 2405 2410 2415

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu  | Ala | Met | Glu | Arg | Met | Val  | Trp | Phe | Phe | Ser | Leu  | Ser | Ala | Arg |
| 2420 |     |     |     |     |     | 2425 |     |     |     |     | 2430 |     |     |     |
| Ser  | Leu | Ala | Ala | Met | Leu | Ser  | Cys | Thr | Tyr | Ser | Arg  | Ala | Thr | His |
| 2435 |     |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |
| Phe  | His | Ser | Gly | Lys | Thr | Val  | Val | Ser | Ser | Ser | Gly  | Thr | Ile | Leu |
| 2450 |     |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |
| Thr  | Arg | Gln | Pro | Arg | Leu | Cys  | Arg | Val | Met | Arg | Ser  | Thr | Leu | Val |
| 2465 |     |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |
| Ala  | Thr | Ser | Pro | Arg | Arg | Gly  | Ser | Leu | Val | Gln | Gln  | Arg | Arg | Pro |
| 2480 |     |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Pro  | Leu | Arg | Glu | Gln | Lys | Gly  | Gly | Ser | Gly | Ser | Ser  | Met | Ser | Ser |
| 2495 |     |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Ser  | Gly | Gly | Ser | Ala | Ser | Thr  | Val | Lys | Met | Pro | Gly  | Arg | Ser | Ser |
| 2510 |     |     |     |     |     | 2515 |     |     |     |     | 2520 |     |     |     |
| Gly  | Ser | Lys | Leu | Met | Gln | Val  | Pro | Arg | Leu | Ser | Ser  | Ala | Ala | Cys |
| 2525 |     |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Gln  | Ser | Arg | Thr | Ala | Ser | Ala  | Arg | Ser | Gly | Leu | Arg  | Gly | Val | Pro |
| 2540 |     |     |     |     |     | 2545 |     |     |     |     | 2550 |     |     |     |
| Gln  | Gly | Met | Gly | Cys | Val | Ser  | Ala | Glu | Ala | Tyr | Met  | Pro | Gln | Met |
| 2555 |     |     |     |     |     | 2560 |     |     |     |     | 2565 |     |     |     |
| Ser  | Thr | Arg | Gly | Ser | Ser | Arg  | Thr | Pro | Met | Val | Gly  | Gln | Arg | Pro |
| 2570 |     |     |     |     |     | 2575 |     |     |     |     | 2580 |     |     |     |
| Pro  | Arg | Met | Leu | Ala | Arg | Thr  | Ser | Tyr | Ser | Ser | Cys  | Glu | Gly | Ala |
| 2585 |     |     |     |     |     | 2590 |     |     |     |     | 2595 |     |     |     |
| Arg  | Ser | Pro | Val | Pro | Arg | Leu  | Glu | Arg | Cys | Gly | Phe  | Ser | Ala | Arg |
| 2600 |     |     |     |     |     | 2605 |     |     |     |     | 2610 |     |     |     |
| Thr  | Ile | Trp | Arg | Lys | Met | Ala  | Trp | Glu | Leu | Glu | Glu  | Met | Val | Gly |
| 2615 |     |     |     |     |     | 2620 |     |     |     |     | 2625 |     |     |     |
| Leu  | Trp | Lys | Met | Leu | Lys | Trp  | Ala | Trp | Gly | Arg | Pro  | Thr | Glu | Ser |
| 2630 |     |     |     |     |     | 2635 |     |     |     |     | 2640 |     |     |     |
| Leu  | Met | Lys | Trp | Ala | Glu | Ser  | Cys | Ser | Leu | Ala | Thr  | Ser | Ser | Ala |
| 2645 |     |     |     |     |     | 2650 |     |     |     |     | 2655 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val | Thr  | Arg | Thr | Ser | Arg | Ala  | Gln | Ser | Arg | Val | Ser  | Trp | Met | Met |
|     | 2660 |     |     |     |     | 2665 |     |     |     |     | 2670 |     |     |     |
| Ser | Tyr  | Leu | Ser | Trp | Pro | Phe  | Cys | Phe | His | Ser | Ser  | Arg | Leu | Arg |
|     | 2675 |     |     |     |     | 2680 |     |     |     |     | 2685 |     |     |     |
| Arg | Asn  | Ser | Ser | Arg | Ser | Phe  | Gln | Tyr | Ser | Ser | Arg  | Gly | Asn | Pro |
|     | 2690 |     |     |     |     | 2695 |     |     |     |     | 2700 |     |     |     |
| Ser | Ser  | Ala | Arg | Glu | Pro | Thr  | Met | Asn | Trp | Leu | Thr  | Ala | Leu | Ala |
|     | 2705 |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |
| Gln | Gln  | Pro | Phe | Ser | Thr | Gly  | Arg | Ala | Ala | Cys | Ala  | Ala | Leu | Arg |
|     | 2720 |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |
| Arg | Glu  | Val | Trp | Val | Arg | Ala  | Lys | Val | Ser | Arg | Thr  | Met | Thr | Leu |
|     | 2735 |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |
| Arg | Asn  | Trp | Cys | Leu | Lys | Ser  | Arg | Ser | Ser | Gln | Pro  | Pro | Cys | Ser |
|     | 2750 |     |     |     |     | 2755 |     |     |     |     | 2760 |     |     |     |
| Gln | Ser  | Trp | Lys | Ser | Val | Arg  | Phe | Leu | Ala | Gly | Leu  | Gly | Lys | Ala |
|     | 2765 |     |     |     |     | 2770 |     |     |     |     | 2775 |     |     |     |
| Lys | Val  | Thr | Ser | Leu | Lys | Arg  | Ile | Leu | Pro | Ala | Arg  | Gly | Met | Lys |
|     | 2780 |     |     |     |     | 2785 |     |     |     |     | 2790 |     |     |     |
| Leu | Arg  | Val | Met | Arg | Lys | Gly  | Trp | Gly | Thr | Ser | Ala  | Arg | Leu | Leu |
|     | 2795 |     |     |     |     | 2800 |     |     |     |     | 2805 |     |     |     |
| Met | Thr  | Trp | Ala | Ala | Arg | Thr  | Ile | Ser | Ser | Lys | Pro  | Leu | Met | Leu |
|     | 2810 |     |     |     |     | 2815 |     |     |     |     | 2820 |     |     |     |
| Cys | Pro  | Thr | Met | Ser | Ser | Thr  | Asn | Arg | Gly | Arg | Pro  | Leu | Thr | Trp |
|     | 2825 |     |     |     |     | 2830 |     |     |     |     | 2835 |     |     |     |
| Gly | Ser  | Phe | Leu | Ser | Ser | Ser  | Val | Ser | Ser | Ala | Gly  | Ser | Leu | Ser |
|     | 2840 |     |     |     |     | 2845 |     |     |     |     | 2850 |     |     |     |
| Pro | Cys  | Cys | Ser | Arg | Ala | Gln  | Ser | Ala | Thr | Trp | Gly  | Leu | Ala | Leu |
|     | 2855 |     |     |     |     | 2860 |     |     |     |     | 2865 |     |     |     |
| Arg | Lys  | Glu | Val | Gln | Arg | Ser  | Thr | Ala | Arg | Ala | Val  | Cys | Lys | Arg |
|     | 2870 |     |     |     |     | 2875 |     |     |     |     | 2880 |     |     |     |
| Ser | Arg  | Tyr | Arg | Asn | Cys | Trp  | Pro | Thr | Ala | Ile | Phe  | Ser | Gly | Val |

2885

2890

2895

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Gln  | Lys | Val | Arg | Gly | Ser  | Pro | Cys | Gln | Arg | Ser  | His | Leu | Ser |
|     | 2900 |     |     |     |     | 2905 |     |     |     |     | 2910 |     |     |     |
| Trp | Arg  | Ala | Arg | Ser | Trp | Ala  | Ser | Ser | Thr | Ser | Gly  | Gly | Ser | Pro |
|     | 2915 |     |     |     |     | 2920 |     |     |     |     | 2925 |     |     |     |
| Glu | Ser  | Phe | Met | Thr | Ser | Met  | Lys | Gly | Thr | Ser | Cys  | Leu | Pro | Lys |
|     | 2930 |     |     |     |     | 2935 |     |     |     |     | 2940 |     |     |     |
| Asp | Pro  | Ile | Gln | Val | Val | Ser  | Thr | Ser | Val | Arg | Lys  | Ser | Leu | Ser |
|     | 2945 |     |     |     |     | 2950 |     |     |     |     | 2955 |     |     |     |
| Val | Arg  | Gly | Cys | Glu | Pro | Met  | Gly | Lys | Asn | Trp | Ile  | Ser | Cys | His |
|     | 2960 |     |     |     |     | 2965 |     |     |     |     | 2970 |     |     |     |
| Gln | Leu  | Glu | Glu | Trp | Leu | Leu  | Met | Trp | Lys | Lys | Cys  | Arg | Arg | Arg |
|     | 2975 |     |     |     |     | 2980 |     |     |     |     | 2985 |     |     |     |
| Ala | Glu  | His | Ser | Cys | Leu | Cys  | Leu | Tyr | Lys | Arg | Pro  | Gln | Cys | Ser |
|     | 2990 |     |     |     |     | 2995 |     |     |     |     | 3000 |     |     |     |
| Gln | Arg  | Cys | Thr | Gly | Cys | Thr  | Cys | Cys | Thr | Ser | Cys  | Thr | Trp | Val |
|     | 3005 |     |     |     |     | 3010 |     |     |     |     | 3015 |     |     |     |
| Pro | Leu  | Ala | Arg | Asn | Phe | Ser  | Gly | Gln | Trp | Ser | Ala  | Gly | Gly | Cys |
|     | 3020 |     |     |     |     | 3025 |     |     |     |     | 3030 |     |     |     |
| Ile | Ser  | Cys | Cys | Thr | Thr | Ser  | Trp | Pro | Ser | Ala | Trp  | Pro | Ser | Ser |
|     | 3035 |     |     |     |     | 3040 |     |     |     |     | 3045 |     |     |     |
| Ala | Ser  | Met | Val | Val | Met | Leu  | Thr | Ser | Pro | Arg | Gly  | Arg | Gln | Val |
|     | 3050 |     |     |     |     | 3055 |     |     |     |     | 3060 |     |     |     |
| Gln | Thr  | Ser | Ala | Arg | Thr | Gly  | Arg | Arg | Ala | Arg | Thr  | Arg | Ala | Arg |
|     | 3065 |     |     |     |     | 3070 |     |     |     |     | 3075 |     |     |     |
| Arg | Pro  | Glu | Leu | Ser | Arg | Val  | Leu | Arg | Arg | Cys | Gly  | Val | Arg | Ser |
|     | 3080 |     |     |     |     | 3085 |     |     |     |     | 3090 |     |     |     |
| Val | Gly  | Ser | Gly | Gly | Ala | Arg  | Leu | Thr | Cys | Arg | Ser  | Phe | Ser | Arg |
|     | 3095 |     |     |     |     | 3100 |     |     |     |     | 3105 |     |     |     |
| Ala | Arg  | Gly | Arg | Ser | Arg | Trp  | Tyr | Leu | Ile | Ser | Thr  | Ala | Pro | Leu |
|     | 3110 |     |     |     |     | 3115 |     |     |     |     | 3120 |     |     |     |

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Val Ala Thr Ser Thr Ala Cys Arg Val Pro Cys Pro Trp Gly Ala  
 3125 3130 3135  
  
 Thr Thr Val Pro Arg Phe Phe Leu Gly Ala Ala Ser Met Ser Val  
 3140 3145 3150  
  
 Arg Ser Gly Gly Glu Asp Ala Arg Arg Ala Ala Gly Ala Ala Arg  
 3155 3160 3165  
  
 Gly Pro Glu Ala Gly Ala Ala Gly Ala Arg Arg Arg Arg Ala Arg  
 3170 3175 3180  
  
 Ala Gly Ser Gly Thr Ala Pro Gly Glu Asp Trp Arg Glu Arg Arg  
 3185 3190 3195  
  
 Arg Asp Gly Arg Pro Gly Ser Asp Ala Ser Gly Arg Pro Arg Asp  
 3200 3205 3210  
  
 Pro Val Thr Lys Arg Val Arg Gln Asn Gln Ser Arg Tyr Arg Arg  
 3215 3220 3225  
  
 Arg Pro Ala Ala Gly Ser Leu Ala Arg Arg Pro Ser Cys Pro Gly  
 3230 3235 3240  
  
 Arg Arg Ser Arg Ser Thr Ala Arg Ser Pro Pro Pro Glu Gly Leu  
 3245 3250 3255  
  
 Arg Gly Arg Arg Ala Arg Arg Trp Pro Arg Gly Arg Trp Arg Cys  
 3260 3265 3270  
  
 Gly Pro Ala Ala Arg Arg Arg Ser Cys Arg Pro Arg Ser Arg Arg  
 3275 3280 3285  
  
 Gly Cys Arg Pro Arg Leu Arg Arg Gly Arg Ala Arg Ala Pro Pro  
 3290 3295 3300  
  
 Gly Arg Gly Ala Arg Arg Gly Ala Arg Pro Arg Ser Cys Arg Gly  
 3305 3310 3315  
  
 Ala Gly Arg Gly Ser Ala Trp Trp Arg Cys Ala Arg Arg Arg Ser  
 3320 3325 3330  
  
 Thr Ser Ser Gly Gly Ala Ala Ser Arg Arg Arg Pro Gly Leu Pro  
 3335 3340 3345  
  
 Ser Val Pro Trp Pro Arg Arg Ser Pro Arg Arg Ser Lys Thr Gly  
 3350 3355 3360

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser | Cys  | Ala | Pro | Arg | Arg | Ser  | Thr | Pro | Pro | Pro | Glu  | Asp | Gly | Ala |
|     | 3365 |     |     |     |     | 3370 |     |     |     |     | 3375 |     |     |     |
| Arg | Arg  | Trp | Trp | Arg | Ala | Pro  | Arg | Ala | Arg | Arg | Pro  | Arg | Gly | Ala |
|     | 3380 |     |     |     |     | 3385 |     |     |     |     | 3390 |     |     |     |
| Pro | Leu  | Pro | Ser | Pro | Pro | Leu  | Pro | Pro | Pro | Leu | Thr  | Ser | Leu | Leu |
|     | 3395 |     |     |     |     | 3400 |     |     |     |     | 3405 |     |     |     |
| Leu | Pro  | Pro | Gln | Glu | Ala | Val  | Ala | Gly | Glu | Gly | Pro  | Cys | Val | Ala |
|     | 3410 |     |     |     |     | 3415 |     |     |     |     | 3420 |     |     |     |
| Gly | Gly  | Ala | Arg | Ala | Asp | Gly  | Arg | Ser | Ala | Arg | Trp  | Ser | Pro | Arg |
|     | 3425 |     |     |     |     | 3430 |     |     |     |     | 3435 |     |     |     |
| Ala | Gly  | Asp | Ala | Trp | Ser | Arg  | Arg | Arg | Ala | Arg | Pro  | Arg | Gly | Ala |
|     | 3440 |     |     |     |     | 3445 |     |     |     |     | 3450 |     |     |     |
| Ala | Ala  | Arg | Arg | Arg | Arg | Ala  | Ser | Pro | Gly | Gly | Arg  | Arg | Gly | Gly |
|     | 3455 |     |     |     |     | 3460 |     |     |     |     | 3465 |     |     |     |
| Leu | Arg  | Trp | Ala | Gly | Arg | Gly  | Arg | Arg | Cys | Ile | Leu  | Ser | Ile | Asp |
|     | 3470 |     |     |     |     | 3475 |     |     |     |     | 3480 |     |     |     |
| Pro | Gly  | Leu | Arg | Ala | Arg | Thr  | Ala | Ser | Arg | Asp | Pro  | Arg | Asp | Pro |
|     | 3485 |     |     |     |     | 3490 |     |     |     |     | 3495 |     |     |     |
| Lys | Thr  | Ala | Glu | Arg | Arg | Leu  | Arg | Ala | Ser | Arg | Ser  | Arg | Lys | Val |
|     | 3500 |     |     |     |     | 3505 |     |     |     |     | 3510 |     |     |     |
| Gly | Ala  | Arg | Phe | Leu | Val | Leu  | Arg | Val | Phe | Gly | Arg  | Glu | Ala | Gly |
|     | 3515 |     |     |     |     | 3520 |     |     |     |     | 3525 |     |     |     |
| Gly | Arg  | Cys | Cys | Trp | Ser | Ser  | Arg | Arg | Ser | Asp | Gly  | Gly | Trp | Trp |
|     | 3530 |     |     |     |     | 3535 |     |     |     |     | 3540 |     |     |     |
| Arg | Gly  | Ala | Pro | Gly | Pro | Trp  | Ala | Arg | Leu | Ala | Gly  | Cys | Ala | Asp |
|     | 3545 |     |     |     |     | 3550 |     |     |     |     | 3555 |     |     |     |
| Gly | Arg  | Pro | Cys | Pro | Arg | Arg  | Gly | Pro | Asp | Thr | Trp  | Arg | Gly | Pro |
|     | 3560 |     |     |     |     | 3565 |     |     |     |     | 3570 |     |     |     |
| Cys | Ser  | Ser | Pro | Ala | Ala | Ala  | Pro | Arg | Ala | Pro | Pro  | Pro | Arg | Pro |
|     | 3575 |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
| Arg | Gly  | Arg | Ala | Cys | Ala | Ala  | Arg | Thr | Arg | Ala | Ala  | Ala | Gly | Arg |
|     | 3590 |     |     |     |     | 3595 |     |     |     |     | 3600 |     |     |     |



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Pro | Gly | Arg | Arg | Arg | Arg  | Ala | Arg | Gly | Trp | Pro  | Ala | Gly | Ser |
| 3605 |     |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |
| Gly  | Gly | Trp | Ser | Gly | Ser | Arg  | Arg | Ser | Arg | Arg | Ser  | Gly | Gly | Arg |
| 3620 |     |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
| Leu  | Arg | Cys | Trp | Cys | Arg | Ser  | Ser | Trp | Pro | Arg | Thr  | Ser | Arg | Ser |
| 3635 |     |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
| Gly  | Gly | Arg | Val | Ala | Arg | Ala  | Arg | Gly | Thr | Gly | Ala  | Ser | Arg | Arg |
| 3650 |     |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
| Ala  | Cys | Arg | Arg | Cys | Ser | Arg  | Cys | Arg | Arg | Ala | Arg  | Gly | Thr | Gly |
| 3665 |     |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
| Ile  | Arg | Arg | Gly | Ser | Ala | Ala  | Ala | Ala | Gly | Gly | Arg  | Ala | Ala | Ile |
| 3680 |     |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |
| Ala  | Arg | Trp | Arg | Gly | Arg | Arg  | Ala | Arg | Gly | Pro | Arg  | Ala | Gly | Gly |
| 3695 |     |     |     |     |     | 3700 |     |     |     |     | 3705 |     |     |     |
| Gly  | Ser | Arg | Arg | Cys | Thr | Trp  | Thr | Ser | Arg | Cys | Arg  | Arg | Arg | Trp |
| 3710 |     |     |     |     |     | 3715 |     |     |     |     | 3720 |     |     |     |
| Trp  | Arg | Arg | Ala | Gly | Thr | Arg  | Gly | Arg | Gly | Ser | Arg  | Cys | Cys | Ala |
| 3725 |     |     |     |     |     | 3730 |     |     |     |     | 3735 |     |     |     |
| Ala  | Ala | Gly | Ser | Ser | Ser | Trp  | Trp | Pro | Arg | Ser | Gly  | Pro | Gly | Ala |
| 3740 |     |     |     |     |     | 3745 |     |     |     |     | 3750 |     |     |     |
| Arg  | Ser | Arg | Gly | Cys | Ser | Arg  | His | Thr | Gly | Lys | Asn  | Glu | Ser | Gly |
| 3755 |     |     |     |     |     | 3760 |     |     |     |     | 3765 |     |     |     |
| Gln  | Arg | Leu | Asp | Ser | Val | Ala  | Trp | Arg | Leu | Ser | Glu  | Arg | Val | Gly |
| 3770 |     |     |     |     |     | 3775 |     |     |     |     | 3780 |     |     |     |
| Leu  | Arg | Val | Tyr | Pro | Gly | Ser  | Asn | Leu | Glu | Ser | Gly  | Trp | Ser | Arg |
| 3785 |     |     |     |     |     | 3790 |     |     |     |     | 3795 |     |     |     |
| Ser  | Arg | Gly | Thr | Gly | Thr | Pro  | Val | Ser | Thr | Gln | Ala  | Cys | Arg | Asn |
| 3800 |     |     |     |     |     | 3805 |     |     |     |     | 3810 |     |     |     |
| Leu  | Gln | Asp | Thr | Glu | Ala | Gly  | Arg | Phe | Leu | Ala | Leu  | Val | Ala | Gly |
| 3815 |     |     |     |     |     | 3820 |     |     |     |     | 3825 |     |     |     |
| His  | Glu | Lys | Leu | Val | Ser | Ala  | Glu | Ser | Gly | Arg | Pro  | Arg | Trp | Leu |

3830

3835

3840

Ala Ala Val Val Trp Arg Lys Asn Arg Gln Gly Cys Val Ala Val  
 3845 3850 3855

Cys Pro Gly Ser Ser Leu Ser Ala Arg Arg Arg Pro Asp Ser Ala  
 3860 3865 3870

Ala Asn Val Gly Val Ala Ala Pro Ser Phe Pro Arg Pro Leu Ser  
 3875 3880 3885

Gln Pro Thr Ser Pro Val Thr Glu Arg Ala Pro Leu Phe Phe Ser  
 3890 3895 3900

Cys Val Phe Ala Arg Cys Ile Pro Tyr Cys Gly Arg Cys Ala Pro  
 3905 3910 3915

Thr Leu His His Asn Arg Pro Tyr Arg Ser Ser Ser Asn Ser Arg  
 3920 3925 3930

Arg Phe Cys Pro Arg Pro Ser Ser Ser Gln Pro Leu Pro Arg Arg  
 3935 3940 3945

Pro Pro Ala Glu Pro Ala Phe Ser Met Thr Trp Pro Trp Lys Arg  
 3950 3955 3960

Ala Arg Gly Trp Arg Gly Trp Gly Arg Arg Arg Arg Ser Gly Thr  
 3965 3970 3975

Arg Ala Cys Arg Lys Gly Thr Leu Ala Arg Pro Thr Cys Pro Ser  
 3980 3985 3990

Arg Thr Cys Ser Glu Thr Gly Ala Ala Arg Ser Pro Arg Arg Cys  
 3995 4000 4005

Ala Pro Pro Ala Ser Thr Arg Gly Gly Ser Cys Gly Ala Ala Trp  
 4010 4015 4020

Thr Glu Ser Gly Cys Gly Thr Arg Ile Ser Arg Arg Thr Ser Arg  
 4025 4030 4035

Gly Ser Ala Pro Arg Ala Arg Thr Trp Pro Arg Pro Thr Trp Ser  
 4040 4045 4050

Arg Arg Thr Ser Arg Pro Arg Arg Arg Ala Thr Ser Lys Asn Pro  
 4055 4060 4065

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Ser Thr Thr Thr Cys Ala Arg Ser Arg Ala Arg Arg Pro Trp Ala  
 4070 4075 4080  
  
 Cys Thr Cys Gly Thr Cys Trp Arg Pro Ser Cys Arg Thr Pro Arg  
 4085 4090 4095  
  
 Ala Ser Arg Arg Arg Ser Cys Phe Trp Trp Cys Ser Thr Val Gly  
 4100 4105 4110  
  
 Thr Thr Arg Arg Ser Gly Arg Arg Cys Ile Ser Pro Ser Pro Arg  
 4115 4120 4125  
  
 Ala Ala Gly Ser Trp Thr Trp Thr Phe Cys Arg Ala Ser Trp Cys  
 4130 4135 4140  
  
 Arg Ser Ala Gly Cys Arg Cys Pro Arg Ser Trp Arg Pro Ser Thr  
 4145 4150 4155  
  
 Ser Arg Cys Val Trp Ala Ser Thr Thr Leu Gly Arg Ser Thr Arg  
 4160 4165 4170  
  
 Pro Arg Thr Cys Pro Thr Arg Arg Arg Ser Thr Gly Phe Thr Cys  
 4175 4180 4185  
  
 Ala Pro Lys Cys Pro Ala Thr Ile Trp Gly Cys Thr Ala Thr Thr  
 4190 4195 4200  
  
 Gly Cys Thr Ala Arg Ala Pro Ala Ala Gly Ala Ser Ala Thr Arg  
 4205 4210 4215  
  
 Ser Cys Thr Ala Cys Ser Gly Pro Pro Gly Pro Gly Pro Arg Gly  
 4220 4225 4230  
  
 Arg Ala Thr Leu Thr Trp Ala Arg Thr Cys Ala Gly Ser Pro Ala  
 4235 4240 4245  
  
 Ala Gly Pro Trp Lys Leu Pro Ala Val Pro Pro Thr Trp Arg Arg  
 4250 4255 4260  
  
 Trp Thr Met Arg Arg Arg Arg Ala Ser Thr Trp Lys Thr Asp Gly  
 4265 4270 4275  
  
 Ala Thr Val Phe Leu Leu Asp Ala Ala Thr Ala Thr Ala Ala Ala  
 4280 4285 4290  
  
 Ser Ser Arg Asp Ala Gly Gly Ala Ala Glu Pro Ala Val Arg His  
 4295 4300 4305

## 368530-7006W01\_SequenceListing\_ST25.txt

Leu Leu Gly Arg Leu Asp Pro Gly His Ala Thr His His Gly Ala  
 4310 4315 4320  
 Asp Asp Pro Gln Ser Arg Ser Leu Thr Ala Ala Ser Gly Gln Pro  
 4325 4330 4335  
 Ala Leu Gly His Pro Gly Gly Arg Gly Ala Leu Ala Leu Glu Pro  
 4340 4345 4350  
 His Ala Arg Glu Gly Ala Gly His Arg Glu Arg Ala Gly Gly Glu  
 4355 4360 4365  
 Gln Gly His Pro Arg Arg Gly Arg Ala Gly Val Gln Arg Ala Ala  
 4370 4375 4380  
 Gly Ala Arg Gly Pro Leu Gln Gln His Gln Arg Ala Asp Glu Pro  
 4385 4390 4395  
 Gly Pro His Gly Asp Arg Arg Ala Arg Gly Gly Val Ala Ala Arg  
 4400 4405 4410  
 Ala Val Pro Pro Arg Val Glu Pro Gly Leu His Gly Gly Ala Glu  
 4415 4420 4425  
 Arg Leu Pro Glu His Ala Ala Arg Gln Arg Ala Pro Gly Pro Gly  
 4430 4435 4440  
 Gly Leu His Gln Leu His Gln Arg Ala Ala Ala Asp Gly Gly Arg  
 4445 4450 4455  
 Gly Ala Pro Glu Arg Gly Val Pro Val Gly Ala Gly Leu Leu Leu  
 4460 4465 4470  
 Pro Asp Gln Ser Pro Gly Leu Ala Asp Arg Glu Pro Glu Pro Gly  
 4475 4480 4485  
 Phe Gln Glu Leu Ala Gly Thr Val Gly Arg Ala Gly Pro Gly Arg  
 4490 4495 4500  
 Gly Pro Arg Asp Gly Val Glu Pro Ala Asp Ala Glu Leu Ala Pro  
 4505 4510 4515  
 Ala Ala Ala Ala Gly Gly Ala Leu His Gly Gln Arg Gln Arg Glu  
 4520 4525 4530  
 Pro Arg Leu Val Pro Gly Leu Pro Ala Pro Val Pro Arg Gly His  
 4535 4540 4545

## 368530-7006W01\_SequenceListing\_ST25.txt

Arg Thr Gly Ala Arg Gly Arg Ala Asp Leu Pro Gly Asp His Pro  
 4550 4555 4560  
 Arg Glu Pro Arg Ala Gly Pro Gly Gly Pro Gly Gln Pro Gly Gly  
 4565 4570 4575  
 His Pro Glu Leu Pro Ala Asp Gln Pro Val Ala Glu Asp Pro Ala  
 4580 4585 4590  
 Pro Val Arg Ala Glu His Arg Gly Gly Ala His Pro Ala Leu Arg  
 4595 4600 4605  
 Ala Ala Glu Arg Gly Ala Val Pro Asp Ala Gly Gly Gly His Ala  
 4610 4615 4620  
 Gln Arg Gly Ala Arg His Asp Arg Ala Gln His Gly Ala Gln His  
 4625 4630 4635  
 Val Arg Pro Gln Pro Pro Val His Gln Ala Asp Gly Leu Leu Ala  
 4640 4645 4650  
 Ser Gly Gly Arg His Glu Leu Gly Leu Leu Tyr Gln Arg His Leu  
 4655 4660 4665  
 Glu Pro Ala Leu Ala Pro Ala Ala Arg Val Leu His Gly Arg Val  
 4670 4675 4680  
 Arg His Ala Arg Pro Gln Arg Arg Val Pro Val Gly Arg Arg Gly  
 4685 4690 4695  
 Gln Gln Arg Val Leu Ala Ala Ser Arg Asn Gln Cys Arg Val Glu  
 4700 4705 4710  
 Glu Arg Gly Arg Gly Pro Ala Ala Val Leu Gly Ala Val Arg Ser  
 4715 4720 4725  
 Arg Gly Cys Cys Arg Gly Gly Ala Arg Gly Arg Gln Pro Leu Pro  
 4730 4735 4740  
 Glu Pro Ala Leu Phe Ala Glu Gln Arg Ala Gln Gln Arg Ala Gly  
 4745 4750 4755  
 Ser Ala Asp Ala Thr Ala Pro Ala Gly Arg Gly Gly Val Pro Glu  
 4760 4765 4770  
 Arg Leu Leu Val Glu Ala Arg Ala Arg Glu Glu Leu Pro Gln Arg

4775

4780

4785

Asp Arg Glu Pro Gly Gly Gln Asp Glu Pro Leu Glu Asp Val Arg  
 4790 4795 4800

Ala Arg Ala Gln Gly Arg Ala Pro Ser Gln Arg Arg His Pro Thr  
 4805 4810 4815

Pro Ala Ala Arg Gln Ala Ala Gly Thr Gly Val Gly Arg Gly Phe  
 4820 4825 4830

Arg Arg Arg Gln Gln Arg Val Gly Leu Gly Trp Glu Trp Trp Pro  
 4835 4840 4845

Val Arg Ser Pro Ala Pro Pro Tyr Arg Ala Pro Asp Val Arg Ile  
 4850 4855 4860

Lys Asn Lys Arg Arg Tyr Ser Pro Arg Pro Trp Arg Pro Ala Cys  
 4865 4870 4875

Val Leu Leu Cys Cys Leu Tyr Asp Glu Ala Arg Val Pro Gly Gly  
 4880 4885 4890

Ser Ser Ser Leu Val Arg Glu Arg Asp Ala Ala Gly Gly Gly Gly  
 4895 4900 4905

Gly Asp Ala Ala Pro Ala Gly Gly Ala Leu Arg Ala Pro Ala Val  
 4910 4915 4920

Pro Gly Ala Tyr Gly Gly Ala Glu Gln His Ser Leu Leu Gly Ala  
 4925 4930 4935

Gly Thr Leu Val Arg Tyr His Pro Val Val Pro Gly Gly Gln Gln  
 4940 4945 4950

Val Gly Arg His Arg Leu Ala Glu Leu Pro Glu Arg Pro Gln Gln  
 4955 4960 4965

Leu Pro Asp His Arg Gly Ala Glu Gln Arg Phe His Pro His Gly  
 4970 4975 4980

Gly Gln His Pro Asp His Gln Leu Arg Ala Leu Ala Val Gly Arg  
 4985 4990 4995

Pro Ala Glu Asn His His Ala His Gln His Ala Gln Arg Glu Arg  
 5000 5005 5010

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | His | Val | Gln | Gln | Gln | Val  | Gln | Gly | Ala | Gly | Asp  | Gly | Leu | Ala |
| 5015 |     |     |     |     |     | 5020 |     |     |     |     | 5025 |     |     |     |
| Gln  | Asp | Pro | Gln | Arg | Gly | Gly  | Leu | Trp | Ser | Gly | Arg  | Ala | Asp | Leu |
| 5030 |     |     |     |     |     | 5035 |     |     |     |     | 5040 |     |     |     |
| Arg  | Val | Gly | Gly | Val | Ala | Ala  | Arg | Gly | Gln | Leu | Leu  | Gly | Asp | His |
| 5045 |     |     |     |     |     | 5050 |     |     |     |     | 5055 |     |     |     |
| Asp  | His | Arg | Ser | Asp | Glu | Gln  | Arg | His | His | Arg | Gln  | Leu | Leu | Gly |
| 5060 |     |     |     |     |     | 5065 |     |     |     |     | 5070 |     |     |     |
| Gly  | Gly | Ala | Ala | Glu | Arg | Gly  | Ala | Gly | Glu | Arg | His  | Arg | Arg | Glu |
| 5075 |     |     |     |     |     | 5080 |     |     |     |     | 5085 |     |     |     |
| Val  | Arg | His | Ala | Gln | Leu | Pro  | Ala | Gly | Leu | Gly | Pro  | Arg | Asp | Arg |
| 5090 |     |     |     |     |     | 5095 |     |     |     |     | 5100 |     |     |     |
| Ala  | Gly | Asp | Ala | Gly | Arg | Val  | His | Gln | Arg | Gly | Leu  | Pro | Pro | Arg |
| 5105 |     |     |     |     |     | 5110 |     |     |     |     | 5115 |     |     |     |
| His  | Arg | Pro | Ala | Ala | Arg | Leu  | Arg | Arg | Gly | Leu | His  | Arg | Glu | Pro |
| 5120 |     |     |     |     |     | 5125 |     |     |     |     | 5130 |     |     |     |
| Pro  | Gln | Gln | Pro | Ala | Gly | His  | Pro | Gln | Ala | Ala | Ala  | Leu | Pro | Gly |
| 5135 |     |     |     |     |     | 5140 |     |     |     |     | 5145 |     |     |     |
| Gly  | Leu | Pro | Asp | Pro | Val | Arg  | Gly | Pro | Gly | Gly | Gly  | Gln | His | Pro |
| 5150 |     |     |     |     |     | 5155 |     |     |     |     | 5160 |     |     |     |
| Arg  | Ala | Leu | Gly | Cys | Arg | Ser  | Leu | Arg | Glu | Lys | Gln  | Gly | Gly | His |
| 5165 |     |     |     |     |     | 5170 |     |     |     |     | 5175 |     |     |     |
| Arg  | Arg | Gly | Asp | Arg | Ser | Arg  | Gly | His | Arg | Leu | Tyr  | Arg | Gly | Ala |
| 5180 |     |     |     |     |     | 5185 |     |     |     |     | 5190 |     |     |     |
| Gly  | Arg | Phe | Cys | Arg | Cys | Gly  | Ser | Gly | Arg | Gly | Gly  | Asn | Arg | Lys |
| 5195 |     |     |     |     |     | 5200 |     |     |     |     | 5205 |     |     |     |
| Asp  | Ser | His | Pro | Ala | Gly | Gly  | Glu | Gly | Gln | Gln | Gly  | Gln | Glu | Leu |
| 5210 |     |     |     |     |     | 5215 |     |     |     |     | 5220 |     |     |     |
| Gln  | Arg | Ala | Arg | Gly | Gln | Glu  | Lys | His | Arg | Leu | Pro  | Gln | Leu | Val |
| 5225 |     |     |     |     |     | 5230 |     |     |     |     | 5235 |     |     |     |
| Pro  | Gly | Leu | Gln | Leu | Arg | Arg  | Pro | Arg | Glu | Gly | Arg  | Ala | Leu | Leu |
| 5240 |     |     |     |     |     | 5245 |     |     |     |     | 5250 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp  | Ala | Ala | His | His | Leu | Gly  | Arg | His | Leu | Arg | Arg  | Gly | Ala | Ser |
| 5255 |     |     |     |     |     | 5260 |     |     |     |     | 5265 |     |     |     |
| Leu  | Leu | Val | Ala | Ala | Arg | His  | Asp | Ala | Arg | Pro | Gly  | His | Leu | Pro |
| 5270 |     |     |     |     |     | 5275 |     |     |     |     | 5280 |     |     |     |
| Leu  | His | Ala | Ser | Ser | Gln | Leu  | Pro | Gly | Gly | Gly | Arg  | Arg | Ala | Pro |
| 5285 |     |     |     |     |     | 5290 |     |     |     |     | 5295 |     |     |     |
| Ala  | Arg | Leu | Leu | Gln | Glu | Leu  | Leu | Gln | Arg | Ala | Gly  | Arg | Leu | Leu |
| 5300 |     |     |     |     |     | 5305 |     |     |     |     | 5310 |     |     |     |
| Ala  | Ala | Ala | Ala | Arg | Leu | His  | Leu | Ala | His | Ala | Arg  | Leu | Gln | Pro |
| 5315 |     |     |     |     |     | 5320 |     |     |     |     | 5325 |     |     |     |
| Leu  | Pro | Arg | Glu | Pro | Asp | Pro  | Arg | Pro | Pro | Ala | Arg  | Ala | His | His |
| 5330 |     |     |     |     |     | 5335 |     |     |     |     | 5340 |     |     |     |
| Tyr  | His | Arg | Gln | Lys | Arg | Ser  | Cys | Ser | His | Arg | Ser  | Arg | Asp | Pro |
| 5345 |     |     |     |     |     | 5350 |     |     |     |     | 5355 |     |     |     |
| Ala  | Ala | Ala | Gln | Gln | Tyr | Pro  | Gly | Ser | Pro | Ala | Arg  | Asp | Arg | His |
| 5360 |     |     |     |     |     | 5365 |     |     |     |     | 5370 |     |     |     |
| Arg  | Gln | Thr | Pro | His | Leu | Pro  | Leu | Arg | Leu | Gln | Gly  | Pro | Gly | Arg |
| 5375 |     |     |     |     |     | 5380 |     |     |     |     | 5385 |     |     |     |
| Ser  | Arg | Ala | Ala | Arg | Pro | Leu  | Glu | Pro | His | Leu | Leu  | Lys | Asn | Val |
| 5390 |     |     |     |     |     | 5395 |     |     |     |     | 5400 |     |     |     |
| His  | Ser | His | Leu | Ala | Gln | His  | Arg | Leu | Gly | Pro | Ala  | Arg | Ala | Gln |
| 5405 |     |     |     |     |     | 5410 |     |     |     |     | 5415 |     |     |     |
| Gln  | Asp | Val | Arg | Arg | Arg | Ser  | Pro | Thr | Leu | His | Ala  | Thr | Pro | Arg |
| 5420 |     |     |     |     |     | 5425 |     |     |     |     | 5430 |     |     |     |
| Ala  | Arg | Ala | Arg | Ala | Leu | Pro  | Arg | Ser | Leu | Gly | Arg  | Pro | Gln | Gly |
| 5435 |     |     |     |     |     | 5440 |     |     |     |     | 5445 |     |     |     |
| Pro  | Arg | Ala | Leu | Ala | His | His  | Arg | Arg | Arg | Arg | Asp  | Arg | Pro | Gly |
| 5450 |     |     |     |     |     | 5455 |     |     |     |     | 5460 |     |     |     |
| Gly  | Gly | Arg | Arg | Ala | Gln | Leu  | His | Ala | Arg | Arg | Arg  | Ala | Arg | Leu |
| 5465 |     |     |     |     |     | 5470 |     |     |     |     | 5475 |     |     |     |
| His  | Arg | Gly | Arg | Arg | His | Arg  | Gln | Arg | Gly | Gly | Arg  | Arg | Ala | Pro |
| 5480 |     |     |     |     |     | 5485 |     |     |     |     | 5490 |     |     |     |



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | Arg | Pro | His | Gln | Glu | Pro  | Ala | Ala | Ala | His | Arg  | Pro | Ala | Ala |
| 5495 |     |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |
| Pro  | Glu | His | Pro | Arg | His | Ala  | Arg | Gly | Ala | Ser | Leu  | Ala | Ala | Gln |
| 5510 |     |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
| Gly  | Gln | Ala | His | Gly | Thr | Gln  | Gly | His | Ala | Gln | Gly  | Gly | Gln | Thr |
| 5525 |     |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
| Arg  | Gly | Leu | Arg | Gln | Gln | Gln  | Arg | Arg | Gln | Asp | Pro  | Gln | Thr | Arg |
| 5540 |     |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
| Gly  | His | Gly | Gly | Gly | Gly | Gly  | His | Arg | Gln | His | Val  | Pro | Pro | Ala |
| 5555 |     |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
| Ala  | Arg | Gln | Arg | Val | Leu | Gly  | Ala | Arg | Arg | Arg | His  | Arg | Cys | Ala |
| 5570 |     |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |
| Arg  | Ala | Arg | Ala | His | Pro | Pro  | Pro | Ser | His | Leu | Lys  | Met | Leu | Thr |
| 5585 |     |     |     |     |     | 5590 |     |     |     |     | 5595 |     |     |     |
| Ser  | Arg | Cys | Cys | Val | Pro | Ala  | Ala | Arg | Arg | Met | Ser  | Lys | Arg | Lys |
| 5600 |     |     |     |     |     | 5605 |     |     |     |     | 5610 |     |     |     |
| Tyr  | Lys | Glu | Glu | Met | Leu | Gln  | Val | Ile | Ala | Pro | Glu  | Ile | Tyr | Gly |
| 5615 |     |     |     |     |     | 5620 |     |     |     |     | 5625 |     |     |     |
| Pro  | Ala | Ala | Ala | Val | Lys | Glu  | Glu | Arg | Lys | Pro | Arg  | Lys | Leu | Lys |
| 5630 |     |     |     |     |     | 5635 |     |     |     |     | 5640 |     |     |     |
| Arg  | Val | Lys | Lys | Asp | Lys | Lys  | Glu | Glu | Glu | Asp | Asp  | Gly | Leu | Val |
| 5645 |     |     |     |     |     | 5650 |     |     |     |     | 5655 |     |     |     |
| Glu  | Phe | Val | Arg | Glu | Phe | Ala  | Pro | Arg | Arg | Arg | Val  | Gln | Trp | Arg |
| 5660 |     |     |     |     |     | 5665 |     |     |     |     | 5670 |     |     |     |
| Gly  | Arg | Lys | Val | Lys | Pro | Val  | Leu | Arg | Pro | Gly | Thr  | Thr | Val | Val |
| 5675 |     |     |     |     |     | 5680 |     |     |     |     | 5685 |     |     |     |
| Phe  | Thr | Pro | Gly | Glu | Arg | Ser  | Gly | Ser | Ala | Ser | Lys  | Arg | Ser | Tyr |
| 5690 |     |     |     |     |     | 5695 |     |     |     |     | 5700 |     |     |     |
| Asp  | Glu | Val | Tyr | Gly | Asp | Glu  | Asp | Ile | Leu | Glu | Gln  | Ala | Val | Glu |
| 5705 |     |     |     |     |     | 5710 |     |     |     |     | 5715 |     |     |     |
| Arg  | Leu | Gly | Glu | Phe | Ala | Tyr  | Gly | Lys | Arg | Ser | Arg  | Pro | Ala | Pro |

5720

5725

5730

Leu Lys Glu Glu Ala Val Ser Ile Pro Leu Asp His Gly Asn Pro  
 5735 5740 5745

Thr Pro Ser Leu Lys Pro Val Thr Leu Gln Gln Val Leu Pro Ser  
 5750 5755 5760

Ala Ala Pro Arg Arg Gly Phe Lys Arg Glu Gly Gly Glu Asp Leu  
 5765 5770 5775

Tyr Pro Thr Met Gln Leu Met Val Pro Lys Arg Gln Lys Leu Glu  
 5780 5785 5790

Asp Val Leu Glu His Met Lys Val Asp Pro Glu Val Gln Pro Glu  
 5795 5800 5805

Val Lys Val Arg Pro Ile Lys Gln Val Ala Pro Gly Leu Gly Val  
 5810 5815 5820

Gln Thr Val Asp Ile Lys Ile Pro Thr Glu Pro Met Glu Thr Gln  
 5825 5830 5835

Thr Glu Pro Val Lys Pro Ser Thr Ser Thr Met Glu Val Gln Thr  
 5840 5845 5850

Asp Pro Trp Met Pro Ala Pro Ala Ser Thr Ser Thr Arg Arg Arg  
 5855 5860 5865

Arg Lys Tyr Gly Ala Ala Ser Leu Leu Met Pro Asn Tyr Ala Leu  
 5870 5875 5880

His Pro Ser Ile Ile Pro Thr Pro Gly Tyr Arg Gly Thr Arg Phe  
 5885 5890 5895

Tyr Arg Gly Tyr Thr Ser Ser Arg Arg Arg Lys Thr Thr Thr Arg  
 5900 5905 5910

Arg Arg Arg Arg Ser Arg Arg Ser Ser Thr Ala Thr Ser Ala Leu  
 5915 5920 5925

Val Arg Arg Val Tyr Arg Ser Gly Arg Glu Pro Leu Thr Leu Pro  
 5930 5935 5940

Arg Ala Arg Tyr His Pro Ser Ile Ala Ile Leu Pro Pro Pro Thr  
 5945 5950 5955

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Cys  | Arg | Tyr | Gly | Pro | His | Met  | Pro | Pro | Pro | Arg | Pro  | His | Tyr | Gly |
| 5960 |     |     |     |     |     | 5965 |     |     |     |     | 5970 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Leu  | Pro | Arg | Lys | Lys | Ala | Ala  | Pro | Lys | Ala | Asp | Gly  | Glu | Arg | Ala |
| 5975 |     |     |     |     |     | 5980 |     |     |     |     | 5985 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Ser | Pro | Ser | Pro | Pro | Ala  | Ala | Ala | Arg | His | Gln  | Gln | Ala | Val |
| 5990 |     |     |     |     |     | 5995 |     |     |     |     | 6000 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly  | Gly | Arg | Leu | Pro | Ala | Arg  | Ala | Asp | Pro | His | His  | Arg | Arg | Gly |
| 6005 |     |     |     |     |     | 6010 |     |     |     |     | 6015 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asp  | Arg | Gly | Asp | Pro | Arg | His  | Ser | Phe | Arg | Gly | Gly  | Ala | Gly | Leu |
| 6020 |     |     |     |     |     | 6025 |     |     |     |     | 6030 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser  | Ala | Pro | Leu | Arg | His | Lys  | Lys | Ala | Trp | Ile | Cys  | Asn | Lys | Lys |
| 6035 |     |     |     |     |     | 6040 |     |     |     |     | 6045 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Lys  | Asn | Gly | Leu | Thr | Leu | Leu  | Val | Leu | Cys | Val | Phe  | Leu | Asp | Gly |
| 6050 |     |     |     |     |     | 6055 |     |     |     |     | 6060 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | His | Gln | Phe | Phe | Val | Pro  | Gly | Thr | Ala | Thr | Arg  | His | Ala | Ala |
| 6065 |     |     |     |     |     | 6070 |     |     |     |     | 6075 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Val  | Tyr | Gly | His | Leu | Glu | Arg  | His | Arg | Gln | Gln | Pro  | Thr | Glu | Arg |
| 6080 |     |     |     |     |     | 6085 |     |     |     |     | 6090 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly  | Arg | Leu | Gln | Leu | Glu | Gln  | Ser | Leu | Glu | Arg | Ala  | Glu | Phe | Arg |
| 6095 |     |     |     |     |     | 6100 |     |     |     |     | 6105 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Val  | His | Ala | Gln | Asn | Leu | Trp  | Gln | Gln | Gly | Val | Glu  | Gln | Gln | His |
| 6110 |     |     |     |     |     | 6115 |     |     |     |     | 6120 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Ala | Gly | Ala | Glu | Gly | Lys  | Ala | Glu | Arg | Thr | Glu  | Leu | Pro | Ala |
| 6125 |     |     |     |     |     | 6130 |     |     |     |     | 6135 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Glu  | Gly | Gly | Trp | Pro | Gly | Leu  | Arg | His | Gln | Arg | Gly  | Gly | Pro | Gly |
| 6140 |     |     |     |     |     | 6145 |     |     |     |     | 6150 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gln  | Pro | Gly | Arg | Ala | Glu | Thr  | Asp | Gln | Gln | Pro | Pro  | Gly | Arg | Gly |
| 6155 |     |     |     |     |     | 6160 |     |     |     |     | 6165 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Ala | Arg | Gly | Val | Arg | Gly  | Asp | Ala | Pro | Gly | Gly  | Gly | Gly | Ala |
| 6170 |     |     |     |     |     | 6175 |     |     |     |     | 6180 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Ser | Pro | Gly | Gln | Ala | Arg  | Arg | Gln | Ala | Thr | Ala  | Ser | Arg | Arg |
| 6185 |     |     |     |     |     | 6190 |     |     |     |     | 6195 |     |     |     |

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Gly Gly Asp Ala Ala Asp Ala His Gly Arg Ala Ala Pro Val Arg  
 6200 6205 6210  
 Gly Gly Gly Glu Thr Gly Pro Ala His His Ala Ala Arg Gly Ala  
 6215 6220 6225  
 Ser Gly His Arg Ser Ala Glu Thr Gln Gln Gln Pro Ala Arg Asp  
 6230 6235 6240  
 Pro Gly Leu Ala Ser Ala Ser Pro Leu His Ser Gly Ala Pro Ala  
 6245 6250 6255  
 Ala Gly Gly Arg Arg Val Ala Arg Pro Pro Arg Pro Pro Pro Gly  
 6260 6265 6270  
 Glu Leu Ala Glu His Ser Glu Gln His Arg Gly Ser Gly Ser Ala  
 6275 6280 6285  
 Glu Cys Glu Ala Pro Pro Leu Leu Leu Lys Asp Thr Val Ala Leu  
 6290 6295 6300  
 Asn Leu Leu Val Cys Val Tyr Met Tyr Val Arg Arg Pro Glu Gly  
 6305 6310 6315  
 Gly Val Arg Gly Ala Ser Pro Ser Cys Lys Met Ala Thr Pro Ser  
 6320 6325 6330  
 Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala Gly Gln Asp Ala  
 6335 6340 6345  
 Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala Arg Ala Thr  
 6350 6355 6360  
 Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro Thr Val  
 6365 6370 6375  
 Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu Thr  
 6380 6385 6390  
 Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
 6395 6400 6405  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp  
 6410 6415 6420  
 Met Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly  
 6425 6430 6435

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Ser  | Phe | Lys | Pro | Tyr | Ser  | Gly | Thr | Ala | Tyr | Asn  | Ser | Leu | Ala |
|     | 6440 |     |     |     |     | 6445 |     |     |     |     | 6450 |     |     |     |
| Pro | Lys  | Gly | Ala | Pro | Asn | Ser  | Ser | Gln | Trp | Glu | Gln  | Ala | Lys | Thr |
|     | 6455 |     |     |     |     | 6460 |     |     |     |     | 6465 |     |     |     |
| Gly | Asn  | Gly | Gly | Thr | Met | Glu  | Thr | His | Thr | Tyr | Gly  | Val | Ala | Pro |
|     | 6470 |     |     |     |     | 6475 |     |     |     |     | 6480 |     |     |     |
| Met | Gly  | Gly | Glu | Asn | Ile | Thr  | Lys | Asp | Gly | Leu | Gln  | Ile | Gly | Thr |
|     | 6485 |     |     |     |     | 6490 |     |     |     |     | 6495 |     |     |     |
| Asp | Val  | Thr | Ala | Asn | Gln | Asn  | Lys | Pro | Ile | Tyr | Ala  | Asp | Lys | Thr |
|     | 6500 |     |     |     |     | 6505 |     |     |     |     | 6510 |     |     |     |
| Phe | Gln  | Pro | Glu | Pro | Gln | Val  | Gly | Glu | Glu | Asn | Trp  | Gln | Glu | Thr |
|     | 6515 |     |     |     |     | 6520 |     |     |     |     | 6525 |     |     |     |
| Glu | Asn  | Phe | Tyr | Gly | Gly | Arg  | Ala | Leu | Lys | Lys | Asp  | Thr | Asn | Met |
|     | 6530 |     |     |     |     | 6535 |     |     |     |     | 6540 |     |     |     |
| Lys | Pro  | Cys | Tyr | Gly | Ser | Tyr  | Ala | Arg | Pro | Thr | Asn  | Glu | Lys | Gly |
|     | 6545 |     |     |     |     | 6550 |     |     |     |     | 6555 |     |     |     |
| Gly | Gln  | Ala | Lys | Leu | Lys | Val  | Gly | Asp | Asp | Gly | Val  | Pro | Thr | Lys |
|     | 6560 |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Glu | Phe  | Asp | Ile | Asp | Leu | Ala  | Phe | Phe | Asp | Thr | Pro  | Gly | Gly | Thr |
|     | 6575 |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Val | Asn  | Gly | Gln | Asp | Glu | Tyr  | Lys | Ala | Asp | Ile | Val  | Met | Tyr | Thr |
|     | 6590 |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Glu | Asn  | Thr | Tyr | Leu | Glu | Thr  | Pro | Asp | Thr | His | Val  | Val | Tyr | Lys |
|     | 6605 |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Pro | Gly  | Lys | Asp | Asp | Ala | Ser  | Ser | Glu | Ile | Asn | Leu  | Val | Gln | Gln |
|     | 6620 |     |     |     |     | 6625 |     |     |     |     | 6630 |     |     |     |
| Ser | Met  | Pro | Asn | Arg | Pro | Asn  | Tyr | Ile | Gly | Phe | Arg  | Asp | Asn | Phe |
|     | 6635 |     |     |     |     | 6640 |     |     |     |     | 6645 |     |     |     |
| Ile | Gly  | Leu | Met | Tyr | Tyr | Asn  | Ser | Thr | Gly | Asn | Met  | Gly | Val | Leu |
|     | 6650 |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |
| Ala | Gly  | Gln | Ala | Ser | Gln | Leu  | Asn | Ala | Val | Val | Asp  | Leu | Gln | Asp |

6665

6670

6675

Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly  
 6680 6685 6690

Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser  
 6695 6700 6705

Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp  
 6710 6715 6720

Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp Gly Ser Gly Thr Asn  
 6725 6730 6735

Ala Ala Tyr Gln Gly Val Lys Val Lys Asp Gly Gln Asp Gly Asp  
 6740 6745 6750

Val Glu Ser Glu Trp Glu Asn Asp Asp Thr Val Ala Ala Arg Asn  
 6755 6760 6765

Gln Leu Cys Lys Gly Asn Ile Phe Ala Met Glu Ile Asn Leu Gln  
 6770 6775 6780

Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn Val Ala Leu Tyr  
 6785 6790 6795

Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Thr Asn Val Thr Leu Pro  
 6800 6805 6810

Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Thr Pro  
 6815 6820 6825

Pro Ser Leu Val Asp Ala Tyr Leu Asn Ile Gly Ala Arg Trp Ser  
 6830 6835 6840

Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn  
 6845 6850 6855

Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr  
 6860 6865 6870

Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys  
 6875 6880 6885

Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe  
 6890 6895 6900

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Lys  | Asp | Val | Asn | Met | Ile  | Leu | Gln | Ser | Ser | Leu  | Gly | Asn | Asp |
|     | 6905 |     |     |     |     | 6910 |     |     |     |     | 6915 |     |     |     |
| Leu | Arg  | Thr | Asp | Gly | Ala | Ser  | Ile | Ala | Phe | Thr | Ser  | Ile | Asn | Leu |
|     | 6920 |     |     |     |     | 6925 |     |     |     |     | 6930 |     |     |     |
| Tyr | Ala  | Thr | Phe | Phe | Pro | Met  | Ala | His | Asn | Thr | Ala  | Ser | Thr | Leu |
|     | 6935 |     |     |     |     | 6940 |     |     |     |     | 6945 |     |     |     |
| Glu | Ala  | Met | Leu | Arg | Asn | Asp  | Thr | Asn | Asp | Gln | Ser  | Phe | Asn | Asp |
|     | 6950 |     |     |     |     | 6955 |     |     |     |     | 6960 |     |     |     |
| Tyr | Leu  | Ser | Ala | Ala | Asn | Met  | Leu | Tyr | Pro | Ile | Pro  | Ala | Asn | Ala |
|     | 6965 |     |     |     |     | 6970 |     |     |     |     | 6975 |     |     |     |
| Thr | Asn  | Val | Pro | Ile | Ser | Ile  | Pro | Ser | Arg | Asn | Trp  | Ala | Ala | Phe |
|     | 6980 |     |     |     |     | 6985 |     |     |     |     | 6990 |     |     |     |
| Arg | Gly  | Trp | Ser | Phe | Thr | Arg  | Leu | Lys | Thr | Arg | Glu  | Thr | Pro | Ser |
|     | 6995 |     |     |     |     | 7000 |     |     |     |     | 7005 |     |     |     |
| Leu | Gly  | Ser | Gly | Phe | Asp | Pro  | Tyr | Phe | Val | Tyr | Ser  | Gly | Ser | Ile |
|     | 7010 |     |     |     |     | 7015 |     |     |     |     | 7020 |     |     |     |
| Pro | Tyr  | Leu | Asp | Gly | Thr | Phe  | Tyr | Leu | Asn | His | Thr  | Phe | Lys | Lys |
|     | 7025 |     |     |     |     | 7030 |     |     |     |     | 7035 |     |     |     |
| Val | Ser  | Ile | Thr | Phe | Asp | Ser  | Ser | Val | Ser | Trp | Pro  | Gly | Asn | Asp |
|     | 7040 |     |     |     |     | 7045 |     |     |     |     | 7050 |     |     |     |
| Arg | Leu  | Leu | Thr | Pro | Asn | Glu  | Phe | Glu | Ile | Lys | Arg  | Thr | Val | Asp |
|     | 7055 |     |     |     |     | 7060 |     |     |     |     | 7065 |     |     |     |
| Gly | Glu  | Gly | Tyr | Asn | Val | Ala  | Gln | Cys | Asn | Met | Thr  | Lys | Asp | Trp |
|     | 7070 |     |     |     |     | 7075 |     |     |     |     | 7080 |     |     |     |
| Phe | Leu  | Val | Gln | Met | Leu | Ala  | His | Tyr | Asn | Ile | Gly  | Tyr | Gln | Gly |
|     | 7085 |     |     |     |     | 7090 |     |     |     |     | 7095 |     |     |     |
| Phe | Tyr  | Val | Pro | Glu | Gly | Tyr  | Lys | Asp | Arg | Met | Tyr  | Ser | Phe | Phe |
|     | 7100 |     |     |     |     | 7105 |     |     |     |     | 7110 |     |     |     |
| Arg | Asn  | Phe | Gln | Pro | Met | Ser  | Arg | Gln | Val | Val | Asp  | Glu | Val | Asn |
|     | 7115 |     |     |     |     | 7120 |     |     |     |     | 7125 |     |     |     |
| Tyr | Lys  | Asp | Tyr | Gln | Ala | Val  | Thr | Leu | Ala | Tyr | Gln  | His | Asn | Asn |
|     | 7130 |     |     |     |     | 7135 |     |     |     |     | 7140 |     |     |     |

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Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln  
 7145 7150 7155  
  
 Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala  
 7160 7165 7170  
  
 Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met  
 7175 7180 7185  
  
 Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu  
 7190 7195 7200  
  
 Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala  
 7205 7210 7215  
  
 Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu  
 7220 7225 7230  
  
 Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln  
 7235 7240 7245  
  
 Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe  
 7250 7255 7260  
  
 Ser Ala Gly Asn Ala Thr Thr Ala Ala Leu Ala Ser Cys Lys Met  
 7265 7270 7275  
  
 Thr Ala Gly Ser Gly Glu Gln Glu Leu Arg Ala Ile Leu Arg Asp  
 7280 7285 7290  
  
 Leu Gly Cys Gly Pro Cys Phe Leu Gly Thr Phe Asp Lys Arg Phe  
 7295 7300 7305  
  
 Pro Gly Phe Met Ala Pro His Lys Leu Ala Cys Ala Ile Val Asn  
 7310 7315 7320  
  
 Thr Ala Gly Arg Glu Thr Gly Gly Glu His Trp Leu Ala Phe Ala  
 7325 7330 7335  
  
 Trp Asn Pro Arg Ser His Thr Cys Tyr Leu Phe Asp Pro Phe Gly  
 7340 7345 7350  
  
 Phe Ser Asp Glu Arg Leu Lys Gln Ile Tyr Gln Phe Glu Tyr Glu  
 7355 7360 7365  
  
 Gly Leu Leu Arg Arg Ser Ala Leu Ala Thr Glu Asp Arg Cys Val  
 7370 7375 7380



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Thr Leu Glu Lys Ser Thr Gln Thr Val Gln Gly Pro Arg Ser Ala  
 7385 7390 7395  
 Ala Cys Gly Leu Phe Cys Cys Met Phe Leu His Ala Phe Val His  
 7400 7405 7410  
 Trp Pro Asp Arg Pro Met Asp Lys Asn Pro Thr Met Asn Leu Leu  
 7415 7420 7425  
 Thr Gly Val Pro Asn Gly Met Leu Gln Ser Pro Gln Val Glu Pro  
 7430 7435 7440  
 Thr Leu Arg Arg Asn Gln Glu Ala Leu Tyr Arg Phe Leu Asn Ala  
 7445 7450 7455  
 His Ser Ala Tyr Phe Arg Ser His Arg Ala Arg Ile Glu Lys Ala  
 7460 7465 7470  
 Thr Ala Phe Asp Arg Met Asn Gln Asp Met Lys Thr Gly Val Cys  
 7475 7480 7485  
 Met Met Leu Tyr Ser Thr Ala His Val Tyr Ala Thr Phe Ser Glu  
 7490 7495 7500  
 Ala Leu Thr Leu Phe Arg Asn Arg Arg Gly Ser Ala Gly Ser Arg  
 7505 7510 7515  
 His Gly Pro Arg Ala Gly Ile Arg Cys Gly Thr Gly Thr Trp Ala  
 7520 7525 7530  
 Ala Thr Thr Arg Gly Ser Ala Ala Trp Ala Arg Gly Gly Arg Gly  
 7535 7540 7545  
 Thr Ser Arg Ser Thr Ala Cys Ala Val Ala Gly Arg Pro Ala Gly  
 7550 7555 7560  
 Arg Ala Arg Arg Ser Asn Arg Ser Trp Asp Pro Arg Ser Ala Arg  
 7565 7570 7575  
 Glu Ser Cys Gly Thr Arg Gly Cys Ser Thr Gly Thr Pro Ser Gly  
 7580 7585 7590  
 Pro Gly Ala Ser Arg Leu Pro Ala Pro Ser Arg Arg Cys Pro Pro  
 7595 7600 7605  
 Arg Pro Asp Pro Arg Arg Trp Pro Ser Arg Arg Gly Ser Ser Cys

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Ser  | Ala | Ala | Pro | Cys | Trp  | Ala | Arg | Ser | Arg | Ala  | Cys | Gly | Cys |
|     | 7625 |     |     |     |     | 7630 |     |     |     |     | 7635 |     |     |     |
| Asn | Arg  | Ser | Ala | Gly | Gly | Ser  | Ala | Ser | Ser | Gly | Pro  | Ala | Arg | Ser |
|     | 7640 |     |     |     |     | 7645 |     |     |     |     | 7650 |     |     |     |
| Ser | Cys  | Pro | Gly | Thr | Trp | Pro  | Ser | Lys | Pro | Pro | Ala  | Gly | Gly | Arg |
|     | 7655 |     |     |     |     | 7660 |     |     |     |     | 7665 |     |     |     |
| Pro | Ala  | Ala | Pro | Cys | Arg | Pro  | Arg | Arg | Arg | Pro | Arg  | Arg | Thr | Cys |
|     | 7670 |     |     |     |     | 7675 |     |     |     |     | 7680 |     |     |     |
| Arg | Thr  | Gly | Trp | Trp | Arg | Ser  | Arg | Arg | Arg | Ala | Arg  | Ser | Ser | Ala |
|     | 7685 |     |     |     |     | 7690 |     |     |     |     | 7695 |     |     |     |
| Arg | Arg  | Cys | Trp | Pro | Ala | Ala  | Pro | Arg | Cys | Ala | Pro  | Ser | Gly | Ser |
|     | 7700 |     |     |     |     | 7705 |     |     |     |     | 7710 |     |     |     |
| Gly | Ser  | Trp | Pro | Gly | Trp | Gly  | Ser | Pro | Ser | Ala | Arg  | Ala | Ala | Arg |
|     | 7715 |     |     |     |     | 7720 |     |     |     |     | 7725 |     |     |     |
| Ser | Arg  | Ser | Pro | His | Pro | Ser  | Arg | Cys | Ala | Pro | Ser  | Gly | Ser | Ser |
|     | 7730 |     |     |     |     | 7735 |     |     |     |     | 7740 |     |     |     |
| Arg | Ser  | Arg | Ala | Gly | Thr | Ala  | Ala | Cys | Pro | Arg | Leu  | Arg | Cys | Ser |
|     | 7745 |     |     |     |     | 7750 |     |     |     |     | 7755 |     |     |     |
| Arg | Ala  | Ala | Thr | Ala | Arg | Ser  | Arg | Cys | Thr | Pro | Ser  | Ser | Cys | Gly |
|     | 7760 |     |     |     |     | 7765 |     |     |     |     | 7770 |     |     |     |
| Arg | Ser  | Gly | Ser | Ala | Ser | Ala  | Arg | Ser | Pro | Ala | Gly  | Ser | Gly | Pro |
|     | 7775 |     |     |     |     | 7780 |     |     |     |     | 7785 |     |     |     |
| Ser | Ser  | Arg | Ser | Gly | Ser | Cys  | Cys | Trp | Arg | Ser | Ala  | Gly | Cys | Arg |
|     | 7790 |     |     |     |     | 7795 |     |     |     |     | 7800 |     |     |     |
| Gly | Ala  | Pro | Arg | Ser | His | Thr  | Gly | Gly | Arg | Cys | Gly  | Gly | Thr | Pro |
|     | 7805 |     |     |     |     | 7810 |     |     |     |     | 7815 |     |     |     |
| Arg | Pro  | Ala | Arg | Ala | Ser | Ala  | Gly | Arg | Arg | Thr | Ser  | Gly | Arg | Ser |
|     | 7820 |     |     |     |     | 7825 |     |     |     |     | 7830 |     |     |     |
| Pro | Arg  | Gly | Thr | Gly | Pro | Ser  | Ala | Ala | Ser | Ser | Leu  | Pro | Cys | Pro |
|     | 7835 |     |     |     |     | 7840 |     |     |     |     | 7845 |     |     |     |

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Ser Pro Arg Pro Lys Arg Ser Ala Gly Ser Gly Gly Ser Ser Pro  
 7850 7855 7860  
  
 Pro Leu Ser Ser Ser Pro Pro Pro Arg Ser Gly Gly Arg Ser Arg  
 7865 7870 7875  
  
 Pro Gly Ser Gln Thr Leu Ala Cys Arg Pro Ser Arg Cys Ala Arg  
 7880 7885 7890  
  
 Gly Glu Ser Ser Pro Arg Pro Pro Ala Pro Pro Arg Pro Ala Phe  
 7895 7900 7905  
  
 Arg Pro Arg Cys Pro Gly Cys Leu Ala Lys Ala His Ala Trp Ser  
 7910 7915 7920  
  
 Cys Gly Val Ser Phe Trp Ala Ala Glu Ala Ala Ala Met Cys Trp  
 7925 7930 7935  
  
 Glu Ser Ala Ser Ser Arg Ser Pro Arg Leu Phe Leu Leu Leu Gly  
 7940 7945 7950  
  
 Arg Arg Pro Arg Pro Arg Gly Gly Arg His Ala Ser Ser Gly Ala  
 7955 7960 7965  
  
 Glu Ala Glu Ala Thr Gly Ser Arg Gly Ser Ala Gly Gly Trp Gln  
 7970 7975 7980  
  
 Ser Pro Phe Arg Val Arg Gly Cys Ala Pro Gly Gly Ala Ala Leu  
 7985 7990 7995  
  
 Thr Asp Phe Leu Arg Gly Arg Pro Leu Cys Ser Pro Arg Glu Gln  
 8000 8005 8010  
  
 Gln Gln Ala Trp Arg Leu Ser His Arg Arg Gln His Arg His Leu  
 8015 8020 8025  
  
 Pro Pro Pro Pro Pro Thr Arg Thr Ser Ser Arg Met Lys Ala  
 8030 8035 8040  
  
 Pro Pro Arg Arg Pro Ala Pro Pro Pro Thr Pro Arg Pro Gln Thr  
 8045 8050 8055  
  
 Cys Lys Arg Trp Arg Asn Pro Ser Arg Leu Thr Trp Ala Thr Arg  
 8060 8065 8070  
  
 Pro Arg Ser Thr Arg Arg Ser Trp Gln Arg Ala Phe Gln Pro Arg  
 8075 8080 8085

## 368530-7006W01\_SequenceListing\_ST25.txt

Lys Arg Thr Thr Lys Ser Ser Gln Ser Arg Lys Gln Arg Thr Ser  
 8090 8095 8100  
 Arg Thr Arg Leu Gly Thr Ser Met Ala Thr Thr Ala Gly Gln Arg  
 8105 8110 8115  
 Thr Cys Ser Ser Ser Ile Trp Pro Ala Asn Ala Ser Ser Ser Arg  
 8120 8125 8130  
 Thr Arg Cys Ser Thr Ala Pro Arg Cys Pro Ser Ala Trp Arg Ser  
 8135 8140 8145  
 Ser Ala Ala Pro Thr Ser Ala Thr Ser Ser Arg Arg Ala Cys Pro  
 8150 8155 8160  
 Pro Ser Ala Ser Pro Thr Ala Pro Val Ser Pro Thr Arg Ala Ser  
 8165 8170 8175  
 Thr Ser Thr Arg Ser Ser Arg Cys Pro Arg Pro Trp Pro Pro Thr  
 8180 8185 8190  
 Thr Ser Phe Ser Arg Thr Lys Gly Ser Pro Ser Pro Ala Ala Pro  
 8195 8200 8205  
 Thr Ala Pro Ala Pro Thr Pro Cys Ser Thr Trp Ala Pro Ala Pro  
 8210 8215 8220  
 Ala Tyr Leu Ile Ser Pro Pro Trp Lys Arg Phe Pro Arg Ser Ser  
 8225 8230 8235  
 Arg Val Trp Ala Ala Thr Arg Leu Gly Pro Arg Thr Leu Cys Lys  
 8240 8245 8250  
 Glu Ala Glu Arg Ser Met Ser Thr Thr Ala Pro Trp Trp Ser Trp  
 8255 8260 8265  
 Lys Ala Thr Thr Arg Ala Trp Arg Ser Ser Ser Ala Arg Ser Ser  
 8270 8275 8280  
 Pro Thr Ser Pro Thr Arg Arg Ser Thr Cys Pro Pro Arg Ser Ala  
 8285 8290 8295  
 Pro Ser Trp Thr Arg Cys Ser Ser Ser Ala Pro Arg Pro Ser Arg  
 8300 8305 8310  
 Arg Arg Arg Cys Arg Thr Pro Arg Val Arg Thr Arg Ala Ser Pro  
 8315 8320 8325

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Trp  | Ser | Ala | Thr | Ser | Ser | Trp  | Arg | Ala | Gly | Trp | Glu  | Arg | Val | Ala |
| 8330 |     |     |     |     |     | 8335 |     |     |     |     | 8340 |     |     |     |
| Pro  | Pro | Arg | Ala | Trp | Lys | Ser  | Gly | Ala | Ser | Ser | Trp  | Pro | Trp | Ser |
| 8345 |     |     |     |     |     | 8350 |     |     |     |     | 8355 |     |     |     |
| Trp  | Pro | Trp | Ser | Trp | Ser | Val  | Cys | Ala | Ala | Ser | Leu  | Pro | Thr | Arg |
| 8360 |     |     |     |     |     | 8365 |     |     |     |     | 8370 |     |     |     |
| Arg  | Pro | Cys | Ala | Arg | Ser | Arg  | Arg | Thr | Cys | Thr | Thr  | Ser | Ser | Gly |
| 8375 |     |     |     |     |     | 8380 |     |     |     |     | 8385 |     |     |     |
| Thr  | Gly | Ser | Cys | Ala | Arg | Pro  | Ala | Arg | Ser | Pro | Thr  | Trp | Ser | Pro |
| 8390 |     |     |     |     |     | 8395 |     |     |     |     | 8400 |     |     |     |
| Thr  | Trp | Ser | Pro | Thr | Trp | Ala  | Ser | Cys | Thr | Arg | Thr  | Ala | Trp | Gly |
| 8405 |     |     |     |     |     | 8410 |     |     |     |     | 8415 |     |     |     |
| Lys  | Thr | Cys | Cys | Thr | Pro | Pro  | Cys | Ala | Gly | Arg | Pro  | Ala | Ala | Thr |
| 8420 |     |     |     |     |     | 8425 |     |     |     |     | 8430 |     |     |     |
| Thr  | Ser | Ala | Thr | Ala | Ser | Thr  | Cys | Thr | Ser | Ala | Thr  | Pro | Gly | Arg |
| 8435 |     |     |     |     |     | 8440 |     |     |     |     | 8445 |     |     |     |
| Arg  | Ala | Trp | Ala | Cys | Gly | Ser  | Ser | Ala | Trp | Arg | Ser  | Arg | Thr | Lys |
| 8450 |     |     |     |     |     | 8455 |     |     |     |     | 8460 |     |     |     |
| Ser  | Ser | Ala | Ser | Ser | Cys | Arg  | Arg | Thr | Ser | Arg | Pro  | Cys | Gly | Pro |
| 8465 |     |     |     |     |     | 8470 |     |     |     |     | 8475 |     |     |     |
| Gly  | Ser | Thr | Ser | Val | Pro | Pro  | Pro | Arg | Thr | Trp | Pro  | Thr | Ser | Ser |
| 8480 |     |     |     |     |     | 8485 |     |     |     |     | 8490 |     |     |     |
| Ser  | Pro | Ser | Ala | Cys | Gly | Arg  | Cys | Ala | Thr | Gly | Cys  | Pro | Thr | Leu |
| 8495 |     |     |     |     |     | 8500 |     |     |     |     | 8505 |     |     |     |
| Ala  | Lys | Ala | Cys | Cys | Lys | Thr  | Phe | Ala | Leu | Ser | Ser  | Ser | Asn | Ala |
| 8510 |     |     |     |     |     | 8515 |     |     |     |     | 8520 |     |     |     |
| Pro  | Gly | Ser | Cys | Pro | Pro | Pro  | Ala | Pro | Arg | Cys | Pro  | Arg | Thr | Ser |
| 8525 |     |     |     |     |     | 8530 |     |     |     |     | 8535 |     |     |     |
| Cys  | Arg | Pro | Ser | Ala | Ser | Ala  | Pro | Arg | Arg | Ser | Gly  | Ala | Thr | Ala |
| 8540 |     |     |     |     |     | 8545 |     |     |     |     | 8550 |     |     |     |
| Thr  | Cys | Cys | Ala | Trp | Pro | Thr  | Thr | Trp | Pro | Thr | Thr  | Arg | Thr | Ser |

8555

8560

8565

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Thr | Ser | Ala | Ala | Arg | Val  | Cys | Trp | Ser | Ala | Thr  | Ala | Ala | Ala |
| 8570 |     |     |     |     |     | 8575 |     |     |     |     | 8580 |     |     |     |
| Thr  | Ser | Ala | Arg | Arg | Thr | Ala  | Pro | Trp | Pro | Ala | Thr  | Pro | Ser | Cys |
| 8585 |     |     |     |     |     | 8590 |     |     |     |     | 8595 |     |     |     |
| Ala  | Arg | Pro | Arg | Ser | Ser | Ala  | Pro | Ser | Ser | Cys | Lys  | Ala | Pro | Ala |
| 8600 |     |     |     |     |     | 8605 |     |     |     |     | 8610 |     |     |     |
| Thr  | Ala | Arg | Ala | Arg | Gly | Val  | Asn | Ser | Pro | Arg | Gly  | Cys | Gly | Pro |
| 8615 |     |     |     |     |     | 8620 |     |     |     |     | 8625 |     |     |     |
| Arg  | Pro | Thr | Cys | Ala | Ser | Ser  | Cys | Pro | Arg | Thr | Thr  | Ile | Pro | Ser |
| 8630 |     |     |     |     |     | 8635 |     |     |     |     | 8640 |     |     |     |
| Arg  | Ser | Gly | Ser | Thr | Arg | Thr  | Asn | Pro | Ser | Arg | Pro  | Arg | Pro | Ser |
| 8645 |     |     |     |     |     | 8650 |     |     |     |     | 8655 |     |     |     |
| Cys  | Arg | Pro | Ala | Ser | Ser | Pro  | Arg | Gly | Pro | Ser | Trp  | Pro | Asn | Cys |
| 8660 |     |     |     |     |     | 8665 |     |     |     |     | 8670 |     |     |     |
| Lys  | Pro | Ser | Arg | Asn | Pro | Ala  | Lys | Asn | Phe | Cys | Lys  | Arg | Ala | Thr |
| 8675 |     |     |     |     |     | 8680 |     |     |     |     | 8685 |     |     |     |
| Gly  | Ser | Thr | Trp | Thr | Pro | Arg  | Pro | Glu | Arg | Ser | Ser  | Thr | Pro | Ala |
| 8690 |     |     |     |     |     | 8695 |     |     |     |     | 8700 |     |     |     |
| Ser  | Pro | Arg | Met | Pro | Arg | Gly  | Ser | Ser | Lys | Lys | Leu  | Lys | Val | Glu |
| 8705 |     |     |     |     |     | 8710 |     |     |     |     | 8715 |     |     |     |
| Leu  | Pro | Pro | Pro | Glu | Asp | Leu  | Glu | Glu | Asp | Trp | Glu  | Ser | Ser | Gln |
| 8720 |     |     |     |     |     | 8725 |     |     |     |     | 8730 |     |     |     |
| Ala  | Glu | Glu | Glu | Glu | Met | Glu  | Asp | Trp | Asp | Ser | Thr  | Gln | Ala | Glu |
| 8735 |     |     |     |     |     | 8740 |     |     |     |     | 8745 |     |     |     |
| Glu  | Asp | Ser | Leu | Gln | Asp | Ser  | Leu | Glu | Glu | Glu | Asp  | Glu | Val | Glu |
| 8750 |     |     |     |     |     | 8755 |     |     |     |     | 8760 |     |     |     |
| Glu  | Ala | Glu | Glu | Glu | Ala | Ala  | Ala | Ala | Arg | Pro | Ser  | Ser | Ser | Ala |
| 8765 |     |     |     |     |     | 8770 |     |     |     |     | 8775 |     |     |     |
| Glu  | Lys | Ala | Ser | Ser | Thr | Asp  | Thr | Ile | Ser | Ala | Pro  | Gly | Arg | Gly |
| 8780 |     |     |     |     |     | 8785 |     |     |     |     | 8790 |     |     |     |

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|------|-----|-----|
| Arg | Gly  | Gly | Arg | Ala | His | Ser  | Arg | Trp | Asp | Glu | Thr  | Gly  | Arg | Phe |
|     | 8795 |     |     |     |     | 8800 |     |     |     |     |      | 8805 |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Pro | Asn  | Pro | Thr | Thr | Gln | Thr  | Gly | Lys | Lys | Glu | Arg  | Gln  | Gly | Tyr |
|     | 8810 |     |     |     |     | 8815 |     |     |     |     | 8820 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Lys | Ser  | Trp | Arg | Gly | His | Lys  | Asn | Ala | Ile | Val | Ser  | Cys  | Leu | Gln |
|     | 8825 |     |     |     |     | 8830 |     |     |     |     | 8835 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Ala | Cys  | Gly | Gly | Asn | Ile | Ser  | Phe | Thr | Arg | Arg | Tyr  | Leu  | Leu | Phe |
|     | 8840 |     |     |     |     | 8845 |     |     |     |     | 8850 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| His | Arg  | Gly | Val | Asn | Phe | Pro  | Arg | Asn | Ile | Leu | His  | Tyr  | Tyr | Arg |
|     | 8855 |     |     |     |     | 8860 |     |     |     |     | 8865 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| His | Leu  | His | Ser | Pro | Tyr | Tyr  | Cys | Phe | Gln | Glu | Glu  | Ala  | Glu | Thr |
|     | 8870 |     |     |     |     | 8875 |     |     |     |     | 8880 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Gln | Gln  | Gln | Gln | Lys | Thr | Ser  | Gly | Ser | Ser | Ser | Lys  | Ile  | His | Ser |
|     | 8885 |     |     |     |     | 8890 |     |     |     |     | 8895 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Gly | Gly  | Arg | Trp | Thr | Glu | Asp  | Arg | Gly | Glu | Arg | Ala  | Gly  | Ala | Asp |
|     | 8900 |     |     |     |     | 8905 |     |     |     |     | 8910 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Pro | Gly  | Ala | Glu | Glu | Pro | Asp  | Leu | Ser | His | Pro | Leu  | Cys  | His | Leu |
|     | 8915 |     |     |     |     | 8920 |     |     |     |     | 8925 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Pro | Ala  | Glu | Ser | Gly | Ala | Gly  | Ala | Gly | Thr | Glu | Ser  | Gln  | Glu | Pro |
|     | 8930 |     |     |     |     | 8935 |     |     |     |     | 8940 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Phe | Ser  | Ala | Leu | Ala | His | Pro  | Gln | Leu | Ser | Val | Ser  | Gln  | Glu | Arg |
|     | 8945 |     |     |     |     | 8950 |     |     |     |     | 8955 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Arg | Pro  | Thr | Ser | Ala | His | Ser  | Arg | Gly | Arg | Arg | Gly  | Ser  | Leu | Gln |
|     | 8960 |     |     |     |     | 8965 |     |     |     |     | 8970 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Gln | Val  | Leu | Arg | Ala | His | Ser  | Arg | Val | Ala | Arg | Ala  | Arg  | Pro | His |
|     | 8975 |     |     |     |     | 8980 |     |     |     |     | 8985 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Thr | Glu  | Lys | Gly | Gly | Asn | Tyr  | Val | Thr | Thr | Cys | Ala  | Leu  | Arg | Pro |
|     | 8990 |     |     |     |     | 8995 |     |     |     |     | 9000 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Thr | Ile  | Met | Ser | Lys | Glu | Ile  | Pro | Thr | Pro | Tyr | Met  | Trp  | Ser | Tyr |
|     | 9005 |     |     |     |     | 9010 |     |     |     |     | 9015 |      |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
| Gln | Pro  | Gln | Met | Gly | Leu | Ala  | Ala | Gly | Ala | Ala | Gln  | Asp  | Tyr | Ser |
|     | 9020 |     |     |     |     | 9025 |     |     |     |     | 9030 |      |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Arg  | Met | Asn | Trp | Leu | Ser  | Ala | Gly | Pro | Ala | Met  | Ile | Ser | Arg |
|     | 9035 |     |     |     |     | 9040 |     |     |     |     | 9045 |     |     |     |
| Val | Asn  | Asp | Ile | Arg | Ala | His  | Arg | Asn | Gln | Ile | Leu  | Leu | Glu | Gln |
|     | 9050 |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Ser | Ala  | Ile | Thr | Ala | Thr | Pro  | Arg | His | His | Leu | Asn  | Pro | Arg | Asn |
|     | 9065 |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Trp | Pro  | Ala | Ala | Leu | Val | Tyr  | Gln | Glu | Ile | Pro | Gln  | Pro | Thr | Thr |
|     | 9080 |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Val | Leu  | Leu | Pro | Arg | Asp | Ala  | Gln | Ala | Glu | Val | Gln  | Leu | Thr | Asn |
|     | 9095 |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Ser | Gly  | Val | Gln | Leu | Ala | Gly  | Gly | Ala | Ala | Leu | Cys  | Arg | His | Arg |
|     | 9110 |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Pro | Ala  | Gln | Gly | Ile | Lys | Arg  | Leu | Val | Ile | Arg | Gly  | Arg | Gly | Thr |
|     | 9125 |     |     |     |     | 9130 |     |     |     |     | 9135 |     |     |     |
| Gln | Leu  | Asn | Asp | Glu | Val | Val  | Ser | Ser | Ser | Leu | Gly  | Leu | Arg | Pro |
|     | 9140 |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Asp | Gly  | Val | Phe | Gln | Leu | Ala  | Gly | Ser | Gly | Arg | Ser  | Ser | Phe | Thr |
|     | 9155 |     |     |     |     | 9160 |     |     |     |     | 9165 |     |     |     |
| Pro | Arg  | Gln | Ala | Val | Leu | Thr  | Leu | Glu | Ser | Ser | Ser  | Ser | Gln | Pro |
|     | 9170 |     |     |     |     | 9175 |     |     |     |     | 9180 |     |     |     |
| Arg | Ser  | Gly | Gly | Ile | Gly | Thr  | Leu | Gln | Phe | Val | Glu  | Glu | Phe | Thr |
|     | 9185 |     |     |     |     | 9190 |     |     |     |     | 9195 |     |     |     |
| Pro | Ser  | Val | Tyr | Phe | Asn | Pro  | Phe | Ser | Gly | Ser | Pro  | Gly | His | Tyr |
|     | 9200 |     |     |     |     | 9205 |     |     |     |     | 9210 |     |     |     |
| Pro | Asp  | Glu | Phe | Ile | Pro | Asn  | Phe | Asp | Ala | Ile | Ser  | Glu | Ser | Val |
|     | 9215 |     |     |     |     | 9220 |     |     |     |     | 9225 |     |     |     |
| Asp | Gly  | Tyr | Asp | Met | Ser | His  | Gly | Gly | Ala | Ala | Asp  | Leu | Ala | Arg |
|     | 9230 |     |     |     |     | 9235 |     |     |     |     | 9240 |     |     |     |
| Leu | Arg  | His | Leu | Asp | His | Cys  | Arg | Arg | Phe | Arg | Cys  | Phe | Ala | Arg |
|     | 9245 |     |     |     |     | 9250 |     |     |     |     | 9255 |     |     |     |
| Asp | Leu  | Ala | Glu | Phe | Ala | Tyr  | Phe | Glu | Leu | Pro | Glu  | Glu | His | Pro |
|     | 9260 |     |     |     |     | 9265 |     |     |     |     | 9270 |     |     |     |



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Gln Gly Pro Ala His Gly Val Arg Ile Ile Val Glu Gly Gly Leu  
 9275 9280 9285  
 Asp Ser His Leu Leu Arg Ile Phe Ser Gln Arg Pro Ile Leu Val  
 9290 9295 9300  
 Glu Arg Glu Gln Gly Gln Thr Leu Leu Thr Leu Tyr Cys Ile Cys  
 9305 9310 9315  
 Asn His Pro Gly Leu His Glu Ser Leu Cys Cys Leu Leu Cys Thr  
 9320 9325 9330  
 Glu Tyr Asn Lys Ser Asp Gln Arg Leu Leu Arg Thr Arg Leu Trp  
 9335 9340 9345  
 Cys Ser Cys Tyr Gln Pro Val Pro Val Leu His Arg Glu Arg Asp  
 9350 9355 9360  
 Arg Ala Pro Ala Pro Val Ala Pro Gln Glu Val Pro His Leu Ala  
 9365 9370 9375  
 Val Pro Gly Leu Pro Asp Arg Arg Cys Gln Pro Leu Arg Gln Arg  
 9380 9385 9390  
 Arg Ser Pro Ala Glu Arg Pro Cys Gln Pro Tyr Phe Phe His Pro  
 9395 9400 9405  
 Gln Lys Gln Ala Pro Ala Leu Pro Thr Leu Pro Pro Arg Asp Leu  
 9410 9415 9420  
 Ser Val Arg Leu Arg Thr Leu Pro Ser His Leu Pro Pro Asp Pro  
 9425 9430 9435  
 Glu Tyr His Ser Ala Ala Pro Arg Tyr Gln Pro Asn Tyr Pro Pro  
 9440 9445 9450  
 Thr Pro Pro Ser Arg Pro Phe Leu Ile Tyr His Tyr Arg Arg Trp  
 9455 9460 9465  
 Leu Leu Leu Leu Val Leu Pro Arg Pro Val Asp Pro Arg Ser Pro  
 9470 9475 9480  
 Thr Gln Ser Pro Glu Glu Val Arg Lys Cys Lys Phe Gln Glu Pro  
 9485 9490 9495  
 Trp Lys Phe Leu Lys Cys Tyr Arg Gln Lys Ser Asp Met His Pro

9500

9505

9510

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser  | Trp | Ile | Met | Ile | Ile | Gly  | Ile | Val | Asn | Ile | Leu  | Ala | Cys | Thr |
| 9515 |     |     |     |     |     | 9520 |     |     |     |     | 9525 |     |     |     |
| Leu  | Ile | Ser | Phe | Val | Ile | Tyr  | Pro | Cys | Phe | Asp | Phe  | Gly | Trp | Asn |
| 9530 |     |     |     |     |     | 9535 |     |     |     |     | 9540 |     |     |     |
| Ser  | Pro | Glu | Ala | Leu | Tyr | Leu  | Pro | Pro | Glu | Pro | Asp  | Thr | Pro | Pro |
| 9545 |     |     |     |     |     | 9550 |     |     |     |     | 9555 |     |     |     |
| Gln  | Gln | Gln | Pro | Gln | Ala | His  | Ala | Leu | Pro | Pro | Pro  | Gln | Pro | Arg |
| 9560 |     |     |     |     |     | 9565 |     |     |     |     | 9570 |     |     |     |
| Pro  | Gln | Tyr | Met | Pro | Ile | Leu  | Asp | Tyr | Glu | Ala | Glu  | Pro | Gln | Arg |
| 9575 |     |     |     |     |     | 9580 |     |     |     |     | 9585 |     |     |     |
| Pro  | Met | Leu | Pro | Ala | Ile | Ser  | Tyr | Phe | Asn | Leu | Thr  | Gly | Gly | Asp |
| 9590 |     |     |     |     |     | 9595 |     |     |     |     | 9600 |     |     |     |
| Asp  | Pro | Thr | Gly | Gln | Gln | Arg  | Gln | Arg | Pro | Ser | Pro  | Gly | His | Gly |
| 9605 |     |     |     |     |     | 9610 |     |     |     |     | 9615 |     |     |     |
| Arg  | Pro | Arg | Leu | Gly | Ala | Ala  | Thr | Arg | Pro | Thr | Ser  | His | Ser | Ser |
| 9620 |     |     |     |     |     | 9625 |     |     |     |     | 9630 |     |     |     |
| Ala  | Ala | Gly | Glu | Ser | Arg | Gln  | Gly | Ala | Ala | Gly | Arg  | His | Ser | His |
| 9635 |     |     |     |     |     | 9640 |     |     |     |     | 9645 |     |     |     |
| Pro  | Pro | Val | Gln | Glu | Arg | His  | Leu | Leu | Pro | Gly | Glu  | Thr | Gly | Gln |
| 9650 |     |     |     |     |     | 9655 |     |     |     |     | 9660 |     |     |     |
| Asp  | Leu | Leu | Arg | Gly | His | Pro  | Asp | Arg | Pro | Ser | Pro  | Leu | Leu | Arg |
| 9665 |     |     |     |     |     | 9670 |     |     |     |     | 9675 |     |     |     |
| Ala  | Pro | Ala | Ala | Ala | Pro | Glu  | Val | His | Leu | Pro | Gly  | Arg | Ser | Gln |
| 9680 |     |     |     |     |     | 9685 |     |     |     |     | 9690 |     |     |     |
| Pro  | His | Arg | His | His | Pro | Ala  | Val | Gly | Arg | Tyr | Gln  | Gly | Val | His |
| 9695 |     |     |     |     |     | 9700 |     |     |     |     | 9705 |     |     |     |
| Pro  | Leu | Leu | Leu | Arg | Leu | Pro  | Arg | Leu | Arg | Pro | His  | Ser | Asp | Gln |
| 9710 |     |     |     |     |     | 9715 |     |     |     |     | 9720 |     |     |     |
| Asp  | Pro | Leu | Arg | Pro | Pro | Arg  | Pro | Pro | Pro | His | Glu  | Leu | Ile | Thr |
| 9725 |     |     |     |     |     | 9730 |     |     |     |     | 9735 |     |     |     |

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Pro Leu Ser Ser Glu Ile Lys Ile Ile Leu Met Met Ile Ile Lys  
 9740 9745 9750  
  
 Lys Ile Ile Ile Phe Glu Ile Lys Ile Gln Ser Tyr Phe Glu Phe  
 9755 9760 9765  
  
 Asn Lys Asn Lys Glu Ser Leu Thr Asn Leu Ile Pro Gly Leu Cys  
 9770 9775 9780  
  
 Pro Cys Phe Leu Pro Thr Pro Pro His Ser Pro Leu Pro Ser Ser  
 9785 9790 9795  
  
 Gly Thr Ala Gly Pro Gly Gly Leu Gln Thr Ser Ser Thr Arg Arg  
 9800 9805 9810  
  
 Gly Cys Gln Ile Pro Pro Val Pro Gln Ser Ser Phe Tyr Leu Leu  
 9815 9820 9825  
  
 Ser Asp Val Gln Lys Ala Arg Pro Gly Gly Leu Arg Pro Arg Leu  
 9830 9835 9840  
  
 Pro Leu Arg Cys Arg Gln Arg Thr Asp Arg Ala Leu His Gln Pro  
 9845 9850 9855  
  
 Pro Leu Arg Leu Phe Arg Trp Ile Pro Arg Glu Ala Pro Gly Gly  
 9860 9865 9870  
  
 Val Val Pro Ala Thr Gly Pro Arg His His Gln Glu Arg Gly Asn  
 9875 9880 9885  
  
 His Pro Gln Ala Gly Arg Gly Gly Gly Pro Arg Leu Val Gly Lys  
 9890 9895 9900  
  
 Thr His Leu Gln His Gly His Gln Gly Arg Arg Pro Ser Gln Tyr  
 9905 9910 9915  
  
 Phe Lys Gln His His Phe Pro Asn Cys Cys Pro Phe Leu Gln Gln  
 9920 9925 9930  
  
 Gln Trp Asn Phe Lys Pro Gln Cys Leu His Thr Ile Ser Ser Ile  
 9935 9940 9945  
  
 Ser His Ile His Phe Arg His Lys Ser Trp Lys Arg Ser Ser Asp  
 9950 9955 9960  
  
 Phe Lys Val Val Asp Cys Thr Thr Asn Ser Ser Ser Tyr Ile Gln  
 9965 9970 9975

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Leu Lys His His Ser Lys Asn Arg Gln Arg Ala Ile Tyr Leu Gln  
 9980 9985 9990  
 Trp Lys Gln Arg Thr Gly Tyr Lys Pro Lys Lys Arg Thr Ser Phe  
 9995 10000 10005  
 Arg Cys Tyr Cys Asn Ile Tyr Trp Lys Trp Leu Arg Leu Trp Ile  
 10010 10015 10020  
 Leu Trp Lys Asn Lys Thr Arg Asn Tyr Gln Asn Trp Ser Arg Ile  
 10025 10030 10035  
 Lys Phe Cys Gln Ser Asn Ser Cys Gln Thr Arg His Arg Phe Lys  
 10040 10045 10050  
 Phe Leu Arg Trp Cys Leu Asp Ser Trp Lys Gln Thr Gly Gln Ala  
 10055 10060 10065  
 Asn Thr Leu Asp Tyr Pro Pro Lys Pro Leu Ser Ile Thr Phe Arg  
 10070 10075 10080  
 Gln Arg Cys Gln Ile Tyr Ser Leu Ser Tyr Lys Met Arg Ser Asn  
 10085 10090 10095  
 Thr Arg His Cys Gly Ser Gly Gly Cys Tyr Cys Arg Ile Ser Thr  
 10100 10105 10110  
 Lys Ser Asn His Ser Gln Lys Arg His Ser Phe Pro Ile Phe Arg  
 10115 10120 10125  
 Trp Cys Thr His Val Lys Leu Ile Asn Gly Arg Leu Leu Glu Leu  
 10130 10135 10140  
 Gly Gly Thr Asp His Ser Lys Cys Ser Leu Tyr Lys Cys Cys Gly  
 10145 10150 10155  
 Ile His Ala Lys Tyr Arg Cys Ile Ser Lys Asn Pro Lys Asn Thr  
 10160 10165 10170  
 Lys His Ser Gln Ser Gly Ile Phe Asn Trp Arg Asn Tyr Tyr Ala  
 10175 10180 10185  
 Asn Asp Thr Asn His Asn Phe Gln Trp His Lys Arg His Asn Pro  
 10190 10195 10200  
 Ser His Leu Leu Tyr Asp Phe Tyr Met Ala Val Asp Trp Arg Leu  
 10205 10210 10215

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Gly | Gln   | Lys | Tyr | Tyr | Leu | Cys   | Tyr | Gln | Leu | Ile | Leu   | Phe | Phe | Leu |
|     | 10220 |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |
| His | Arg   | Pro | Gly | Ile | Ile | Pro   | Pro | Ser | Lys | Pro | Thr   | Pro | Phe | Pro |
|     | 10235 |     |     |     |     | 10240 |     |     |     |     | 10245 |     |     |     |
| Thr | Thr   | Phe | Val | Tyr | Met | Glu   | Thr | Leu | Lys | Gln | Lys   | Asn | Lys | Val |
|     | 10250 |     |     |     |     | 10255 |     |     |     |     | 10260 |     |     |     |
| Gln | Val   | Phe | Tyr | Ile | Asn | Ser   | Phe | Thr | Gly | Leu | Glu   | Gln | Leu | Phe |
|     | 10265 |     |     |     |     | 10270 |     |     |     |     | 10275 |     |     |     |
| Phe | Leu   | His | Pro | Pro | Arg | Thr   | Trp | Asn | Thr | Pro | Pro   | Ser | Pro | Pro |
|     | 10280 |     |     |     |     | 10285 |     |     |     |     | 10290 |     |     |     |
| Ala | Gln   | Pro | Thr | Ser | Glu | Cys   | His | Trp | Trp | Thr | Cys   | Phe | Trp | Ser |
|     | 10295 |     |     |     |     | 10300 |     |     |     |     | 10305 |     |     |     |
| Pro | Arg   | Ser | Thr | Gln | Phe | Gln   | Ser | Glu | Pro | Val | Ser   | Asp | Arg | Ser |
|     | 10310 |     |     |     |     | 10315 |     |     |     |     | 10320 |     |     |     |
| Gly | Arg   | Asn | Pro | Pro | Gly | Thr   | Pro | Ala | Ser | Ala | Pro   | His | Ser | Ser |
|     | 10325 |     |     |     |     | 10330 |     |     |     |     | 10335 |     |     |     |
| Thr | Ala   | Glu | Asp | Cys | Pro | Arg   | Trp | Ser | Gly | Ser | Arg   | Leu | Ser | Gly |
|     | 10340 |     |     |     |     | 10345 |     |     |     |     | 10350 |     |     |     |
| Arg | Ser   | Arg | Arg | Ala | Ala | Val   | Gly | Ile | Ile | Val | Arg   | Glu | Arg | Asp |
|     | 10355 |     |     |     |     | 10360 |     |     |     |     | 10365 |     |     |     |
| Arg | Pro   | Val | Val | Ser | His | Gln   | Ala | Pro | Gln | Gln | Ser   | Leu | Pro | Pro |
|     | 10370 |     |     |     |     | 10375 |     |     |     |     | 10380 |     |     |     |
| Pro | Leu   | Arg | Gln | Ala | Ala | Ala   | Gln | Gly | Val | Arg | Val   | Gln | Gly | Leu |
|     | 10385 |     |     |     |     | 10390 |     |     |     |     | 10395 |     |     |     |
| Pro | Gln   | His | Asp | Ala | His | Gly   | Pro | Gln | His | Gln | Ser   | Ser | Gly | Ala |
|     | 10400 |     |     |     |     | 10405 |     |     |     |     | 10410 |     |     |     |
| Ala | Gly   | Ala | Ala | Ala | His | Ala   | Asn | Leu | Ala | Gln | Val   | Thr | Ala | Val |
|     | 10415 |     |     |     |     | 10420 |     |     |     |     | 10425 |     |     |     |
| Arg | Ala   | Thr | Gln | Asp | His | Gln   | Val | Val | Gln | Gln | Ser   | Ile | Val | Gln |
|     | 10430 |     |     |     |     | 10435 |     |     |     |     | 10440 |     |     |     |
| His | Ala   | Pro | Ala | Glu | Thr | His   | Arg | Gly | Lys | Asp | Ala   | Thr | His | Val |

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|         |                 |       |                 |       |             |  |  |  |  |       |  |  |  |
|---------|-----------------|-------|-----------------|-------|-------------|--|--|--|--|-------|--|--|--|
| 10445   |                 |       |                 |       | 10450       |  |  |  |  | 10455 |  |  |  |
| Ala Val | Val Pro Asp Pro | Gln   | Val Asn Gln Val | Ala   | Leu Pro Pro |  |  |  |  |       |  |  |  |
| 10460   |                 | 10465 |                 | 10470 |             |  |  |  |  |       |  |  |  |
| Glu Asp | Ala Ala His Val | His   | Asp Leu Leu Gly | His   | Val Ala Val |  |  |  |  |       |  |  |  |
| 10475   |                 | 10480 |                 | 10485 |             |  |  |  |  |       |  |  |  |
| His His | Leu Pro Val Pro | His   | His Pro Leu Val | Glu   | His Ala Ala |  |  |  |  |       |  |  |  |
| 10490   |                 | 10495 |                 | 10500 |             |  |  |  |  |       |  |  |  |
| Pro Asp | Asp Pro Ala Glu | Pro   | Gln Gly Gln His | Arg   | Pro Ala Arg |  |  |  |  |       |  |  |  |
| 10505   |                 | 10510 |                 | 10515 |             |  |  |  |  |       |  |  |  |
| His Ala | Ala Lys Arg Pro | Arg   | Ile Pro Ala Met | Thr   | Met Glu Asp |  |  |  |  |       |  |  |  |
| 10520   |                 | 10525 |                 | 10530 |             |  |  |  |  |       |  |  |  |
| Pro Pro | Leu Val Pro Val | Asp   | His Leu Gly Ala | Glu   | Gln Val Tyr |  |  |  |  |       |  |  |  |
| 10535   |                 | 10540 |                 | 10545 |             |  |  |  |  |       |  |  |  |
| Val Gly | Thr Ala Gln Ala | Tyr   | Ala His Ala Ser | Leu   | Gln His Ser |  |  |  |  |       |  |  |  |
| 10550   |                 | 10555 |                 | 10560 |             |  |  |  |  |       |  |  |  |
| Gln Leu | Leu Gly Gly Gln | Asn   | His Ile Pro Gly | His   | Gly Glu Leu |  |  |  |  |       |  |  |  |
| 10565   |                 | 10570 |                 | 10575 |             |  |  |  |  |       |  |  |  |
| Leu Gln | Asp Ser Glu Pro | Arg   | Arg Thr Gly Gln | Ser   | Ser His Ile |  |  |  |  |       |  |  |  |
| 10580   |                 | 10585 |                 | 10590 |             |  |  |  |  |       |  |  |  |
| Thr Tyr | Ile Val His Gly | Gln   | Gly Ile Ala Ile | Arg   | Gln His Arg |  |  |  |  |       |  |  |  |
| 10595   |                 | 10600 |                 | 10605 |             |  |  |  |  |       |  |  |  |
| Val Ile | Leu His Gln Arg | Ser   | Ala Gly Leu Gly | Leu   | Leu Thr Ala |  |  |  |  |       |  |  |  |
| 10610   |                 | 10615 |                 | 10620 |             |  |  |  |  |       |  |  |  |
| Trp Gly | Gly Arg Pro Ile | Arg   | Val Met Ala Gly | Arg   | Gly Ser Cys |  |  |  |  |       |  |  |  |
| 10625   |                 | 10630 |                 | 10635 |             |  |  |  |  |       |  |  |  |
| Ser Arg | Pro Cys His Asp | Ala   | Val Ala Phe Gly | His   | Phe Arg Thr |  |  |  |  |       |  |  |  |
| 10640   |                 | 10645 |                 | 10650 |             |  |  |  |  |       |  |  |  |
| Cys Cys | Ser Arg Thr Trp | Ser   | Gly Arg Cys Thr | Pro   | Ile Ala Gly |  |  |  |  |       |  |  |  |
| 10655   |                 | 10660 |                 | 10665 |             |  |  |  |  |       |  |  |  |
| Gly Gly | Leu Gly Ala Trp | Asn   | Ala Arg Cys Ser | Cys   | Lys Thr Ala |  |  |  |  |       |  |  |  |
| 10670   |                 | 10675 |                 | 10680 |             |  |  |  |  |       |  |  |  |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Thr | Leu   | Ser | Asp | Arg | Ala | Ala   | Asp | Leu | Gly | Pro | Gln   | Glu | Arg | Ser |
|     | 10685 |     |     |     |     | 10690 |     |     |     |     | 10695 |     |     |     |
| His | His   | Ala | Leu | Ser | His | Arg   | Pro | Pro | Trp | Asn | Gly   | Pro | Gly | Pro |
|     | 10700 |     |     |     |     | 10705 |     |     |     |     | 10710 |     |     |     |
| Ala | Arg   | Cys | Asn | Phe | Val | Gly   | Phe | Arg | Arg | Arg | Gly   | Arg | Glu | Glu |
|     | 10715 |     |     |     |     | 10720 |     |     |     |     | 10725 |     |     |     |
| Gln | Glu   | Glu | Pro | Leu | Thr | Phe   | Asn | Pro | Asn | Gly | Leu   | Gly | Ala | Leu |
|     | 10730 |     |     |     |     | 10735 |     |     |     |     | 10740 |     |     |     |
| Gln | Asn   | Glu | Gly | His | Gly | Asp   | Gly | Thr | Ser | Arg | Pro   | Arg | Cys | Val |
|     | 10745 |     |     |     |     | 10750 |     |     |     |     | 10755 |     |     |     |
| Gly | Gly   | Lys | Gln | Pro | Gly | Gln   | Arg | Tyr | Gly | Ser | Arg   | Asp | Val | Pro |
|     | 10760 |     |     |     |     | 10765 |     |     |     |     | 10770 |     |     |     |
| Arg | Trp   | Leu | Pro | Ala | Lys | Pro   | Pro | Arg | Ala | His | Pro   | Glu | Thr | Arg |
|     | 10775 |     |     |     |     | 10780 |     |     |     |     | 10785 |     |     |     |
| Gln | Arg   | Lys | Arg | Glu | Gly | Ser   | Leu | Ile | Pro | Gln | Pro   | Ser | Cys | Tyr |
|     | 10790 |     |     |     |     | 10795 |     |     |     |     | 10800 |     |     |     |
| Thr | Pro   | Ala | Pro | Ser | Pro | Asp   | Asn | Phe | His | Phe | Ser   | Ser | Leu | Glu |
|     | 10805 |     |     |     |     | 10810 |     |     |     |     | 10815 |     |     |     |
| Phe | Glu   | Leu | Val | Pro | Glu | Val   | Asn | Pro | Ser | Gln | Pro   | Lys | Ala | Arg |
|     | 10820 |     |     |     |     | 10825 |     |     |     |     | 10830 |     |     |     |
| Ala | Glu   | His | Pro | Pro | Pro | Ala   | Phe | Leu | Ser | Thr | Pro   | Ser | Phe | Gln |
|     | 10835 |     |     |     |     | 10840 |     |     |     |     | 10845 |     |     |     |
| Asp | Ile   | Leu | Leu | Leu | Val | His   | Leu | Gln | Gln | Ile | Asp   | Lys | Arg | Asn |
|     | 10850 |     |     |     |     | 10855 |     |     |     |     | 10860 |     |     |     |
| Ile | Lys   | Ile | Ser | Ala | Ala | Ile   | Pro | Glu | Leu | Leu | Pro   | Gln | Gln | Leu |
|     | 10865 |     |     |     |     | 10870 |     |     |     |     | 10875 |     |     |     |
| Val | Leu   | Phe | His | Ile | Val | Ser   | Glu | Ile | Phe | Ser | His   | Arg | Thr | Pro |
|     | 10880 |     |     |     |     | 10885 |     |     |     |     | 10890 |     |     |     |
| Arg | Asn   | Lys | Arg | Arg | Ala | Ser   | His | Ile | Thr | Asp | Lys   | Pro | Lys | Ser |
|     | 10895 |     |     |     |     | 10900 |     |     |     |     | 10905 |     |     |     |
| Pro | Pro   | Val | Ser | Ile | Ala | Lys   | Cys | Lys | Ile | Glu | Ile   | Ser | Met | Leu |
|     | 10910 |     |     |     |     | 10915 |     |     |     |     | 10920 |     |     |     |

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|                  |                              |                              |             |
|------------------|------------------------------|------------------------------|-------------|
| Ala Arg<br>10925 | Pro Gly Asp Ile Phe<br>10930 | Gln Ile Thr Gly Gln<br>10935 | Lys Ile Gly |
| Ala Ile<br>10940 | Phe Lys Lys Ile Asn<br>10945 | Lys Arg Lys Ile Phe<br>10950 | Gln Val His |
| Val Gly<br>10955 | Leu Gly Asn Asn Asp<br>10960 | Gly Val Ser Ala Arg<br>10965 | Gly Ala Phe |
| Gln His<br>10970 | Gly Leu Ala Asp Leu<br>10975 | Lys Asn Lys Lys Asn<br>10980 | Ile Lys Pro |
| Cys Pro<br>10985 | Gly Glu Gln Val Gly<br>10990 | Lys Ser Phe Ser Pro<br>10995 | Ala Pro Gly |
| Arg Pro<br>11000 | Arg Gly Leu Arg Arg<br>11005 | Asp Pro Arg Lys Asn<br>11010 | Cys Arg Tyr |
| Asp Lys<br>11015 | Pro Ser Gln Arg Asp<br>11020 | Val Pro Gly Gly Arg<br>11025 | Arg Glu Phe |
| Glu Lys<br>11030 | Lys His Thr Pro Pro<br>11035 | Glu His Trp Ser Pro<br>11040 | Val Lys Lys |
| Ser Gly<br>11045 | Arg Gly Ser Asn Glu<br>11050 | Ala Leu Gln Arg Ser<br>11055 | Leu Ser Ser |
| Pro Ala<br>11060 | Lys Arg Cys His Ala<br>11065 | Asp Glu Ala Gln Asn<br>11070 | Phe Gln Val |
| Arg Lys<br>11075 | Lys Cys Asn Tyr Ser<br>11080 | Pro Pro Ala Gln Ala<br>11085 | Ala Lys Leu |
| Pro Ile<br>11090 | Pro Pro Asp Thr His<br>11095 | Thr Lys Pro Gln Arg<br>11100 | Pro Leu Thr |
| Glu Arg<br>11105 | Gln Gln Gln Arg His<br>11110 | Thr Thr Gly Ala Arg<br>11115 | Val Arg Glu |
| Lys Thr<br>11120 | Glu Leu Pro Val Arg<br>11125 | Pro Leu Ser Ala Gln<br>11130 | Tyr Ile Ala |
| Pro Asp<br>11135 | Leu His Arg Lys Gly<br>11140 | Gln Ser Leu Lys Ile<br>11145 | Pro Ala Lys |
| Ser His<br>11150 | Thr Pro Ser Thr Arg<br>11155 | Pro Glu Thr Gly Asp<br>11160 | Thr Leu Arg |



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Lys Ile Arg Ala Leu Pro Gln Thr Ala Lys Leu Pro Ser Phe Pro  
11165 11170 11175

Gly Ser His Ala Thr Ser Ser Lys His Asp Phe Gln Ile Pro Ser  
11180 11185 11190

Thr Val Lys Asn Ile Thr Arg Pro Ala Pro Asn Gly Arg Arg Ser  
11195 11200 11205

Arg Ser Gln Ser Pro Ser Ser Leu Pro Lys Phe Lys Gln Leu Ile  
11210 11215 11220

Cys Ile Leu Thr Arg Thr Lys Ser Leu Arg Tyr Ile Ile Asp Asp  
11225 11230 11235

<210> 14  
<211> 11224  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Artificially Synthesized

<400> 14

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Cys Gly Ser Gly Asp Arg  
20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Met Arg Arg Ser Arg Phe  
35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg  
50 55 60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
85 90 95

Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
115 120 125

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Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
 130 135 140  
 Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
 145 150 155 160  
 Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
 165 170 175  
 Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
 180 185 190  
 Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
 195 200 205  
 Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
 210 215 220  
 Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
 225 230 235 240  
 Ser Met Pro Ser Thr Pro Pro Ile Asp Val Asn Asp Gly Lys Trp Pro  
 245 250 255  
 Ala Trp His Tyr Ala Gln Tyr Met Thr Leu Trp Asp Phe Pro Thr Trp  
 260 265 270  
 Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile Thr Met Val Met Arg Phe  
 275 280 285  
 Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe Asp Ser Arg Gly Phe Pro  
 290 295 300  
 Ser Leu His Pro Ile Asp Val Asn Gly Ser Leu Phe Trp His Gln Asn  
 305 310 315 320  
 Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn Ser Ala Pro Leu Thr Gln  
 325 330 335  
 Met Gly Gly Arg Arg Val Arg Trp Glu Val Tyr Ile Ser Arg Ala Arg  
 340 345 350  
 Leu Val Asn Arg Gln Ile Thr Arg Ser Phe Ile Ala Val Val Tyr His  
 355 360 365  
 Ser Ile Ala Asn Ala Val Ser Ala Ser Asp Thr Thr Val Ser Asn Leu  
 370 375 380

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Arg Leu Glu Phe Asp Ala Thr Met Arg Val Arg Gly Ile Pro Arg Asn  
385 390 395 400

Trp Pro Gln Trp Trp Ile Trp Gly Ile Leu Gly Phe Trp Met Ile Ile  
405 410 415

Ile Cys Arg Val Val Gly Asn Leu Asp Leu Trp Val Thr Val Tyr Tyr  
420 425 430

Gly Val Pro Val Trp Lys Glu Ala Lys Thr Thr Leu Phe Cys Ala Ser  
435 440 445

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

Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu Glu Asn  
465 470 475 480

Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met Val Asp Gln Met  
485 490 495

His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val  
500 505 510

Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Lys Asn Val Asn Ile  
515 520 525

Ser Ala Asn Ala Asn Ala Thr Ala Thr Leu Asn Ser Ser Met Asn Gly  
530 535 540

Glu Ile Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Leu Arg Asp Lys  
545 550 555 560

Lys Gln Lys Val Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu  
565 570 575

Asn Gly Gly Glu His Asn Glu Thr Gly Glu Tyr Ile Leu Ile Asn Cys  
580 585 590

Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro  
595 600 605

Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys  
610 615 620

Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr

```

625                               630           635           640
Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu
      645                               650
Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Val Arg Ser Glu Asn
      660                               665           670
Leu Thr Asn Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser Val
      675                               680           685
Glu Ile Lys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg
      690                               695           700
Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp
705                               710           715           720
Ile Arg Glu Ala His Cys Asn Ile Ser Arg Glu Thr Trp Asn Ser Thr
      725                               730           735
Leu Ile Gln Val Lys Glu Lys Leu Arg Glu His Tyr Asn Lys Thr Ile
      740                               745           750
Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Val Thr Thr His Ser
      755                               760           765
Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Thr Lys Leu Phe
      770                               775           780
Asn Glu Thr Lys Leu Phe Asn Glu Ser Glu Tyr Val Asp Asn Lys Thr
785                               790           795           800
Ile Ile Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu
      805                               810           815
Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys
      820                               825           830
Lys Ser Asn Ile Thr Gly Leu Leu Leu Thr Trp Asp Gly Gly Glu Asn
      835                               840           845
Ser Thr Glu Gly Val Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn
      850                               855           860
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu
865                               870           875           880

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Gly Val Ala Pro Thr Lys Ser Lys Arg Lys Val Val Gly Arg Glu Lys  
885 890 895

Arg Ala Val Gly Leu Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala  
900 905 910

Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg  
915 920 925

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala  
930 935 940

Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys  
945 950 955 960

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

Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys Ala Thr  
980 985 990

Ala Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Leu Gly Asp Ile  
995 1000 1005

Trp Asp Asn Met Thr Trp Met Gln Trp Asp Arg Glu Ile Ser Asn  
1010 1015 1020

Tyr Thr Asn Thr Ile Phe Arg Leu Leu Glu Asp Ser Gln Asn Gln  
1025 1030 1035

Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys  
1040 1045 1050

Asn Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr Ile  
1055 1060 1065

Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile  
1070 1075 1080

Ile Phe Gly Val Leu Ala Ile Val Lys Arg Val Arg Gln Gly Tyr  
1085 1090 1095

Ser Pro Leu Ser Phe Gln Thr Leu Ile Pro Asn Pro Arg Gly Pro  
1100 1105 1110

Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Lys  
1115 1120 1125

368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp | Arg  | Ser | Ile | Arg | Leu | Val  | Ser | Gly | Phe | Leu | Ala  | Leu | Ala | Trp |
|     | 1130 |     |     |     |     | 1135 |     |     |     |     | 1140 |     |     |     |
| Asp | Asp  | Leu | Arg | Ser | Leu | Cys  | Leu | Phe | Ser | Tyr | His  | Gln | Leu | Arg |
|     | 1145 |     |     |     |     | 1150 |     |     |     |     | 1155 |     |     |     |
| Asp | Phe  | Ile | Leu | Thr | Ala | Ala  | Arg | Ala | Ala | Glu | Leu  | Leu | Gly | Arg |
|     | 1160 |     |     |     |     | 1165 |     |     |     |     | 1170 |     |     |     |
| Ser | Ser  | Leu | Arg | Gly | Leu | Gln  | Arg | Gly | Trp | Glu | Val  | Leu | Lys | Tyr |
|     | 1175 |     |     |     |     | 1180 |     |     |     |     | 1185 |     |     |     |
| Leu | Gly  | Asn | Leu | Val | Gln | Tyr  | Trp | Gly | Leu | Glu | Leu  | Lys | Arg | Ser |
|     | 1190 |     |     |     |     | 1195 |     |     |     |     | 1200 |     |     |     |
| Ala | Ile  | Asn | Leu | Phe | Asp | Thr  | Ile | Ala | Ile | Ala | Val  | Ala | Glu | Gly |
|     | 1205 |     |     |     |     | 1210 |     |     |     |     | 1215 |     |     |     |
| Thr | Asp  | Arg | Ile | Ile | Glu | Val  | Ile | Gln | Arg | Ile | Cys  | Arg | Ala | Ile |
|     | 1220 |     |     |     |     | 1225 |     |     |     |     | 1230 |     |     |     |
| Arg | Tyr  | Ile | Pro | Thr | Arg | Ile  | Arg | Gln | Gly | Phe | Glu  | Ala | Ala | Leu |
|     | 1235 |     |     |     |     | 1240 |     |     |     |     | 1245 |     |     |     |
| Leu | Gly  | Thr | Ser | Arg | Val | Asp  | Pro | Gly | Gly | Gln | Thr  | Ala | Asp | Gln |
|     | 1250 |     |     |     |     | 1255 |     |     |     |     | 1260 |     |     |     |
| Pro | Arg  | Leu | Cys | Leu | Leu | Val  | Ala | Ser | His | Leu | Leu  | Phe | Ala | Pro |
|     | 1265 |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |
| Pro | Pro  | Cys | Leu | Pro | Pro | Trp  | Lys | Val | Pro | Leu | Pro  | Leu | Ser | Phe |
|     | 1280 |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |
| Pro | Asn  | Lys | Met | Arg | Lys | Leu  | His | Arg | Ile | Val | Val  | Gly | Val | Ile |
|     | 1295 |     |     |     |     | 1300 |     |     |     |     | 1305 |     |     |     |
| Leu | Phe  | Trp | Gly | Val | Gly | Trp  | Gly | Arg | Thr | Ala | Arg  | Gly | Arg | Ile |
|     | 1310 |     |     |     |     | 1315 |     |     |     |     | 1320 |     |     |     |
| Gly | Lys  | Thr | Ile | Ala | Gly | Met  | Leu | Gly | Met | Arg | Trp  | Ala | Leu | Trp |
|     | 1325 |     |     |     |     | 1330 |     |     |     |     | 1335 |     |     |     |
| Leu | Leu  | Arg | Arg | Lys | Glu | Pro  | Ala | Asp | Leu | Gln | Ile  | Ile | His | Leu |
|     | 1340 |     |     |     |     | 1345 |     |     |     |     | 1350 |     |     |     |
| Cys | Arg  | Val | Arg | Arg | Lys | Arg  | Asn | Gly | Ile | Met | Gly  | Ile | Met | Gly |
|     | 1355 |     |     |     |     | 1360 |     |     |     |     | 1365 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu | His  | Ile | Gly | Gln | Ile | Ser  | Thr | Tyr | Ala | Gly | His  | Arg | Ala | Cys |
|     | 1370 |     |     |     |     | 1375 |     |     |     |     | 1380 |     |     |     |
| Gly | Leu  | Ala | Pro | Pro | Gln | Asp  | Met | Ala | Arg | Val | Arg  | Ala | Gln | Arg |
|     | 1385 |     |     |     |     | 1390 |     |     |     |     | 1395 |     |     |     |
| His | Asp  | Pro | Leu | Gln | Cys | Ala  | Pro | Gly | Leu | Pro | Pro  | Arg | His | Val |
|     | 1400 |     |     |     |     | 1405 |     |     |     |     | 1410 |     |     |     |
| His | Ala  | Leu | Pro | Val | Gln | His  | Ala | Ile | Cys | Glu | Gly  | Ala | Ala | Gly |
|     | 1415 |     |     |     |     | 1420 |     |     |     |     | 1425 |     |     |     |
| Ala | Arg  | Cys | His | Val | Gln | Ser  | Glu | Pro | Asp | Gly | Gly  | Val | His | Glu |
|     | 1430 |     |     |     |     | 1435 |     |     |     |     | 1440 |     |     |     |
| Cys | Gly  | Ala | Val | Glu | Asn | Ser  | Glu | Ile | Ile | Gln | Asp  | Gln | Val | Pro |
|     | 1445 |     |     |     |     | 1450 |     |     |     |     | 1455 |     |     |     |
| Gly | Leu  | Arg | Met | Arg | Arg | Gln  | Ala | Arg | Gln | Ala | Ser  | Ala | Arg | Val |
|     | 1460 |     |     |     |     | 1465 |     |     |     |     | 1470 |     |     |     |
| Cys | Gly  | Gly | Asp | Gly | Gly | Pro  | Ala | Thr | Arg | Ser | Phe  | Gly | Val | Val |
|     | 1475 |     |     |     |     | 1480 |     |     |     |     | 1485 |     |     |     |
| Leu | Gln  | Arg | Asp | Gly | Val | Arg  | Leu | Gln | Arg | Gly | Arg  | Ile | Leu | Glu |
|     | 1490 |     |     |     |     | 1495 |     |     |     |     | 1500 |     |     |     |
| Val | Val  | Phe | Gly | Ala | Gly | Cys  | Glu | Pro | Ala | Gly | Ala  | Glu | Leu | Lys |
|     | 1505 |     |     |     |     | 1510 |     |     |     |     | 1515 |     |     |     |
| Ser | Val  | Val | Phe | Cys | Val | Leu  | Gln | Gln | His | Glu | Arg  | Lys | Arg | Leu |
|     | 1520 |     |     |     |     | 1525 |     |     |     |     | 1530 |     |     |     |
| Leu | Gly  | Arg | Gly | Ile | Gln | Pro  | Leu | Ser | Asp | Gly | Ala  | Ser | Pro | Leu |
|     | 1535 |     |     |     |     | 1540 |     |     |     |     | 1545 |     |     |     |
| Leu | Gly  | Gly | Ser | Ala | Ser | Glu  | Cys | Asp | Gly | Ile | His  | Gly | Gly | Arg |
|     | 1550 |     |     |     |     | 1555 |     |     |     |     | 1560 |     |     |     |
| Pro | Ala  | Arg | Ala | Ala | Arg | Glu  | Leu | Phe | Asn | Pro | Asp  | Leu | Arg | Asp |
|     | 1565 |     |     |     |     | 1570 |     |     |     |     | 1575 |     |     |     |
| Pro | Glu  | Leu | Leu | Val | Arg | Gly  | Arg | Ser | Cys | Arg | Arg  | Ser | Cys | Cys |
|     | 1580 |     |     |     |     | 1585 |     |     |     |     | 1590 |     |     |     |
| Phe | Arg  | Arg | Gln | Arg | Arg | Ala  | Arg | Asn | Gly | Pro | Gly  | Arg | Arg | Leu |

1595

1600

1605

Leu Gln Leu Ser Gly Gly Gln Leu Glu Phe His Gln Ser Arg Gln  
 1610 1615 1620

Pro Glu Arg Gly Glu Ala Ala Ala Ala Asp Gly Pro Ala Arg Gly  
 1625 1630 1635

Pro Asp Pro Ala Pro Gly Arg Ala Asp Pro Ala Gly Gly Ser Ala  
 1640 1645 1650

Ala Gly Gly Asp Ala Gly Arg Gly Cys His Gly Glu Asn Gln Ile  
 1655 1660 1665

Lys Asn Glu Ser Ile Asn Lys Arg Arg Arg Leu Leu Ile Leu Thr  
 1670 1675 1680

Gln Ser Leu Glu Ser Leu Phe Asp Phe Ser Arg Ala Val Gly Pro  
 1685 1690 1695

Gly Pro Pro Val Ser Ile Ile Glu His Pro Val Asp Leu Phe Gln  
 1700 1705 1710

Asp Pro Val Glu Val Gly Leu Asp Val Glu Val His Gly His Glu  
 1715 1720 1725

Pro Val Pro Gly Val Glu Val Ala Pro Leu Gln Gly Leu Val Leu  
 1730 1735 1740

Gly Asp Gly Val Val Asn His Pro Val Ile Ala Gly Ala Gln Gly  
 1745 1750 1755

Val Val Leu His Asp Val Leu Glu Glu Glu Thr Asp Gly His Gly  
 1760 1765 1770

Gln Pro Leu Gly Val Gly Val Asp Glu Pro Val Glu Leu Gly Gly  
 1775 1780 1785

Met His Ala Gly Gly Asp Glu Met His Leu Gly Leu Asp Leu Glu  
 1790 1795 1800

Ile Gly Asp Val Pro Ala Gln Ile Pro Pro Gly Val His Val Val  
 1805 1810 1815

Gln Asp His Gln His Gly Val Ser Gly Ala Leu Gly Glu Phe Val  
 1820 1825 1830



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Met  | Gln | Leu | Gly | Arg | Glu | Gly  | Val | Lys | Glu | Phe | Gly  | Asp | Ala | Leu |
| 1835 |     |     |     |     |     | 1840 |     |     |     |     | 1845 |     |     |     |
| Val  | Thr | Ala | Gln | Val | Phe | His  | Ala | Leu | Ile | His | Asp  | Asp | Gly | Asp |
| 1850 |     |     |     |     |     | 1855 |     |     |     |     | 1860 |     |     |     |
| Gly  | Pro | Val | Gly | Gly | Gly | Leu  | Gly | Lys | Asp | Val | Ser  | Gly | Val | Gly |
| 1865 |     |     |     |     |     | 1870 |     |     |     |     | 1875 |     |     |     |
| His  | Ile | Val | Val | Val | Val | Leu  | Gly | Glu | Leu | Val | Ile  | Gly | His | Phe |
| 1880 |     |     |     |     |     | 1885 |     |     |     |     | 1890 |     |     |     |
| Asn  | Glu | Phe | Gly | Ala | Glu | Gly  | Ala | Arg | Leu | Gly | Asp  | Glu | Gly | Ala |
| 1895 |     |     |     |     |     | 1900 |     |     |     |     | 1905 |     |     |     |
| Leu  | Asp | Pro | Gly | Gly | Val | Val  | Ala | Leu | Ala | Asp | Leu  | His | Leu | Pro |
| 1910 |     |     |     |     |     | 1915 |     |     |     |     | 1920 |     |     |     |
| Gly  | Leu | Glu | Leu | Gly | Gly | Gly  | Asp | His | Val | His | Leu  | Arg | Gly | Asp |
| 1925 |     |     |     |     |     | 1930 |     |     |     |     | 1935 |     |     |     |
| Glu  | Lys | Asn | Gly | Phe | Arg | Gly  | Gly | Gly | Asp | Glu | Leu  | Gly | Arg | Lys |
| 1940 |     |     |     |     |     | 1945 |     |     |     |     | 1950 |     |     |     |
| Gln  | Val | Pro | Glu | Gln | Leu | Gly  | Leu | Ala | Ala | Thr | Gly  | Gly | Ala | Val |
| 1955 |     |     |     |     |     | 1960 |     |     |     |     | 1965 |     |     |     |
| Asp  | Asp | Pro | Asp | Asp | Arg | Leu  | Gln | Val | Val | Val | Glu  | Gly | Glu | Thr |
| 1970 |     |     |     |     |     | 1975 |     |     |     |     | 1980 |     |     |     |
| Ala  | Ala | Val | Leu | Ala | Glu | Glu  | Gly | Gly | His | Leu | Val  | His | His | Leu |
| 1985 |     |     |     |     |     | 1990 |     |     |     |     | 1995 |     |     |     |
| Ala  | His | Met | His | Val | Leu | Ala  | His | Glu | Phe | Arg | Gln  | Glu | Ala | Leu |
| 2000 |     |     |     |     |     | 2005 |     |     |     |     | 2010 |     |     |     |
| Ala  | Pro | Gln | Arg | Glu | Glu | Leu  | Leu | Gln | Arg | Gly | Glu  | Val | Phe | Gln |
| 2015 |     |     |     |     |     | 2020 |     |     |     |     | 2025 |     |     |     |
| Arg  | Leu | Glu | Ser | Val | Gly | His  | Gly | His | Phe | Gly | Glu  | Gly | Leu | Leu |
| 2030 |     |     |     |     |     | 2035 |     |     |     |     | 2040 |     |     |     |
| Gln  | Glu | Phe | Gln | Thr | Val | Pro  | Glu | Leu | Gly | Asp | Val  | Leu | Gly | Ile |
| 2045 |     |     |     |     |     | 2050 |     |     |     |     | 2055 |     |     |     |
| Ser  | Ile | Gln | Gln | Thr | Ser | Ser  | Phe | Arg | Gly | Leu | Gly  | Arg | Leu | Arg |
| 2060 |     |     |     |     |     | 2065 |     |     |     |     | 2070 |     |     |     |

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Glu Gly Thr Arg Arg Trp Ala Ser Ser Glu Ala Arg Val Arg Ser  
 2075 2080 2085  
 Phe Gln Gly Arg Arg Val Arg Val Ser Val Val Ser Val Thr Val  
 2090 2095 2100  
 Lys Gly Cys Ala Pro Gly Trp Ala Leu Ala Arg Val Arg Phe Arg  
 2105 2110 2115  
 Leu Ile Arg Leu Val Glu Asn Arg Ser Arg Ser Ala Pro Cys Ala  
 2120 2125 2130  
 Ser Ala Arg Gln Leu Ser Met Ser Ser Leu Ser Ala Ser Ala Ala  
 2135 2140 2145  
 Trp Pro Leu Ala Arg Ser Leu Pro Leu Glu Val Cys Pro Gln Thr  
 2150 2155 2160  
 Gly Gln Arg Arg Asp Leu Arg Ala Ser Leu Gly Ala Arg Lys Thr  
 2165 2170 2175  
 Asp Ser Gly Ala Ala Ser Ala Pro Gln Leu Ala Gln Thr Val Ser  
 2180 2185 2190  
 His Ser Thr Ser Gln Val Arg Ser Gly Arg Leu Gly Ser Lys Thr  
 2195 2200 2205  
 Arg Phe Pro Pro Cys Phe Leu Met Arg Phe Leu Pro Leu Val Ser  
 2210 2215 2220  
 Met Ser Ser Cys Pro Arg Trp Val Thr Lys Arg Leu Ser Val Ser  
 2225 2230 2235  
 Pro Thr Asp Phe Met Gly Arg Ser Ser Ser Gly Val Pro Arg Ser  
 2240 2245 2250  
 Ser Ser Arg Asn Pro Ala His Ser Glu Thr Lys Ala Arg Val Gln  
 2255 2260 2265  
 Ala Ser Thr Lys Glu Ala Thr Trp Glu Gly Arg Ser Leu Ser Thr  
 2270 2275 2280  
 Ser Gly Ser Thr Phe Ser Arg Val Cys Lys His Met Ser Pro Ser  
 2285 2290 2295  
 Ser Thr Ser Arg Lys Val Ile Gly Leu Val Ala Thr Pro Gly Val  
 2300 2305 2310

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Ala  | Gly | Gly | Val | Lys | Gly  | Ala | Gly | Pro | Cys | Ser  | Ser | Ser | Leu |
|     | 2315 |     |     |     |     | 2320 |     |     |     |     | 2325 |     |     |     |
| Ser | Ser  | Gly | Ser | Leu | Ser | Arg  | Ser | Ala | Ser | Cys | Trp  | Gly | Arg | Tyr |
|     | 2330 |     |     |     |     | 2335 |     |     |     |     | 2340 |     |     |     |
| Ser | Leu  | Ser | Lys | Ala | Gly | Met  | Thr | Ser | Ala | Leu | Arg  | Leu | Ser | Val |
|     | 2345 |     |     |     |     | 2350 |     |     |     |     | 2355 |     |     |     |
| Ser | Arg  | Asn | Glu | Glu | Asp | Leu  | Ile | Leu | Thr | Val | Pro  | Leu | Glu | Thr |
|     | 2360 |     |     |     |     | 2365 |     |     |     |     | 2370 |     |     |     |
| Pro | Phe  | Met | Ser | Pro | Ser | Ser  | Ile | Trp | Ser | Glu | Lys  | Thr | Ile | Phe |
|     | 2375 |     |     |     |     | 2380 |     |     |     |     | 2385 |     |     |     |
| Leu | Leu  | Ser | Ser | Leu | Val | Ala  | Lys | Glu | Pro | Arg | Ala  | Leu | Glu | Ser |
|     | 2390 |     |     |     |     | 2395 |     |     |     |     | 2400 |     |     |     |
| Ser | Leu  | Ala | Met | Glu | Arg | Met  | Val | Trp | Phe | Phe | Ser  | Leu | Ser | Ala |
|     | 2405 |     |     |     |     | 2410 |     |     |     |     | 2415 |     |     |     |
| Arg | Ser  | Leu | Ala | Ala | Met | Leu  | Ser | Cys | Thr | Tyr | Ser  | Arg | Ala | Thr |
|     | 2420 |     |     |     |     | 2425 |     |     |     |     | 2430 |     |     |     |
| His | Phe  | His | Ser | Gly | Lys | Thr  | Val | Val | Ser | Ser | Ser  | Gly | Thr | Ile |
|     | 2435 |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |
| Leu | Thr  | Arg | Gln | Pro | Arg | Leu  | Cys | Arg | Val | Met | Arg  | Ser | Thr | Leu |
|     | 2450 |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |
| Val | Ala  | Thr | Ser | Pro | Arg | Arg  | Gly | Ser | Leu | Val | Gln  | Gln | Arg | Arg |
|     | 2465 |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |
| Pro | Pro  | Leu | Arg | Glu | Gln | Lys  | Gly | Gly | Ser | Gly | Ser  | Ser | Met | Ser |
|     | 2480 |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Ser | Ser  | Gly | Gly | Ser | Ala | Ser  | Thr | Val | Lys | Met | Pro  | Gly | Arg | Ser |
|     | 2495 |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Ser | Gly  | Ser | Lys | Leu | Met | Gln  | Val | Pro | Arg | Leu | Ser  | Ser | Ala | Ala |
|     | 2510 |     |     |     |     | 2515 |     |     |     |     | 2520 |     |     |     |
| Cys | Gln  | Ser | Arg | Thr | Ala | Ser  | Ala | Arg | Ser | Gly | Leu  | Arg | Gly | Val |
|     | 2525 |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Pro | Gln  | Gly | Met | Gly | Cys | Val  | Ser | Ala | Glu | Ala | Tyr  | Met | Pro | Gln |

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Met Ser Thr Arg Gly Ser Ser Arg Thr Pro Met Val Gly Gln Arg  
 2555 2560 2565

Pro Pro Arg Met Leu Ala Arg Thr Ser Tyr Ser Ser Cys Glu Gly  
 2570 2575 2580

Ala Arg Ser Pro Val Pro Arg Leu Glu Arg Cys Gly Phe Ser Ala  
 2585 2590 2595

Arg Thr Ile Trp Arg Lys Met Ala Trp Glu Leu Glu Glu Met Val  
 2600 2605 2610

Gly Leu Trp Lys Met Leu Lys Trp Ala Trp Gly Arg Pro Thr Glu  
 2615 2620 2625

Ser Leu Met Lys Trp Ala Glu Ser Cys Ser Leu Ala Thr Ser Ser  
 2630 2635 2640

Ala Val Thr Arg Thr Ser Arg Ala Gln Ser Arg Val Ser Trp Met  
 2645 2650 2655

Met Ser Tyr Leu Ser Trp Pro Phe Cys Phe His Ser Ser Arg Leu  
 2660 2665 2670

Arg Arg Asn Ser Ser Arg Ser Phe Gln Tyr Ser Ser Arg Gly Asn  
 2675 2680 2685

Pro Ser Ser Ala Arg Glu Pro Thr Met Asn Trp Leu Thr Ala Leu  
 2690 2695 2700

Ala Gln Gln Pro Phe Ser Thr Gly Arg Ala Ala Cys Ala Ala Leu  
 2705 2710 2715

Arg Arg Glu Val Trp Val Arg Ala Lys Val Ser Arg Thr Met Thr  
 2720 2725 2730

Leu Arg Asn Trp Cys Leu Lys Ser Arg Ser Ser Gln Pro Pro Cys  
 2735 2740 2745

Ser Gln Ser Trp Lys Ser Val Arg Phe Leu Ala Gly Leu Gly Lys  
 2750 2755 2760

Ala Lys Val Thr Ser Leu Lys Arg Ile Leu Pro Ala Arg Gly Met  
 2765 2770 2775

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Lys Leu Arg Val Met Arg Lys Gly Trp Gly Thr Ser Ala Arg Leu  
 2780 2785 2790  
  
 Leu Met Thr Trp Ala Ala Arg Thr Ile Ser Ser Lys Pro Leu Met  
 2795 2800 2805  
  
 Leu Cys Pro Thr Met Ser Ser Thr Asn Arg Gly Arg Pro Leu Thr  
 2810 2815 2820  
  
 Trp Gly Ser Phe Leu Ser Ser Ser Val Ser Ser Ala Gly Ser Leu  
 2825 2830 2835  
  
 Ser Pro Cys Cys Ser Arg Ala Gln Ser Ala Thr Trp Gly Leu Ala  
 2840 2845 2850  
  
 Leu Arg Lys Glu Val Gln Arg Ser Thr Ala Arg Ala Val Cys Lys  
 2855 2860 2865  
  
 Arg Ser Arg Tyr Arg Asn Cys Trp Pro Thr Ala Ile Phe Ser Gly  
 2870 2875 2880  
  
 Val Thr Gln Lys Val Arg Gly Ser Pro Cys Gln Arg Ser His Leu  
 2885 2890 2895  
  
 Ser Trp Arg Ala Arg Ser Trp Ala Ser Ser Thr Ser Gly Gly Ser  
 2900 2905 2910  
  
 Pro Glu Ser Phe Met Thr Ser Met Lys Gly Thr Ser Cys Leu Pro  
 2915 2920 2925  
  
 Lys Asp Pro Ile Gln Val Val Ser Thr Ser Val Arg Lys Ser Leu  
 2930 2935 2940  
  
 Ser Val Arg Gly Cys Glu Pro Met Gly Lys Asn Trp Ile Ser Cys  
 2945 2950 2955  
  
 His Gln Leu Glu Glu Trp Leu Leu Met Trp Lys Lys Cys Arg Arg  
 2960 2965 2970  
  
 Arg Ala Glu His Ser Cys Leu Cys Leu Tyr Lys Arg Pro Gln Cys  
 2975 2980 2985  
  
 Ser Gln Arg Cys Thr Gly Cys Thr Cys Cys Thr Ser Cys Thr Trp  
 2990 2995 3000  
  
 Val Pro Leu Ala Arg Asn Phe Ser Gly Gln Trp Ser Ala Gly Gly  
 3005 3010 3015

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Cys Ile Ser Cys Cys Thr Thr Ser Trp Pro Ser Ala Trp Pro Ser  
 3020 3025 3030  
 Ser Ala Ser Met Val Val Met Leu Thr Ser Pro Arg Gly Arg Gln  
 3035 3040 3045  
 Val Gln Thr Ser Ala Arg Thr Gly Arg Arg Ala Arg Thr Arg Ala  
 3050 3055 3060  
 Arg Arg Pro Glu Leu Ser Arg Val Leu Arg Arg Cys Gly Val Arg  
 3065 3070 3075  
 Ser Val Gly Ser Gly Gly Ala Arg Leu Thr Cys Arg Ser Phe Ser  
 3080 3085 3090  
 Arg Ala Arg Gly Arg Ser Arg Trp Tyr Leu Ile Ser Thr Ala Pro  
 3095 3100 3105  
 Leu Val Ala Thr Ser Thr Ala Cys Arg Val Pro Cys Pro Trp Gly  
 3110 3115 3120  
 Ala Thr Thr Val Pro Arg Phe Phe Leu Gly Ala Ala Ser Met Ser  
 3125 3130 3135  
 Val Arg Ser Gly Gly Glu Asp Ala Arg Arg Ala Ala Gly Ala Ala  
 3140 3145 3150  
 Arg Gly Pro Glu Ala Gly Ala Ala Gly Ala Arg Arg Arg Arg Ala  
 3155 3160 3165  
 Arg Ala Gly Ser Gly Thr Ala Pro Gly Glu Asp Trp Arg Glu Arg  
 3170 3175 3180  
 Arg Arg Asp Gly Arg Pro Gly Ser Asp Ala Ser Gly Arg Pro Arg  
 3185 3190 3195  
 Asp Pro Val Thr Lys Arg Val Arg Gln Asn Gln Ser Arg Tyr Arg  
 3200 3205 3210  
 Arg Arg Pro Ala Ala Gly Ser Leu Ala Arg Arg Pro Ser Cys Pro  
 3215 3220 3225  
 Gly Arg Arg Ser Arg Ser Thr Ala Arg Ser Pro Pro Pro Glu Gly  
 3230 3235 3240  
 Leu Arg Gly Arg Arg Ala Arg Arg Trp Pro Arg Gly Arg Trp Arg  
 3245 3250 3255

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Cys Gly Pro Ala Ala Arg Arg Arg Ser Cys Arg Pro Arg Ser Arg  
 3260 3265 3270  
 Arg Gly Cys Arg Pro Arg Leu Arg Arg Gly Arg Ala Arg Ala Pro  
 3275 3280 3285  
 Pro Gly Arg Gly Ala Arg Arg Gly Ala Arg Pro Arg Ser Cys Arg  
 3290 3295 3300  
 Gly Ala Gly Arg Gly Ser Ala Trp Trp Arg Cys Ala Arg Arg Arg  
 3305 3310 3315  
 Ser Thr Ser Ser Gly Gly Ala Ala Ser Arg Arg Arg Pro Gly Leu  
 3320 3325 3330  
 Pro Ser Val Pro Trp Pro Arg Arg Ser Pro Arg Arg Ser Lys Thr  
 3335 3340 3345  
 Gly Ser Cys Ala Pro Arg Arg Ser Thr Pro Pro Pro Glu Asp Gly  
 3350 3355 3360  
 Ala Arg Arg Trp Trp Arg Ala Pro Arg Ala Arg Arg Pro Arg Gly  
 3365 3370 3375  
 Ala Pro Leu Pro Ser Pro Pro Leu Pro Pro Pro Leu Thr Ser Leu  
 3380 3385 3390  
 Leu Leu Pro Pro Gln Glu Ala Val Ala Gly Glu Gly Pro Cys Val  
 3395 3400 3405  
 Ala Gly Gly Ala Arg Ala Asp Gly Arg Ser Ala Arg Trp Ser Pro  
 3410 3415 3420  
 Arg Ala Gly Asp Ala Trp Ser Arg Arg Arg Ala Arg Pro Arg Gly  
 3425 3430 3435  
 Ala Ala Ala Arg Arg Arg Arg Ala Ser Pro Gly Gly Arg Arg Gly  
 3440 3445 3450  
 Gly Leu Arg Trp Ala Gly Arg Gly Arg Arg Cys Ile Leu Ser Ile  
 3455 3460 3465  
 Asp Pro Gly Leu Arg Ala Arg Thr Ala Ser Arg Asp Pro Arg Asp  
 3470 3475 3480  
 Pro Lys Thr Ala Glu Arg Arg Leu Arg Ala Ser Arg Ser Arg Lys

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val | Gly  | Ala | Arg | Phe | Leu | Val  | Leu | Arg | Val | Phe | Gly  | Arg | Glu | Ala |
|     | 3500 |     |     |     |     | 3505 |     |     |     |     | 3510 |     |     |     |
| Gly | Gly  | Arg | Cys | Cys | Trp | Ser  | Ser | Arg | Arg | Ser | Asp  | Gly | Gly | Trp |
|     | 3515 |     |     |     |     | 3520 |     |     |     |     | 3525 |     |     |     |
| Trp | Arg  | Gly | Ala | Pro | Gly | Pro  | Trp | Ala | Arg | Leu | Ala  | Gly | Cys | Ala |
|     | 3530 |     |     |     |     | 3535 |     |     |     |     | 3540 |     |     |     |
| Asp | Gly  | Arg | Pro | Cys | Pro | Arg  | Arg | Gly | Pro | Asp | Thr  | Trp | Arg | Gly |
|     | 3545 |     |     |     |     | 3550 |     |     |     |     | 3555 |     |     |     |
| Pro | Cys  | Ser | Ser | Pro | Ala | Ala  | Ala | Pro | Arg | Ala | Pro  | Pro | Pro | Arg |
|     | 3560 |     |     |     |     | 3565 |     |     |     |     | 3570 |     |     |     |
| Pro | Arg  | Gly | Arg | Ala | Cys | Ala  | Ala | Arg | Thr | Arg | Ala  | Ala | Ala | Gly |
|     | 3575 |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
| Arg | Ala  | Pro | Gly | Arg | Arg | Arg  | Arg | Ala | Arg | Gly | Trp  | Pro | Ala | Gly |
|     | 3590 |     |     |     |     | 3595 |     |     |     |     | 3600 |     |     |     |
| Ser | Gly  | Gly | Trp | Ser | Gly | Ser  | Arg | Arg | Ser | Arg | Arg  | Ser | Gly | Gly |
|     | 3605 |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |
| Arg | Leu  | Arg | Cys | Trp | Cys | Arg  | Ser | Ser | Trp | Pro | Arg  | Thr | Ser | Arg |
|     | 3620 |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
| Ser | Gly  | Gly | Arg | Val | Ala | Arg  | Ala | Arg | Gly | Thr | Gly  | Ala | Ser | Arg |
|     | 3635 |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
| Arg | Ala  | Cys | Arg | Arg | Cys | Ser  | Arg | Cys | Arg | Arg | Ala  | Arg | Gly | Thr |
|     | 3650 |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
| Gly | Ile  | Arg | Arg | Gly | Ser | Ala  | Ala | Ala | Ala | Gly | Gly  | Arg | Ala | Ala |
|     | 3665 |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
| Ile | Ala  | Arg | Trp | Arg | Gly | Arg  | Arg | Ala | Arg | Gly | Pro  | Arg | Ala | Gly |
|     | 3680 |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |
| Gly | Gly  | Ser | Arg | Arg | Cys | Thr  | Trp | Thr | Ser | Arg | Cys  | Arg | Arg | Arg |
|     | 3695 |     |     |     |     | 3700 |     |     |     |     | 3705 |     |     |     |
| Trp | Trp  | Arg | Arg | Ala | Gly | Thr  | Arg | Gly | Arg | Gly | Ser  | Arg | Cys | Cys |
|     | 3710 |     |     |     |     | 3715 |     |     |     |     | 3720 |     |     |     |



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Ala Ala Ala Gly Ser Ser Ser Trp Trp Pro Arg Ser Gly Pro Gly  
 3725 3730 3735  
  
 Ala Arg Ser Arg Gly Cys Ser Arg His Thr Gly Lys Asn Glu Ser  
 3740 3745 3750  
  
 Gly Gln Arg Leu Asp Ser Val Ala Trp Arg Leu Ser Glu Arg Val  
 3755 3760 3765  
  
 Gly Leu Arg Val Tyr Pro Gly Ser Asn Leu Glu Ser Gly Trp Ser  
 3770 3775 3780  
  
 Arg Ser Arg Gly Thr Gly Thr Pro Val Ser Thr Gln Ala Cys Arg  
 3785 3790 3795  
  
 Asn Leu Gln Asp Thr Glu Ala Gly Arg Phe Leu Ala Leu Val Ala  
 3800 3805 3810  
  
 Gly His Glu Lys Leu Val Ser Ala Glu Ser Gly Arg Pro Arg Trp  
 3815 3820 3825  
  
 Leu Ala Ala Val Val Trp Arg Lys Asn Arg Gln Gly Cys Val Ala  
 3830 3835 3840  
  
 Val Cys Pro Gly Ser Ser Leu Ser Ala Arg Arg Arg Pro Asp Ser  
 3845 3850 3855  
  
 Ala Ala Asn Val Gly Val Ala Ala Pro Ser Phe Pro Arg Pro Leu  
 3860 3865 3870  
  
 Ser Gln Pro Thr Ser Pro Val Thr Glu Arg Ala Pro Leu Phe Phe  
 3875 3880 3885  
  
 Ser Cys Val Phe Ala Arg Cys Ile Pro Tyr Cys Gly Arg Cys Ala  
 3890 3895 3900  
  
 Pro Thr Leu His His Asn Arg Pro Tyr Arg Ser Ser Ser Asn Ser  
 3905 3910 3915  
  
 Arg Arg Phe Cys Pro Arg Pro Ser Ser Ser Gln Pro Leu Pro Arg  
 3920 3925 3930  
  
 Arg Pro Pro Ala Glu Pro Ala Phe Ser Met Thr Trp Pro Trp Lys  
 3935 3940 3945  
  
 Arg Ala Arg Gly Trp Arg Gly Trp Gly Arg Arg Arg Arg Ser Gly  
 3950 3955 3960

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Arg  | Ala | Cys | Arg | Lys | Gly  | Thr | Leu | Ala | Arg | Pro  | Thr | Cys | Pro |
|     | 3965 |     |     |     |     | 3970 |     |     |     |     | 3975 |     |     |     |
| Ser | Arg  | Thr | Cys | Ser | Glu | Thr  | Gly | Ala | Ala | Arg | Ser  | Pro | Arg | Arg |
|     | 3980 |     |     |     |     | 3985 |     |     |     |     | 3990 |     |     |     |
| Cys | Ala  | Pro | Pro | Ala | Ser | Thr  | Arg | Gly | Gly | Ser | Cys  | Gly | Ala | Ala |
|     | 3995 |     |     |     |     | 4000 |     |     |     |     | 4005 |     |     |     |
| Trp | Thr  | Glu | Ser | Gly | Cys | Gly  | Thr | Arg | Ile | Ser | Arg  | Arg | Thr | Ser |
|     | 4010 |     |     |     |     | 4015 |     |     |     |     | 4020 |     |     |     |
| Arg | Gly  | Ser | Ala | Pro | Arg | Ala  | Arg | Thr | Trp | Pro | Arg  | Pro | Thr | Trp |
|     | 4025 |     |     |     |     | 4030 |     |     |     |     | 4035 |     |     |     |
| Ser | Arg  | Arg | Thr | Ser | Arg | Pro  | Arg | Arg | Arg | Ala | Thr  | Ser | Lys | Asn |
|     | 4040 |     |     |     |     | 4045 |     |     |     |     | 4050 |     |     |     |
| Pro | Ser  | Thr | Thr | Thr | Cys | Ala  | Arg | Ser | Arg | Ala | Arg  | Arg | Pro | Trp |
|     | 4055 |     |     |     |     | 4060 |     |     |     |     | 4065 |     |     |     |
| Ala | Cys  | Thr | Cys | Gly | Thr | Cys  | Trp | Arg | Pro | Ser | Cys  | Arg | Thr | Pro |
|     | 4070 |     |     |     |     | 4075 |     |     |     |     | 4080 |     |     |     |
| Arg | Ala  | Ser | Arg | Arg | Arg | Ser  | Cys | Phe | Trp | Trp | Cys  | Ser | Thr | Val |
|     | 4085 |     |     |     |     | 4090 |     |     |     |     | 4095 |     |     |     |
| Gly | Thr  | Thr | Arg | Arg | Ser | Gly  | Arg | Arg | Cys | Ile | Ser  | Pro | Ser | Pro |
|     | 4100 |     |     |     |     | 4105 |     |     |     |     | 4110 |     |     |     |
| Arg | Ala  | Ala | Gly | Ser | Trp | Thr  | Trp | Thr | Phe | Cys | Arg  | Ala | Ser | Trp |
|     | 4115 |     |     |     |     | 4120 |     |     |     |     | 4125 |     |     |     |
| Cys | Arg  | Ser | Ala | Gly | Cys | Arg  | Cys | Pro | Arg | Ser | Trp  | Arg | Pro | Ser |
|     | 4130 |     |     |     |     | 4135 |     |     |     |     | 4140 |     |     |     |
| Thr | Ser  | Arg | Cys | Val | Trp | Ala  | Ser | Thr | Thr | Leu | Gly  | Arg | Ser | Thr |
|     | 4145 |     |     |     |     | 4150 |     |     |     |     | 4155 |     |     |     |
| Arg | Pro  | Arg | Thr | Cys | Pro | Thr  | Arg | Arg | Arg | Ser | Thr  | Gly | Phe | Thr |
|     | 4160 |     |     |     |     | 4165 |     |     |     |     | 4170 |     |     |     |
| Cys | Ala  | Pro | Lys | Cys | Pro | Ala  | Thr | Ile | Trp | Gly | Cys  | Thr | Ala | Thr |
|     | 4175 |     |     |     |     | 4180 |     |     |     |     | 4185 |     |     |     |
| Thr | Gly  | Cys | Thr | Ala | Arg | Ala  | Pro | Ala | Ala | Gly | Ala  | Ser | Ala | Thr |
|     | 4190 |     |     |     |     | 4195 |     |     |     |     | 4200 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Ser | Cys | Thr | Ala | Cys | Ser  | Gly | Pro | Pro | Gly | Pro  | Gly | Pro | Arg |
| 4205 |     |     |     |     |     | 4210 |     |     |     |     | 4215 |     |     |     |
| Gly  | Arg | Ala | Thr | Leu | Thr | Trp  | Ala | Arg | Thr | Cys | Ala  | Gly | Ser | Pro |
| 4220 |     |     |     |     |     | 4225 |     |     |     |     | 4230 |     |     |     |
| Ala  | Ala | Gly | Pro | Trp | Lys | Leu  | Pro | Ala | Val | Pro | Pro  | Thr | Trp | Arg |
| 4235 |     |     |     |     |     | 4240 |     |     |     |     | 4245 |     |     |     |
| Arg  | Trp | Thr | Met | Arg | Arg | Arg  | Arg | Ala | Ser | Thr | Trp  | Lys | Thr | Asp |
| 4250 |     |     |     |     |     | 4255 |     |     |     |     | 4260 |     |     |     |
| Gly  | Ala | Thr | Val | Phe | Leu | Leu  | Asp | Ala | Ala | Thr | Ala  | Thr | Ala | Ala |
| 4265 |     |     |     |     |     | 4270 |     |     |     |     | 4275 |     |     |     |
| Ala  | Ser | Ser | Arg | Asp | Ala | Gly  | Gly | Ala | Ala | Glu | Pro  | Ala | Val | Arg |
| 4280 |     |     |     |     |     | 4285 |     |     |     |     | 4290 |     |     |     |
| His  | Leu | Leu | Gly | Arg | Leu | Asp  | Pro | Gly | His | Ala | Thr  | His | His | Gly |
| 4295 |     |     |     |     |     | 4300 |     |     |     |     | 4305 |     |     |     |
| Ala  | Asp | Asp | Pro | Gln | Ser | Arg  | Ser | Leu | Thr | Ala | Ala  | Ser | Gly | Gln |
| 4310 |     |     |     |     |     | 4315 |     |     |     |     | 4320 |     |     |     |
| Pro  | Ala | Leu | Gly | His | Pro | Gly  | Gly | Arg | Gly | Ala | Leu  | Ala | Leu | Glu |
| 4325 |     |     |     |     |     | 4330 |     |     |     |     | 4335 |     |     |     |
| Pro  | His | Ala | Arg | Glu | Gly | Ala  | Gly | His | Arg | Glu | Arg  | Ala | Gly | Gly |
| 4340 |     |     |     |     |     | 4345 |     |     |     |     | 4350 |     |     |     |
| Glu  | Gln | Gly | His | Pro | Arg | Arg  | Gly | Arg | Ala | Gly | Val  | Gln | Arg | Ala |
| 4355 |     |     |     |     |     | 4360 |     |     |     |     | 4365 |     |     |     |
| Ala  | Gly | Ala | Arg | Gly | Pro | Leu  | Gln | Gln | His | Gln | Arg  | Ala | Asp | Glu |
| 4370 |     |     |     |     |     | 4375 |     |     |     |     | 4380 |     |     |     |
| Pro  | Gly | Pro | His | Gly | Asp | Arg  | Arg | Ala | Arg | Gly | Gly  | Val | Ala | Ala |
| 4385 |     |     |     |     |     | 4390 |     |     |     |     | 4395 |     |     |     |
| Arg  | Ala | Val | Pro | Pro | Arg | Val  | Glu | Pro | Gly | Leu | His  | Gly | Gly | Ala |
| 4400 |     |     |     |     |     | 4405 |     |     |     |     | 4410 |     |     |     |
| Glu  | Arg | Leu | Pro | Glu | His | Ala  | Ala | Arg | Gln | Arg | Ala  | Pro | Gly | Pro |
| 4415 |     |     |     |     |     | 4420 |     |     |     |     | 4425 |     |     |     |
| Gly  | Gly | Leu | His | Gln | Leu | His  | Gln | Arg | Ala | Ala | Ala  | Asp | Gly | Gly |

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4435

4440

Arg Gly Ala Pro Glu Arg Gly Val Pro Val Gly Ala Gly Leu Leu  
 4445 4450 4455

Leu Pro Asp Gln Ser Pro Gly Leu Ala Asp Arg Glu Pro Glu Pro  
 4460 4465 4470

Gly Phe Gln Glu Leu Ala Gly Thr Val Gly Arg Ala Gly Pro Gly  
 4475 4480 4485

Arg Gly Pro Arg Asp Gly Val Glu Pro Ala Asp Ala Glu Leu Ala  
 4490 4495 4500

Pro Ala Ala Ala Ala Gly Gly Ala Leu His Gly Gln Arg Gln Arg  
 4505 4510 4515

Glu Pro Arg Leu Val Pro Gly Leu Pro Ala Pro Val Pro Arg Gly  
 4520 4525 4530

His Arg Thr Gly Ala Arg Gly Arg Ala Asp Leu Pro Gly Asp His  
 4535 4540 4545

Pro Arg Glu Pro Arg Ala Gly Pro Gly Gly Pro Gly Gln Pro Gly  
 4550 4555 4560

Gly His Pro Glu Leu Pro Ala Asp Gln Pro Val Ala Glu Asp Pro  
 4565 4570 4575

Ala Pro Val Arg Ala Glu His Arg Gly Gly Ala His Pro Ala Leu  
 4580 4585 4590

Arg Ala Ala Glu Arg Gly Ala Val Pro Asp Ala Gly Gly Gly His  
 4595 4600 4605

Ala Gln Arg Gly Ala Arg His Asp Arg Ala Gln His Gly Ala Gln  
 4610 4615 4620

His Val Arg Pro Gln Pro Pro Val His Gln Ala Asp Gly Leu Leu  
 4625 4630 4635

Ala Ser Gly Gly Arg His Glu Leu Gly Leu Leu Tyr Gln Arg His  
 4640 4645 4650

Leu Glu Pro Ala Leu Ala Pro Ala Ala Arg Val Leu His Gly Arg  
 4655 4660 4665

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Val Arg His Ala Arg Pro Gln Arg Arg Val Pro Val Gly Arg Arg  
 4670 4675 4680  
  
 Gly Gln Gln Arg Val Leu Ala Ala Ser Arg Asn Gln Cys Arg Val  
 4685 4690 4695  
  
 Glu Glu Arg Gly Arg Gly Pro Ala Ala Val Leu Gly Ala Val Arg  
 4700 4705 4710  
  
 Ser Arg Gly Cys Cys Arg Gly Gly Ala Arg Gly Arg Gln Pro Leu  
 4715 4720 4725  
  
 Pro Glu Pro Ala Leu Phe Ala Glu Gln Arg Ala Gln Gln Arg Ala  
 4730 4735 4740  
  
 Gly Ser Ala Asp Ala Thr Ala Pro Ala Gly Arg Gly Gly Val Pro  
 4745 4750 4755  
  
 Glu Arg Leu Leu Val Glu Ala Arg Ala Arg Glu Glu Leu Pro Gln  
 4760 4765 4770  
  
 Arg Asp Arg Glu Pro Gly Gly Gln Asp Glu Pro Leu Glu Asp Val  
 4775 4780 4785  
  
 Arg Ala Arg Ala Gln Gly Arg Ala Pro Ser Gln Arg Arg His Pro  
 4790 4795 4800  
  
 Thr Pro Ala Ala Arg Gln Ala Ala Gly Thr Gly Val Gly Arg Gly  
 4805 4810 4815  
  
 Phe Arg Arg Arg Gln Gln Arg Val Gly Leu Gly Trp Glu Trp Trp  
 4820 4825 4830  
  
 Pro Val Arg Ser Pro Ala Pro Pro Tyr Arg Ala Pro Asp Val Arg  
 4835 4840 4845  
  
 Ile Lys Asn Lys Arg Arg Tyr Ser Pro Arg Pro Trp Arg Pro Ala  
 4850 4855 4860  
  
 Cys Val Leu Leu Cys Cys Leu Tyr Asp Glu Ala Arg Val Pro Gly  
 4865 4870 4875  
  
 Gly Ser Ser Ser Leu Val Arg Glu Arg Asp Ala Ala Gly Gly Gly  
 4880 4885 4890  
  
 Gly Gly Asp Ala Ala Pro Ala Gly Gly Ala Leu Arg Ala Pro Ala  
 4895 4900 4905

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Val Pro Gly Ala Tyr Gly Gly Ala Glu Gln His Ser Leu Leu Gly  
 4910 4915 4920  
 Ala Gly Thr Leu Val Arg Tyr His Pro Val Val Pro Gly Gly Gln  
 4925 4930 4935  
 Gln Val Gly Arg His Arg Leu Ala Glu Leu Pro Glu Arg Pro Gln  
 4940 4945 4950  
 Gln Leu Pro Asp His Arg Gly Ala Glu Gln Arg Phe His Pro His  
 4955 4960 4965  
 Gly Gly Gln His Pro Asp His Gln Leu Arg Ala Leu Ala Val Gly  
 4970 4975 4980  
 Arg Pro Ala Glu Asn His His Ala His Gln His Ala Gln Arg Glu  
 4985 4990 4995  
 Arg Val His Val Gln Gln Gln Val Gln Gly Ala Gly Asp Gly Leu  
 5000 5005 5010  
 Ala Gln Asp Pro Gln Arg Gly Gly Leu Trp Ser Gly Arg Ala Asp  
 5015 5020 5025  
 Leu Arg Val Gly Gly Val Ala Ala Arg Gly Gln Leu Leu Gly Asp  
 5030 5035 5040  
 His Asp His Arg Ser Asp Glu Gln Arg His His Arg Gln Leu Leu  
 5045 5050 5055  
 Gly Gly Gly Ala Ala Glu Arg Gly Ala Gly Glu Arg His Arg Arg  
 5060 5065 5070  
 Glu Val Arg His Ala Gln Leu Pro Ala Gly Leu Gly Pro Arg Asp  
 5075 5080 5085  
 Arg Ala Gly Asp Ala Gly Arg Val His Gln Arg Gly Leu Pro Pro  
 5090 5095 5100  
 Arg His Arg Pro Ala Ala Arg Leu Arg Arg Gly Leu His Arg Glu  
 5105 5110 5115  
 Pro Pro Gln Gln Pro Ala Gly His Pro Gln Ala Ala Ala Leu Pro  
 5120 5125 5130  
 Gly Gly Leu Pro Asp Pro Val Arg Gly Pro Gly Gly Gly Gln His  
 5135 5140 5145

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro  | Arg | Ala | Leu | Gly | Cys | Arg  | Ser | Leu | Arg | Glu | Lys  | Gln | Gly | Gly |
| 5150 |     |     |     |     |     | 5155 |     |     |     |     | 5160 |     |     |     |
| His  | Arg | Arg | Gly | Asp | Arg | Ser  | Arg | Gly | His | Arg | Leu  | Tyr | Arg | Gly |
| 5165 |     |     |     |     |     | 5170 |     |     |     |     | 5175 |     |     |     |
| Ala  | Gly | Arg | Phe | Cys | Arg | Cys  | Gly | Ser | Gly | Arg | Gly  | Gly | Asn | Arg |
| 5180 |     |     |     |     |     | 5185 |     |     |     |     | 5190 |     |     |     |
| Lys  | Asp | Ser | His | Pro | Ala | Gly  | Gly | Glu | Gly | Gln | Gln  | Gly | Gln | Glu |
| 5195 |     |     |     |     |     | 5200 |     |     |     |     | 5205 |     |     |     |
| Leu  | Gln | Arg | Ala | Arg | Gly | Gln  | Glu | Lys | His | Arg | Leu  | Pro | Gln | Leu |
| 5210 |     |     |     |     |     | 5215 |     |     |     |     | 5220 |     |     |     |
| Val  | Pro | Gly | Leu | Gln | Leu | Arg  | Arg | Pro | Arg | Glu | Gly  | Arg | Ala | Leu |
| 5225 |     |     |     |     |     | 5230 |     |     |     |     | 5235 |     |     |     |
| Leu  | Asp | Ala | Ala | His | His | Leu  | Gly | Arg | His | Leu | Arg  | Arg | Gly | Ala |
| 5240 |     |     |     |     |     | 5245 |     |     |     |     | 5250 |     |     |     |
| Ser  | Leu | Leu | Val | Ala | Ala | Arg  | His | Asp | Ala | Arg | Pro  | Gly | His | Leu |
| 5255 |     |     |     |     |     | 5260 |     |     |     |     | 5265 |     |     |     |
| Pro  | Leu | His | Ala | Ser | Ser | Gln  | Leu | Pro | Gly | Gly | Gly  | Arg | Arg | Ala |
| 5270 |     |     |     |     |     | 5275 |     |     |     |     | 5280 |     |     |     |
| Pro  | Ala | Arg | Leu | Leu | Gln | Glu  | Leu | Leu | Gln | Arg | Ala  | Gly | Arg | Leu |
| 5285 |     |     |     |     |     | 5290 |     |     |     |     | 5295 |     |     |     |
| Leu  | Ala | Ala | Ala | Ala | Arg | Leu  | His | Leu | Ala | His | Ala  | Arg | Leu | Gln |
| 5300 |     |     |     |     |     | 5305 |     |     |     |     | 5310 |     |     |     |
| Pro  | Leu | Pro | Arg | Glu | Pro | Asp  | Pro | Arg | Pro | Pro | Ala  | Arg | Ala | His |
| 5315 |     |     |     |     |     | 5320 |     |     |     |     | 5325 |     |     |     |
| His  | Tyr | His | Arg | Gln | Lys | Arg  | Ser | Cys | Ser | His | Arg  | Ser | Arg | Asp |
| 5330 |     |     |     |     |     | 5335 |     |     |     |     | 5340 |     |     |     |
| Pro  | Ala | Ala | Ala | Gln | Gln | Tyr  | Pro | Gly | Ser | Pro | Ala  | Arg | Asp | Arg |
| 5345 |     |     |     |     |     | 5350 |     |     |     |     | 5355 |     |     |     |
| His  | Arg | Gln | Thr | Pro | His | Leu  | Pro | Leu | Arg | Leu | Gln  | Gly | Pro | Gly |
| 5360 |     |     |     |     |     | 5365 |     |     |     |     | 5370 |     |     |     |
| Arg  | Ser | Arg | Ala | Ala | Arg | Pro  | Leu | Glu | Pro | His | Leu  | Leu | Lys | Asn |

5375

5380

5385

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | His | Ser | His | Leu | Ala | Gln  | His | Arg | Leu | Gly | Pro  | Ala | Arg | Ala |
| 5390 |     |     |     |     |     | 5395 |     |     |     |     | 5400 |     |     |     |
| Gln  | Gln | Asp | Val | Arg | Arg | Arg  | Ser | Pro | Thr | Leu | His  | Ala | Thr | Pro |
| 5405 |     |     |     |     |     | 5410 |     |     |     |     | 5415 |     |     |     |
| Arg  | Ala | Arg | Ala | Arg | Ala | Leu  | Pro | Arg | Ser | Leu | Gly  | Arg | Pro | Gln |
| 5420 |     |     |     |     |     | 5425 |     |     |     |     | 5430 |     |     |     |
| Gly  | Pro | Arg | Ala | Leu | Ala | His  | His | Arg | Arg | Arg | Arg  | Asp | Arg | Pro |
| 5435 |     |     |     |     |     | 5440 |     |     |     |     | 5445 |     |     |     |
| Gly  | Gly | Gly | Arg | Arg | Ala | Gln  | Leu | His | Ala | Arg | Arg  | Arg | Ala | Arg |
| 5450 |     |     |     |     |     | 5455 |     |     |     |     | 5460 |     |     |     |
| Leu  | His | Arg | Gly | Arg | Arg | His  | Arg | Gln | Arg | Gly | Gly  | Arg | Arg | Ala |
| 5465 |     |     |     |     |     | 5470 |     |     |     |     | 5475 |     |     |     |
| Pro  | Val | Arg | Pro | His | Gln | Glu  | Pro | Ala | Ala | Ala | His  | Arg | Pro | Ala |
| 5480 |     |     |     |     |     | 5485 |     |     |     |     | 5490 |     |     |     |
| Ala  | Pro | Glu | His | Pro | Arg | His  | Ala | Arg | Gly | Ala | Ser  | Leu | Ala | Ala |
| 5495 |     |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |
| Gln  | Gly | Gln | Ala | His | Gly | Thr  | Gln | Gly | His | Ala | Gln  | Gly | Gly | Gln |
| 5510 |     |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
| Thr  | Arg | Gly | Leu | Arg | Gln | Gln  | Gln | Arg | Arg | Gln | Asp  | Pro | Gln | Thr |
| 5525 |     |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
| Arg  | Gly | His | Gly | Gly | Gly | Gly  | Gly | His | Arg | Gln | His  | Val | Pro | Pro |
| 5540 |     |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
| Ala  | Ala | Arg | Gln | Arg | Val | Leu  | Gly | Ala | Arg | Arg | Arg  | His | Arg | Cys |
| 5555 |     |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
| Ala  | Arg | Ala | Arg | Ala | His | Pro  | Pro | Pro | Ser | His | Leu  | Lys | Met | Leu |
| 5570 |     |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |
| Thr  | Ser | Arg | Cys | Cys | Val | Pro  | Ala | Ala | Arg | Arg | Met  | Ser | Lys | Arg |
| 5585 |     |     |     |     |     | 5590 |     |     |     |     | 5595 |     |     |     |
| Lys  | Tyr | Lys | Glu | Glu | Met | Leu  | Gln | Val | Ile | Ala | Pro  | Glu | Ile | Tyr |
| 5600 |     |     |     |     |     | 5605 |     |     |     |     | 5610 |     |     |     |



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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly  | Pro | Ala | Ala | Ala | Val | Lys  | Glu | Glu | Arg | Lys | Pro  | Arg | Lys | Leu |
| 5615 |     |     |     |     |     | 5620 |     |     |     |     | 5625 |     |     |     |
| Lys  | Arg | Val | Lys | Lys | Asp | Lys  | Lys | Glu | Glu | Glu | Asp  | Asp | Gly | Leu |
| 5630 |     |     |     |     |     | 5635 |     |     |     |     | 5640 |     |     |     |
| Val  | Glu | Phe | Val | Arg | Glu | Phe  | Ala | Pro | Arg | Arg | Arg  | Val | Gln | Trp |
| 5645 |     |     |     |     |     | 5650 |     |     |     |     | 5655 |     |     |     |
| Arg  | Gly | Arg | Lys | Val | Lys | Pro  | Val | Leu | Arg | Pro | Gly  | Thr | Thr | Val |
| 5660 |     |     |     |     |     | 5665 |     |     |     |     | 5670 |     |     |     |
| Val  | Phe | Thr | Pro | Gly | Glu | Arg  | Ser | Gly | Ser | Ala | Ser  | Lys | Arg | Ser |
| 5675 |     |     |     |     |     | 5680 |     |     |     |     | 5685 |     |     |     |
| Tyr  | Asp | Glu | Val | Tyr | Gly | Asp  | Glu | Asp | Ile | Leu | Glu  | Gln | Ala | Val |
| 5690 |     |     |     |     |     | 5695 |     |     |     |     | 5700 |     |     |     |
| Glu  | Arg | Leu | Gly | Glu | Phe | Ala  | Tyr | Gly | Lys | Arg | Ser  | Arg | Pro | Ala |
| 5705 |     |     |     |     |     | 5710 |     |     |     |     | 5715 |     |     |     |
| Pro  | Leu | Lys | Glu | Glu | Ala | Val  | Ser | Ile | Pro | Leu | Asp  | His | Gly | Asn |
| 5720 |     |     |     |     |     | 5725 |     |     |     |     | 5730 |     |     |     |
| Pro  | Thr | Pro | Ser | Leu | Lys | Pro  | Val | Thr | Leu | Gln | Gln  | Val | Leu | Pro |
| 5735 |     |     |     |     |     | 5740 |     |     |     |     | 5745 |     |     |     |
| Ser  | Ala | Ala | Pro | Arg | Arg | Gly  | Phe | Lys | Arg | Glu | Gly  | Gly | Glu | Asp |
| 5750 |     |     |     |     |     | 5755 |     |     |     |     | 5760 |     |     |     |
| Leu  | Tyr | Pro | Thr | Met | Gln | Leu  | Met | Val | Pro | Lys | Arg  | Gln | Lys | Leu |
| 5765 |     |     |     |     |     | 5770 |     |     |     |     | 5775 |     |     |     |
| Glu  | Asp | Val | Leu | Glu | His | Met  | Lys | Val | Asp | Pro | Glu  | Val | Gln | Pro |
| 5780 |     |     |     |     |     | 5785 |     |     |     |     | 5790 |     |     |     |
| Glu  | Val | Lys | Val | Arg | Pro | Ile  | Lys | Gln | Val | Ala | Pro  | Gly | Leu | Gly |
| 5795 |     |     |     |     |     | 5800 |     |     |     |     | 5805 |     |     |     |
| Val  | Gln | Thr | Val | Asp | Ile | Lys  | Ile | Pro | Thr | Glu | Pro  | Met | Glu | Thr |
| 5810 |     |     |     |     |     | 5815 |     |     |     |     | 5820 |     |     |     |
| Gln  | Thr | Glu | Pro | Val | Lys | Pro  | Ser | Thr | Ser | Thr | Met  | Glu | Val | Gln |
| 5825 |     |     |     |     |     | 5830 |     |     |     |     | 5835 |     |     |     |
| Thr  | Asp | Pro | Trp | Met | Pro | Ala  | Pro | Ala | Ser | Thr | Ser  | Thr | Arg | Arg |
| 5840 |     |     |     |     |     | 5845 |     |     |     |     | 5850 |     |     |     |

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Arg Arg Lys Tyr Gly Ala Ala Ser Leu Leu Met Pro Asn Tyr Ala  
 5855 5860 5865  
 Leu His Pro Ser Ile Ile Pro Thr Pro Gly Tyr Arg Gly Thr Arg  
 5870 5875 5880  
 Phe Tyr Arg Gly Tyr Thr Ser Ser Arg Arg Arg Lys Thr Thr Thr  
 5885 5890 5895  
 Arg Arg Arg Arg Arg Ser Arg Arg Ser Ser Thr Ala Thr Ser Ala  
 5900 5905 5910  
 Leu Val Arg Arg Val Tyr Arg Ser Gly Arg Glu Pro Leu Thr Leu  
 5915 5920 5925  
 Pro Arg Ala Arg Tyr His Pro Ser Ile Ala Ile Leu Pro Pro Pro  
 5930 5935 5940  
 Thr Cys Arg Tyr Gly Pro His Met Pro Pro Pro Arg Pro His Tyr  
 5945 5950 5955  
 Gly Leu Pro Arg Lys Lys Ala Ala Pro Lys Ala Asp Gly Glu Arg  
 5960 5965 5970  
 Ala Ala Ser Pro Ser Pro Pro Ala Ala Ala Arg His Gln Gln Ala  
 5975 5980 5985  
 Val Gly Gly Arg Leu Pro Ala Arg Ala Asp Pro His His Arg Arg  
 5990 5995 6000  
 Gly Asp Arg Gly Asp Pro Arg His Ser Phe Arg Gly Gly Ala Gly  
 6005 6010 6015  
 Leu Ser Ala Pro Leu Arg His Lys Lys Ala Trp Ile Cys Asn Lys  
 6020 6025 6030  
 Lys Lys Asn Gly Leu Thr Leu Leu Val Leu Cys Val Phe Leu Asp  
 6035 6040 6045  
 Gly Arg His Gln Phe Phe Val Pro Gly Thr Ala Thr Arg His Ala  
 6050 6055 6060  
 Ala Val Tyr Gly His Leu Glu Arg His Arg Gln Gln Pro Thr Glu  
 6065 6070 6075  
 Arg Gly Arg Leu Gln Leu Glu Gln Ser Leu Glu Arg Ala Glu Phe  
 6080 6085 6090

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Val | His | Ala | Gln | Asn | Leu  | Trp | Gln | Gln | Gly | Val  | Glu | Gln | Gln |
| 6095 |     |     |     |     |     | 6100 |     |     |     |     | 6105 |     |     |     |
| His  | Arg | Ala | Gly | Ala | Glu | Gly  | Lys | Ala | Glu | Arg | Thr  | Glu | Leu | Pro |
| 6110 |     |     |     |     |     | 6115 |     |     |     |     | 6120 |     |     |     |
| Ala  | Glu | Gly | Gly | Trp | Pro | Gly  | Leu | Arg | His | Gln | Arg  | Gly | Gly | Pro |
| 6125 |     |     |     |     |     | 6130 |     |     |     |     | 6135 |     |     |     |
| Gly  | Gln | Pro | Gly | Arg | Ala | Glu  | Thr | Asp | Gln | Gln | Pro  | Pro | Gly | Arg |
| 6140 |     |     |     |     |     | 6145 |     |     |     |     | 6150 |     |     |     |
| Gly  | Pro | Ala | Arg | Gly | Val | Arg  | Gly | Asp | Ala | Pro | Gly  | Gly | Gly | Gly |
| 6155 |     |     |     |     |     | 6160 |     |     |     |     | 6165 |     |     |     |
| Ala  | Ala | Ser | Pro | Gly | Gln | Ala  | Arg | Arg | Gln | Ala | Thr  | Ala | Ser | Arg |
| 6170 |     |     |     |     |     | 6175 |     |     |     |     | 6180 |     |     |     |
| Arg  | Gly | Gly | Asp | Ala | Ala | Asp  | Ala | His | Gly | Arg | Ala  | Ala | Pro | Val |
| 6185 |     |     |     |     |     | 6190 |     |     |     |     | 6195 |     |     |     |
| Arg  | Gly | Gly | Gly | Glu | Thr | Gly  | Pro | Ala | His | His | Ala  | Ala | Arg | Gly |
| 6200 |     |     |     |     |     | 6205 |     |     |     |     | 6210 |     |     |     |
| Ala  | Ser | Gly | His | Arg | Ser | Ala  | Glu | Thr | Gln | Gln | Gln  | Pro | Ala | Arg |
| 6215 |     |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Asp  | Pro | Gly | Leu | Ala | Ser | Ala  | Ser | Pro | Leu | His | Ser  | Gly | Ala | Pro |
| 6230 |     |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Ala  | Ala | Gly | Gly | Arg | Arg | Val  | Ala | Arg | Pro | Pro | Arg  | Pro | Pro | Pro |
| 6245 |     |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |
| Gly  | Glu | Leu | Ala | Glu | His | Ser  | Glu | Gln | His | Arg | Gly  | Ser | Gly | Ser |
| 6260 |     |     |     |     |     | 6265 |     |     |     |     | 6270 |     |     |     |
| Ala  | Glu | Cys | Glu | Ala | Pro | Pro  | Leu | Leu | Leu | Lys | Asp  | Thr | Val | Ala |
| 6275 |     |     |     |     |     | 6280 |     |     |     |     | 6285 |     |     |     |
| Leu  | Asn | Leu | Leu | Val | Cys | Val  | Tyr | Met | Tyr | Val | Arg  | Arg | Pro | Glu |
| 6290 |     |     |     |     |     | 6295 |     |     |     |     | 6300 |     |     |     |
| Gly  | Gly | Val | Arg | Gly | Ala | Ser  | Pro | Ser | Cys | Lys | Met  | Ala | Thr | Pro |
| 6305 |     |     |     |     |     | 6310 |     |     |     |     | 6315 |     |     |     |
| Ser  | Met | Leu | Pro | Gln | Trp | Ala  | Tyr | Met | His | Ile | Ala  | Gly | Gln | Asp |

6320

6325

6330

Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala Arg Ala  
6335 6340 6345

Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro Thr  
6350 6355 6360

Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
6365 6370 6375

Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser  
6380 6385 6390

Tyr Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu  
6395 6400 6405

Asp Met Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg  
6410 6415 6420

Gly Pro Ser Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu  
6425 6430 6435

Ala Pro Lys Gly Ala Pro Asn Ser Ser Gln Trp Glu Gln Ala Lys  
6440 6445 6450

Thr Gly Asn Gly Gly Thr Met Glu Thr His Thr Tyr Gly Val Ala  
6455 6460 6465

Pro Met Gly Gly Glu Asn Ile Thr Lys Asp Gly Leu Gln Ile Gly  
6470 6475 6480

Thr Asp Val Thr Ala Asn Gln Asn Lys Pro Ile Tyr Ala Asp Lys  
6485 6490 6495

Thr Phe Gln Pro Glu Pro Gln Val Gly Glu Glu Asn Trp Gln Glu  
6500 6505 6510

Thr Glu Asn Phe Tyr Gly Gly Arg Ala Leu Lys Lys Asp Thr Asn  
6515 6520 6525

Met Lys Pro Cys Tyr Gly Ser Tyr Ala Arg Pro Thr Asn Glu Lys  
6530 6535 6540

Gly Gly Gln Ala Lys Leu Lys Val Gly Asp Asp Gly Val Pro Thr  
6545 6550 6555

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Lys  | Glu | Phe | Asp | Ile | Asp | Leu  | Ala | Phe | Phe | Asp | Thr  | Pro | Gly | Gly |
| 6560 |     |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Thr  | Val | Asn | Gly | Gln | Asp | Glu  | Tyr | Lys | Ala | Asp | Ile  | Val | Met | Tyr |
| 6575 |     |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Thr  | Glu | Asn | Thr | Tyr | Leu | Glu  | Thr | Pro | Asp | Thr | His  | Val | Val | Tyr |
| 6590 |     |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Lys  | Pro | Gly | Lys | Asp | Asp | Ala  | Ser | Ser | Glu | Ile | Asn  | Leu | Val | Gln |
| 6605 |     |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Gln  | Ser | Met | Pro | Asn | Arg | Pro  | Asn | Tyr | Ile | Gly | Phe  | Arg | Asp | Asn |
| 6620 |     |     |     |     |     | 6625 |     |     |     |     | 6630 |     |     |     |
| Phe  | Ile | Gly | Leu | Met | Tyr | Tyr  | Asn | Ser | Thr | Gly | Asn  | Met | Gly | Val |
| 6635 |     |     |     |     |     | 6640 |     |     |     |     | 6645 |     |     |     |
| Leu  | Ala | Gly | Gln | Ala | Ser | Gln  | Leu | Asn | Ala | Val | Val  | Asp | Leu | Gln |
| 6650 |     |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |
| Asp  | Arg | Asn | Thr | Glu | Leu | Ser  | Tyr | Gln | Leu | Leu | Leu  | Asp | Ser | Leu |
| 6665 |     |     |     |     |     | 6670 |     |     |     |     | 6675 |     |     |     |
| Gly  | Asp | Arg | Thr | Arg | Tyr | Phe  | Ser | Met | Trp | Asn | Gln  | Ala | Val | Asp |
| 6680 |     |     |     |     |     | 6685 |     |     |     |     | 6690 |     |     |     |
| Ser  | Tyr | Asp | Pro | Asp | Val | Arg  | Ile | Ile | Glu | Asn | His  | Gly | Val | Glu |
| 6695 |     |     |     |     |     | 6700 |     |     |     |     | 6705 |     |     |     |
| Asp  | Glu | Leu | Pro | Asn | Tyr | Cys  | Phe | Pro | Leu | Asp | Gly  | Ser | Gly | Thr |
| 6710 |     |     |     |     |     | 6715 |     |     |     |     | 6720 |     |     |     |
| Asn  | Ala | Ala | Tyr | Gln | Gly | Val  | Lys | Val | Lys | Asp | Gly  | Gln | Asp | Gly |
| 6725 |     |     |     |     |     | 6730 |     |     |     |     | 6735 |     |     |     |
| Asp  | Val | Glu | Ser | Glu | Trp | Glu  | Asn | Asp | Asp | Thr | Val  | Ala | Ala | Arg |
| 6740 |     |     |     |     |     | 6745 |     |     |     |     | 6750 |     |     |     |
| Asn  | Gln | Leu | Cys | Lys | Gly | Asn  | Ile | Phe | Ala | Met | Glu  | Ile | Asn | Leu |
| 6755 |     |     |     |     |     | 6760 |     |     |     |     | 6765 |     |     |     |
| Gln  | Ala | Asn | Leu | Trp | Arg | Ser  | Phe | Leu | Tyr | Ser | Asn  | Val | Ala | Leu |
| 6770 |     |     |     |     |     | 6775 |     |     |     |     | 6780 |     |     |     |
| Tyr  | Leu | Pro | Asp | Ser | Tyr | Lys  | Tyr | Thr | Pro | Thr | Asn  | Val | Thr | Leu |
| 6785 |     |     |     |     |     | 6790 |     |     |     |     | 6795 |     |     |     |

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Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Thr  
 6800 6805 6810  
 Pro Pro Ser Leu Val Asp Ala Tyr Leu Asn Ile Gly Ala Arg Trp  
 6815 6820 6825  
 Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg  
 6830 6835 6840  
 Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg  
 6845 6850 6855  
 Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile  
 6860 6865 6870  
 Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn  
 6875 6880 6885  
 Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn  
 6890 6895 6900  
 Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn  
 6905 6910 6915  
 Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr  
 6920 6925 6930  
 Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn  
 6935 6940 6945  
 Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn  
 6950 6955 6960  
 Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala  
 6965 6970 6975  
 Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro  
 6980 6985 6990  
 Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser  
 6995 7000 7005  
 Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys  
 7010 7015 7020  
 Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn  
 7025 7030 7035

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp | Arg  | Leu | Leu | Thr | Pro | Asn  | Glu | Phe | Glu | Ile | Lys  | Arg | Thr | Val |
|     | 7040 |     |     |     |     | 7045 |     |     |     |     | 7050 |     |     |     |
| Asp | Gly  | Glu | Gly | Tyr | Asn | Val  | Ala | Gln | Cys | Asn | Met  | Thr | Lys | Asp |
|     | 7055 |     |     |     |     | 7060 |     |     |     |     | 7065 |     |     |     |
| Trp | Phe  | Leu | Val | Gln | Met | Leu  | Ala | His | Tyr | Asn | Ile  | Gly | Tyr | Gln |
|     | 7070 |     |     |     |     | 7075 |     |     |     |     | 7080 |     |     |     |
| Gly | Phe  | Tyr | Val | Pro | Glu | Gly  | Tyr | Lys | Asp | Arg | Met  | Tyr | Ser | Phe |
|     | 7085 |     |     |     |     | 7090 |     |     |     |     | 7095 |     |     |     |
| Phe | Arg  | Asn | Phe | Gln | Pro | Met  | Ser | Arg | Gln | Val | Val  | Asp | Glu | Val |
|     | 7100 |     |     |     |     | 7105 |     |     |     |     | 7110 |     |     |     |
| Asn | Tyr  | Lys | Asp | Tyr | Gln | Ala  | Val | Thr | Leu | Ala | Tyr  | Gln | His | Asn |
|     | 7115 |     |     |     |     | 7120 |     |     |     |     | 7125 |     |     |     |
| Asn | Ser  | Gly | Phe | Val | Gly | Tyr  | Leu | Ala | Pro | Thr | Met  | Arg | Gln | Gly |
|     | 7130 |     |     |     |     | 7135 |     |     |     |     | 7140 |     |     |     |
| Gln | Pro  | Tyr | Pro | Ala | Asn | Tyr  | Pro | Tyr | Pro | Leu | Ile  | Gly | Lys | Ser |
|     | 7145 |     |     |     |     | 7150 |     |     |     |     | 7155 |     |     |     |
| Ala | Val  | Ala | Ser | Val | Thr | Gln  | Lys | Lys | Phe | Leu | Cys  | Asp | Arg | Val |
|     | 7160 |     |     |     |     | 7165 |     |     |     |     | 7170 |     |     |     |
| Met | Trp  | Arg | Ile | Pro | Phe | Ser  | Ser | Asn | Phe | Met | Ser  | Met | Gly | Ala |
|     | 7175 |     |     |     |     | 7180 |     |     |     |     | 7185 |     |     |     |
| Leu | Thr  | Asp | Leu | Gly | Gln | Asn  | Met | Leu | Tyr | Ala | Asn  | Ser | Ala | His |
|     | 7190 |     |     |     |     | 7195 |     |     |     |     | 7200 |     |     |     |
| Ala | Leu  | Asp | Met | Asn | Phe | Glu  | Val | Asp | Pro | Met | Asp  | Glu | Ser | Thr |
|     | 7205 |     |     |     |     | 7210 |     |     |     |     | 7215 |     |     |     |
| Leu | Leu  | Tyr | Val | Val | Phe | Glu  | Val | Phe | Asp | Val | Val  | Arg | Val | His |
|     | 7220 |     |     |     |     | 7225 |     |     |     |     | 7230 |     |     |     |
| Gln | Pro  | His | Arg | Gly | Val | Ile  | Glu | Ala | Val | Tyr | Leu  | Arg | Thr | Pro |
|     | 7235 |     |     |     |     | 7240 |     |     |     |     | 7245 |     |     |     |
| Phe | Ser  | Ala | Gly | Asn | Ala | Thr  | Thr | Ala | Ala | Leu | Ala  | Ser | Cys | Lys |
|     | 7250 |     |     |     |     | 7255 |     |     |     |     | 7260 |     |     |     |
| Met | Thr  | Ala | Gly | Ser | Gly | Glu  | Gln | Glu | Leu | Arg | Ala  | Ile | Leu | Arg |

7265

7270

7275

Asp Leu Gly Cys Gly Pro Cys Phe Leu Gly Thr Phe Asp Lys Arg  
 7280 7285 7290

Phe Pro Gly Phe Met Ala Pro His Lys Leu Ala Cys Ala Ile Val  
 7295 7300 7305

Asn Thr Ala Gly Arg Glu Thr Gly Gly Glu His Trp Leu Ala Phe  
 7310 7315 7320

Ala Trp Asn Pro Arg Ser His Thr Cys Tyr Leu Phe Asp Pro Phe  
 7325 7330 7335

Gly Phe Ser Asp Glu Arg Leu Lys Gln Ile Tyr Gln Phe Glu Tyr  
 7340 7345 7350

Glu Gly Leu Leu Arg Arg Ser Ala Leu Ala Thr Glu Asp Arg Cys  
 7355 7360 7365

Val Thr Leu Glu Lys Ser Thr Gln Thr Val Gln Gly Pro Arg Ser  
 7370 7375 7380

Ala Ala Cys Gly Leu Phe Cys Cys Met Phe Leu His Ala Phe Val  
 7385 7390 7395

His Trp Pro Asp Arg Pro Met Asp Lys Asn Pro Thr Met Asn Leu  
 7400 7405 7410

Leu Thr Gly Val Pro Asn Gly Met Leu Gln Ser Pro Gln Val Glu  
 7415 7420 7425

Pro Thr Leu Arg Arg Asn Gln Glu Ala Leu Tyr Arg Phe Leu Asn  
 7430 7435 7440

Ala His Ser Ala Tyr Phe Arg Ser His Arg Ala Arg Ile Glu Lys  
 7445 7450 7455

Ala Thr Ala Phe Asp Arg Met Asn Gln Asp Met Lys Thr Gly Val  
 7460 7465 7470

Cys Met Met Leu Tyr Ser Thr Ala His Val Tyr Ala Thr Phe Ser  
 7475 7480 7485

Glu Ala Leu Thr Leu Phe Arg Asn Arg Arg Gly Ser Ala Gly Ser  
 7490 7495 7500



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Arg His Gly Pro Arg Ala Gly Ile Arg Cys Gly Thr Gly Thr Trp  
 7505 7510 7515  
 Ala Ala Thr Thr Arg Gly Ser Ala Ala Trp Ala Arg Gly Gly Arg  
 7520 7525 7530  
 Gly Thr Ser Arg Ser Thr Ala Cys Ala Val Ala Gly Arg Pro Ala  
 7535 7540 7545  
 Gly Arg Ala Arg Arg Ser Asn Arg Ser Trp Asp Pro Arg Ser Ala  
 7550 7555 7560  
 Arg Glu Ser Cys Gly Thr Arg Gly Cys Ser Thr Gly Thr Pro Ser  
 7565 7570 7575  
 Gly Pro Gly Ala Ser Arg Leu Pro Ala Pro Ser Arg Arg Cys Pro  
 7580 7585 7590  
 Pro Arg Pro Asp Pro Arg Arg Trp Pro Ser Arg Arg Gly Ser Ser  
 7595 7600 7605  
 Cys Arg Ser Ala Ala Pro Cys Trp Ala Arg Ser Arg Ala Cys Gly  
 7610 7615 7620  
 Cys Asn Arg Ser Ala Gly Gly Ser Ala Ser Ser Gly Pro Ala Arg  
 7625 7630 7635  
 Ser Ser Cys Pro Gly Thr Trp Pro Ser Lys Pro Pro Ala Gly Gly  
 7640 7645 7650  
 Arg Pro Ala Ala Pro Cys Arg Pro Arg Arg Arg Pro Arg Arg Thr  
 7655 7660 7665  
 Cys Arg Thr Gly Trp Trp Arg Ser Arg Arg Arg Ala Arg Ser Ser  
 7670 7675 7680  
 Ala Arg Arg Cys Trp Pro Ala Ala Pro Arg Cys Ala Pro Ser Gly  
 7685 7690 7695  
 Ser Gly Ser Trp Pro Gly Trp Gly Ser Pro Ser Ala Arg Ala Ala  
 7700 7705 7710  
 Arg Ser Arg Ser Pro His Pro Ser Arg Cys Ala Pro Ser Gly Ser  
 7715 7720 7725  
 Ser Arg Ser Arg Ala Gly Thr Ala Ala Cys Pro Arg Leu Arg Cys  
 7730 7735 7740

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Ser Arg Ala Ala Thr Ala Arg Ser Arg Cys Thr Pro Ser Ser Cys  
7745 7750 7755

Gly Arg Ser Gly Ser Ala Ser Ala Arg Ser Pro Ala Gly Ser Gly  
7760 7765 7770

Pro Ser Ser Arg Ser Gly Ser Cys Cys Trp Arg Ser Ala Gly Cys  
7775 7780 7785

Arg Gly Ala Pro Arg Ser His Thr Gly Gly Arg Cys Gly Gly Thr  
7790 7795 7800

Pro Arg Pro Ala Arg Ala Ser Ala Gly Arg Arg Thr Ser Gly Arg  
7805 7810 7815

Ser Pro Arg Gly Thr Gly Pro Ser Ala Ala Ser Ser Leu Pro Cys  
7820 7825 7830

Pro Ser Pro Arg Pro Lys Arg Ser Ala Gly Ser Gly Gly Ser Ser  
7835 7840 7845

Pro Pro Leu Ser Ser Ser Pro Pro Pro Arg Ser Gly Gly Arg Ser  
7850 7855 7860

Arg Pro Gly Ser Gln Thr Leu Ala Cys Arg Pro Ser Arg Cys Ala  
7865 7870 7875

Arg Gly Glu Ser Ser Pro Arg Pro Pro Ala Pro Pro Arg Pro Ala  
7880 7885 7890

Phe Arg Pro Arg Cys Pro Gly Cys Leu Ala Lys Ala His Ala Trp  
7895 7900 7905

Ser Cys Gly Val Ser Phe Trp Ala Ala Glu Ala Ala Ala Met Cys  
7910 7915 7920

Trp Glu Ser Ala Ser Ser Arg Ser Pro Arg Leu Phe Leu Leu Leu  
7925 7930 7935

Gly Arg Arg Pro Arg Pro Arg Gly Gly Arg His Ala Ser Ser Gly  
7940 7945 7950

Ala Glu Ala Glu Ala Thr Gly Ser Arg Gly Ser Ala Gly Gly Trp  
7955 7960 7965

Gln Ser Pro Phe Arg Val Arg Gly Cys Ala Pro Gly Gly Ala Ala  
7970 7975 7980

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Leu  | Thr | Asp | Phe | Leu | Arg | Gly  | Arg | Pro | Leu | Cys | Ser  | Pro | Arg | Glu |
| 7985 |     |     |     |     |     | 7990 |     |     |     |     | 7995 |     |     |     |
| Gln  | Gln | Gln | Ala | Trp | Arg | Leu  | Ser | His | Arg | Arg | Gln  | His | Arg | His |
| 8000 |     |     |     |     |     | 8005 |     |     |     |     | 8010 |     |     |     |
| Leu  | Pro | Pro | Pro | Pro | Pro | Pro  | Thr | Arg | Thr | Ser | Ser  | Arg | Met | Lys |
| 8015 |     |     |     |     |     | 8020 |     |     |     |     | 8025 |     |     |     |
| Ala  | Pro | Pro | Arg | Arg | Pro | Ala  | Pro | Pro | Pro | Thr | Pro  | Arg | Pro | Gln |
| 8030 |     |     |     |     |     | 8035 |     |     |     |     | 8040 |     |     |     |
| Thr  | Cys | Lys | Arg | Trp | Arg | Asn  | Pro | Ser | Arg | Leu | Thr  | Trp | Ala | Thr |
| 8045 |     |     |     |     |     | 8050 |     |     |     |     | 8055 |     |     |     |
| Arg  | Pro | Arg | Ser | Thr | Arg | Arg  | Ser | Trp | Gln | Arg | Ala  | Phe | Gln | Pro |
| 8060 |     |     |     |     |     | 8065 |     |     |     |     | 8070 |     |     |     |
| Arg  | Lys | Arg | Thr | Thr | Lys | Ser  | Ser | Gln | Ser | Arg | Lys  | Gln | Arg | Thr |
| 8075 |     |     |     |     |     | 8080 |     |     |     |     | 8085 |     |     |     |
| Ser  | Arg | Thr | Arg | Leu | Gly | Thr  | Ser | Met | Ala | Thr | Thr  | Ala | Gly | Gln |
| 8090 |     |     |     |     |     | 8095 |     |     |     |     | 8100 |     |     |     |
| Arg  | Thr | Cys | Ser | Ser | Ser | Ile  | Trp | Pro | Ala | Asn | Ala  | Ser | Ser | Ser |
| 8105 |     |     |     |     |     | 8110 |     |     |     |     | 8115 |     |     |     |
| Arg  | Thr | Arg | Cys | Ser | Thr | Ala  | Pro | Arg | Cys | Pro | Ser  | Ala | Trp | Arg |
| 8120 |     |     |     |     |     | 8125 |     |     |     |     | 8130 |     |     |     |
| Ser  | Ser | Ala | Ala | Pro | Thr | Ser  | Ala | Thr | Ser | Ser | Arg  | Arg | Ala | Cys |
| 8135 |     |     |     |     |     | 8140 |     |     |     |     | 8145 |     |     |     |
| Pro  | Pro | Ser | Ala | Ser | Pro | Thr  | Ala | Pro | Val | Ser | Pro  | Thr | Arg | Ala |
| 8150 |     |     |     |     |     | 8155 |     |     |     |     | 8160 |     |     |     |
| Ser  | Thr | Ser | Thr | Arg | Ser | Ser  | Arg | Cys | Pro | Arg | Pro  | Trp | Pro | Pro |
| 8165 |     |     |     |     |     | 8170 |     |     |     |     | 8175 |     |     |     |
| Thr  | Thr | Ser | Phe | Ser | Arg | Thr  | Lys | Gly | Ser | Pro | Ser  | Pro | Ala | Ala |
| 8180 |     |     |     |     |     | 8185 |     |     |     |     | 8190 |     |     |     |
| Pro  | Thr | Ala | Pro | Ala | Pro | Thr  | Pro | Cys | Ser | Thr | Trp  | Ala | Pro | Ala |
| 8195 |     |     |     |     |     | 8200 |     |     |     |     | 8205 |     |     |     |
| Pro  | Ala | Tyr | Leu | Ile | Ser | Pro  | Pro | Trp | Lys | Arg | Phe  | Pro | Arg | Ser |

8210

8215

8220

Ser Arg Val Trp Ala Ala Thr Arg Leu Gly Pro Arg Thr Leu Cys  
 8225 8230 8235

Lys Glu Ala Glu Arg Ser Met Ser Thr Thr Ala Pro Trp Trp Ser  
 8240 8245 8250

Trp Lys Ala Thr Thr Arg Ala Trp Arg Ser Ser Ser Ala Arg Ser  
 8255 8260 8265

Ser Pro Thr Ser Pro Thr Arg Arg Ser Thr Cys Pro Pro Arg Ser  
 8270 8275 8280

Ala Pro Ser Trp Thr Arg Cys Ser Ser Ser Ala Pro Arg Pro Ser  
 8285 8290 8295

Arg Arg Arg Arg Cys Arg Thr Pro Arg Val Arg Thr Arg Ala Ser  
 8300 8305 8310

Pro Trp Ser Ala Thr Ser Ser Trp Arg Ala Gly Trp Glu Arg Val  
 8315 8320 8325

Ala Pro Pro Arg Ala Trp Lys Ser Gly Ala Ser Ser Trp Pro Trp  
 8330 8335 8340

Ser Trp Pro Trp Ser Trp Ser Val Cys Ala Ala Ser Leu Pro Thr  
 8345 8350 8355

Arg Arg Pro Cys Ala Arg Ser Arg Arg Thr Cys Thr Thr Ser Ser  
 8360 8365 8370

Gly Thr Gly Ser Cys Ala Arg Pro Ala Arg Ser Pro Thr Trp Ser  
 8375 8380 8385

Pro Thr Trp Ser Pro Thr Trp Ala Ser Cys Thr Arg Thr Ala Trp  
 8390 8395 8400

Gly Lys Thr Cys Cys Thr Pro Pro Cys Ala Gly Arg Pro Ala Ala  
 8405 8410 8415

Thr Thr Ser Ala Thr Ala Ser Thr Cys Thr Ser Ala Thr Pro Gly  
 8420 8425 8430

Arg Arg Ala Trp Ala Cys Gly Ser Ser Ala Trp Arg Ser Arg Thr  
 8435 8440 8445

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Lys Ser Ser Ala Ser Ser Cys Arg Arg Thr Ser Arg Pro Cys Gly  
 8450 8455 8460  
 Pro Gly Ser Thr Ser Val Pro Pro Pro Arg Thr Trp Pro Thr Ser  
 8465 8470 8475  
 Ser Ser Pro Ser Ala Cys Gly Arg Cys Ala Thr Gly Cys Pro Thr  
 8480 8485 8490  
 Leu Ala Lys Ala Cys Cys Lys Thr Phe Ala Leu Ser Ser Ser Asn  
 8495 8500 8505  
 Ala Pro Gly Ser Cys Pro Pro Pro Ala Pro Arg Cys Pro Arg Thr  
 8510 8515 8520  
 Ser Cys Arg Pro Ser Ala Ser Ala Pro Arg Arg Ser Gly Ala Thr  
 8525 8530 8535  
 Ala Thr Cys Cys Ala Trp Pro Thr Thr Trp Pro Thr Thr Arg Thr  
 8540 8545 8550  
 Ser Arg Thr Ser Ala Ala Arg Val Cys Trp Ser Ala Thr Ala Ala  
 8555 8560 8565  
 Ala Thr Ser Ala Arg Arg Thr Ala Pro Trp Pro Ala Thr Pro Ser  
 8570 8575 8580  
 Cys Ala Arg Pro Arg Ser Ser Ala Pro Ser Ser Cys Lys Ala Pro  
 8585 8590 8595  
 Ala Thr Ala Arg Ala Arg Gly Val Asn Ser Pro Arg Gly Cys Gly  
 8600 8605 8610  
 Pro Arg Pro Thr Cys Ala Ser Ser Cys Pro Arg Thr Thr Ile Pro  
 8615 8620 8625  
 Ser Arg Ser Gly Ser Thr Arg Thr Asn Pro Ser Arg Pro Arg Pro  
 8630 8635 8640  
 Ser Cys Arg Pro Ala Ser Ser Pro Arg Gly Pro Ser Trp Pro Asn  
 8645 8650 8655  
 Cys Lys Pro Ser Arg Asn Pro Ala Lys Asn Phe Cys Lys Arg Ala  
 8660 8665 8670  
 Thr Gly Ser Thr Trp Thr Pro Arg Pro Glu Arg Ser Ser Thr Pro  
 8675 8680 8685

## 368530-7006W01\_SequenceListing\_ST25.txt

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Ser | Pro | Arg | Met | Pro | Arg  | Gly | Ser | Ser | Lys | Lys  | Leu | Lys | Val |
| 8690 |     |     |     |     |     | 8695 |     |     |     |     | 8700 |     |     |     |
| Glu  | Leu | Pro | Pro | Pro | Glu | Asp  | Leu | Glu | Glu | Asp | Trp  | Glu | Ser | Ser |
| 8705 |     |     |     |     |     | 8710 |     |     |     |     | 8715 |     |     |     |
| Gln  | Ala | Glu | Glu | Glu | Glu | Met  | Glu | Asp | Trp | Asp | Ser  | Thr | Gln | Ala |
| 8720 |     |     |     |     |     | 8725 |     |     |     |     | 8730 |     |     |     |
| Glu  | Glu | Asp | Ser | Leu | Gln | Asp  | Ser | Leu | Glu | Glu | Glu  | Asp | Glu | Val |
| 8735 |     |     |     |     |     | 8740 |     |     |     |     | 8745 |     |     |     |
| Glu  | Glu | Ala | Glu | Glu | Glu | Ala  | Ala | Ala | Ala | Arg | Pro  | Ser | Ser | Ser |
| 8750 |     |     |     |     |     | 8755 |     |     |     |     | 8760 |     |     |     |
| Ala  | Glu | Lys | Ala | Ser | Ser | Thr  | Asp | Thr | Ile | Ser | Ala  | Pro | Gly | Arg |
| 8765 |     |     |     |     |     | 8770 |     |     |     |     | 8775 |     |     |     |
| Gly  | Arg | Gly | Gly | Arg | Ala | His  | Ser | Arg | Trp | Asp | Glu  | Thr | Gly | Arg |
| 8780 |     |     |     |     |     | 8785 |     |     |     |     | 8790 |     |     |     |
| Phe  | Pro | Asn | Pro | Thr | Thr | Gln  | Thr | Gly | Lys | Lys | Glu  | Arg | Gln | Gly |
| 8795 |     |     |     |     |     | 8800 |     |     |     |     | 8805 |     |     |     |
| Tyr  | Lys | Ser | Trp | Arg | Gly | His  | Lys | Asn | Ala | Ile | Val  | Ser | Cys | Leu |
| 8810 |     |     |     |     |     | 8815 |     |     |     |     | 8820 |     |     |     |
| Gln  | Ala | Cys | Gly | Gly | Asn | Ile  | Ser | Phe | Thr | Arg | Arg  | Tyr | Leu | Leu |
| 8825 |     |     |     |     |     | 8830 |     |     |     |     | 8835 |     |     |     |
| Phe  | His | Arg | Gly | Val | Asn | Phe  | Pro | Arg | Asn | Ile | Leu  | His | Tyr | Tyr |
| 8840 |     |     |     |     |     | 8845 |     |     |     |     | 8850 |     |     |     |
| Arg  | His | Leu | His | Ser | Pro | Tyr  | Tyr | Cys | Phe | Gln | Glu  | Glu | Ala | Glu |
| 8855 |     |     |     |     |     | 8860 |     |     |     |     | 8865 |     |     |     |
| Thr  | Gln | Gln | Gln | Gln | Lys | Thr  | Ser | Gly | Ser | Ser | Ser  | Lys | Ile | His |
| 8870 |     |     |     |     |     | 8875 |     |     |     |     | 8880 |     |     |     |
| Ser  | Gly | Gly | Arg | Trp | Thr | Glu  | Asp | Arg | Gly | Glu | Arg  | Ala | Gly | Ala |
| 8885 |     |     |     |     |     | 8890 |     |     |     |     | 8895 |     |     |     |
| Asp  | Pro | Gly | Ala | Glu | Glu | Pro  | Asp | Leu | Ser | His | Pro  | Leu | Cys | His |
| 8900 |     |     |     |     |     | 8905 |     |     |     |     | 8910 |     |     |     |
| Leu  | Pro | Ala | Glu | Ser | Gly | Ala  | Gly | Ala | Gly | Thr | Glu  | Ser | Gln | Glu |
| 8915 |     |     |     |     |     | 8920 |     |     |     |     | 8925 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Phe  | Ser | Ala | Leu | Ala | His  | Pro | Gln | Leu | Ser | Val  | Ser | Gln | Glu |
|     | 8930 |     |     |     |     | 8935 |     |     |     |     | 8940 |     |     |     |
| Arg | Arg  | Pro | Thr | Ser | Ala | His  | Ser | Arg | Gly | Arg | Arg  | Gly | Ser | Leu |
|     | 8945 |     |     |     |     | 8950 |     |     |     |     | 8955 |     |     |     |
| Gln | Gln  | Val | Leu | Arg | Ala | His  | Ser | Arg | Val | Ala | Arg  | Ala | Arg | Pro |
|     | 8960 |     |     |     |     | 8965 |     |     |     |     | 8970 |     |     |     |
| His | Thr  | Glu | Lys | Gly | Gly | Asn  | Tyr | Val | Thr | Thr | Cys  | Ala | Leu | Arg |
|     | 8975 |     |     |     |     | 8980 |     |     |     |     | 8985 |     |     |     |
| Pro | Thr  | Ile | Met | Ser | Lys | Glu  | Ile | Pro | Thr | Pro | Tyr  | Met | Trp | Ser |
|     | 8990 |     |     |     |     | 8995 |     |     |     |     | 9000 |     |     |     |
| Tyr | Gln  | Pro | Gln | Met | Gly | Leu  | Ala | Ala | Gly | Ala | Ala  | Gln | Asp | Tyr |
|     | 9005 |     |     |     |     | 9010 |     |     |     |     | 9015 |     |     |     |
| Ser | Thr  | Arg | Met | Asn | Trp | Leu  | Ser | Ala | Gly | Pro | Ala  | Met | Ile | Ser |
|     | 9020 |     |     |     |     | 9025 |     |     |     |     | 9030 |     |     |     |
| Arg | Val  | Asn | Asp | Ile | Arg | Ala  | His | Arg | Asn | Gln | Ile  | Leu | Leu | Glu |
|     | 9035 |     |     |     |     | 9040 |     |     |     |     | 9045 |     |     |     |
| Gln | Ser  | Ala | Ile | Thr | Ala | Thr  | Pro | Arg | His | His | Leu  | Asn | Pro | Arg |
|     | 9050 |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Asn | Trp  | Pro | Ala | Ala | Leu | Val  | Tyr | Gln | Glu | Ile | Pro  | Gln | Pro | Thr |
|     | 9065 |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Thr | Val  | Leu | Leu | Pro | Arg | Asp  | Ala | Gln | Ala | Glu | Val  | Gln | Leu | Thr |
|     | 9080 |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Asn | Ser  | Gly | Val | Gln | Leu | Ala  | Gly | Gly | Ala | Ala | Leu  | Cys | Arg | His |
|     | 9095 |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Arg | Pro  | Ala | Gln | Gly | Ile | Lys  | Arg | Leu | Val | Ile | Arg  | Gly | Arg | Gly |
|     | 9110 |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Thr | Gln  | Leu | Asn | Asp | Glu | Val  | Val | Ser | Ser | Ser | Leu  | Gly | Leu | Arg |
|     | 9125 |     |     |     |     | 9130 |     |     |     |     | 9135 |     |     |     |
| Pro | Asp  | Gly | Val | Phe | Gln | Leu  | Ala | Gly | Ser | Gly | Arg  | Ser | Ser | Phe |
|     | 9140 |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Thr | Pro  | Arg | Gln | Ala | Val | Leu  | Thr | Leu | Glu | Ser | Ser  | Ser | Ser | Gln |

|          |     |     |     |     |     |          |     |     |     |     |          |     |     |     |
|----------|-----|-----|-----|-----|-----|----------|-----|-----|-----|-----|----------|-----|-----|-----|
| Pro 9170 | Arg | Ser | Gly | Gly | Ile | Gly 9175 | Thr | Leu | Gln | Phe | Val 9180 | Glu | Glu | Phe |
| Thr 9185 | Pro | Ser | Val | Tyr | Phe | Asn 9190 | Pro | Phe | Ser | Gly | Ser 9195 | Pro | Gly | His |
| Tyr 9200 | Pro | Asp | Glu | Phe | Ile | Pro 9205 | Asn | Phe | Asp | Ala | Ile 9210 | Ser | Glu | Ser |
| Val 9215 | Asp | Gly | Tyr | Asp | Met | Ser 9220 | His | Gly | Gly | Ala | Ala 9225 | Asp | Leu | Ala |
| Arg 9230 | Leu | Arg | His | Leu | Asp | His 9235 | Cys | Arg | Arg | Phe | Arg 9240 | Cys | Phe | Ala |
| Arg 9245 | Asp | Leu | Ala | Glu | Phe | Ala 9250 | Tyr | Phe | Glu | Leu | Pro 9255 | Glu | Glu | His |
| Pro 9260 | Gln | Gly | Pro | Ala | His | Gly 9265 | Val | Arg | Ile | Ile | Val 9270 | Glu | Gly | Gly |
| Leu 9275 | Asp | Ser | His | Leu | Leu | Arg 9280 | Ile | Phe | Ser | Gln | Arg 9285 | Pro | Ile | Leu |
| Val 9290 | Glu | Arg | Glu | Gln | Gly | Gln 9295 | Thr | Leu | Leu | Thr | Leu 9300 | Tyr | Cys | Ile |
| Cys 9305 | Asn | His | Pro | Gly | Leu | His 9310 | Glu | Ser | Leu | Cys | Cys 9315 | Leu | Leu | Cys |
| Thr 9320 | Glu | Tyr | Asn | Lys | Ser | Asp 9325 | Gln | Arg | Leu | Leu | Arg 9330 | Thr | Arg | Leu |
| Trp 9335 | Cys | Ser | Cys | Tyr | Gln | Pro 9340 | Val | Pro | Val | Leu | His 9345 | Arg | Glu | Arg |
| Asp 9350 | Arg | Ala | Pro | Ala | Pro | Val 9355 | Ala | Pro | Gln | Glu | Val 9360 | Pro | His | Leu |
| Ala 9365 | Val | Pro | Gly | Leu | Pro | Asp 9370 | Arg | Arg | Cys | Gln | Pro 9375 | Leu | Arg | Gln |
| Arg 9380 | Arg | Ser | Pro | Ala | Glu | Arg 9385 | Pro | Cys | Gln | Pro | Tyr 9390 | Phe | Phe | His |



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Pro Gln Lys Gln Ala Pro Ala Leu Pro Thr Leu Pro Pro Arg Asp  
 9395 9400 9405  
  
 Leu Ser Val Arg Leu Arg Thr Leu Pro Ser His Leu Pro Pro Asp  
 9410 9415 9420  
  
 Pro Glu Tyr His Ser Ala Ala Pro Arg Tyr Gln Pro Asn Tyr Pro  
 9425 9430 9435  
  
 Pro Thr Pro Pro Ser Arg Pro Phe Leu Ile Tyr His Tyr Arg Arg  
 9440 9445 9450  
  
 Trp Leu Leu Leu Leu Val Leu Pro Arg Pro Val Asp Pro Arg Ser  
 9455 9460 9465  
  
 Pro Thr Gln Ser Pro Glu Glu Val Arg Lys Cys Lys Phe Gln Glu  
 9470 9475 9480  
  
 Pro Trp Lys Phe Leu Lys Cys Tyr Arg Gln Lys Ser Asp Met His  
 9485 9490 9495  
  
 Pro Ser Trp Ile Met Ile Ile Gly Ile Val Asn Ile Leu Ala Cys  
 9500 9505 9510  
  
 Thr Leu Ile Ser Phe Val Ile Tyr Pro Cys Phe Asp Phe Gly Trp  
 9515 9520 9525  
  
 Asn Ser Pro Glu Ala Leu Tyr Leu Pro Pro Glu Pro Asp Thr Pro  
 9530 9535 9540  
  
 Pro Gln Gln Gln Pro Gln Ala His Ala Leu Pro Pro Pro Gln Pro  
 9545 9550 9555  
  
 Arg Pro Gln Tyr Met Pro Ile Leu Asp Tyr Glu Ala Glu Pro Gln  
 9560 9565 9570  
  
 Arg Pro Met Leu Pro Ala Ile Ser Tyr Phe Asn Leu Thr Gly Gly  
 9575 9580 9585  
  
 Asp Asp Pro Thr Gly Gln Gln Arg Gln Arg Pro Ser Pro Gly His  
 9590 9595 9600  
  
 Gly Arg Pro Arg Leu Gly Ala Ala Thr Arg Pro Thr Ser His Ser  
 9605 9610 9615  
  
 Ser Ala Ala Gly Glu Ser Arg Gln Gly Ala Ala Gly Arg His Ser  
 9620 9625 9630

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His Pro Pro Val Gln Glu Arg His Leu Leu Pro Gly Glu Thr Gly  
 9635 9640 9645  
 Gln Asp Leu Leu Arg Gly His Pro Asp Arg Pro Ser Pro Leu Leu  
 9650 9655 9660  
 Arg Ala Pro Ala Ala Ala Pro Glu Val His Leu Pro Gly Arg Ser  
 9665 9670 9675  
 Gln Pro His Arg His His Pro Ala Val Gly Arg Tyr Gln Gly Val  
 9680 9685 9690  
 His Pro Leu Leu Leu Arg Leu Pro Arg Leu Arg Pro His Ser Asp  
 9695 9700 9705  
 Gln Asp Pro Leu Arg Pro Pro Arg Pro Pro Pro His Glu Leu Ile  
 9710 9715 9720  
 Thr Pro Leu Ser Ser Glu Ile Lys Ile Ile Leu Met Met Ile Ile  
 9725 9730 9735  
 Lys Lys Ile Ile Ile Phe Glu Ile Lys Ile Gln Ser Tyr Phe Glu  
 9740 9745 9750  
 Phe Asn Lys Asn Lys Glu Ser Leu Thr Asn Leu Ile Pro Gly Leu  
 9755 9760 9765  
 Cys Pro Cys Phe Leu Pro Thr Pro Pro His Ser Pro Leu Pro Ser  
 9770 9775 9780  
 Ser Gly Thr Ala Gly Pro Gly Gly Leu Gln Thr Ser Ser Thr Arg  
 9785 9790 9795  
 Arg Gly Cys Gln Ile Pro Pro Val Pro Gln Ser Ser Phe Tyr Leu  
 9800 9805 9810  
 Leu Ser Asp Val Gln Lys Ala Arg Pro Gly Gly Leu Arg Pro Arg  
 9815 9820 9825  
 Leu Pro Leu Arg Cys Arg Gln Arg Thr Asp Arg Ala Leu His Gln  
 9830 9835 9840  
 Pro Pro Leu Arg Leu Phe Arg Trp Ile Pro Arg Glu Ala Pro Gly  
 9845 9850 9855  
 Gly Val Val Pro Ala Thr Gly Pro Arg His His Gln Glu Arg Gly  
 9860 9865 9870

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Asn His Pro Gln Ala Gly Arg Gly Gly Gly Pro Arg Leu Val Gly  
 9875 9880 9885  
 Lys Thr His Leu Gln His Gly His Gln Gly Arg Arg Pro Ser Gln  
 9890 9895 9900  
 Tyr Phe Lys Gln His His Phe Pro Asn Cys Cys Pro Phe Leu Gln  
 9905 9910 9915  
 Gln Gln Trp Asn Phe Lys Pro Gln Cys Leu His Thr Ile Ser Ser  
 9920 9925 9930  
 Ile Ser His Ile His Phe Arg His Lys Ser Trp Lys Arg Ser Ser  
 9935 9940 9945  
 Asp Phe Lys Val Val Asp Cys Thr Thr Asn Ser Ser Ser Tyr Ile  
 9950 9955 9960  
 Gln Leu Lys His His Ser Lys Asn Arg Gln Arg Ala Ile Tyr Leu  
 9965 9970 9975  
 Gln Trp Lys Gln Arg Thr Gly Tyr Lys Pro Lys Lys Arg Thr Ser  
 9980 9985 9990  
 Phe Arg Cys Tyr Cys Asn Ile Tyr Trp Lys Trp Leu Arg Leu Trp  
 9995 10000 10005  
 Ile Leu Trp Lys Asn Lys Thr Arg Asn Tyr Gln Asn Trp Ser Arg  
 10010 10015 10020  
 Ile Lys Phe Cys Gln Ser Asn Ser Cys Gln Thr Arg His Arg Phe  
 10025 10030 10035  
 Lys Phe Leu Arg Trp Cys Leu Asp Ser Trp Lys Gln Thr Gly Gln  
 10040 10045 10050  
 Ala Asn Thr Leu Asp Tyr Pro Pro Lys Pro Leu Ser Ile Thr Phe  
 10055 10060 10065  
 Arg Gln Arg Cys Gln Ile Tyr Ser Leu Ser Tyr Lys Met Arg Ser  
 10070 10075 10080  
 Asn Thr Arg His Cys Gly Ser Gly Gly Cys Tyr Cys Arg Ile Ser  
 10085 10090 10095  
 Thr Lys Ser Asn His Ser Gln Lys Arg His Ser Phe Pro Ile Phe

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|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| 10100 |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
| Arg   | Trp | Cys | Thr | His | Val | Lys   | Leu | Ile | Asn | Gly | Arg   | Leu | Leu | Glu |
| 10115 |     |     |     |     |     | 10120 |     |     |     |     | 10125 |     |     |     |
| Leu   | Gly | Gly | Thr | Asp | His | Ser   | Lys | Cys | Ser | Leu | Tyr   | Lys | Cys | Cys |
| 10130 |     |     |     |     |     | 10135 |     |     |     |     | 10140 |     |     |     |
| Gly   | Ile | His | Ala | Lys | Tyr | Arg   | Cys | Ile | Ser | Lys | Asn   | Pro | Lys | Asn |
| 10145 |     |     |     |     |     | 10150 |     |     |     |     | 10155 |     |     |     |
| Thr   | Lys | His | Ser | Gln | Ser | Gly   | Ile | Phe | Asn | Trp | Arg   | Asn | Tyr | Tyr |
| 10160 |     |     |     |     |     | 10165 |     |     |     |     | 10170 |     |     |     |
| Ala   | Asn | Asp | Thr | Asn | His | Asn   | Phe | Gln | Trp | His | Lys   | Arg | His | Asn |
| 10175 |     |     |     |     |     | 10180 |     |     |     |     | 10185 |     |     |     |
| Pro   | Ser | His | Leu | Leu | Tyr | Asp   | Phe | Tyr | Met | Ala | Val   | Asp | Trp | Arg |
| 10190 |     |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| Leu   | Gly | Gln | Lys | Tyr | Tyr | Leu   | Cys | Tyr | Gln | Leu | Ile   | Leu | Phe | Phe |
| 10205 |     |     |     |     |     | 10210 |     |     |     |     | 10215 |     |     |     |
| Leu   | His | Arg | Pro | Gly | Ile | Ile   | Pro | Pro | Ser | Lys | Pro   | Thr | Pro | Phe |
| 10220 |     |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |
| Pro   | Thr | Thr | Phe | Val | Tyr | Met   | Glu | Thr | Leu | Lys | Gln   | Lys | Asn | Lys |
| 10235 |     |     |     |     |     | 10240 |     |     |     |     | 10245 |     |     |     |
| Val   | Gln | Val | Phe | Tyr | Ile | Asn   | Ser | Phe | Thr | Gly | Leu   | Glu | Gln | Leu |
| 10250 |     |     |     |     |     | 10255 |     |     |     |     | 10260 |     |     |     |
| Phe   | Phe | Leu | His | Pro | Pro | Arg   | Thr | Trp | Asn | Thr | Pro   | Pro | Ser | Pro |
| 10265 |     |     |     |     |     | 10270 |     |     |     |     | 10275 |     |     |     |
| Pro   | Ala | Gln | Pro | Thr | Ser | Glu   | Cys | His | Trp | Trp | Thr   | Cys | Phe | Trp |
| 10280 |     |     |     |     |     | 10285 |     |     |     |     | 10290 |     |     |     |
| Ser   | Pro | Arg | Ser | Thr | Gln | Phe   | Gln | Ser | Glu | Pro | Val   | Ser | Asp | Arg |
| 10295 |     |     |     |     |     | 10300 |     |     |     |     | 10305 |     |     |     |
| Ser   | Gly | Arg | Asn | Pro | Pro | Gly   | Thr | Pro | Ala | Ser | Ala   | Pro | His | Ser |
| 10310 |     |     |     |     |     | 10315 |     |     |     |     | 10320 |     |     |     |
| Ser   | Thr | Ala | Glu | Asp | Cys | Pro   | Arg | Trp | Ser | Gly | Ser   | Arg | Leu | Ser |
| 10325 |     |     |     |     |     | 10330 |     |     |     |     | 10335 |     |     |     |

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|       |     |     |     |     |       |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-------|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Gly   | Arg | Ser | Arg | Arg | Ala   | Ala   | Val | Gly | Ile | Ile | Val   | Arg | Glu | Arg |
| 10340 |     |     |     |     | 10345 |       |     |     |     |     | 10350 |     |     |     |
| Asp   | Arg | Pro | Val | Val | Ser   | His   | Gln | Ala | Pro | Gln | Gln   | Ser | Leu | Pro |
| 10355 |     |     |     |     |       | 10360 |     |     |     |     | 10365 |     |     |     |
| Pro   | Pro | Leu | Arg | Gln | Ala   | Ala   | Ala | Gln | Gly | Val | Arg   | Val | Gln | Gly |
| 10370 |     |     |     |     | 10375 |       |     |     |     |     | 10380 |     |     |     |
| Leu   | Pro | Gln | His | Asp | Ala   | His   | Gly | Pro | Gln | His | Gln   | Ser | Ser | Gly |
| 10385 |     |     |     |     |       | 10390 |     |     |     |     | 10395 |     |     |     |
| Ala   | Ala | Gly | Ala | Ala | Ala   | His   | Ala | Asn | Leu | Ala | Gln   | Val | Thr | Ala |
| 10400 |     |     |     |     |       | 10405 |     |     |     |     | 10410 |     |     |     |
| Val   | Arg | Ala | Thr | Gln | Asp   | His   | Gln | Val | Val | Gln | Gln   | Ser | Ile | Val |
| 10415 |     |     |     |     |       | 10420 |     |     |     |     | 10425 |     |     |     |
| Gln   | His | Ala | Pro | Ala | Glu   | Thr   | His | Arg | Gly | Lys | Asp   | Ala | Thr | His |
| 10430 |     |     |     |     |       | 10435 |     |     |     |     | 10440 |     |     |     |
| Val   | Ala | Val | Val | Pro | Asp   | Pro   | Gln | Val | Asn | Gln | Val   | Ala | Leu | Pro |
| 10445 |     |     |     |     |       | 10450 |     |     |     |     | 10455 |     |     |     |
| Pro   | Glu | Asp | Ala | Ala | His   | Val   | His | Asp | Leu | Leu | Gly   | His | Val | Ala |
| 10460 |     |     |     |     |       | 10465 |     |     |     |     | 10470 |     |     |     |
| Val   | His | His | Leu | Pro | Val   | Pro   | His | His | Pro | Leu | Val   | Glu | His | Ala |
| 10475 |     |     |     |     |       | 10480 |     |     |     |     | 10485 |     |     |     |
| Ala   | Pro | Asp | Asp | Pro | Ala   | Glu   | Pro | Gln | Gly | Gln | His   | Arg | Pro | Ala |
| 10490 |     |     |     |     |       | 10495 |     |     |     |     | 10500 |     |     |     |
| Arg   | His | Ala | Ala | Lys | Arg   | Pro   | Arg | Ile | Pro | Ala | Met   | Thr | Met | Glu |
| 10505 |     |     |     |     |       | 10510 |     |     |     |     | 10515 |     |     |     |
| Asp   | Pro | Pro | Leu | Val | Pro   | Val   | Asp | His | Leu | Gly | Ala   | Glu | Gln | Val |
| 10520 |     |     |     |     |       | 10525 |     |     |     |     | 10530 |     |     |     |
| Tyr   | Val | Gly | Thr | Ala | Gln   | Ala   | Tyr | Ala | His | Ala | Ser   | Leu | Gln | His |
| 10535 |     |     |     |     |       | 10540 |     |     |     |     | 10545 |     |     |     |
| Ser   | Gln | Leu | Leu | Gly | Gly   | Gln   | Asn | His | Ile | Pro | Gly   | His | Gly | Glu |
| 10550 |     |     |     |     |       | 10555 |     |     |     |     | 10560 |     |     |     |
| Leu   | Leu | Gln | Asp | Ser | Glu   | Pro   | Arg | Arg | Thr | Gly | Gln   | Ser | Ser | His |
| 10565 |     |     |     |     |       | 10570 |     |     |     |     | 10575 |     |     |     |

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|                  |                              |                              |             |
|------------------|------------------------------|------------------------------|-------------|
| Ile Thr<br>10580 | Tyr Ile Val His Gly<br>10585 | Gln Gly Ile Ala Ile<br>10590 | Arg Gln His |
| Arg Val<br>10595 | Ile Leu His Gln Arg<br>10600 | Ser Ala Gly Leu Gly<br>10605 | Leu Leu Thr |
| Ala Trp<br>10610 | Gly Gly Arg Pro Ile<br>10615 | Arg Val Met Ala Gly<br>10620 | Arg Gly Ser |
| Cys Ser<br>10625 | Arg Pro Cys His Asp<br>10630 | Ala Val Ala Phe Gly<br>10635 | His Phe Arg |
| Thr Cys<br>10640 | Cys Ser Arg Thr Trp<br>10645 | Ser Gly Arg Cys Thr<br>10650 | Pro Ile Ala |
| Gly Gly<br>10655 | Gly Leu Gly Ala Trp<br>10660 | Asn Ala Arg Cys Ser<br>10665 | Cys Lys Thr |
| Ala Thr<br>10670 | Leu Ser Asp Arg Ala<br>10675 | Ala Asp Leu Gly Pro<br>10680 | Gln Glu Arg |
| Ser His<br>10685 | His Ala Leu Ser His<br>10690 | Arg Pro Pro Trp Asn<br>10695 | Gly Pro Gly |
| Pro Ala<br>10700 | Arg Cys Asn Phe Val<br>10705 | Gly Phe Arg Arg Arg<br>10710 | Gly Arg Glu |
| Glu Gln<br>10715 | Glu Glu Pro Leu Thr<br>10720 | Phe Asn Pro Asn Gly<br>10725 | Leu Gly Ala |
| Leu Gln<br>10730 | Asn Glu Gly His Gly<br>10735 | Asp Gly Thr Ser Arg<br>10740 | Pro Arg Cys |
| Val Gly<br>10745 | Gly Lys Gln Pro Gly<br>10750 | Gln Arg Tyr Gly Ser<br>10755 | Arg Asp Val |
| Pro Arg<br>10760 | Trp Leu Pro Ala Lys<br>10765 | Pro Pro Arg Ala His<br>10770 | Pro Glu Thr |
| Arg Gln<br>10775 | Arg Lys Arg Glu Gly<br>10780 | Ser Leu Ile Pro Gln<br>10785 | Pro Ser Cys |
| Tyr Thr<br>10790 | Pro Ala Pro Ser Pro<br>10795 | Asp Asn Phe His Phe<br>10800 | Ser Ser Leu |
| Glu Phe<br>10805 | Glu Leu Val Pro Glu<br>10810 | Val Asn Pro Ser Gln<br>10815 | Pro Lys Ala |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Arg | Ala   | Glu | His | Pro | Pro | Pro   | Ala | Phe | Leu | Ser | Thr   | Pro | Ser | Phe |
|     | 10820 |     |     |     |     | 10825 |     |     |     |     | 10830 |     |     |     |
| Gln | Asp   | Ile | Leu | Leu | Leu | Val   | His | Leu | Gln | Gln | Ile   | Asp | Lys | Arg |
|     | 10835 |     |     |     |     | 10840 |     |     |     |     | 10845 |     |     |     |
| Asn | Ile   | Lys | Ile | Ser | Ala | Ala   | Ile | Pro | Glu | Leu | Leu   | Pro | Gln | Gln |
|     | 10850 |     |     |     |     | 10855 |     |     |     |     | 10860 |     |     |     |
| Leu | Val   | Leu | Phe | His | Ile | Val   | Ser | Glu | Ile | Phe | Ser   | His | Arg | Thr |
|     | 10865 |     |     |     |     | 10870 |     |     |     |     | 10875 |     |     |     |
| Pro | Arg   | Asn | Lys | Arg | Arg | Ala   | Ser | His | Ile | Thr | Asp   | Lys | Pro | Lys |
|     | 10880 |     |     |     |     | 10885 |     |     |     |     | 10890 |     |     |     |
| Ser | Pro   | Pro | Val | Ser | Ile | Ala   | Lys | Cys | Lys | Ile | Glu   | Ile | Ser | Met |
|     | 10895 |     |     |     |     | 10900 |     |     |     |     | 10905 |     |     |     |
| Leu | Ala   | Arg | Pro | Gly | Asp | Ile   | Phe | Gln | Ile | Thr | Gly   | Gln | Lys | Ile |
|     | 10910 |     |     |     |     | 10915 |     |     |     |     | 10920 |     |     |     |
| Gly | Ala   | Ile | Phe | Lys | Lys | Ile   | Asn | Lys | Arg | Lys | Ile   | Phe | Gln | Val |
|     | 10925 |     |     |     |     | 10930 |     |     |     |     | 10935 |     |     |     |
| His | Val   | Gly | Leu | Gly | Asn | Asn   | Asp | Gly | Val | Ser | Ala   | Arg | Gly | Ala |
|     | 10940 |     |     |     |     | 10945 |     |     |     |     | 10950 |     |     |     |
| Phe | Gln   | His | Gly | Leu | Ala | Asp   | Leu | Lys | Asn | Lys | Lys   | Asn | Ile | Lys |
|     | 10955 |     |     |     |     | 10960 |     |     |     |     | 10965 |     |     |     |
| Pro | Cys   | Pro | Gly | Glu | Gln | Val   | Gly | Lys | Ser | Phe | Ser   | Pro | Ala | Pro |
|     | 10970 |     |     |     |     | 10975 |     |     |     |     | 10980 |     |     |     |
| Gly | Arg   | Pro | Arg | Gly | Leu | Arg   | Arg | Asp | Pro | Arg | Lys   | Asn | Cys | Arg |
|     | 10985 |     |     |     |     | 10990 |     |     |     |     | 10995 |     |     |     |
| Tyr | Asp   | Lys | Pro | Ser | Gln | Arg   | Asp | Val | Pro | Gly | Gly   | Arg | Arg | Glu |
|     | 11000 |     |     |     |     | 11005 |     |     |     |     | 11010 |     |     |     |
| Phe | Glu   | Lys | Lys | His | Thr | Pro   | Pro | Glu | His | Trp | Ser   | Pro | Val | Lys |
|     | 11015 |     |     |     |     | 11020 |     |     |     |     | 11025 |     |     |     |
| Lys | Ser   | Gly | Arg | Gly | Ser | Asn   | Glu | Ala | Leu | Gln | Arg   | Ser | Leu | Ser |
|     | 11030 |     |     |     |     | 11035 |     |     |     |     | 11040 |     |     |     |
| Ser | Pro   | Ala | Lys | Arg | Cys | His   | Ala | Asp | Glu | Ala | Gln   | Asn | Phe | Gln |

11045

11050

11055

|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Val | Arg   | Lys | Lys | Cys | Asn | Tyr   | Ser | Pro | Pro | Ala | Gln   | Ala | Ala | Lys |
|     | 11060 |     |     |     |     | 11065 |     |     |     |     | 11070 |     |     |     |
| Leu | Pro   | Ile | Pro | Pro | Asp | Thr   | His | Thr | Lys | Pro | Gln   | Arg | Pro | Leu |
|     | 11075 |     |     |     |     | 11080 |     |     |     |     | 11085 |     |     |     |
| Thr | Glu   | Arg | Gln | Gln | Gln | Arg   | His | Thr | Thr | Gly | Ala   | Arg | Val | Arg |
|     | 11090 |     |     |     |     | 11095 |     |     |     |     | 11100 |     |     |     |
| Glu | Lys   | Thr | Glu | Leu | Pro | Val   | Arg | Pro | Leu | Ser | Ala   | Gln | Tyr | Ile |
|     | 11105 |     |     |     |     | 11110 |     |     |     |     | 11115 |     |     |     |
| Ala | Pro   | Asp | Leu | His | Arg | Lys   | Gly | Gln | Ser | Leu | Lys   | Ile | Pro | Ala |
|     | 11120 |     |     |     |     | 11125 |     |     |     |     | 11130 |     |     |     |
| Lys | Ser   | His | Thr | Pro | Ser | Thr   | Arg | Pro | Glu | Thr | Gly   | Asp | Thr | Leu |
|     | 11135 |     |     |     |     | 11140 |     |     |     |     | 11145 |     |     |     |
| Arg | Lys   | Ile | Arg | Ala | Leu | Pro   | Gln | Thr | Ala | Lys | Leu   | Pro | Ser | Phe |
|     | 11150 |     |     |     |     | 11155 |     |     |     |     | 11160 |     |     |     |
| Pro | Gly   | Ser | His | Ala | Thr | Ser   | Ser | Lys | His | Asp | Phe   | Gln | Ile | Pro |
|     | 11165 |     |     |     |     | 11170 |     |     |     |     | 11175 |     |     |     |
| Ser | Thr   | Val | Lys | Asn | Ile | Thr   | Arg | Pro | Ala | Pro | Asn   | Gly | Arg | Arg |
|     | 11180 |     |     |     |     | 11185 |     |     |     |     | 11190 |     |     |     |
| Ser | Arg   | Ser | Gln | Ser | Pro | Ser   | Ser | Leu | Pro | Lys | Phe   | Lys | Gln | Leu |
|     | 11195 |     |     |     |     | 11200 |     |     |     |     | 11205 |     |     |     |
| Ile | Cys   | Ile | Leu | Thr | Arg | Thr   | Lys | Ser | Leu | Arg | Tyr   | Ile | Ile | Asp |
|     | 11210 |     |     |     |     | 11215 |     |     |     |     | 11220 |     |     |     |

Asp

<210> 15  
 <211> 11142  
 <212> PRT  
 <213> Artificial Sequence  
  
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 <223> Artificially Synthesized  
  
 <220>  
 <221> misc\_feature  
 <222> (2011)..(2011)



<223> Xaa can be any naturally occurring amino acid

<400> 15

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Arg Glu Thr Gly Asp Arg  
20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Val Arg Arg Ser Arg Phe  
35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg  
50 55 60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
85 90 95

Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
115 120 125

Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
130 135 140

Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
145 150 155 160

Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
165 170 175

Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
180 185 190

Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
195 200 205

Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
210 215 220

Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
225 230 235 240

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Ser Met Pro Ser Thr Pro Pro Ile Asp Val Asn Asp Gly Lys Trp Pro  
245 250 255

Ala Trp His Tyr Ala Gln Tyr Met Thr Leu Trp Asp Phe Pro Thr Trp  
260 265 270

Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile Thr Met Val Met Arg Phe  
275 280 285

Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe Asp Ser Arg Gly Phe Pro  
290 295 300

Ser Leu His Pro Ile Asp Val Asn Gly Ser Leu Phe Trp His Gln Asn  
305 310 315 320

Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn Ser Ala Pro Leu Thr Gln  
325 330 335

Met Gly Gly Arg Arg Val Arg Trp Glu Val Tyr Ile Ser Arg Ala Arg  
340 345 350

Leu Val Asn Arg Gln Ile Thr Arg Ser Phe Ile Ala Val Val Tyr His  
355 360 365

Ser Ile Ala Asn Ala Val Ser Ala Ser Asp Thr Thr Val Ser Asn Leu  
370 375 380

Arg Leu Glu Tyr Leu Ile Arg Leu Thr Ile Gly Leu Arg Leu Glu Phe  
385 390 395 400

Asp Ala Thr Met Arg Val Met Gly Ile Leu Arg Ser Tyr Gln Gln Trp  
405 410 415

Trp Ile Trp Gly Ile Leu Gly Phe Trp Met Leu Met Ile Cys Asn Val  
420 425 430

Trp Gly Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys  
435 440 445

Glu Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala His Lys  
450 455 460

Glu Glu Val His Asn Ile Trp Ala Thr His Ala Cys Val Pro Thr Asp  
465 470 475 480

Pro Asn Pro Gln Glu Ile Val Leu Lys Asn Val Thr Glu Asn Phe Asn  
485 490 495

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Met Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser  
500 505 510

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys  
515 520 525

Val Thr Leu Asn Cys Ser Asp Val Lys Ile Lys Gly Thr Asn Ala Thr  
530 535 540

Tyr Asn Asn Ala Thr Tyr Asn Asn Asn Asn Thr Ile Ser Asp Met Lys  
545 550 555 560

Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Thr Asp Lys Lys Lys Lys  
565 570 575

Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Ala Leu Asp Gly Lys  
580 585 590

Glu Thr Asn Ser Thr Asn Ser Ser Glu Tyr Arg Leu Ile Asn Cys Asn  
595 600 605

Thr Ser Ala Val Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile  
610 615 620

Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn  
625 630 635 640

Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val  
645 650 655

Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu  
660 665 670

Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Phe Glu Asn Leu  
675 680 685

Thr Asn Asn Ala Lys Ile Ile Ile Val His Leu Asn Glu Ser Val Glu  
690 695 700

Ile Asn Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Val Arg Ile  
705 710 715 720

Gly Pro Gly Gln Thr Phe Phe Ala Thr Gly Asp Ile Ile Gly Asp Ile  
725 730 735

Arg Gln Ala His Cys Asn Ile Ser Arg Lys Lys Trp Asn Thr Thr Leu

740

745

750

Gln Arg Val Lys Glu Lys Leu Lys Glu Lys Phe Pro Asn Lys Thr Ile  
 755 760 765

Gln Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser  
 770 775 780

Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Tyr Thr Ser Asp Leu Phe  
 785 790 795 800

Asn Ser Thr Tyr Met Ser Asn Asn Thr Gly Gly Ala Asn Ile Thr Leu  
 805 810 815

Gln Cys Arg Ile Lys Gln Ile Ile Arg Met Trp Gln Gly Val Gly Gln  
 820 825 830

Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn  
 835 840 845

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Glu Lys Asn Asp  
 850 855 860

Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg  
 865 870 875 880

Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile  
 885 890 895

Ala Pro Asp Lys Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala  
 900 905 910

Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser  
 915 920 925

Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu  
 930 935 940

Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu  
 945 950 955 960

Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu  
 965 970 975

Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu  
 980 985 990

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Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val  
 995 1000 1005

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Tyr Glu Glu Ile Trp  
 1010 1015 1020

Gly Asn Met Thr Trp Met Gln Trp Asp Arg Glu Ile Asn Asn Tyr  
 1025 1030 1035

Thr Asn Thr Ile Tyr Ser Leu Leu Glu Glu Ser Gln Asn Gln Gln  
 1040 1045 1050

Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Glu Ser  
 1055 1060 1065

Leu Trp Ser Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Arg  
 1070 1075 1080

Ile Phe Ile Ile Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile  
 1085 1090 1095

Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser  
 1100 1105 1110

Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser Pro Arg Glu Pro Asp  
 1115 1120 1125

Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Ala  
 1130 1135 1140

Arg Ser Val Arg Leu Val Asn Gly Phe Leu Ala Leu Ala Trp Glu  
 1145 1150 1155

Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp  
 1160 1165 1170

Leu Ile Leu Ile Ala Ala Arg Ala Ala Ala Leu Leu Gly Arg Ser  
 1175 1180 1185

Ser Leu Trp Gly Leu Gln Lys Gly Trp Glu Ala Leu Lys Tyr Leu  
 1190 1195 1200

Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala  
 1205 1210 1215

Ile Ser Leu Phe Asp Ala Ile Ala Ile Thr Val Ala Glu Gly Thr  
 1220 1225 1230

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp | Arg  | Ile | Ile | Asn | Ile | Val  | Gln | Arg | Ile | Ser | Arg  | Ala | Phe | Tyr |
|     | 1235 |     |     |     |     | 1240 |     |     |     |     | 1245 |     |     |     |
| Asn | Ile  | Pro | Arg | Arg | Ile | Arg  | Gln | Gly | Phe | Glu | Ala  | Thr | Leu | Gln |
|     | 1250 |     |     |     |     | 1255 |     |     |     |     | 1260 |     |     |     |
| Gly | Thr  | Ser | Arg | Val | Asp | Pro  | Gly | Gly | Gln | Thr | Ala  | Asp | Gln | Pro |
|     | 1265 |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |
| Arg | Leu  | Cys | Leu | Leu | Val | Ala  | Ser | His | Leu | Leu | Phe  | Ala | Pro | Pro |
|     | 1280 |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |
| Pro | Cys  | Leu | Pro | Pro | Trp | Lys  | Val | Pro | Leu | Pro | Leu  | Ser | Phe | Pro |
|     | 1295 |     |     |     |     | 1300 |     |     |     |     | 1305 |     |     |     |
| Asn | Lys  | Met | Arg | Lys | Leu | His  | Arg | Ile | Val | Val | Gly  | Val | Ile | Leu |
|     | 1310 |     |     |     |     | 1315 |     |     |     |     | 1320 |     |     |     |
| Phe | Trp  | Gly | Val | Gly | Trp | Gly  | Arg | Thr | Ala | Arg | Gly  | Arg | Ile | Gly |
|     | 1325 |     |     |     |     | 1330 |     |     |     |     | 1335 |     |     |     |
| Lys | Thr  | Ile | Ala | Gly | Met | Leu  | Gly | Met | Arg | Trp | Ala  | Leu | Trp | Leu |
|     | 1340 |     |     |     |     | 1345 |     |     |     |     | 1350 |     |     |     |
| Leu | Arg  | Arg | Lys | Glu | Pro | Ala  | Asp | Leu | Gln | Ile | Ile  | His | Leu | Cys |
|     | 1355 |     |     |     |     | 1360 |     |     |     |     | 1365 |     |     |     |
| Arg | Val  | Arg | Arg | Lys | Arg | Asn  | Gly | Ile | Met | Gly | Ile  | Met | Gly | Leu |
|     | 1370 |     |     |     |     | 1375 |     |     |     |     | 1380 |     |     |     |
| His | Ile  | Gly | Gln | Ile | Ser | Ile  | Cys | Trp | Pro | Pro | Cys  | Met | Pro | Arg |
|     | 1385 |     |     |     |     | 1390 |     |     |     |     | 1395 |     |     |     |
| Thr | Pro  | Ala | Arg | His | Gly | Pro  | Ser | Ser | Ser | Thr | Thr  | Ser | Pro | Asp |
|     | 1400 |     |     |     |     | 1405 |     |     |     |     | 1410 |     |     |     |
| Ala | Met  | Cys | Thr | Trp | Gly | Pro  | Ala | Glu | Ala | Cys | Ser  | Cys | Pro | Thr |
|     | 1415 |     |     |     |     | 1420 |     |     |     |     | 1425 |     |     |     |
| Ser | Ala  | Thr | Cys | Asn | Leu | Arg  | Cys | Cys | Trp | Ser | Pro  | Met | Pro | Cys |
|     | 1430 |     |     |     |     | 1435 |     |     |     |     | 1440 |     |     |     |
| Pro | Glu  | Ala | Arg | Gly | Cys | Leu  | Thr | Met | Trp | Ser | Cys  | Gly | Lys | Phe |
|     | 1445 |     |     |     |     | 1450 |     |     |     |     | 1455 |     |     |     |
| Asp | Met  | Met | Asn | Pro | Arg | Pro  | Gly | Ala | Gly | Pro | Ala  | Asn | Ala | Glu |
|     | 1460 |     |     |     |     | 1465 |     |     |     |     | 1470 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala  | Ser | Thr | Pro | Gly | Phe | Ser  | Pro | Cys | Val | Trp | Arg  | Arg | Arg | Thr |
| 1475 |     |     |     |     |     | 1480 |     |     |     |     | 1485 |     |     |     |
| Cys  | Asp | Pro | Ile | Ile | Trp | Cys  | Cys | Pro | Ala | Thr | Gly  | Arg | Ser | Ser |
| 1490 |     |     |     |     |     | 1495 |     |     |     |     | 1500 |     |     |     |
| Ala  | Pro | Ala | Gly | Lys | Asn | Leu  | Thr | Arg | Val | Ser | Ser  | Val | Trp | Gly |
| 1505 |     |     |     |     |     | 1510 |     |     |     |     | 1515 |     |     |     |
| Arg  | Trp | Arg | Ala | Cys | Met | Arg  | Gly | Arg | Met | Thr | Lys  | Ile | Cys | Val |
| 1520 |     |     |     |     |     | 1525 |     |     |     |     | 1530 |     |     |     |
| Phe  | Leu | Cys | Val | Ala | Ala | Ala  | Ala | Glu | Ala | Pro | Pro  | Leu | Arg | Glu |
| 1535 |     |     |     |     |     | 1540 |     |     |     |     | 1545 |     |     |     |
| Gly  | Tyr | Ser | Ala | Leu | Ile | Arg  | Gly | Val | Ser | Pro | Pro  | Gly | Arg | Glu |
| 1550 |     |     |     |     |     | 1555 |     |     |     |     | 1560 |     |     |     |
| Cys  | Val | Arg | Met | Trp | Asp | Pro  | Arg | Trp | Thr | Ala | Gly  | Pro | Cys | Ser |
| 1565 |     |     |     |     |     | 1570 |     |     |     |     | 1575 |     |     |     |
| Pro  | Arg | Thr | Leu | Gln | Pro | Pro  | Thr | Arg | Pro | Ala | Pro  | Arg | Pro | Trp |
| 1580 |     |     |     |     |     | 1585 |     |     |     |     | 1590 |     |     |     |
| Thr  | Gln | Leu | Pro | Pro | Gln | Leu  | Leu | Leu | Pro | Pro | Pro  | Ala | Pro | Cys |
| 1595 |     |     |     |     |     | 1600 |     |     |     |     | 1605 |     |     |     |
| Ala  | Glu | Trp | Pro | Trp | Ala | Pro  | Ala | Thr | Thr | Ala | Leu  | Trp | Trp | Pro |
| 1610 |     |     |     |     |     | 1615 |     |     |     |     | 1620 |     |     |     |
| Thr  | Arg | Leu | Pro | Pro | Ile | Ile  | Pro | Pro | Ala | Thr | Arg  | Arg | Ser | Cys |
| 1625 |     |     |     |     |     | 1630 |     |     |     |     | 1635 |     |     |     |
| Cys  | Cys | Trp | Pro | Ser | Ser | Arg  | Pro | Pro | Ser | Ala | Trp  | Ala | Ser | Pro |
| 1640 |     |     |     |     |     | 1645 |     |     |     |     | 1650 |     |     |     |
| Ser  | Arg | Trp | Leu | Ser | Cys | Arg  | Arg | Arg | Arg | Gly | Pro  | Arg | Leu | Pro |
| 1655 |     |     |     |     |     | 1660 |     |     |     |     | 1665 |     |     |     |
| Arg  | Lys | Pro | Asn | Lys | Lys | Ile  | Asn | Lys | Thr | Glu | Thr  | Val | Val | Asp |
| 1670 |     |     |     |     |     | 1675 |     |     |     |     | 1680 |     |     |     |
| Phe  | Asn | Thr | Glu | Ser | Ile | Phe  | Ile | Phe | Phe | Ala | Arg  | Gly | Arg | Pro |
| 1685 |     |     |     |     |     | 1690 |     |     |     |     | 1695 |     |     |     |
| Trp  | Thr | Thr | Gly | Leu | Asp | His  | Ala | Pro | Gly | Gly | Phe  | Phe | Pro | Gly |

1700

1705

1710

Pro Gly Arg Gly Gly Leu Gly Cys Gly Thr Trp Ala Ala Arg Pro  
 1715 1720 1725

Gly Gly Gly Gly Ser Ser Ile Ala Gly Pro Arg Ala Arg Gly Trp  
 1730 1735 1740

Cys Cys Lys Ser Pro Ser His Ser Arg Gly Ala Gly Arg Gly Ala  
 1745 1750 1755

Ala Arg Cys Pro Gly Gly Asp Trp Pro Arg Ala Ala Pro Trp Cys  
 1760 1765 1770

Arg Cys Arg Thr Cys Ala Gly Arg Asp Ala Cys Gly Gly Arg Asp  
 1775 1780 1785

Ala Ser Trp Pro Gly Ser Asp Trp Arg Cys Ser Arg Pro Asp Pro  
 1790 1795 1800

Ala Gly Gly Ser Cys Cys Ala Gly Pro Pro Ala Arg Cys Ile Arg  
 1805 1810 1815

Arg Thr Trp Gly Ile Cys His Ala Thr Trp Lys Gly Arg Arg Glu  
 1820 1825 1830

Arg Ile Trp Arg Arg Pro Cys Asp Arg Pro Gly Phe Pro Cys Thr  
 1835 1840 1845

His Pro Trp Arg Trp Ala Arg Gly Arg Arg Pro Gly Gln Arg Arg  
 1850 1855 1860

Phe Gly Gly Arg Thr His Arg Ser Cys Gly Pro Gly Ala Arg His  
 1865 1870 1875

Arg Pro Phe Ile Trp Gly Gly Gly Cys Pro Thr Gly Gly Arg Arg  
 1880 1885 1890

Cys Pro Arg Ser Arg Gly Arg Ser Cys Pro Arg Arg Ser Ala Ser  
 1895 1900 1905

Pro Arg Pro Ala Arg Arg Gly Gly Ser Cys Pro Pro Ala Gly Arg  
 1910 1915 1920

Lys Lys Arg Phe Pro Gly Arg Gly Arg Ala Gly Pro Lys Ala Gly  
 1925 1930 1935



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Ser Gly Ala Ala Gly Thr Cys Arg Ser Arg Trp Gly Arg Arg Pro  
 1940 1945 1950  
 Arg Pro Ala Ala Gly Gly Ser Gly Arg Asp Ser Cys Arg Pro Arg  
 1955 1960 1965  
 Gly Gly Gly Gly Pro Pro Arg Ser Ser Ser Arg Ala His Ala Cys  
 1970 1975 1980  
 Ser Arg Ala Arg Val Pro Pro Gly Gly Ala Arg Pro Pro Ala Arg  
 1985 1990 1995  
 Gly Ala Leu Ala Ala Arg Arg Ser Phe Ser Ala Ala Xaa Arg Arg  
 2000 2005 2010  
 Pro Trp Ala Phe Trp Arg Gly Ser Val Ala Arg Val Pro Asp Gly  
 2015 2020 2025  
 Pro Arg Ala Arg Cys Ala Leu Gly His Leu Asp Pro Ala Asp Leu  
 2030 2035 2040  
 Leu Val Ser Arg Val Gly Ala Thr Ala Gly Val Gly His Gln Ala  
 2045 2050 2055  
 Met Gly Val Gln Arg Gly Gln Gly Pro Val Leu Pro Gly Ser Gln  
 2060 2065 2070  
 Gly Pro Arg Gln Arg Gly Leu Arg His Gly Glu Gly Val Arg Ala  
 2075 2080 2085  
 Gly Leu Gly Ala Cys Glu Gly Ala Leu Gln Ala His Pro Ala Gly  
 2090 2095 2100  
 Arg Glu Pro Leu Pro Val Gly Ala Leu Arg Val Gly Gln Val Ala  
 2105 2110 2115  
 Ile Glu His Glu Phe Val Val Glu Arg Leu Gly Arg Val Ala Leu  
 2120 2125 2130  
 Gly Ala Glu Leu Thr Phe Gly Ser Val Ser Ala Asp Gly Thr Glu  
 2135 2140 2145  
 Glu Gly Leu Glu Gly Val Glu Leu Gly Gly Glu Glu Asp Gly Leu  
 2150 2155 2160  
 Gly Gly Val Gly Val Arg Ala Ala Ala Gly Ala Asp Gly Leu Ala  
 2165 2170 2175

## 368530-7006W01\_SequenceListing\_ST25.txt

Leu His Glu Pro Gly Glu Val Gly Pro Val Gly Val Lys Asn Glu  
 2180 2185 2190  
 Val Ser Ser Val Leu Phe Asp Ala Phe Leu Thr Ser Gly Leu His  
 2195 2200 2205  
 Glu Leu Val Ser Pro Leu Gly Asp Lys Glu Ala Val Arg Val Pro  
 2210 2215 2220  
 Val Asp Arg Leu Tyr Gly Pro Val Leu Glu Arg Gly Ala Ala Val  
 2225 2230 2235  
 Leu Val Val Glu Glu Pro Arg Pro Leu Arg Asp Glu Gly Pro Gly  
 2240 2245 2250  
 Pro Gly Gln His Glu Gly Gly His Val Gly Gly Val Ala Val Val  
 2255 2260 2265  
 Val His Gln Arg Val His Leu Leu Gln Gly Met Gln Ala His Val  
 2270 2275 2280  
 Pro Leu Val His Ile Gln Glu Gly Asp Trp Leu Val Ser Val Gly  
 2285 2290 2295  
 His Val Thr Gly Gly Pro Gly Arg Gly Gly Ile Lys Gly Gly Gly  
 2300 2305 2310  
 Pro Leu Leu Val Leu Thr Val Phe Arg Ile Ala Val Gln Glu Arg  
 2315 2320 2325  
 Gln Leu Leu Gly Val Phe Pro Leu Glu Gly Trp His Asn Leu Gly  
 2330 2335 2340  
 Thr Gln Val Val Ser Phe Lys Arg Gly Gly Phe Asp Ile Asp Gly  
 2345 2350 2355  
 Ala Val Gly Asp Ala Phe His Glu Pro Leu Val His Leu Val Arg  
 2360 2365 2370  
 Lys Asp Asp Leu Phe Val Val Glu Leu Gly Gly Glu Gly Ala Val  
 2375 2380 2385  
 Glu Gly Val Gly Glu Glu Leu Gly Asp Gly Ala His Gly Leu Val  
 2390 2395 2400  
 Leu Phe Leu Val Gly Ala Leu Leu Gly Gly Asp Val Glu Leu His  
 2405 2410 2415

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | Leu | Ala | Arg | His | Ala | Leu  | Pro | Phe | Gly | Glu | Asp  | Gly | Gly | Glu |
| 2420 |     |     |     |     |     | 2425 |     |     |     |     | 2430 |     |     |     |
| Leu  | Val | Gly | His | Asp | Ser | Asp  | Pro | Pro | Ala | Ala | Val  | Val | Gln | Gly |
| 2435 |     |     |     |     |     | 2440 |     |     |     |     | 2445 |     |     |     |
| Asp  | Glu | Val | His | Ala | Gly | Gly  | His | Leu | Ala | Ala | Gln  | Gly | Leu | Val |
| 2450 |     |     |     |     |     | 2455 |     |     |     |     | 2460 |     |     |     |
| Gly  | Pro | Ala | Glu | Ala | Pro | Ala  | Leu | Ala | Arg | Ala | Glu  | Gly | Gly | Gln |
| 2465 |     |     |     |     |     | 2470 |     |     |     |     | 2475 |     |     |     |
| Arg  | Val | Gln | His | Glu | Leu | Val  | Gly | Gly | Val | Gly | Val  | His | Gly | Glu |
| 2480 |     |     |     |     |     | 2485 |     |     |     |     | 2490 |     |     |     |
| Asp  | Ala | Gly | Gln | Lys | Leu | Gly  | Val | Glu | Val | Ala | Asp  | Ala | Gly | Val |
| 2495 |     |     |     |     |     | 2500 |     |     |     |     | 2505 |     |     |     |
| Gln  | Ile | Val | Gln | Arg | Arg | Leu  | Pro | Val | Ala | His | Gly  | Gln | Arg | Ala |
| 2510 |     |     |     |     |     | 2515 |     |     |     |     | 2520 |     |     |     |
| Leu  | Val | Gly | Ala | Glu | Gly | Arg  | Ala | Pro | Gly | His | Gly  | Val | Arg | Glu |
| 2525 |     |     |     |     |     | 2530 |     |     |     |     | 2535 |     |     |     |
| Arg  | Gly | Gly | Val | His | Ala | Ala  | Asp | Val | Val | Asp | Val  | Glu | Gly | Leu |
| 2540 |     |     |     |     |     | 2545 |     |     |     |     | 2550 |     |     |     |
| Leu  | Glu | Asp | Ala | Asp | Val | Gly  | Gly | Val | Ala | Ala | Pro  | Pro | Ala | Asp |
| 2555 |     |     |     |     |     | 2560 |     |     |     |     | 2565 |     |     |     |
| Ala  | Gly | Ala | His | Val | Val | Val  | Gln | Leu | Val | Arg | Gly  | Arg | Glu | Glu |
| 2570 |     |     |     |     |     | 2575 |     |     |     |     | 2580 |     |     |     |
| Pro  | Arg | Ala | Glu | Val | Gly | Ala  | Leu | Arg | Leu | Phe | Gly  | Ala | Val | Asp |
| 2585 |     |     |     |     |     | 2590 |     |     |     |     | 2595 |     |     |     |
| Asp  | Leu | Ala | Glu | Asp | Gly | Val  | Gly | Val | Gly | Gly | Asp  | Gly | Gly | Pro |
| 2600 |     |     |     |     |     | 2605 |     |     |     |     | 2610 |     |     |     |
| Leu  | Glu | Asp | Val | Glu | Val | Gly  | Val | Gly | Gln | Ala | Asp  | Arg | Val | Pro |
| 2615 |     |     |     |     |     | 2620 |     |     |     |     | 2625 |     |     |     |
| Asp  | Glu | Val | Gly | Val | Gly | Val  | Leu | Gln | Leu | Gly | Asp  | Glu | Leu | Gly |
| 2630 |     |     |     |     |     | 2635 |     |     |     |     | 2640 |     |     |     |
| Gly  | Asp | Glu | Asp | Val | Gln | Gly  | Ala | Val | Val | Glu | Gly  | Leu | Leu | Asp |

2645

2650

2655

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp | Val  | Val | Leu | Glu | Leu | Ala  | Leu | Leu | Leu | Pro | Gln  | Leu | Ala | Val |
|     | 2660 |     |     |     |     | 2665 |     |     |     |     | 2670 |     |     |     |
| Glu | Lys  | Glu | Leu | Phe | Ala | Val  | Leu | Pro | Val | Leu | Phe  | Glu | Gly | Glu |
|     | 2675 |     |     |     |     | 2680 |     |     |     |     | 2685 |     |     |     |
| Pro | Val  | Leu | Ile | Gly | Thr | Val  | Arg | Ala | His | His | Val  | Glu | Leu | Val |
|     | 2690 |     |     |     |     | 2695 |     |     |     |     | 2700 |     |     |     |
| Asp | Gly  | Leu | Val | Gly | Ala | Ala  | Ala | Leu | Leu | His | Gly  | Glu | Gly | Val |
|     | 2705 |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |
| Ser | Leu  | Cys | Gly | Leu | Ala | Gln  | Gly | Gly | Val | Gly | Glu  | Gly | Glu | Gly |
|     | 2720 |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |
| Val | Ala  | His | His | Asp | Leu | Glu  | Glu | Leu | Val | Leu | Glu  | Val | Glu | Val |
|     | 2735 |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |
| Val | Ala  | Ala | Ala | Leu | Leu | Pro  | Glu | Leu | Glu | Val | Arg  | Ala | Leu | Leu |
|     | 2750 |     |     |     |     | 2755 |     |     |     |     | 2760 |     |     |     |
| Val | Gly  | Gly | Val | Gly | Gln | Ser  | Glu | Ser | Asn | Ile | Val  | Glu | Glu | Asp |
|     | 2765 |     |     |     |     | 2770 |     |     |     |     | 2775 |     |     |     |
| Leu | Ala  | Arg | Ala | Gly | His | Glu  | Val | Ala | Ser | Asp | Ala  | Glu | Arg | Leu |
|     | 2780 |     |     |     |     | 2785 |     |     |     |     | 2790 |     |     |     |
| Gly | His  | Leu | Gly | Pro | Val | Val  | Asp | Asp | Leu | Gly | Gly  | Glu | Asp | Asp |
|     | 2795 |     |     |     |     | 2800 |     |     |     |     | 2805 |     |     |     |
| Leu | Val  | Glu | Ala | Val | Asp | Val  | Val | Pro | Asp | Asp | Val  | Glu | Phe | His |
|     | 2810 |     |     |     |     | 2815 |     |     |     |     | 2820 |     |     |     |
| Glu | Ser  | Arg | Ala | Ala | Leu | Asn  | Val | Gly | Gln | Leu | Leu  | Glu | Leu | Val |
|     | 2825 |     |     |     |     | 2830 |     |     |     |     | 2835 |     |     |     |
| Val | Gly  | Glu | Leu | Gly | Gly | Val  | Ala | Glu | Pro | Val | Leu  | Leu | Glu | Gly |
|     | 2840 |     |     |     |     | 2845 |     |     |     |     | 2850 |     |     |     |
| Pro | Val  | Gly | Asp | Val | Gly | Val  | Gly | Ala | Glu | Glu | Gly  | Ser | Pro | Glu |
|     | 2855 |     |     |     |     | 2860 |     |     |     |     | 2865 |     |     |     |
| Ile | His  | Gly | Gln | Gly | Gly | Leu  | Gln | Ala | Val | Pro | Val  | Leu | Thr | Glu |
|     | 2870 |     |     |     |     | 2875 |     |     |     |     | 2880 |     |     |     |

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Leu Leu Ala His Gly His Phe Phe Gly Gly Asp Ala Val Glu Gly  
 2885 2890 2895  
  
 Ala Gly Val Ala Val Pro Ala Val Pro Leu Glu Leu Glu Gly Glu  
 2900 2905 2910  
  
 Val Val Gly Glu Leu Asp Glu Arg Arg Val Pro Gly Glu Phe His  
 2915 2920 2925  
  
 Asp Gln His Glu Gly Asp Glu Leu Leu Ala Glu Gly Pro His Pro  
 2930 2935 2940  
  
 Gly Val Gly Phe His Ile Val Gly Glu Glu Glu Pro Phe Gly Ala  
 2945 2950 2955  
  
 Arg Met Arg Ala Asp Gly Glu Glu Leu Asp Leu Leu Pro Pro Val  
 2960 2965 2970  
  
 Gly Gly Met Ala Val Asp Val Met Glu Val Glu Met Pro Thr Ala  
 2975 2980 2985  
  
 Arg Arg Ala Leu Val Leu Val Phe Ile Gln Ala Ser Ala Val Leu  
 2990 2995 3000  
  
 Ala Thr Leu His Gly Met His Val Leu His Glu Leu Tyr Leu Gly  
 3005 3010 3015  
  
 Ser Phe Asp Glu Glu Phe Gln Trp Ala Val Glu Arg Trp Arg Leu  
 3020 3025 3030  
  
 His Leu Val Leu Tyr Tyr Val Leu Ala Ile Gly Val Ala Ile Val  
 3035 3040 3045  
  
 Cys Leu Asp Gly Gly His Ala Asp Glu Pro Ala Arg Glu Ala Gly  
 3050 3055 3060  
  
 Pro Asp Phe Gly Ser Asp Gly Ser Glu Ser Glu Asp Glu Gly Ala  
 3065 3070 3075  
  
 Gln Ala Gly Ala Val Gln Gly Pro Glu Thr Leu Arg Ser Gln Val  
 3080 3085 3090  
  
 Ser Gly Gln Arg Arg Arg Ala Val Asp Leu Gln Glu Leu Phe Gln  
 3095 3100 3105  
  
 Gly Ala Arg Glu Val Gln Met Val Leu Asp Leu His Gly Ala Val  
 3110 3115 3120

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Gly Gly Asp Val His Gly Leu Gln Gly Pro Val Pro Leu Gly Arg  
 3125 3130 3135  
 His His Arg Ala Pro Phe Leu Leu Gly Arg Cys Phe His Ala Gly  
 3140 3145 3150  
 Gln Lys Arg Arg Arg Gly Arg Ala Pro Gly Gly Arg Gly Gly Ser  
 3155 3160 3165  
 Gly Pro Gly Gly Arg Gly Gly Arg Gly Thr Ser Ala Pro Arg Ala  
 3170 3175 3180  
 Gly Arg Phe Trp Tyr Cys Ala Arg Arg Arg Leu Ala Ala Thr Thr  
 3185 3190 3195  
 Arg Arg Leu Thr Ser Trp Ile Arg Leu Trp Val Lys Ala Thr Gly  
 3200 3205 3210  
 Pro Val Ser Leu Asn Leu Lys Glu Ser Ser Thr Glu Ser Ile Ser  
 3215 3220 3225  
 Val Ser Leu Thr Ala Ala Cys Arg Arg Ile Ser Cys Thr Ser Pro  
 3230 3235 3240  
 Glu Leu Ser Trp Ala Ile Ser Val Met Asn Cys Ser Ile Ser Ser  
 3245 3250 3255  
 Ser Arg Ser Pro Arg Pro Ala Arg Ser Thr Val Ala Ala Arg Ser  
 3260 3265 3270  
 Leu Glu Met Arg Pro Met Ser Cys Glu Lys Ala Phe Met Pro Ala  
 3275 3280 3285  
 Ser Phe Gln Thr Arg Leu Thr Thr Ala Pro Ser Gly Ser Arg Ala  
 3290 3295 3300  
 Arg Met Thr Thr Trp Ala Arg Leu Ser Ser Thr Trp Arg Val Lys  
 3305 3310 3315  
 Thr Ala Leu Gln Arg Arg Trp Arg Leu Ser Val Val Ala Met Cys  
 3320 3325 3330  
 Ser Val Thr Lys Lys Tyr Met Ile Gln Arg Arg Ser Gly Ile Ser  
 3335 3340 3345  
 Leu Thr Ser Pro Arg Ala Ser Lys Arg Ser Met Ala Ser Lys Ser  
 3350 3355 3360

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Ala  | Lys | Leu | Lys | Asn | Trp  | Glu | Leu | Arg | Ala | Glu  | Thr | Val | Asn |
|     | 3365 |     |     |     |     | 3370 |     |     |     |     | 3375 |     |     |     |
| Ser | Ser  | Ser | Arg | Arg | Arg | Met  | Ser | Ser | Ala | Met | Val  | Ala | Arg | Thr |
|     | 3380 |     |     |     |     | 3385 |     |     |     |     | 3390 |     |     |     |
| Ser | Arg  | Ser | Lys | Ala | Pro | Gly  | Gly | Ser | Ser | Ser | Ser  | Ile | Ser | Ser |
|     | 3395 |     |     |     |     | 3400 |     |     |     |     | 3405 |     |     |     |
| Ser | Ser  | Thr | Asn | Ile | Ser | Ser  | Thr | Ser | Ser | Ser | Gly  | Gly | Gly | Gly |
|     | 3410 |     |     |     |     | 3415 |     |     |     |     | 3420 |     |     |     |
| Gly | Gly  | Gly | Ala | Leu | Arg | Arg  | Arg | Arg | Arg | Thr | Gly  | Arg | Arg | Ser |
|     | 3425 |     |     |     |     | 3430 |     |     |     |     | 3435 |     |     |     |
| Met | Lys  | Arg | Ser | Met | Val | Ser  | Pro | Arg | Arg | Arg | Arg  | Met | Val | Ser |
|     | 3440 |     |     |     |     | 3445 |     |     |     |     | 3450 |     |     |     |
| Val | Thr  | Ala | Arg | Pro | Ser | Ser  | Arg | Gly | Arg | Ser | Val  | Lys | Thr | Pro |
|     | 3455 |     |     |     |     | 3460 |     |     |     |     | 3465 |     |     |     |
| Pro | Arg  | Ile | Ser | Arg | Trp | Pro  | Pro | Gly | Gly | Ser | Pro  | Leu | Gly | Arg |
|     | 3470 |     |     |     |     | 3475 |     |     |     |     | 3480 |     |     |     |
| Glu | Arg  | Ala | Leu | Thr | Met | His  | Leu | Ile | Asn | Trp | Pro  | Val | Gly | Thr |
|     | 3485 |     |     |     |     | 3490 |     |     |     |     | 3495 |     |     |     |
| Pro | Arg  | Lys | Asp | Leu | Ser | Val  | Ser | Arg | Ser | Thr | Gly  | Ser | Glu | Asn |
|     | 3500 |     |     |     |     | 3505 |     |     |     |     | 3510 |     |     |     |
| Arg | Thr  | Lys | Ala | Ser | Ser | Gln  | Ser | Gln | Ser | Gln | Gly  | Arg | Leu | Ser |
|     | 3515 |     |     |     |     | 3520 |     |     |     |     | 3525 |     |     |     |
| Pro | Val  | Ser | Cys | Ser | Ser | Gly  | Ile | Ser | Gly | Gly | Gly  | Arg | Ala | Met |
|     | 3530 |     |     |     |     | 3535 |     |     |     |     | 3540 |     |     |     |
| Leu | Leu  | Val | Met | Lys | Leu | Lys  | Ala | Val | Leu | Arg | Arg  | Arg | Met | Val |
|     | 3545 |     |     |     |     | 3550 |     |     |     |     | 3555 |     |     |     |
| Ala | Arg  | Ser | Thr | Arg | Ser | Leu  | Gly | Pro | Ala | Cys | Trp  | Met | Arg | Arg |
|     | 3560 |     |     |     |     | 3565 |     |     |     |     | 3570 |     |     |     |
| Arg | Ser  | Ala | Met | Pro | Gln | Ala  | Trp | Ser | His | Leu | Ala  | Arg | Ser | Leu |
|     | 3575 |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
| Ser | Cys  | Met | Ser | Arg | Ser | Thr  | Gly | Thr | Ser | Ser | Ser  | Pro | Ala | Arg |

3590

3595

3600

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Cys  | Met | Arg | Val | Ser | Pro  | Asn | Pro | Arg | Trp | Gly  | Trp | Thr | Ser |
|     | 3605 |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |
| Ala | Arg  | Ser | Ala | Thr | Thr | Arg  | Ser | Ala | Arg | Met | Ala  | Cys | Cys | Ile |
|     | 3620 |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
| Trp | Val  | Arg | Val | Val | Trp | Lys  | Ser | Ser | Lys | Ser | Thr  | Lys | Arg | Trp |
|     | 3635 |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
| Ala | Pro  | Val | Leu | Met | Val | Glu  | Gln | Leu | Ala | Met | Thr  | Asp | Gln | Leu |
|     | 3650 |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
| Thr | Val  | Trp | Trp | Pro | Gly | Arg  | Thr | Ser | Ser | Trp | Tyr  | Leu | Arg | Arg |
|     | 3665 |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
| Glu | Ala  | Arg | Val | Ser | Lys | Met  | Ser | Leu | Gln | Val | Arg  | Thr | Arg | Tyr |
|     | 3680 |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |
| Trp | Tyr  | Pro | Thr | Arg | Lys | Cys  | Gly | Gly | Gly | Trp | Arg  | Ser | Gly | His |
|     | 3695 |     |     |     |     | 3700 |     |     |     |     | 3705 |     |     |     |
| Arg | Ser  | Val | Ala | Gly | Ala | Pro  | Gly | Ala | Arg | Ser | Ser  | Ser | Met | Arg |
|     | 3710 |     |     |     |     | 3715 |     |     |     |     | 3720 |     |     |     |
| Arg | Trp  | Pro | Met | Tyr | Leu | Asp  | Ile | Gln | Val | Met | Pro  | Ala | Ala | Val |
|     | 3725 |     |     |     |     | 3730 |     |     |     |     | 3735 |     |     |     |
| Val | Glu  | Ala | Arg | Gly | Asn | Ser  | Arg | Thr | Arg | Phe | Gln  | Met | Leu | Arg |
|     | 3740 |     |     |     |     | 3745 |     |     |     |     | 3750 |     |     |     |
| Ser | Gly  | Arg | Lys | Phe | Met | Val  | Ala | Ala | Val | Trp | Pro  | Val | Arg | Arg |
|     | 3755 |     |     |     |     | 3760 |     |     |     |     | 3765 |     |     |     |
| Ala | Gln  | Ser | Trp | Met | Leu | Thr  | Tyr | Gly | Gln | Lys | Arg  | Lys | Arg | Ser |
|     | 3770 |     |     |     |     | 3775 |     |     |     |     | 3780 |     |     |     |
| Ala | Ala  | Arg | Leu | Arg | Gly | Leu  | Glu | Ala | Lys | Arg | Thr  | Gly | Trp | Ala |
|     | 3785 |     |     |     |     | 3790 |     |     |     |     | 3795 |     |     |     |
| Ala | Arg  | Val | Pro | Arg | Phe | Glu  | Ser | Arg | Ile | Arg | Leu  | Glu | Pro | Gln |
|     | 3800 |     |     |     |     | 3805 |     |     |     |     | 3810 |     |     |     |
| Leu | Thr  | Trp | Tyr | Trp | His | Ser  | Arg | Leu | Asp | Pro | Ser  | Leu | Leu | Thr |
|     | 3815 |     |     |     |     | 3820 |     |     |     |     | 3825 |     |     |     |



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Lys Pro Pro Gly Tyr Gly Gly Gly Ser Phe Phe Gly Leu Gly Arg  
 3830 3835 3840  
 Trp Ser Lys Thr Ser Lys Arg Gly Lys Arg Pro Pro Ala Met Ala  
 3845 3850 3855  
 Arg Cys Arg Ser Leu Glu Lys Glu Ser Pro Gly Leu Arg Cys Gly  
 3860 3865 3870  
 Val Pro Arg Phe Glu Pro Gln Arg Ser Ala Pro Ala Gly Phe Arg  
 3875 3880 3885  
 Gly Arg Gly Arg Gly Cys Pro Val Val Ser Lys Thr Pro Pro Ala  
 3890 3895 3900  
 Asp Phe Ser Ser Tyr Gly Ala Ser Pro Ser Phe Ser Cys Val Phe  
 3905 3910 3915  
 Ala Arg Cys Ile Pro Tyr Cys Gly Arg Cys Ala Pro Thr Leu His  
 3920 3925 3930  
 Leu Asn Arg Pro Tyr Arg Arg Ser Ser Ser Asn Ser Arg Arg Phe  
 3935 3940 3945  
 Cys Pro Arg Pro Ser Ser Ser Gln Pro Leu Pro Arg Arg Pro Pro  
 3950 3955 3960  
 Ala Glu Pro Ala Phe Ser Met Thr Trp Pro Trp Lys Arg Ala Arg  
 3965 3970 3975  
 Gly Trp Arg Gly Trp Gly Arg Arg Arg Arg Ser Gly Thr Arg Ala  
 3980 3985 3990  
 Cys Arg Lys Gly Thr Leu Ala Arg Pro Thr Cys Pro Ser Arg Thr  
 3995 4000 4005  
 Cys Ser Glu Thr Gly Ala Ala Arg Ser Pro Arg Arg Cys Ala Pro  
 4010 4015 4020  
 Pro Ala Ser Thr Arg Gly Gly Ser Cys Gly Ala Ala Trp Thr Glu  
 4025 4030 4035  
 Ser Gly Cys Gly Thr Arg Ile Ser Arg Arg Thr Ser Arg Gly Ser  
 4040 4045 4050  
 Ala Pro Arg Ala Arg Thr Trp Pro Arg Pro Thr Trp Ser Arg Arg  
 4055 4060 4065

## 368530-7006W01\_SequenceListing\_ST25.txt

Thr Ser Arg Pro Arg Arg Arg Ala Thr Ser Lys Asn Pro Ser Thr  
 4070 4075 4080  
 Thr Thr Cys Ala Arg Ser Arg Ala Arg Arg Pro Trp Ala Cys Thr  
 4085 4090 4095  
 Cys Gly Thr Cys Trp Arg Pro Ser Cys Arg Thr Pro Arg Ala Ser  
 4100 4105 4110  
 Arg Arg Arg Ser Cys Phe Trp Trp Cys Ser Thr Val Gly Thr Thr  
 4115 4120 4125  
 Arg Arg Ser Gly Arg Arg Cys Ile Ser Pro Ser Pro Arg Ala Ala  
 4130 4135 4140  
 Gly Ser Trp Thr Trp Thr Phe Cys Arg Ala Ser Trp Cys Arg Ser  
 4145 4150 4155  
 Ala Gly Cys Arg Cys Pro Arg Ser Trp Arg Leu Ser Thr Ser Arg  
 4160 4165 4170  
 Cys Ala Trp Ala Ser Thr Thr Leu Gly Arg Ser Thr Arg Pro Arg  
 4175 4180 4185  
 Thr Cys Pro Thr Arg Arg Arg Ser Thr Gly Phe Thr Cys Ala Pro  
 4190 4195 4200  
 Lys Cys Pro Ala Thr Ile Trp Gly Cys Thr Ala Thr Thr Gly Cys  
 4205 4210 4215  
 Thr Ala Arg Ala Pro Ala Ala Gly Ala Ser Ala Thr Arg Ser Cys  
 4220 4225 4230  
 Thr Ala Cys Ser Gly Pro Pro Gly Pro Gly Pro Arg Gly Arg Ala  
 4235 4240 4245  
 Thr Leu Thr Trp Ala Arg Thr Cys Ala Gly Ser Pro Ala Ala Gly  
 4250 4255 4260  
 Pro Trp Lys Leu Pro Ala Val Pro Pro Thr Trp Arg Arg Trp Thr  
 4265 4270 4275  
 Met Arg Arg Arg Arg Ala Ser Thr Trp Lys Thr Asp Gly Ala Thr  
 4280 4285 4290  
 Val Phe Leu Leu Asp Ala Ala Thr Ala Thr Ala Ser Ser Arg Asp  
 4295 4300 4305

368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ala | Gly  | Gly | Ala | Ala | Glu | Pro  | Ala | Val | Arg | His | Leu  | Leu | Gly | Arg |
|     | 4310 |     |     |     |     | 4315 |     |     |     |     | 4320 |     |     |     |
| Leu | Asp  | Pro | Gly | His | Ala | Thr  | His | His | Gly | Ala | Asp  | Asp | Pro | Gln |
|     | 4325 |     |     |     |     | 4330 |     |     |     |     | 4335 |     |     |     |
| Ser | Arg  | Ser | Leu | Thr | Ala | Ala  | Ser | Gly | Gln | Pro | Ala  | Leu | Gly | His |
|     | 4340 |     |     |     |     | 4345 |     |     |     |     | 4350 |     |     |     |
| Pro | Gly  | Gly | Arg | Gly | Ala | Leu  | Ala | Leu | Glu | Pro | His  | Ala | Arg | Glu |
|     | 4355 |     |     |     |     | 4360 |     |     |     |     | 4365 |     |     |     |
| Gly | Ala  | Gly | His | Arg | Glu | Arg  | Ala | Gly | Gly | Glu | Gln  | Gly | His | Pro |
|     | 4370 |     |     |     |     | 4375 |     |     |     |     | 4380 |     |     |     |
| Arg | Arg  | Arg | Gly | Arg | Ala | Gly  | Val | Gln | Arg | Ala | Ala  | Gly | Ala | Arg |
|     | 4385 |     |     |     |     | 4390 |     |     |     |     | 4395 |     |     |     |
| Gly | Pro  | Leu | Gln | Gln | His | Gln  | Arg | Ala | Asp | Glu | Pro  | Gly | Pro | His |
|     | 4400 |     |     |     |     | 4405 |     |     |     |     | 4410 |     |     |     |
| Gly | Asp  | Arg | Arg | Ala | Arg | Gly  | Gly | Val | Ala | Ala | Arg  | Ala | Val | Pro |
|     | 4415 |     |     |     |     | 4420 |     |     |     |     | 4425 |     |     |     |
| Pro | Arg  | Val | Glu | Pro | Gly | Leu  | His | Gly | Gly | Ala | Glu  | Arg | Leu | Pro |
|     | 4430 |     |     |     |     | 4435 |     |     |     |     | 4440 |     |     |     |
| Glu | His  | Ala | Ala | Arg | Gln | Arg  | Ala | Pro | Gly | Pro | Gly  | Gly | Leu | His |
|     | 4445 |     |     |     |     | 4450 |     |     |     |     | 4455 |     |     |     |
| Gln | Leu  | His | Gln | Arg | Ala | Ala  | Ala | Asp | Gly | Gly | Arg  | Gly | Ala | Pro |
|     | 4460 |     |     |     |     | 4465 |     |     |     |     | 4470 |     |     |     |
| Glu | Arg  | Gly | Val | Pro | Val | Gly  | Ala | Gly | Leu | Leu | Leu  | Pro | Asp | Gln |
|     | 4475 |     |     |     |     | 4480 |     |     |     |     | 4485 |     |     |     |
| Ser | Pro  | Gly | Leu | Ala | Asp | Arg  | Glu | Pro | Glu | Pro | Gly  | Phe | Gln | Glu |
|     | 4490 |     |     |     |     | 4495 |     |     |     |     | 4500 |     |     |     |
| Leu | Ala  | Gly | Thr | Val | Gly | Arg  | Ala | Gly | Pro | Gly | Arg  | Gly | Pro | Arg |
|     | 4505 |     |     |     |     | 4510 |     |     |     |     | 4515 |     |     |     |
| Asp | Gly  | Val | Glu | Pro | Ala | Asp  | Ala | Glu | Leu | Ala | Pro  | Ala | Ala | Ala |
|     | 4520 |     |     |     |     | 4525 |     |     |     |     | 4530 |     |     |     |
| Ala | Gly  | Gly | Ala | Leu | His | Gly  | Gln | Arg | Gln | Arg | Glu  | Pro | Arg | Leu |

4535

4540

4545

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Val  | Pro | Gly | Leu | Pro | Ala | Pro  | Val | Pro | Arg | Gly | His  | Arg | Ala | Gly |
| 4550 |     |     |     |     |     | 4555 |     |     |     |     | 4560 |     |     |     |
| Ala  | Arg | Gly | Arg | Ala | Asp | Leu  | Pro | Gly | Asp | His | Pro  | Arg | Glu | Pro |
| 4565 |     |     |     |     |     | 4570 |     |     |     |     | 4575 |     |     |     |
| Arg  | Ala | Gly | Pro | Gly | Gly | Pro  | Gly | Gln | Pro | Gly | Gly  | His | Pro | Glu |
| 4580 |     |     |     |     |     | 4585 |     |     |     |     | 4590 |     |     |     |
| Leu  | Pro | Ala | Asp | Gln | Pro | Val  | Ala | Glu | Asp | Pro | Ala  | Pro | Val | Arg |
| 4595 |     |     |     |     |     | 4600 |     |     |     |     | 4605 |     |     |     |
| Ala  | Glu | His | Arg | Gly | Gly | Ala  | His | Pro | Ala | Leu | Arg  | Ala | Ala | Glu |
| 4610 |     |     |     |     |     | 4615 |     |     |     |     | 4620 |     |     |     |
| Arg  | Gly | Ala | Val | Pro | Asp | Ala  | Gly | Gly | Gly | His | Ala  | Gln | Arg | Arg |
| 4625 |     |     |     |     |     | 4630 |     |     |     |     | 4635 |     |     |     |
| Ala  | Arg | His | Asp | Arg | Ala | Gln  | His | Gly | Ala | Gln | His  | Val | Arg | Ser |
| 4640 |     |     |     |     |     | 4645 |     |     |     |     | 4650 |     |     |     |
| Gln  | Pro | Pro | Val | His | Gln | Ala  | Asp | Gly | Leu | Leu | Ala  | Ser | Gly | Gly |
| 4655 |     |     |     |     |     | 4660 |     |     |     |     | 4665 |     |     |     |
| Arg  | His | Glu | Leu | Gly | Leu | Leu  | Tyr | Gln | Arg | His | Leu  | Glu | Pro | Ala |
| 4670 |     |     |     |     |     | 4675 |     |     |     |     | 4680 |     |     |     |
| Leu  | Ala | Pro | Ala | Ala | Arg | Val  | Leu | His | Gly | Arg | Val  | Arg | His | Ala |
| 4685 |     |     |     |     |     | 4690 |     |     |     |     | 4695 |     |     |     |
| Arg  | Pro | Gln | Arg | Arg | Val | Pro  | Val | Gly | Arg | Arg | Gly  | Gln | Gln | Arg |
| 4700 |     |     |     |     |     | 4705 |     |     |     |     | 4710 |     |     |     |
| Val  | Leu | Ala | Ala | Pro | Arg | His  | His | Arg | Val | Glu | Glu  | Arg | Gly | Arg |
| 4715 |     |     |     |     |     | 4720 |     |     |     |     | 4725 |     |     |     |
| Gly  | Pro | Ala | Ala | Val | Leu | Gly  | Ala | Val | Arg | Ser | Arg  | Gly | Cys | Cys |
| 4730 |     |     |     |     |     | 4735 |     |     |     |     | 4740 |     |     |     |
| Arg  | Gly | Gly | Ala | Gly | Arg | Gln  | Pro | Leu | Pro | Glu | Pro  | Ala | Leu | Phe |
| 4745 |     |     |     |     |     | 4750 |     |     |     |     | 4755 |     |     |     |
| Ala  | Glu | Gln | Arg | Ala | Gln | Gln  | Arg | Ala | Gly | Ser | Ala  | Asp | Ala | Ala |
| 4760 |     |     |     |     |     | 4765 |     |     |     |     | 4770 |     |     |     |

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|                 |                             |                             |             |
|-----------------|-----------------------------|-----------------------------|-------------|
| Ala Pro<br>4775 | Ala Gly Arg Gly Gly<br>4780 | Val Pro Glu Arg Leu<br>4785 | Leu Val Glu |
| Ala Arg<br>4790 | Ala Arg Glu Glu Leu<br>4795 | Pro Gln Arg Asp Arg<br>4800 | Glu Pro Gly |
| Gly Gln<br>4805 | Asp Glu Pro Leu Glu<br>4810 | Asp Val Arg Ala Arg<br>4815 | Ala Gln Gly |
| Arg Ala<br>4820 | Pro Ser Gln Gln Arg<br>4825 | Arg His Pro Thr Pro<br>4830 | Ala Thr Arg |
| Gln Ala<br>4835 | Ala Gly Ser Gly Val<br>4840 | Gly Arg Gly Phe Arg<br>4845 | Arg Arg Gln |
| Gln Arg<br>4850 | Val Gly Leu Gly Trp<br>4855 | Glu Trp Trp Trp Pro<br>4860 | Val Arg Ser |
| Leu Ala<br>4865 | Pro Pro Tyr Arg Ala<br>4870 | Pro Asp Val Arg Ile<br>4875 | Lys Asn Lys |
| Lys Arg<br>4880 | Tyr Ser Pro Arg Pro<br>4885 | Trp Arg Pro Ala Cys<br>4890 | Val Leu Leu |
| Cys Cys<br>4895 | Leu Tyr Asp Glu Ala<br>4900 | Arg Val Pro Gly Gly<br>4905 | Ser Ser Ser |
| Leu Val<br>4910 | Arg Glu Arg Asp Ala<br>4915 | Ala Gly Gly Gly Gly<br>4920 | Gly Asp Ala |
| Ala Pro<br>4925 | Ala Gly Gly Ala Leu<br>4930 | Arg Ala Pro Ala Val<br>4935 | Pro Gly Ala |
| Tyr Gly<br>4940 | Gly Ala Glu Gln His<br>4945 | Ser Leu Leu Gly Ala<br>4950 | Gly Thr Leu |
| Val Arg<br>4955 | Tyr His Pro Val Val<br>4960 | Pro Gly Gly Gln Gln<br>4965 | Val Gly Gly |
| His Arg<br>4970 | Leu Ala Glu Leu Pro<br>4975 | Glu Arg Pro Gln Gln<br>4980 | Leu Pro Asp |
| His Arg<br>4985 | Gly Ala Glu Gln Arg<br>4990 | Phe His Pro His Gly<br>4995 | Gly Gln His |
| Pro Asp<br>5000 | His Gln Leu Arg Ala<br>5005 | Leu Ala Val Gly Arg<br>5010 | Pro Ala Glu |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asn | His  | His | Ala | His | Gln | His  | Ala | Gln | Arg | Glu | Arg  | Val | His | Val |
|     | 5015 |     |     |     |     | 5020 |     |     |     |     | 5025 |     |     |     |
| Gln | Gln  | Gln | Val | Gln | Gly | Ala  | Gly | Asp | Gly | Leu | Ala  | Gln | Asp | Pro |
|     | 5030 |     |     |     |     | 5035 |     |     |     |     | 5040 |     |     |     |
| Gln | Trp  | Gly | Arg | Gly | Gly | Glu  | Leu | Trp | Ser | Gly | Arg  | Ala | Asp | Leu |
|     | 5045 |     |     |     |     | 5050 |     |     |     |     | 5055 |     |     |     |
| Arg | Val  | Gly | Gly | Val | Ala | Ala  | Arg | Gly | Gln | Leu | Leu  | Gly | Asp | His |
|     | 5060 |     |     |     |     | 5065 |     |     |     |     | 5070 |     |     |     |
| Asp | His  | Arg | Ser | Asp | Glu | Gln  | Arg | His | His | Arg | Gln  | Leu | Leu | Gly |
|     | 5075 |     |     |     |     | 5080 |     |     |     |     | 5085 |     |     |     |
| Gly | Gly  | Ala | Ser | Glu | Arg | Gly  | Ala | Gly | Glu | Arg | His  | Arg | Arg | Glu |
|     | 5090 |     |     |     |     | 5095 |     |     |     |     | 5100 |     |     |     |
| Val | Arg  | His | Ala | Gln | Leu | Pro  | Ala | Gly | Leu | Gly | Pro  | Arg | Asp | Arg |
|     | 5105 |     |     |     |     | 5110 |     |     |     |     | 5115 |     |     |     |
| Ala | Gly  | Asp | Ala | Gly | Arg | Val  | His | Gln | Arg | Gly | Leu  | Pro | Pro | Arg |
|     | 5120 |     |     |     |     | 5125 |     |     |     |     | 5130 |     |     |     |
| His | Arg  | Pro | Ala | Ala | Arg | Leu  | Arg | Arg | Gly | Leu | His  | Arg | Glu | Pro |
|     | 5135 |     |     |     |     | 5140 |     |     |     |     | 5145 |     |     |     |
| Pro | Gln  | Gln | Pro | Ala | Gly | His  | Pro | Gln | Ala | Ala | Ala  | Leu | Pro | Gly |
|     | 5150 |     |     |     |     | 5155 |     |     |     |     | 5160 |     |     |     |
| Gly | Leu  | Pro | Asp | Pro | Val | Arg  | Gly | Pro | Gly | Gly | Gly  | Gln | His | Pro |
|     | 5165 |     |     |     |     | 5170 |     |     |     |     | 5175 |     |     |     |
| Arg | Ala  | Leu | Gly | Cys | Arg | Ser  | Leu | Glu | Lys | Gln | Gly  | Gly | Gly | Arg |
|     | 5180 |     |     |     |     | 5185 |     |     |     |     | 5190 |     |     |     |
| Arg | Ser  | Gly | Asp | Arg | Ser | Arg  | Gly | His | Arg | Leu | Tyr  | Arg | Gly | Ala |
|     | 5195 |     |     |     |     | 5200 |     |     |     |     | 5205 |     |     |     |
| Gly | Arg  | Phe | Cys | Arg | Arg | Gly  | Ser | Gly | Arg | Gly | Gly  | Asn | Arg | Lys |
|     | 5210 |     |     |     |     | 5215 |     |     |     |     | 5220 |     |     |     |
| Asp | Ser  | His | Pro | Ala | Gly | Gly  | Glu | Gly | Gln | Gln | Gly  | Gln | Glu | Leu |
|     | 5225 |     |     |     |     | 5230 |     |     |     |     | 5235 |     |     |     |
| Gln | Arg  | Ala | Arg | Gly | Gln | Glu  | Lys | His | Arg | Leu | Pro  | Gln | Leu | Val |
|     | 5240 |     |     |     |     | 5245 |     |     |     |     | 5250 |     |     |     |

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Pro Gly Leu Gln Leu Arg Arg Pro Arg Glu Gly Arg Ala Leu Leu  
5255 5260 5265

Asp Ala Ala His His Leu Gly Arg His Leu Arg Arg Gly Ala Ser  
5270 5275 5280

Leu Leu Val Ala Ala Arg His Asp Ala Arg Pro Gly His Leu Pro  
5285 5290 5295

Leu His Ala Ser Ser Gln Leu Pro Gly Gly Gly Arg Arg Ala Pro  
5300 5305 5310

Ala Arg Leu Leu Gln Glu Leu Leu Gln Arg Ala Gly Arg Leu Leu  
5315 5320 5325

Ala Ala Ala Ala Arg Leu His Leu Ala His Ala Arg Leu Gln Pro  
5330 5335 5340

Leu Pro Arg Glu Pro Asp Pro Arg Pro Pro Ala Arg Ala His His  
5345 5350 5355

Tyr His Arg Gln Lys Arg Ser Cys Ser His Arg Ser Arg Asp Pro  
5360 5365 5370

Ala Ala Ala Gln Gln Tyr Pro Gly Ser Pro Ala Arg Asp Arg His  
5375 5380 5385

Arg Gln Thr Pro His Leu Pro Leu Arg Leu Gln Gly Pro Gly Arg  
5390 5395 5400

Ser Arg Ala Ala Arg Pro Leu Glu Pro His Leu Leu Lys Asn Val  
5405 5410 5415

His Ser His Leu Ala Gln His Arg Leu Gly Pro Ala Arg Ala Gln  
5420 5425 5430

Gln Asp Val Arg Arg Arg Ser Pro Thr Leu His Ala Thr Pro Arg  
5435 5440 5445

Ala Arg Ala Arg Ala Leu Pro Arg Ser Leu Gly Arg Pro Gln Gly  
5450 5455 5460

Pro Arg Ala Leu Ala His His Arg Arg Arg Arg Asp Arg Pro Gly  
5465 5470 5475

Gly Gly Arg Arg Ala Gln Leu His Ala Arg Arg Arg Ala Arg Leu

5480

5485

5490

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| His  | Arg | Gly | Arg | Arg | His | Arg  | Gln | Arg | Gly | Gly | Arg  | Cys | Ala | Pro |
| 5495 |     |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |
| Val  | Arg | Pro | Arg | Gln | Glu | Pro  | Ala | Ala | Ala | His | Arg  | Pro | Ala | Ala |
| 5510 |     |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
| Pro  | Glu | His | Pro | Arg | His | Ala  | Arg | Gly | Ala | Ser | Leu  | Ala | Ala | Gln |
| 5525 |     |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
| Gly  | Gln | Ala | His | Gly | Thr | Gln  | Gly | His | Ala | Gln | Gly  | Gly | Gln | Thr |
| 5540 |     |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
| Arg  | Gly | Leu | Arg | Gln | Gln | Gln  | Arg | Arg | Gln | Asp | Pro  | Gln | Thr | Arg |
| 5555 |     |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
| Gly  | His | Gly | Gly | Gly | Gly | Gly  | His | Arg | Gln | His | Val  | Pro | Pro | Ala |
| 5570 |     |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |
| Ala  | Arg | Gln | Arg | Val | Leu | Gly  | Ala | Arg | Arg | Arg | His  | Arg | Cys | Ala |
| 5585 |     |     |     |     |     | 5590 |     |     |     |     | 5595 |     |     |     |
| Arg  | Ala | Arg | Ala | His | Pro | Pro  | Pro | Ser | His | Leu | Lys  | Met | Leu | Thr |
| 5600 |     |     |     |     |     | 5605 |     |     |     |     | 5610 |     |     |     |
| Ser  | Arg | Cys | Cys | Val | Pro | Ala  | Ala | Arg | Arg | Met | Ser  | Lys | Arg | Lys |
| 5615 |     |     |     |     |     | 5620 |     |     |     |     | 5625 |     |     |     |
| Tyr  | Lys | Glu | Glu | Met | Leu | Gln  | Val | Ile | Ala | Pro | Glu  | Ile | Tyr | Gly |
| 5630 |     |     |     |     |     | 5635 |     |     |     |     | 5640 |     |     |     |
| Pro  | Ala | Val | Lys | Glu | Glu | Arg  | Lys | Pro | Arg | Lys | Leu  | Lys | Arg | Val |
| 5645 |     |     |     |     |     | 5650 |     |     |     |     | 5655 |     |     |     |
| Lys  | Lys | Asp | Lys | Lys | Glu | Glu  | Glu | Asp | Val | Asp | Gly  | Leu | Val | Glu |
| 5660 |     |     |     |     |     | 5665 |     |     |     |     | 5670 |     |     |     |
| Phe  | Val | Arg | Glu | Phe | Ala | Pro  | Arg | Arg | Arg | Val | Gln  | Trp | Arg | Gly |
| 5675 |     |     |     |     |     | 5680 |     |     |     |     | 5685 |     |     |     |
| Arg  | Lys | Val | Lys | Pro | Val | Leu  | Arg | Pro | Gly | Thr | Thr  | Val | Val | Phe |
| 5690 |     |     |     |     |     | 5695 |     |     |     |     | 5700 |     |     |     |
| Thr  | Pro | Gly | Glu | Arg | Ser | Gly  | Ser | Ala | Ser | Lys | Arg  | Ser | Tyr | Asp |
| 5705 |     |     |     |     |     | 5710 |     |     |     |     | 5715 |     |     |     |



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Glu Val Tyr Gly Asp Glu Asp Ile Leu Glu Gln Ala Val Glu Arg  
 5720 5725 5730  
 Leu Gly Glu Phe Ala Tyr Gly Lys Arg Ser Arg Pro Ala Pro Leu  
 5735 5740 5745  
 Lys Glu Glu Ala Val Ser Ile Pro Leu Asp His Gly Asn Pro Thr  
 5750 5755 5760  
 Pro Ser Leu Lys Pro Val Thr Leu Gln Gln Val Leu Pro Ser Ala  
 5765 5770 5775  
 Ala Pro Arg Arg Gly Phe Lys Arg Glu Gly Gly Glu Asp Leu Tyr  
 5780 5785 5790  
 Pro Thr Met Gln Leu Met Val Pro Lys Arg Gln Lys Leu Glu Asp  
 5795 5800 5805  
 Val Leu Glu His Met Lys Val Asp Pro Glu Val Gln Pro Glu Val  
 5810 5815 5820  
 Lys Val Arg Pro Ile Lys Gln Val Ala Pro Gly Leu Gly Val Gln  
 5825 5830 5835  
 Thr Val Asp Ile Lys Ile Pro Thr Glu Pro Met Glu Thr Gln Thr  
 5840 5845 5850  
 Glu Pro Val Lys Pro Ser Thr Ser Thr Met Glu Val Gln Thr Asp  
 5855 5860 5865  
 Pro Trp Met Pro Ala Pro Ala Ser Thr Thr Arg Arg Arg Arg Lys  
 5870 5875 5880  
 Tyr Gly Ala Ala Ser Leu Leu Met Pro Asn Tyr Ala Leu His Pro  
 5885 5890 5895  
 Ser Ile Ile Pro Thr Pro Gly Tyr Arg Gly Thr Arg Phe Tyr Arg  
 5900 5905 5910  
 Gly Tyr Thr Ser Ser Arg Arg Lys Thr Thr Thr Arg Arg Arg Arg  
 5915 5920 5925  
 Arg Arg Thr Arg Arg Ser Ser Thr Ala Thr Ser Ala Ala Ala Leu  
 5930 5935 5940  
 Val Arg Arg Val Tyr Arg Ser Gly Arg Glu Pro Leu Thr Leu Pro  
 5945 5950 5955

## 368530-7006W01\_SequenceListing\_ST25.txt

Arg Ala Arg Tyr His Pro Ser Ile Ala Ile Leu Cys Arg Arg Leu  
 5960 5965 5970  
 Leu Leu Ala Asp Met Ala Leu Thr Cys Arg Leu Arg Val Pro Ile  
 5975 5980 5985  
 Thr Gly Tyr Arg Gly Arg Lys Pro Arg Arg Arg Arg Leu Thr Gly  
 5990 5995 6000  
 Asn Gly Leu Arg Arg His His His Arg Arg Arg Arg Ala Ile Ser  
 6005 6010 6015  
 Lys Arg Leu Gly Gly Gly Phe Leu Pro Ala Leu Ile Pro Ile Ile  
 6020 6025 6030  
 Ala Ala Ala Ile Gly Ala Ile Pro Gly Ile Ala Ser Val Ala Val  
 6035 6040 6045  
 Gln Ala Ser Gln Arg His Asp Thr Ala Trp Lys Ile Cys Asn Lys  
 6050 6055 6060  
 Lys Met Asp Arg Ser Trp Ser Cys Asp Val Cys Phe Met Glu Asp  
 6065 6070 6075  
 Ile Asn Phe Ser Ser Leu Ala Pro Arg His Gly Thr Arg Pro Phe  
 6080 6085 6090  
 Met Gly Thr Trp Ser Asp Ile Gly Asn Ser Gln Leu Asn Gly Gly  
 6095 6100 6105  
 Ala Phe Asn Trp Ser Ser Leu Trp Ser Gly Leu Lys Asn Phe Gly  
 6110 6115 6120  
 Ser Thr Leu Lys Thr Tyr Gly Asn Lys Ala Trp Asn Ser Ser Thr  
 6125 6130 6135  
 Gly Gln Ala Leu Arg Glu Lys Leu Lys Glu Gln Asn Phe Gln Gln  
 6140 6145 6150  
 Lys Val Val Asp Gly Leu Ala Ser Gly Ile Asn Gly Val Val Asp  
 6155 6160 6165  
 Leu Ala Asn Gln Ala Val Gln Lys Gln Ile Asn Ser Arg Leu Asp  
 6170 6175 6180  
 Ala Val Pro Pro Ala Gly Ser Val Glu Met Pro Gln Val Glu Glu  
 6185 6190 6195

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Glu  | Leu | Pro | Pro | Leu | Asp | Lys  | Arg | Gly | Asp | Lys | Arg  | Pro | Arg | Pro |
| 6200 |     |     |     |     |     | 6205 |     |     |     |     | 6210 |     |     |     |
| Asp  | Ala | Glu | Glu | Thr | Leu | Leu  | Thr | His | Thr | Asp | Glu  | Pro | Pro | Pro |
| 6215 |     |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Tyr  | Glu | Glu | Ala | Val | Lys | Leu  | Gly | Leu | Pro | Thr | Thr  | Arg | Pro | Val |
| 6230 |     |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Ala  | Pro | Leu | Ala | Thr | Gly | Val  | Leu | Lys | Pro | Ser | Ser  | Ser | Ser | Gln |
| 6245 |     |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |
| Pro  | Ala | Thr | Leu | Asp | Leu | Pro  | Pro | Pro | Ala | Ser | Arg  | Pro | Ser | Thr |
| 6260 |     |     |     |     |     | 6265 |     |     |     |     | 6270 |     |     |     |
| Val  | Ala | Lys | Pro | Leu | Pro | Pro  | Val | Ala | Val | Ala | Ser  | Arg | Ala | Pro |
| 6275 |     |     |     |     |     | 6280 |     |     |     |     | 6285 |     |     |     |
| Arg  | Gly | Arg | Pro | Gln | Ala | Asn  | Trp | Gln | Ser | Thr | Leu  | Asn | Ser | Ile |
| 6290 |     |     |     |     |     | 6295 |     |     |     |     | 6300 |     |     |     |
| Val  | Gly | Leu | Gly | Val | Gln | Ser  | Val | Lys | Arg | Arg | Arg  | Cys | Tyr | Lys |
| 6305 |     |     |     |     |     | 6310 |     |     |     |     | 6315 |     |     |     |
| Thr  | Leu | Arg | Leu | Thr | Cys | Leu  | Ser | Val | Cys | Ile | Cys  | Met | Ser | Ala |
| 6320 |     |     |     |     |     | 6325 |     |     |     |     | 6330 |     |     |     |
| Asp  | Gln | Lys | Glu | Glu | Glu | Ala  | Arg | Arg | Arg | Val | Ala  | Arg | Trp | Pro |
| 6335 |     |     |     |     |     | 6340 |     |     |     |     | 6345 |     |     |     |
| Pro  | His | Arg | Cys | Cys | Pro | Ser  | Gly | Arg | Thr | Cys | Thr  | Ser | Pro | Asp |
| 6350 |     |     |     |     |     | 6355 |     |     |     |     | 6360 |     |     |     |
| Arg  | Thr | Leu | Arg | Ser | Thr | Val  | Arg | Val | Trp | Cys | Ser  | Ser | Pro | Ala |
| 6365 |     |     |     |     |     | 6370 |     |     |     |     | 6375 |     |     |     |
| Pro  | Gln | Thr | Pro | Thr | Ser | Val  | Trp | Gly | Thr | Ser | Leu  | Gly | Thr | Pro |
| 6380 |     |     |     |     |     | 6385 |     |     |     |     | 6390 |     |     |     |
| Arg  | Trp | Arg | Pro | Arg | Thr | Met  | Pro | Pro | Thr | Ala | Ala  | Ser | Gly | Arg |
| 6395 |     |     |     |     |     | 6400 |     |     |     |     | 6405 |     |     |     |
| Cys  | Ala | Ser | Cys | Pro | Trp | Thr  | Ala | Arg | Thr | Thr | Pro  | Thr | Arg | Thr |
| 6410 |     |     |     |     |     | 6415 |     |     |     |     | 6420 |     |     |     |
| Lys  | Cys | Ala | Thr | Arg | Trp | Pro  | Trp | Ala | Thr | Thr | Ala  | Cys | Trp | Thr |

6425

6430

6435

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Trp  | Pro | Ala | Pro | Thr | Leu | Thr  | Ser | Ala | Ala | Cys | Trp  | Ile | Gly | Gly |
| 6440 |     |     |     |     |     | 6445 |     |     |     |     | 6450 |     |     |     |
| Pro  | Ala | Ser | Asn | Pro | Thr | Pro  | Ala | Pro | Pro | Thr | Thr  | Ala | Trp | Leu |
| 6455 |     |     |     |     |     | 6460 |     |     |     |     | 6465 |     |     |     |
| Pro  | Arg | Glu | Arg | Pro | Thr | Leu  | Ala | Ser | Gly | His | Ile  | Lys | Leu | Val |
| 6470 |     |     |     |     |     | 6475 |     |     |     |     | 6480 |     |     |     |
| Ile  | Leu | Ile | Gln | Lys | Lys | Pro  | Ile | His | Met | Glu | Met  | His | Leu | Cys |
| 6485 |     |     |     |     |     | 6490 |     |     |     |     | 6495 |     |     |     |
| Lys  | Ala | Leu | Ala | Leu | Gln | Arg  | Met | Val | Phe | Asn | Leu  | Glu | Leu | Thr |
| 6500 |     |     |     |     |     | 6505 |     |     |     |     | 6510 |     |     |     |
| Ala  | Met | Val | Arg | Gln | Ser | Met  | Gln | Thr | Lys | Leu | Ile  | Asn | Gln | Ser |
| 6515 |     |     |     |     |     | 6520 |     |     |     |     | 6525 |     |     |     |
| Leu  | Lys | Trp | Val | Met | Leu | Asn  | Gly | Met | Thr | Ser | Leu  | Val | Leu | Met |
| 6530 |     |     |     |     |     | 6535 |     |     |     |     | 6540 |     |     |     |
| Lys  | Asn | Met | Glu | Ala | Glu | Leu  | Leu | Ser | Leu | Thr | Pro  | Lys | Ser | Leu |
| 6545 |     |     |     |     |     | 6550 |     |     |     |     | 6555 |     |     |     |
| Ala  | Met | Val | Leu | Leu | Pro | Ser  | Leu | Pro | Ile | Lys | Lys  | Glu | Ala | Arg |
| 6560 |     |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Gln  | Met | Lys | Pro | Lys | Gln | Ala  | Val | Pro | Lys | Asn | Met  | Thr | Leu | Thr |
| 6575 |     |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Trp  | His | Ser | Ser | Ile | Ile | Glu  | Val | Gln | Leu | Pro | Pro  | Ala | Pro | Gln |
| 6590 |     |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Lys  | Leu | Phe | Cys | Ile | Leu | Arg  | Met | Trp | Ile | Trp | Lys  | Leu | Gln | Ile |
| 6605 |     |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Pro  | Ile | Leu | Tyr | Thr | Arg | Gln  | Val | Gln | Met | Thr | Val  | Ala | Leu | Leu |
| 6620 |     |     |     |     |     | 6625 |     |     |     |     | 6630 |     |     |     |
| Ser  | Ile | Trp | Val | Ser | Ser | Pro  | Cys | Pro | Thr | Asp | Pro  | Thr | Thr | Leu |
| 6635 |     |     |     |     |     | 6640 |     |     |     |     | 6645 |     |     |     |
| Ala  | Ser | Glu | Thr | Thr | Leu | Ser  | Val | Cys | Thr | Thr | Thr  | Ala | Leu | Ala |
| 6650 |     |     |     |     |     | 6655 |     |     |     |     | 6660 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ile  | Trp | Val | Tyr | Trp | Leu | Asp  | Arg | Pro | Pro | Ser | Met  | Leu | Trp | Trp |
| 6665 |     |     |     |     |     | 6670 |     |     |     |     | 6675 |     |     |     |
| Thr  | Cys | Arg | Thr | Glu | Thr | Pro  | Asn | Cys | Pro | Thr | Ser  | Ser | Cys | Leu |
| 6680 |     |     |     |     |     | 6685 |     |     |     |     | 6690 |     |     |     |
| Thr  | Leu | Trp | Val | Thr | Glu | Pro  | Gly | Ile | Ser | Val | Cys  | Gly | Ile | Arg |
| 6695 |     |     |     |     |     | 6700 |     |     |     |     | 6705 |     |     |     |
| Arg  | Trp | Thr | Val | Met | Thr | Pro  | Met | Cys | Ala | Leu | Leu  | Lys | Ile | Thr |
| 6710 |     |     |     |     |     | 6715 |     |     |     |     | 6720 |     |     |     |
| Val  | Trp | Arg | Met | Asn | Phe | Leu  | Thr | Ile | Ala | Ser | Pro  | Trp | Met | Leu |
| 6725 |     |     |     |     |     | 6730 |     |     |     |     | 6735 |     |     |     |
| Trp  | Val | Glu | Leu | Ile | Leu | Thr  | Arg | Glu | Leu | Arg | Pro  | Met | Val | Ile |
| 6740 |     |     |     |     |     | 6745 |     |     |     |     | 6750 |     |     |     |
| Ile  | Lys | Pro | Pro | Gly | Pro | Lys  | Met | Ile | Leu | Leu | Met  | Met | Leu | Met |
| 6755 |     |     |     |     |     | 6760 |     |     |     |     | 6765 |     |     |     |
| Asn  | Trp | Ala | Arg | Ala | Ile | Leu  | Ser | Pro | Trp | Arg | Ser  | Thr | Ser | Arg |
| 6770 |     |     |     |     |     | 6775 |     |     |     |     | 6780 |     |     |     |
| Pro  | Thr | Cys | Gly | Gly | Thr | Ser  | Ser | Thr | Arg | Thr | Trp  | Arg | Cys | Thr |
| 6785 |     |     |     |     |     | 6790 |     |     |     |     | 6795 |     |     |     |
| Cys  | Pro | Thr | Pro | Thr | Ser | Thr  | Arg | Arg | Pro | Thr | Ser  | Arg | Cys | Pro |
| 6800 |     |     |     |     |     | 6805 |     |     |     |     | 6810 |     |     |     |
| Pro  | Thr | Pro | Thr | Pro | Thr | Ile  | Thr | Thr | Ala | Ala | Trp  | Trp | Arg | Pro |
| 6815 |     |     |     |     |     | 6820 |     |     |     |     | 6825 |     |     |     |
| Arg  | Trp | Trp | Thr | Pro | Thr | Ser  | Thr | Ser | Gly | Arg | Ala  | Gly | Arg | Trp |
| 6830 |     |     |     |     |     | 6835 |     |     |     |     | 6840 |     |     |     |
| Thr  | Pro | Trp | Thr | Thr | Ser | Thr  | Pro | Ser | Thr | Thr | Thr  | Ala | Thr | Arg |
| 6845 |     |     |     |     |     | 6850 |     |     |     |     | 6855 |     |     |     |
| Ala  | Cys | Asp | Thr | Ala | Pro | Cys  | Ser | Trp | Ala | Thr | Gly  | Ala | Thr | Cys |
| 6860 |     |     |     |     |     | 6865 |     |     |     |     | 6870 |     |     |     |
| Pro  | Ser | Thr | Ser | Arg | Cys | Pro  | Lys | Ser | Phe | Ser | Pro  | Ser | Arg | Ala |
| 6875 |     |     |     |     |     | 6880 |     |     |     |     | 6885 |     |     |     |
| Ser  | Cys | Ser | Cys | Pro | Gly | Pro  | Thr | Pro | Thr | Ser | Gly  | Thr | Ser | Ala |
| 6890 |     |     |     |     |     | 6895 |     |     |     |     | 6900 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Thr  | Ser | Thr | Ser | Cys | Arg  | Ala | Pro | Ser | Ala | Thr  | Thr | Cys | Ala |
|     | 6905 |     |     |     |     | 6910 |     |     |     |     | 6915 |     |     |     |
| Arg | Thr  | Gly | Pro | Pro | Ser | Pro  | Ser | Pro | Ala | Ser | Thr  | Ser | Thr | Pro |
|     | 6920 |     |     |     |     | 6925 |     |     |     |     | 6930 |     |     |     |
| Pro | Ser  | Ser | Pro | Trp | Arg | Thr  | Thr | Pro | Pro | Pro | Arg  | Ser | Arg | Pro |
|     | 6935 |     |     |     |     | 6940 |     |     |     |     | 6945 |     |     |     |
| Cys | Cys  | Ala | Thr | Thr | Pro | Thr  | Thr | Ser | Pro | Ser | Thr  | Thr | Thr | Ser |
|     | 6950 |     |     |     |     | 6955 |     |     |     |     | 6960 |     |     |     |
| Arg | Arg  | Pro | Thr | Cys | Ser | Thr  | Pro | Ser | Arg | Pro | Thr  | Pro | Pro | Thr |
|     | 6965 |     |     |     |     | 6970 |     |     |     |     | 6975 |     |     |     |
| Cys | Pro  | Ser | Pro | Ser | Pro | Arg  | Ala | Thr | Gly | Pro | Pro  | Ser | Ala | Ala |
|     | 6980 |     |     |     |     | 6985 |     |     |     |     | 6990 |     |     |     |
| Gly | Pro  | Ser | Arg | Ala | Ser | Arg  | Pro | Ala | Arg | Arg | Pro  | Arg | Ser | Ala |
|     | 6995 |     |     |     |     | 7000 |     |     |     |     | 7005 |     |     |     |
| Pro | Gly  | Ser | Thr | Pro | Thr | Ser  | Ser | Thr | Arg | Ala | Pro  | Ser | Pro | Thr |
|     | 7010 |     |     |     |     | 7015 |     |     |     |     | 7020 |     |     |     |
| Ser | Thr  | Ala | Pro | Ser | Thr | Ser  | Thr | Thr | Pro | Ser | Arg  | Arg | Ser | Pro |
|     | 7025 |     |     |     |     | 7030 |     |     |     |     | 7035 |     |     |     |
| Ser | Pro  | Ser | Thr | Pro | Pro | Ser  | Ala | Gly | Pro | Ala | Thr  | Thr | Ala | Ser |
|     | 7040 |     |     |     |     | 7045 |     |     |     |     | 7050 |     |     |     |
| Arg | Pro  | Thr | Ser | Ser | Lys | Ser  | Ser | Ala | Pro | Ser | Thr  | Glu | Arg | Gly |
|     | 7055 |     |     |     |     | 7060 |     |     |     |     | 7065 |     |     |     |
| Thr | Thr  | Trp | Pro | Ser | Ala | Thr  | Pro | Arg | Thr | Gly | Ser  | Trp | Ser | Arg |
|     | 7070 |     |     |     |     | 7075 |     |     |     |     | 7080 |     |     |     |
| Cys | Trp  | Pro | Thr | Thr | Thr | Ser  | Ala | Thr | Arg | Ala | Ser  | Thr | Cys | Pro |
|     | 7085 |     |     |     |     | 7090 |     |     |     |     | 7095 |     |     |     |
| Arg | Ala  | Thr | Arg | Thr | Ala | Cys  | Thr | Pro | Ser | Ser | Ala  | Thr | Ser | Ser |
|     | 7100 |     |     |     |     | 7105 |     |     |     |     | 7110 |     |     |     |
| Pro | Ala  | Ala | Arg | Ser | Trp | Thr  | Arg | Ser | Thr | Thr | Arg  | Thr | Thr | Arg |
|     | 7115 |     |     |     |     | 7120 |     |     |     |     | 7125 |     |     |     |
| Pro | Ser  | Pro | Trp | Pro | Thr | Ser  | Thr | Thr | Thr | Arg | Ala  | Ser | Ser | Ala |
|     | 7130 |     |     |     |     | 7135 |     |     |     |     | 7140 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr  | Ser | Arg | Pro | Pro | Cys | Ala  | Arg | Ala | Ser | Pro | Thr  | Pro | Pro | Thr |
| 7145 |     |     |     |     |     | 7150 |     |     |     |     | 7155 |     |     |     |
| Thr  | Pro | Thr | Arg | Ser | Ser | Ala  | Arg | Ala | Pro | Ser | Pro  | Ala | Ser | Pro |
| 7160 |     |     |     |     |     | 7165 |     |     |     |     | 7170 |     |     |     |
| Arg  | Lys | Ser | Ser | Ser | Ala | Thr  | Gly | Ser | Cys | Gly | Ala  | Ser | Pro | Ser |
| 7175 |     |     |     |     |     | 7180 |     |     |     |     | 7185 |     |     |     |
| Pro  | Ala | Thr | Ser | Cys | Pro | Trp  | Ala | Arg | Ser | Pro | Thr  | Ser | Ala | Arg |
| 7190 |     |     |     |     |     | 7195 |     |     |     |     | 7200 |     |     |     |
| Thr  | Cys | Ser | Thr | Pro | Thr | Pro  | Pro | Thr | Arg | Thr | Ile  | Ser | Lys | Ser |
| 7205 |     |     |     |     |     | 7210 |     |     |     |     | 7215 |     |     |     |
| Thr  | Pro | Trp | Met | Ser | Pro | Pro  | Phe | Ser | Met | Leu | Ser  | Ser | Lys | Ser |
| 7220 |     |     |     |     |     | 7225 |     |     |     |     | 7230 |     |     |     |
| Ser  | Thr | Ser | Ser | Glu | Cys | Thr  | Ser | Pro | Thr | Ala | Ala  | Ser | Ser | Arg |
| 7235 |     |     |     |     |     | 7240 |     |     |     |     | 7245 |     |     |     |
| Pro  | Ser | Thr | Cys | Ala | Arg | Pro  | Ser | Arg | Pro | Ala | Thr  | Pro | Pro | Pro |
| 7250 |     |     |     |     |     | 7255 |     |     |     |     | 7260 |     |     |     |
| Lys  | Pro | Leu | Ala | Ser | Cys | Lys  | Met | Thr | Ala | Cys | Ala  | Gly | Ser | Gly |
| 7265 |     |     |     |     |     | 7270 |     |     |     |     | 7275 |     |     |     |
| Glu  | Gln | Glu | Leu | Arg | Ala | Ile  | Leu | Arg | Asp | Leu | Gly  | Cys | Gly | Pro |
| 7280 |     |     |     |     |     | 7285 |     |     |     |     | 7290 |     |     |     |
| Cys  | Phe | Leu | Gly | Thr | Phe | Asp  | Lys | Arg | Phe | Pro | Gly  | Phe | Met | Ala |
| 7295 |     |     |     |     |     | 7300 |     |     |     |     | 7305 |     |     |     |
| Pro  | His | Lys | Leu | Ala | Cys | Ala  | Ile | Val | Asn | Thr | Ala  | Gly | Arg | Glu |
| 7310 |     |     |     |     |     | 7315 |     |     |     |     | 7320 |     |     |     |
| Thr  | Gly | Gly | Glu | His | Trp | Leu  | Ala | Phe | Ala | Trp | Asn  | Pro | Arg | Ser |
| 7325 |     |     |     |     |     | 7330 |     |     |     |     | 7335 |     |     |     |
| His  | Thr | Cys | Tyr | Leu | Phe | Asp  | Pro | Phe | Gly | Phe | Ser  | Asp | Glu | Arg |
| 7340 |     |     |     |     |     | 7345 |     |     |     |     | 7350 |     |     |     |
| Leu  | Lys | Gln | Ile | Tyr | Gln | Phe  | Glu | Tyr | Glu | Gly | Leu  | Leu | Arg | Arg |
| 7355 |     |     |     |     |     | 7360 |     |     |     |     | 7365 |     |     |     |
| Ser  | Ala | Leu | Ala | Thr | Glu | Asp  | Arg | Cys | Val | Thr | Leu  | Glu | Lys | Ser |

7370

7375

7380

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr  | Gln | Thr | Val | Gln | Gly | Pro  | Arg | Ser | Ala | Ala | Cys  | Gly | Leu | Phe |
| 7385 |     |     |     |     |     | 7390 |     |     |     |     | 7395 |     |     |     |
| Cys  | Cys | Met | Phe | Leu | His | Ala  | Phe | Val | His | Trp | Pro  | Asp | Arg | Pro |
| 7400 |     |     |     |     |     | 7405 |     |     |     |     | 7410 |     |     |     |
| Met  | Asp | Lys | Asn | Pro | Thr | Met  | Asn | Leu | Leu | Thr | Gly  | Val | Pro | Asn |
| 7415 |     |     |     |     |     | 7420 |     |     |     |     | 7425 |     |     |     |
| Gly  | Met | Leu | Gln | Ser | Pro | Gln  | Val | Glu | Pro | Thr | Leu  | Arg | Arg | Asn |
| 7430 |     |     |     |     |     | 7435 |     |     |     |     | 7440 |     |     |     |
| Gln  | Glu | Ala | Leu | Tyr | Arg | Phe  | Leu | Asn | Ala | His | Ser  | Ala | Tyr | Phe |
| 7445 |     |     |     |     |     | 7450 |     |     |     |     | 7455 |     |     |     |
| Arg  | Ser | His | Arg | Ala | Arg | Ile  | Glu | Lys | Ala | Thr | Ala  | Phe | Asp | Arg |
| 7460 |     |     |     |     |     | 7465 |     |     |     |     | 7470 |     |     |     |
| Met  | Asn | Gln | Asp | Met | Ser | Gly  | Val | Cys | Met | Met | Leu  | Tyr | Ser | Ser |
| 7475 |     |     |     |     |     | 7480 |     |     |     |     | 7485 |     |     |     |
| Thr  | Ala | His | Val | Tyr | Ala | Thr  | Phe | Ser | Glu | Ala | Leu  | Thr | Leu | Phe |
| 7490 |     |     |     |     |     | 7495 |     |     |     |     | 7500 |     |     |     |
| Arg  | Asn | Arg | Arg | Gly | Ser | Ala  | Gly | Ser | Arg | His | Gly  | Pro | Arg | Ala |
| 7505 |     |     |     |     |     | 7510 |     |     |     |     | 7515 |     |     |     |
| Gly  | Ile | Arg | Cys | Gly | Thr | Gly  | Thr | Trp | Ala | Ala | Thr  | Thr | Arg | Gly |
| 7520 |     |     |     |     |     | 7525 |     |     |     |     | 7530 |     |     |     |
| Ser  | Ala | Ala | Ser | Ala | Arg | Gly  | Gly | Arg | Gly | Thr | Ser  | Arg | Ser | Thr |
| 7535 |     |     |     |     |     | 7540 |     |     |     |     | 7545 |     |     |     |
| Ala  | Cys | Ala | Val | Ala | Gly | Arg  | Pro | Ala | Gly | Arg | Ala  | Arg | Arg | Ser |
| 7550 |     |     |     |     |     | 7555 |     |     |     |     | 7560 |     |     |     |
| Asn  | Arg | Ser | Trp | Asp | Pro | Arg  | Ser | Ala | Arg | Glu | Ser  | Tyr | Gly | Thr |
| 7565 |     |     |     |     |     | 7570 |     |     |     |     | 7575 |     |     |     |
| Arg  | Gly | Cys | Ser | Thr | Gly | Thr  | Pro | Ser | Gly | Pro | Gly  | Ala | Ser | Arg |
| 7580 |     |     |     |     |     | 7585 |     |     |     |     | 7590 |     |     |     |
| Ser  | Pro | Ala | Pro | Ser | Arg | Arg  | Cys | Pro | Pro | Arg | Pro  | Asp | Pro | Arg |
| 7595 |     |     |     |     |     | 7600 |     |     |     |     | 7605 |     |     |     |



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Arg Trp Pro Ser Arg Arg Gly Ser Ser Cys Arg Ser Ala Ala Pro  
 7610 7615 7620  
 Cys Trp Ala Arg Ser Arg Ala Cys Gly Cys Asn Arg Ser Ala Gly  
 7625 7630 7635  
 Gly Ser Ala Ser Ser Gly Pro Ala Arg Ser Ser Cys Pro Gly Thr  
 7640 7645 7650  
 Trp Pro Ser Lys Pro Pro Ala Gly Gly Arg Pro Ala Ala Pro Cys  
 7655 7660 7665  
 Arg Pro Arg Arg Arg Pro Arg Arg Thr Cys Arg Thr Gly Trp Trp  
 7670 7675 7680  
 Arg Ser Gln Arg Arg Ala Arg Ser Ser Ala Arg Arg Cys Trp Pro  
 7685 7690 7695  
 Ala Ala Pro Arg Cys Ala Pro Ser Gly Ser Gly Ser Trp Pro Gly  
 7700 7705 7710  
 Arg Gly Ser Pro Ser Ala Arg Ala Ala Arg Ser Arg Ser Pro His  
 7715 7720 7725  
 Pro Ser Arg Ser Cys Ala Pro Ser Gly Ser Ser Arg Ser Arg Ala  
 7730 7735 7740  
 Gly Thr Ala Ala Cys Pro Arg Pro Arg Cys Thr Arg Ala Ala Thr  
 7745 7750 7755  
 Ala Arg Ser Arg Cys Ser Pro Ser Ser Cys Gly Arg Ser Gly Ser  
 7760 7765 7770  
 Ala Ser Ala Arg Ser Pro Ala Gly Ser Gly Pro Ser Ser Trp Ser  
 7775 7780 7785  
 Gly Ser Cys Cys Trp Arg Ser Ala Glu Cys Arg Gly Ala Pro Arg  
 7790 7795 7800  
 Ser His Thr Gly Gly Arg Tyr Gly Gly Thr Pro Arg Pro Ala Arg  
 7805 7810 7815  
 Ala Ser Ala Gly Arg Arg Thr Ser Gly Arg Ser Pro Arg Gly Thr  
 7820 7825 7830  
 Gly Pro Ser Ala Ala Ser Ser Leu Pro Cys Pro Ser Pro Arg Pro  
 7835 7840 7845

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Lys Arg Ser Ala Gly Ser Gly Gly Ser Ser Pro Leu Ser Ser Ser  
 7850 7855 7860  
 Pro Pro Pro Lys Ser Gly Gly Arg Ser Arg Pro Gly Ser Gln Thr  
 7865 7870 7875  
 Leu Ala Cys Arg Pro Ser Arg Cys Ala Arg Gly Glu Ser Ser Pro  
 7880 7885 7890  
 Arg Pro Pro Ala Pro Pro Arg Pro Ala Phe Arg Pro Arg Cys Pro  
 7895 7900 7905  
 Gly Cys Leu Ala Lys Ala His Ala Trp Ser Cys Gly Val Ser Phe  
 7910 7915 7920  
 Trp Ala Ala Glu Ala Ala Ala Glu Thr Cys Trp Ala Ser Ala Ser  
 7925 7930 7935  
 Ser Arg Ser Pro Arg Leu Phe Leu Leu Leu Gly Arg Arg Pro Arg  
 7940 7945 7950  
 Pro Arg Gly Gly Arg His Ala Ser Ser Gly Ala Glu Ala Glu Ala  
 7955 7960 7965  
 Thr Gly Ser Arg Gly Ser Ala Gly Gly Trp Gln Ser Pro Phe Arg  
 7970 7975 7980  
 Val Arg Gly Cys Ala Pro Gly Gly Ala Ala Leu Thr Asp Phe Leu  
 7985 7990 7995  
 Arg Gly Arg Pro Leu Cys Ser Pro Arg Glu Gln Ala Trp Arg Leu  
 8000 8005 8010  
 Ser His Arg Arg Gln His Arg His Leu Pro Pro Pro Pro Pro Thr  
 8015 8020 8025  
 Arg Thr Ser Ser Ser Arg Met Lys Ala Pro Pro Arg Arg Pro Ala  
 8030 8035 8040  
 Pro Pro Pro Thr Pro Gln Pro Gln Thr Cys Lys Arg Trp Arg Asn  
 8045 8050 8055  
 Pro Ser Arg Leu Thr Trp Ala Thr Arg Pro Arg Ser Thr Arg Arg  
 8060 8065 8070  
 Ser Trp Gln Arg Ala Phe Gln Pro Arg Lys Arg Thr Thr Lys Ser  
 8075 8080 8085

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser  | Gln | Ser | Arg | Lys | Gln | Arg  | Ala | Ser | Arg | Thr | Arg  | Leu | Gly | Ser |
| 8090 |     |     |     |     |     | 8095 |     |     |     |     | 8100 |     |     |     |
| Ser  | Met | Ala | Thr | Thr | Ala | Gly  | Gln | Arg | Thr | Cys | Ser  | Ser | Ser | Ile |
| 8105 |     |     |     |     |     | 8110 |     |     |     |     | 8115 |     |     |     |
| Trp  | Pro | Ala | Asn | Ala | Ser | Ser  | Ser | Arg | Thr | Arg | Cys  | Ser | Thr | Ala |
| 8120 |     |     |     |     |     | 8125 |     |     |     |     | 8130 |     |     |     |
| Pro  | Arg | Cys | Pro | Ser | Ala | Trp  | Arg | Ser | Ser | Ala | Ala  | Pro | Thr | Ser |
| 8135 |     |     |     |     |     | 8140 |     |     |     |     | 8145 |     |     |     |
| Ala  | Thr | Ser | Ser | Arg | Arg | Ala  | Cys | Pro | Pro | Ser | Ala  | Ser | Pro | Thr |
| 8150 |     |     |     |     |     | 8155 |     |     |     |     | 8160 |     |     |     |
| Ala  | Pro | Ala | Ser | Pro | Thr | Arg  | Ala | Ser | Thr | Ser | Thr  | Arg | Ser | Ser |
| 8165 |     |     |     |     |     | 8170 |     |     |     |     | 8175 |     |     |     |
| Arg  | Cys | Pro | Arg | Pro | Trp | Pro  | Pro | Thr | Thr | Ser | Phe  | Ser | Arg | Thr |
| 8180 |     |     |     |     |     | 8185 |     |     |     |     | 8190 |     |     |     |
| Lys  | Gly | Ser | Pro | Ser | Pro | Ala  | Ala | Pro | Thr | Ala | Pro  | Ala | Pro | Thr |
| 8195 |     |     |     |     |     | 8200 |     |     |     |     | 8205 |     |     |     |
| Pro  | Cys | Ser | Thr | Trp | Ala | Pro  | Ala | Pro | Ala | Tyr | Leu  | Ile | Ser | Pro |
| 8210 |     |     |     |     |     | 8215 |     |     |     |     | 8220 |     |     |     |
| Pro  | Trp | Lys | Arg | Phe | Pro | Arg  | Ser | Ser | Arg | Val | Trp  | Ala | Ala | Thr |
| 8225 |     |     |     |     |     | 8230 |     |     |     |     | 8235 |     |     |     |
| Arg  | Leu | Gly | Pro | Arg | Thr | Leu  | Cys | Lys | Glu | Ala | Glu  | Arg | Ser | Met |
| 8240 |     |     |     |     |     | 8245 |     |     |     |     | 8250 |     |     |     |
| Ser  | Thr | Thr | Ala | Pro | Trp | Trp  | Ser | Trp | Lys | Ala | Thr  | Thr | Arg | Ala |
| 8255 |     |     |     |     |     | 8260 |     |     |     |     | 8265 |     |     |     |
| Trp  | Arg | Ser | Ser | Ser | Ala | Arg  | Ser | Ser | Pro | Thr | Ser  | Pro | Thr | Arg |
| 8270 |     |     |     |     |     | 8275 |     |     |     |     | 8280 |     |     |     |
| Arg  | Ser | Thr | Cys | Pro | Pro | Arg  | Ser | Ala | Pro | Ser | Trp  | Thr | Arg | Cys |
| 8285 |     |     |     |     |     | 8290 |     |     |     |     | 8295 |     |     |     |
| Ser  | Ser | Ser | Ala | Pro | Arg | Pro  | Ser | Arg | Arg | Arg | Arg  | Cys | Arg | Thr |
| 8300 |     |     |     |     |     | 8305 |     |     |     |     | 8310 |     |     |     |
| Pro  | Arg | Ala | Arg | Thr | Arg | Ala  | Ser | Pro | Trp | Ser | Ala  | Thr | Ser | Ser |

8315

8320

8325

Trp Arg Ala Gly Trp Glu Arg Val Ala Pro Pro Arg Ala Trp Lys  
 8330 8335 8340  
 Ser Gly Ala Ser Ser Trp Pro Trp Ser Trp Pro Trp Ser Trp Ser  
 8345 8350 8355  
 Val Cys Ala Ala Ser Ser Pro Thr Arg Arg Pro Cys Ala Arg Ser  
 8360 8365 8370  
 Arg Arg Thr Cys Thr Thr Ser Ser Asp Thr Gly Ser Cys Ala Arg  
 8375 8380 8385  
 Pro Ala Arg Ser Pro Thr Trp Ser Pro Thr Trp Ser Pro Thr Trp  
 8390 8395 8400  
 Ala Ser Cys Thr Arg Thr Ala Trp Gly Arg Thr Cys Cys Thr Pro  
 8405 8410 8415  
 Pro Cys Ala Gly Arg Pro Ala Ala Thr Thr Ser Ala Thr Ala Ser  
 8420 8425 8430  
 Thr Cys Thr Ser Ala Thr Pro Gly Arg Arg Ala Trp Ala Cys Gly  
 8435 8440 8445  
 Ser Ser Ala Trp Arg Ser Arg Thr Lys Ser Ser Ala Ser Ser Cys  
 8450 8455 8460  
 Arg Arg Thr Ser Arg Pro Cys Gly Pro Gly Ser Thr Ser Ala Pro  
 8465 8470 8475  
 Pro Pro Arg Thr Trp Pro Thr Ser Ser Ser Pro Ser Ala Cys Gly  
 8480 8485 8490  
 Arg Cys Ala Thr Gly Cys Pro Thr Leu Ala Lys Ala Cys Cys Lys  
 8495 8500 8505  
 Thr Phe Ala Leu Ser Ser Ser Asn Ala Pro Gly Ser Cys Pro Pro  
 8510 8515 8520  
 Pro Ala Pro Arg Cys Pro Arg Thr Ser Cys Arg Pro Ser Ala Ser  
 8525 8530 8535  
 Ala Pro Arg Arg Ser Gly Ala Thr Ala Thr Cys Cys Ala Trp Pro  
 8540 8545 8550

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Thr  | Trp | Pro | Thr | Thr | Arg  | Thr | Ser | Arg | Thr | Ser  | Ala | Ala | Arg |
|     | 8555 |     |     |     |     | 8560 |     |     |     |     | 8565 |     |     |     |
| Ala | Cys  | Ser | Ser | Ala | Thr | Ala  | Ala | Ala | Thr | Ser | Ala  | Arg | Arg | Thr |
|     | 8570 |     |     |     |     | 8575 |     |     |     |     | 8580 |     |     |     |
| Ala | Pro  | Trp | Pro | Ala | Thr | Pro  | Ser | Cys | Ala | Arg | Pro  | Arg | Ser | Ser |
|     | 8585 |     |     |     |     | 8590 |     |     |     |     | 8595 |     |     |     |
| Ala | Pro  | Ser | Ser | Cys | Lys | Ala  | Pro | Ala | Arg | Ala | Arg  | Gly | Val | Asn |
|     | 8600 |     |     |     |     | 8605 |     |     |     |     | 8610 |     |     |     |
| Ser | Pro  | Arg | Gly | Cys | Gly | Pro  | Arg | Pro | Thr | Cys | Ala  | Ser | Ser | Cys |
|     | 8615 |     |     |     |     | 8620 |     |     |     |     | 8625 |     |     |     |
| Pro | Arg  | Thr | Thr | Ile | Pro | Ser  | Arg | Ser | Gly | Ser | Thr  | Arg | Thr | Asn |
|     | 8630 |     |     |     |     | 8635 |     |     |     |     | 8640 |     |     |     |
| Pro | Ser  | Arg | Pro | Arg | Pro | Ser  | Cys | Arg | Pro | Ala | Ser  | Ser | Pro | Arg |
|     | 8645 |     |     |     |     | 8650 |     |     |     |     | 8655 |     |     |     |
| Gly | Pro  | Ser | Trp | Pro | Asn | Cys  | Lys | Pro | Ser | Arg | Asn  | Pro | Ala | Lys |
|     | 8660 |     |     |     |     | 8665 |     |     |     |     | 8670 |     |     |     |
| Asn | Phe  | Cys | Lys | Arg | Ala | Thr  | Gly | Ser | Thr | Trp | Thr  | Pro | Arg | Pro |
|     | 8675 |     |     |     |     | 8680 |     |     |     |     | 8685 |     |     |     |
| Glu | Arg  | Ser | Ser | Thr | Pro | Ala  | Ser | Pro | Arg | Met | Pro  | Arg | Gly | Ser |
|     | 8690 |     |     |     |     | 8695 |     |     |     |     | 8700 |     |     |     |
| Ser | Lys  | Lys | Leu | Lys | Val | Glu  | Leu | Pro | Pro | Pro | Pro  | Glu | Asp | Leu |
|     | 8705 |     |     |     |     | 8710 |     |     |     |     | 8715 |     |     |     |
| Glu | Glu  | Asp | Trp | Glu | Ser | Ser  | Gln | Ala | Glu | Glu | Glu  | Glu | Met | Glu |
|     | 8720 |     |     |     |     | 8725 |     |     |     |     | 8730 |     |     |     |
| Asp | Trp  | Asp | Ser | Thr | Gln | Ala  | Glu | Glu | Asp | Ser | Leu  | Gln | Asp | Ser |
|     | 8735 |     |     |     |     | 8740 |     |     |     |     | 8745 |     |     |     |
| Leu | Glu  | Glu | Glu | Asp | Glu | Val  | Glu | Glu | Ala | Glu | Glu  | Glu | Ala | Ala |
|     | 8750 |     |     |     |     | 8755 |     |     |     |     | 8760 |     |     |     |
| Ala | Ala  | Arg | Pro | Ser | Ser | Ser  | Ala | Glu | Glu | Glu | Lys  | Ala | Ser | Ser |
|     | 8765 |     |     |     |     | 8770 |     |     |     |     | 8775 |     |     |     |
| Thr | Asp  | Thr | Ile | Ser | Ala | Pro  | Gly | Arg | Gly | Arg | Gly  | Gly | Arg | Ala |
|     | 8780 |     |     |     |     | 8785 |     |     |     |     | 8790 |     |     |     |

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His Ser Arg Trp Asp Glu Thr Gly Arg Phe Pro Asn Pro Thr Thr  
 8795 8800 8805  
  
 Gln Thr Gly Lys Lys Glu Arg Gln Gly Tyr Lys Ser Trp Arg Gly  
 8810 8815 8820  
  
 His Lys Asn Ala Ile Val Ser Cys Leu Gln Ala Cys Gly Gly Asn  
 8825 8830 8835  
  
 Ile Ser Phe Thr Arg Arg Tyr Leu Leu Phe His Arg Gly Val Asn  
 8840 8845 8850  
  
 Phe Pro Arg Asn Ile Leu His Tyr Tyr Arg His Leu His Ser Pro  
 8855 8860 8865  
  
 Tyr Tyr Cys Phe Gln Glu Glu Ala Glu Thr Gln Gln Gln Gln Gln  
 8870 8875 8880  
  
 Gln Gln Lys Thr Ser Gly Ser Ser Lys Ile His Ser Gly Gly Arg  
 8885 8890 8895  
  
 Trp Thr Glu Asp Arg Gly Glu Arg Ala Gly Ala Asp Pro Gly Ala  
 8900 8905 8910  
  
 Glu Glu Pro Asp Leu Ser His Pro Leu Cys His Leu Pro Ala Glu  
 8915 8920 8925  
  
 Ser Gly Ala Arg Ala Gly Thr Glu Ser Gln Glu Pro Phe Ser Ala  
 8930 8935 8940  
  
 Leu Ala His Pro Gln Leu Ser Val Ser Gln Glu Arg Arg Pro Thr  
 8945 8950 8955  
  
 Ser Ala His Ser Arg Gly Arg Arg Gly Ser Leu Gln Gln Val Leu  
 8960 8965 8970  
  
 Arg Ala His Ser Arg Val Ala Arg Ala Arg Pro His Thr Glu Lys  
 8975 8980 8985  
  
 Gly Gly Asn Tyr Val Thr Thr Cys Ala Leu Arg Pro Thr Ile Ile  
 8990 8995 9000  
  
 Met Ser Lys Glu Ile Pro Thr Pro Tyr Met Trp Ser Tyr Gln Pro  
 9005 9010 9015  
  
 Gln Met Gly Leu Ala Ala Gly Ala Ala Gln Asp Tyr Ser Thr Arg  
 9020 9025 9030

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Met | Asn  | Trp | Leu | Ser | Ala | Gly  | Pro | Ala | Met | Ile | Ser  | Arg | Val | Asn |
|     | 9035 |     |     |     |     | 9040 |     |     |     |     | 9045 |     |     |     |
| Asp | Ile  | Arg | Ala | His | Arg | Asn  | Gln | Ile | Leu | Leu | Glu  | Gln | Ser | Ala |
|     | 9050 |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Ile | Thr  | Ala | Thr | Pro | Arg | His  | His | Leu | Asn | Pro | Arg  | Asn | Trp | Pro |
|     | 9065 |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Ala | Ala  | Leu | Val | Tyr | Gln | Glu  | Ile | Pro | Gln | Pro | Thr  | Thr | Val | Leu |
|     | 9080 |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Leu | Pro  | Arg | Asp | Ala | Gln | Ala  | Glu | Val | Gln | Leu | Thr  | Asn | Ser | Gly |
|     | 9095 |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Val | Gln  | Leu | Ala | Gly | Gly | Ala  | Ala | Leu | Cys | Arg | His  | Arg | Pro | Ala |
|     | 9110 |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Gln | Gly  | Ile | Lys | Arg | Leu | Val  | Ile | Arg | Gly | Arg | Gly  | Thr | Gln | Leu |
|     | 9125 |     |     |     |     | 9130 |     |     |     |     | 9135 |     |     |     |
| Asn | Asp  | Glu | Val | Val | Ser | Ser  | Ser | Leu | Gly | Leu | Arg  | Pro | Asp | Gly |
|     | 9140 |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Val | Phe  | Gln | Leu | Ala | Gly | Ser  | Gly | Arg | Ser | Ser | Phe  | Thr | Pro | Arg |
|     | 9155 |     |     |     |     | 9160 |     |     |     |     | 9165 |     |     |     |
| Gln | Ala  | Val | Leu | Thr | Leu | Glu  | Ser | Ser | Ser | Ser | Gln  | Pro | Arg | Ser |
|     | 9170 |     |     |     |     | 9175 |     |     |     |     | 9180 |     |     |     |
| Gly | Gly  | Ile | Gly | Thr | Leu | Gln  | Phe | Val | Glu | Glu | Phe  | Thr | Pro | Ser |
|     | 9185 |     |     |     |     | 9190 |     |     |     |     | 9195 |     |     |     |
| Val | Tyr  | Phe | Asn | Pro | Phe | Ser  | Gly | Ser | Pro | Gly | His  | Tyr | Pro | Asp |
|     | 9200 |     |     |     |     | 9205 |     |     |     |     | 9210 |     |     |     |
| Glu | Phe  | Ile | Pro | Asn | Phe | Asp  | Ala | Ile | Ser | Glu | Ser  | Val | Asp | Gly |
|     | 9215 |     |     |     |     | 9220 |     |     |     |     | 9225 |     |     |     |
| Tyr | Asp  | Met | Ser | His | Gly | Gly  | Ala | Ala | Asp | Leu | Ala  | Arg | Leu | Arg |
|     | 9230 |     |     |     |     | 9235 |     |     |     |     | 9240 |     |     |     |
| His | Leu  | Asp | His | Cys | Arg | Arg  | Phe | Arg | Cys | Phe | Ala  | Arg | Asp | Leu |
|     | 9245 |     |     |     |     | 9250 |     |     |     |     | 9255 |     |     |     |
| Ala | Glu  | Phe | Ala | Tyr | Phe | Glu  | Leu | Pro | Glu | Glu | His  | Pro | Gln | Gly |

9260

9265

9270

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Ala  | His | Gly | Val | Arg | Ile  | Val | Val | Glu | Gly | Gly  | Leu | Asp | Ser |
|     | 9275 |     |     |     |     | 9280 |     |     |     |     | 9285 |     |     |     |
| His | Leu  | Leu | Arg | Ile | Phe | Ser  | Gln | Arg | Pro | Ile | Leu  | Ala | Glu | Arg |
|     | 9290 |     |     |     |     | 9295 |     |     |     |     | 9300 |     |     |     |
| Glu | Gln  | Gly | Gln | Thr | Leu | Leu  | Thr | Leu | Tyr | Cys | Ile  | Cys | Asn | His |
|     | 9305 |     |     |     |     | 9310 |     |     |     |     | 9315 |     |     |     |
| Pro | Gly  | Leu | His | Glu | Ser | Leu  | Cys | Cys | Leu | Leu | Cys  | Thr | Glu | Tyr |
|     | 9320 |     |     |     |     | 9325 |     |     |     |     | 9330 |     |     |     |
| Asn | Lys  | Ser | Asp | Gln | Arg | Leu  | Leu | Arg | Thr | Ser | Val  | Cys | Ser | Cys |
|     | 9335 |     |     |     |     | 9340 |     |     |     |     | 9345 |     |     |     |
| Tyr | Gln  | Pro | Val | Pro | Val | Leu  | His | Arg | Glu | Arg | Asp  | Arg | Ala | Pro |
|     | 9350 |     |     |     |     | 9355 |     |     |     |     | 9360 |     |     |     |
| Ala | Pro  | Val | Ala | Pro | Gln | Glu  | Val | Pro | His | Leu | Ala  | Val | Pro | Gly |
|     | 9365 |     |     |     |     | 9370 |     |     |     |     | 9375 |     |     |     |
| Leu | Ser  | Asp | Arg | Arg | Cys | Gln  | Pro | Leu | Arg | Gln | Arg  | Arg | Ser | Pro |
|     | 9380 |     |     |     |     | 9385 |     |     |     |     | 9390 |     |     |     |
| Ala | Glu  | Arg | Pro | Cys | Gln | Pro  | Tyr | Phe | Phe | His | Pro  | Gln | Lys | Gln |
|     | 9395 |     |     |     |     | 9400 |     |     |     |     | 9405 |     |     |     |
| Ala | Pro  | Ala | Leu | Pro | Thr | Leu  | Pro | Pro | Arg | Asp | Leu  | Ser | Val | Arg |
|     | 9410 |     |     |     |     | 9415 |     |     |     |     | 9420 |     |     |     |
| Leu | Gly  | Thr | Leu | Pro | Ser | His  | Leu | Pro | Pro | Asp | Pro  | Glu | Tyr | His |
|     | 9425 |     |     |     |     | 9430 |     |     |     |     | 9435 |     |     |     |
| Ser | Val  | Ala | Pro | Arg | Tyr | Gln  | Pro | Asn | Tyr | Pro | Pro  | Thr | Pro | Pro |
|     | 9440 |     |     |     |     | 9445 |     |     |     |     | 9450 |     |     |     |
| Ser | Arg  | Pro | Arg | Thr | Cys | Thr  | Glu | Leu | Glu | Lys | Tyr  | Ala | Thr | Ile |
|     | 9455 |     |     |     |     | 9460 |     |     |     |     | 9465 |     |     |     |
| His | Ala  | His | Ile | Arg | Leu | Gly  | Arg | Ala | Thr | Ala | Thr  | His | Ala | Pro |
|     | 9470 |     |     |     |     | 9475 |     |     |     |     | 9480 |     |     |     |
| Arg | Tyr  | Leu | Leu | Gln | Ser | Asn  | Arg | Arg | Arg | Leu | Thr  | His | Trp | Pro |
|     | 9485 |     |     |     |     | 9490 |     |     |     |     | 9495 |     |     |     |



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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Thr  | Thr | Ser | Thr | Thr | Phe  | Ser | Trp | Thr | Trp | Thr  | Ala | Ala | Pro |
|     | 9500 |     |     |     |     | 9505 |     |     |     |     | 9510 |     |     |     |
| Arg | Ser  | Ser | Asp | Ser | Pro | Asn  | Phe | Ala | Phe | Ala | Ser  | Ser | Arg | Arg |
|     | 9515 |     |     |     |     | 9520 |     |     |     |     | 9525 |     |     |     |
| Glu | Pro  | Ser | Arg | Ser | Cys | Arg  | Thr | Ala | Pro | Ser | Thr  | Ser | Ala | Arg |
|     | 9530 |     |     |     |     | 9535 |     |     |     |     | 9540 |     |     |     |
| Lys | Ala  | Ser | Ser | Ala | Trp | Asn  | Arg | Pro | Arg | Ser | Pro  | Thr | Arg | Ser |
|     | 9545 |     |     |     |     | 9550 |     |     |     |     | 9555 |     |     |     |
| Pro | Arg  | Pro | Thr | Ile | Ala | Ser  | Pro | Thr | Ser | Ser | Cys  | Ser | Ser | Ala |
|     | 9560 |     |     |     |     | 9565 |     |     |     |     | 9570 |     |     |     |
| Arg | Ser  | Ser | Pro | Ala | Trp | Ser  | Glu | Ser | Thr | Pro | Ser  | Ser | Ser | Pro |
|     | 9575 |     |     |     |     | 9580 |     |     |     |     | 9585 |     |     |     |
| Ser | Ser  | Arg | Ala | Ile | Pro | Arg  | Gly | Ala | Ser | Thr | Ala  | Pro | Ala | Thr |
|     | 9590 |     |     |     |     | 9595 |     |     |     |     | 9600 |     |     |     |
| Pro | Pro  | Thr | Ala | Ser | Thr | Leu  | Ser | Arg | Pro | Ser | Ala  | Ala | Ser | Ala |
|     | 9605 |     |     |     |     | 9610 |     |     |     |     | 9615 |     |     |     |
| Thr | Ser  | Ser | Pro | Thr | Asn | His  | Pro | Leu | Ile | Gln | Asn  | Lys | Tyr | His |
|     | 9620 |     |     |     |     | 9625 |     |     |     |     | 9630 |     |     |     |
| Ile | Asp  | Asp | Asp | Leu | Asn | Lys  | Lys | Ser | Phe | Asp | Leu  | Lys | Arg | Tyr |
|     | 9635 |     |     |     |     | 9640 |     |     |     |     | 9645 |     |     |     |
| Asn | His  | Ile | Asp | Asp | Leu | Ser  | Phe | Lys | Lys | Arg | Ile  | Thr | Tyr | Leu |
|     | 9650 |     |     |     |     | 9655 |     |     |     |     | 9660 |     |     |     |
| Lys | Ser  | Asp | Thr | Arg | Ser | Leu  | Ser | Met | Phe | Ser | Ala  | Asn | Thr | Thr |
|     | 9665 |     |     |     |     | 9670 |     |     |     |     | 9675 |     |     |     |
| Ser | Leu  | Pro | Ser | Ser | Gln | Leu  | Trp | Tyr | Cys | Arg | Pro  | Arg | Arg | Ala |
|     | 9680 |     |     |     |     | 9685 |     |     |     |     | 9690 |     |     |     |
| Ala | Asn  | Phe | Leu | His | Thr | Leu  | Lys | Gly | Met | Ser | Asn  | Ser | Ser | Cys |
|     | 9695 |     |     |     |     | 9700 |     |     |     |     | 9705 |     |     |     |
| Pro | Ser  | Ile | Phe | Ile | Leu | Ser  | Ser | Ile | Arg | Cys | Pro  | Lys | Ser | Ala |
|     | 9710 |     |     |     |     | 9715 |     |     |     |     | 9720 |     |     |     |
| Ser | Gly  | Trp | Met | Met | Thr | Ser  | Thr | Pro | Ser | Thr | Pro  | Thr | Met | Gln |
|     | 9725 |     |     |     |     | 9730 |     |     |     |     | 9735 |     |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Thr  | His | Arg | Pro | Cys | Pro  | Ser | Ser | Thr | Pro | Pro  | Ser | Ser | Leu |
|     | 9740 |     |     |     |     | 9745 |     |     |     |     | 9750 |     |     |     |
| Gln | Met  | Asp | Ser | Lys | Arg | Ser  | Pro | Trp | Gly | Cys | Cys  | Pro | Cys | Asp |
|     | 9755 |     |     |     |     | 9760 |     |     |     |     | 9765 |     |     |     |
| Trp | Leu  | Thr | Pro | Ser | Pro | Pro  | Arg | Thr | Gly | Lys | Ser  | Pro | Ser | Ser |
|     | 9770 |     |     |     |     | 9775 |     |     |     |     | 9780 |     |     |     |
| Trp | Glu  | Arg | Gly | Trp | Thr | Ser  | Thr | Pro | Arg | Glu | Asn  | Ser | Ser | Pro |
|     | 9785 |     |     |     |     | 9790 |     |     |     |     | 9795 |     |     |     |
| Thr | Arg  | Pro | Pro | Arg | Pro | Pro  | Pro | Leu | Ser | Val | Phe  | Pro | Thr | Thr |
|     | 9800 |     |     |     |     | 9805 |     |     |     |     | 9810 |     |     |     |
| Pro | Phe  | Pro | Leu | Thr | Trp | Ile  | Pro | Leu | Phe | Ile | Pro  | Lys | Met | Glu |
|     | 9815 |     |     |     |     | 9820 |     |     |     |     | 9825 |     |     |     |
| Asn | Tyr  | Pro | Tyr | Lys | Phe | Leu  | His | Arg | Thr | Tyr | Asn  | Gln | Pro | Phe |
|     | 9830 |     |     |     |     | 9835 |     |     |     |     | 9840 |     |     |     |
| Thr | His  | Leu | Leu | Met | Asp | Gln  | Val | Asp | Val | Val | Ala  | Leu | Leu | Leu |
|     | 9845 |     |     |     |     | 9850 |     |     |     |     | 9855 |     |     |     |
| Gln | Tyr  | Ser | Trp | Pro | Leu | His  | Ser | Leu | Leu | Met | Lys  | Lys | Glu | Ile |
|     | 9860 |     |     |     |     | 9865 |     |     |     |     | 9870 |     |     |     |
| Leu | Lys  | Leu | Thr | Pro | Val | Val  | His | Gln | Leu | Met | Gln  | Val | Asp | Leu |
|     | 9875 |     |     |     |     | 9880 |     |     |     |     | 9885 |     |     |     |
| Val | Ser  | Thr | Ala | Lys | Glu | Gly  | Ser | Leu | Ser | Leu | Pro  | Gln | Glu | Met |
|     | 9890 |     |     |     |     | 9895 |     |     |     |     | 9900 |     |     |     |
| Gln | Leu  | Lys | Ala | Thr | Ala | Gly  | Leu | Lys | Val | Asp | Leu  | Lys | Val | Met |
|     | 9905 |     |     |     |     | 9910 |     |     |     |     | 9915 |     |     |     |
| Ala | Leu  | Gln | Thr | Leu | Ala | Glu  | Asp | Trp | Asn | Leu | Glu  | Pro | Leu | Val |
|     | 9920 |     |     |     |     | 9925 |     |     |     |     | 9930 |     |     |     |
| Gln | Arg  | Leu | Met | Ser | Gln | Met  | His | Thr | Gln | Phe | Lys  | Leu | Asn | Trp |
|     | 9935 |     |     |     |     | 9940 |     |     |     |     | 9945 |     |     |     |
| Val | Leu  | Ala | Leu | Pro | Leu | Thr  | Val | Gln | Ala | Pro | Leu  | Leu | Leu | Gly |
|     | 9950 |     |     |     |     | 9955 |     |     |     |     | 9960 |     |     |     |
| Thr | Lys  | Arg | Met | Ile | Asn | Leu  | His | Tyr | Gly | Pro | Gln  | Pro | Thr | Pro |
|     | 9965 |     |     |     |     | 9970 |     |     |     |     | 9975 |     |     |     |

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|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Arg   | Gln | Ile | Ala | Lys | Tyr | Thr   | Leu | Lys | Lys | Met | Pro   | Asn | Ser | His |
| 9980  |     |     |     |     |     | 9985  |     |     |     |     | 9990  |     |     |     |
| Phe   | Ala | Gln | Ser | Val | Glu | Val   | Lys | Phe | Trp | Val | Leu   | Leu | Tyr | Trp |
| 9995  |     |     |     |     |     | 10000 |     |     |     |     | 10005 |     |     |     |
| Gln   | Ile | Met | Glu | Val | Ser | Thr   | Gln | Ser | Gln | Thr | Gln   | Ala | Leu | His |
| 10010 |     |     |     |     |     | 10015 |     |     |     |     | 10020 |     |     |     |
| Ser   | Ser | Pro | Ser | Ser | Leu | Met   | Gln | Val | Glu | Phe | Cys   | Ala | Ala | Pro |
| 10025 |     |     |     |     |     | 10030 |     |     |     |     | 10035 |     |     |     |
| His   | Thr | Lys | Asn | Ile | Gly | Thr   | Ser | Glu | Arg | Glu | Met   | Leu | His | Leu |
| 10040 |     |     |     |     |     | 10045 |     |     |     |     | 10050 |     |     |     |
| Leu   | Ser | Pro | Ile | Leu | Met | Leu   | Val | Leu | Cys | Leu | Thr   | Arg | Pro | Ile |
| 10055 |     |     |     |     |     | 10060 |     |     |     |     | 10065 |     |     |     |
| Leu   | Lys | Thr | His | Leu | Gln | Leu   | Gln | Lys | Ala | Ile | Leu   | Ser | Val | Lys |
| 10070 |     |     |     |     |     | 10075 |     |     |     |     | 10080 |     |     |     |
| Phe   | Ile | Ser | Met | Gly | Met | Arg   | Pro | Asn | His | Cys | Leu   | Leu | Leu | Leu |
| 10085 |     |     |     |     |     | 10090 |     |     |     |     | 10095 |     |     |     |
| Met   | Lys | Leu | Arg | Met | Gln | Leu   | Ala | Pro | Thr | Val | Ser   | Leu | Phe | Asn |
| 10100 |     |     |     |     |     | 10105 |     |     |     |     | 10110 |     |     |     |
| Gly   | Asn | Gly | Ile | Val | Leu | Ser   | Thr | Gln | Val | Lys | His   | Leu | Leu | Pro |
| 10115 |     |     |     |     |     | 10120 |     |     |     |     | 10125 |     |     |     |
| Ala   | Pro | Ser | Pro | Ser | Pro | Thr   | Ser | Pro | Lys | Asn | Glu   | His | Cys | Ile |
| 10130 |     |     |     |     |     | 10135 |     |     |     |     | 10140 |     |     |     |
| Pro   | Pro | Cys | Met | Pro | Thr | Leu   | Pro | Thr | Pro | Leu | Cys   | Leu | Trp | Lys |
| 10145 |     |     |     |     |     | 10150 |     |     |     |     | 10155 |     |     |     |
| Lys   | Leu | Ser | Thr | Lys | Asn | Lys   | Val | Gln | Val | Phe | Tyr   | Phe | Asn | Ser |
| 10160 |     |     |     |     |     | 10165 |     |     |     |     | 10170 |     |     |     |
| Phe   | Thr | Gly | Phe | Glu | Gln | Leu   | Phe | Phe | Leu | His | Pro   | Pro | Arg | Thr |
| 10175 |     |     |     |     |     | 10180 |     |     |     |     | 10185 |     |     |     |
| Trp   | Asn | Thr | Pro | Pro | Ser | Pro   | Pro | Ala | Gln | Pro | Thr   | Ser | Glu | Cys |
| 10190 |     |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| His   | Trp | Trp | Thr | Cys | Phe | Trp   | Ser | Pro | Arg | Ser | Thr   | Gln | Phe | Gln |

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|       |     |     |     |     |     |       |     |     |     |     |       |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|
| 10205 |     |     |     |     |     |       |     |     |     |     |       |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Ser   | Glu | Pro | Val | Ser | Gly | Arg   | Ser | Gly | Arg | Asn | Pro   |
| 10220 |     |     |     |     |     | 10225 |     |     |     |     | 10230 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Pro   | Ala | Ser | Ala | Pro | His | Ser   | Ser | Thr | Ala | Glu | Asp   |
| 10235 |     |     |     |     |     | 10240 |     |     |     |     | 10245 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Trp   | Ser | Gly | Ser | Arg | Leu | Ser   | Gly | Arg | Ser | Arg | Arg   |
| 10250 |     |     |     |     |     | 10255 |     |     |     |     | 10260 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Gly   | Ile | Ile | Val | Arg | Glu | Arg   | Asp | Arg | Pro | Val | Val   |
| 10265 |     |     |     |     |     | 10270 |     |     |     |     | 10275 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Ala   | Pro | Gln | Gln | Ser | Leu | Pro   | Pro | Pro | Leu | Arg | Gln   |
| 10280 |     |     |     |     |     | 10285 |     |     |     |     | 10290 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Gln   | Gly | Val | Arg | Val | Gln | Gly   | Leu | Pro | Gln | His | Asp   |
| 10295 |     |     |     |     |     | 10300 |     |     |     |     | 10305 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Pro   | Gln | His | Gln | Ser | Ser | Gly   | Ala | Ala | Gly | Ala | Ala   |
| 10310 |     |     |     |     |     | 10315 |     |     |     |     | 10320 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Asp   | Leu | Ala | Gln | Val | Ala | Ala   | Val | Arg | Ala | Thr | Gln   |
| 10325 |     |     |     |     |     | 10330 |     |     |     |     | 10335 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Val   | Val | Gln | Gln | Ser | Ile | Val   | Gln | His | Ala | Pro | Ala   |
| 10340 |     |     |     |     |     | 10345 |     |     |     |     | 10350 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Arg   | Gly | Lys | Asp | Ala | Thr | His   | Val | Ala | Val | Val | Pro   |
| 10355 |     |     |     |     |     | 10360 |     |     |     |     | 10365 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Val   | Asn | Gln | Val | Ala | Leu | Pro   | Pro | Glu | His | Ala | Ala   |
| 10370 |     |     |     |     |     | 10375 |     |     |     |     | 10380 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Asp   | Leu | Leu | Gly | His | Val | Ala   | Val | His | His | Leu | Pro   |
| 10385 |     |     |     |     |     | 10390 |     |     |     |     | 10395 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| His   | Pro | Leu | Val | Glu | His | Ala   | Ala | Pro | Asp | Asp | Pro   |
| 10400 |     |     |     |     |     | 10405 |     |     |     |     | 10410 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Gln   | Gly | Gln | His | Arg | Pro | Ala   | Arg | His | Ala | Ala | Lys   |
| 10415 |     |     |     |     |     | 10420 |     |     |     |     | 10425 |
|       |     |     |     |     |     |       |     |     |     |     |       |
| Val   | Pro | Ala | Met | Ala | Met | Glu   | Asp | Pro | Pro | Leu | Val   |
| 10430 |     |     |     |     |     | 10435 |     |     |     |     | 10440 |
|       |     |     |     |     |     |       |     |     |     |     |       |

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|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| His   | Leu | Gly | Ala | Glu | Gln | Val   | Tyr | Val | Gly | Thr | Ala   | Gln | Ala | Tyr |
| 10445 |     |     |     |     |     | 10450 |     |     |     |     | 10455 |     |     |     |
| Ala   | His | Ala | Ser | Leu | Gln | His   | Ser | Gln | Leu | Leu | Gly   | Gly | Gln | Asn |
| 10460 |     |     |     |     |     | 10465 |     |     |     |     | 10470 |     |     |     |
| His   | Ile | Pro | Gly | His | Gly | Glu   | Leu | Leu | Gln | Asp | Ser   | Glu | Pro | Arg |
| 10475 |     |     |     |     |     | 10480 |     |     |     |     | 10485 |     |     |     |
| Arg   | Thr | Gly | Gln | Ser | Ser | His   | Ile | Thr | Tyr | Ile | Val   | His | Gly | Gln |
| 10490 |     |     |     |     |     | 10495 |     |     |     |     | 10500 |     |     |     |
| Gly   | Ile | Ala | Ile | Arg | Gln | His   | Arg | Val | Ile | Leu | His   | Gln | Arg | Ser |
| 10505 |     |     |     |     |     | 10510 |     |     |     |     | 10515 |     |     |     |
| Ala   | Gly | Leu | Gly | Leu | Leu | Thr   | Ala | Trp | Gly | Gly | Arg   | Pro | Ile | Arg |
| 10520 |     |     |     |     |     | 10525 |     |     |     |     | 10530 |     |     |     |
| Val   | Met | Ala | Gly | Arg | Gly | Ser   | Cys | Ser | Arg | Pro | Cys   | His | Asp | Ala |
| 10535 |     |     |     |     |     | 10540 |     |     |     |     | 10545 |     |     |     |
| Val   | Ala | Phe | Gly | His | Phe | Arg   | Thr | Cys | Cys | Ser | Arg   | Thr | Trp | Ser |
| 10550 |     |     |     |     |     | 10555 |     |     |     |     | 10560 |     |     |     |
| Gly   | Arg | Cys | Thr | Pro | Ile | Ala   | Gly | Gly | Gly | Pro | Gly   | Ala | Trp | Asn |
| 10565 |     |     |     |     |     | 10570 |     |     |     |     | 10575 |     |     |     |
| Ala   | Arg | Cys | Asn | Cys | Lys | Thr   | Ala | Thr | Leu | Ser | Asp   | Arg | Ala | Ala |
| 10580 |     |     |     |     |     | 10585 |     |     |     |     | 10590 |     |     |     |
| Asp   | Leu | Gly | Pro | Gln | Glu | Arg   | Ser | His | His | Ala | Leu   | Ser | His | Arg |
| 10595 |     |     |     |     |     | 10600 |     |     |     |     | 10605 |     |     |     |
| Pro   | Pro | Trp | Asn | Gly | Pro | Asp   | Pro | Ala | Arg | Cys | Asn   | Phe | Val | Gly |
| 10610 |     |     |     |     |     | 10615 |     |     |     |     | 10620 |     |     |     |
| Phe   | Arg | Arg | Arg | Gly | Arg | Glu   | Glu | Gln | Glu | Glu | Pro   | Leu | Thr | Phe |
| 10625 |     |     |     |     |     | 10630 |     |     |     |     | 10635 |     |     |     |
| Asn   | Pro | Asn | Gly | Leu | Gly | Ala   | Leu | Gln | Asn | Glu | Gly   | Arg | Gly | Asp |
| 10640 |     |     |     |     |     | 10645 |     |     |     |     | 10650 |     |     |     |
| Gly   | Thr | Ser | Arg | Pro | Arg | Cys   | Val | Gly | Gly | Lys | Gln   | Pro | Gly | Gln |
| 10655 |     |     |     |     |     | 10660 |     |     |     |     | 10665 |     |     |     |
| Arg   | Tyr | Gly | Ser | Arg | Asp | Val   | Pro | Arg | Trp | Leu | Pro   | Ala | Lys | Pro |
| 10670 |     |     |     |     |     | 10675 |     |     |     |     | 10680 |     |     |     |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Pro | Arg   | Ala | His | Pro | Glu | Thr   | Arg | Gln | Arg | Lys | Arg   | Glu | Gly | Ser |
|     | 10685 |     |     |     |     | 10690 |     |     |     |     | 10695 |     |     |     |
| Leu | Ile   | Pro | Gln | Ser | Ser | Cys   | Tyr | Thr | Pro | Ala | Pro   | Ser | Pro | Asp |
|     | 10700 |     |     |     |     | 10705 |     |     |     |     | 10710 |     |     |     |
| Asn | Phe   | His | Phe | Ser | Ser | Leu   | Glu | Phe | Glu | Leu | Val   | Pro | Glu | Val |
|     | 10715 |     |     |     |     | 10720 |     |     |     |     | 10725 |     |     |     |
| Asn | Pro   | Ser | Gln | Pro | Arg | Ala   | Arg | Ala | Glu | Arg | Pro   | Pro | Pro | Ala |
|     | 10730 |     |     |     |     | 10735 |     |     |     |     | 10740 |     |     |     |
| Phe | Leu   | Ser | Thr | Pro | Ser | Phe   | Gln | Asp | Ile | Leu | Leu   | Leu | Val | His |
|     | 10745 |     |     |     |     | 10750 |     |     |     |     | 10755 |     |     |     |
| Leu | Gln   | Gln | Ile | Asp | Lys | Arg   | Asn | Ile | Lys | Ile | Ser   | Ala | Ala | Ile |
|     | 10760 |     |     |     |     | 10765 |     |     |     |     | 10770 |     |     |     |
| Pro | Lys   | Leu | Leu | Pro | Gln | Gln   | Leu | Val | Leu | Phe | His   | Ile | Leu | Ser |
|     | 10775 |     |     |     |     | 10780 |     |     |     |     | 10785 |     |     |     |
| Glu | Ile   | Phe | Ser | His | Arg | Thr   | Thr | Arg | Asn | Lys | Ile   | Arg | Ala | Ser |
|     | 10790 |     |     |     |     | 10795 |     |     |     |     | 10800 |     |     |     |
| His | Ser   | Thr | Asp | Lys | Pro | Lys   | Ser | Ser | Pro | Val | Ser   | Ile | Ala | Lys |
|     | 10805 |     |     |     |     | 10810 |     |     |     |     | 10815 |     |     |     |
| Cys | Lys   | Thr | Ala | Ile | Ser | Met   | Leu | Ala | Arg | Pro | Gly   | Asp | Ile | Phe |
|     | 10820 |     |     |     |     | 10825 |     |     |     |     | 10830 |     |     |     |
| Gln | Ile   | Thr | Gly | Gln | Lys | Ile   | Thr | Gln | Ala | Ile | Phe   | Lys | Lys | Ile |
|     | 10835 |     |     |     |     | 10840 |     |     |     |     | 10845 |     |     |     |
| Asn | Lys   | Arg | Lys | Ile | Leu | Gln   | Val | His | Val | Ser | Leu   | Gly | Asn | Asn |
|     | 10850 |     |     |     |     | 10855 |     |     |     |     | 10860 |     |     |     |
| Asp | Glu   | Val | Asn | Ala | Ser | Gly   | Ala | Phe | Gln | His | Gly   | Leu | Ala | Asp |
|     | 10865 |     |     |     |     | 10870 |     |     |     |     | 10875 |     |     |     |
| Leu | Lys   | Thr | Lys | Asn | Lys | Thr   | Leu | Asn | His | Ala | Ser   | Leu | Ala | Asn |
|     | 10880 |     |     |     |     | 10885 |     |     |     |     | 10890 |     |     |     |
| Arg | Trp   | Val | Asn | Arg | Ser | Leu   | Gln | His | Gln | Ala | Gly   | His | Gly | Val |
|     | 10895 |     |     |     |     | 10900 |     |     |     |     | 10905 |     |     |     |
| Ser | Gly   | Ala | Thr | Leu | Val | Lys   | Ile | Val | Ala | Met | Ile   | Glu | Asn | His |
|     | 10910 |     |     |     |     | 10915 |     |     |     |     | 10920 |     |     |     |

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| His | Arg   | Glu | Thr | Phe | Pro | Val   | Ala | Gly | Val | Asn | Asp   | Ser | Thr | Arg |
|     | 10925 |     |     |     |     | 10930 |     |     |     |     | 10935 |     |     |     |
| Ile | His   | Pro | Arg | Asn | Ile | Gly   | Val | Arg | Glu | Lys | Lys   | Ala | Pro | Glu |
|     | 10940 |     |     |     |     | 10945 |     |     |     |     | 10950 |     |     |     |
| Glu | Ala   | Ile | Arg | His | Tyr | Asn   | Ala | Gln | Ser | Gln | Val   | Gln | Gln | Ser |
|     | 10955 |     |     |     |     | 10960 |     |     |     |     | 10965 |     |     |     |
| Asp | Ala   | Met | Arg | Met | Lys | His   | Lys | Ile | Leu | Arg | Cys   | Val | Gln | Asn |
|     | 10970 |     |     |     |     | 10975 |     |     |     |     | 10980 |     |     |     |
| Val | Ile   | Thr | Pro | Leu | Leu | His   | Arg | Gln | Arg | Ser | Pro   | Arg | Ser | Leu |
|     | 10985 |     |     |     |     | 10990 |     |     |     |     | 10995 |     |     |     |
| Gln | Ile   | His | Ile | Gln | Ser | Leu   | Ser | Val | His | Ser | Leu   | Pro | Ser | Ser |
|     | 11000 |     |     |     |     | 11005 |     |     |     |     | 11010 |     |     |     |
| Ser | Thr   | Gln | Gln | Ala | Gln | Glu   | Ser | Glu | Lys | Gly | Ala   | Leu | Thr | Cys |
|     | 11015 |     |     |     |     | 11020 |     |     |     |     | 11025 |     |     |     |
| Pro | Pro   | Ala | Leu | Cys | Ser | Ile   | Tyr | Ser | Pro | Asp | Leu   | His | Arg | Lys |
|     | 11030 |     |     |     |     | 11035 |     |     |     |     | 11040 |     |     |     |
| Gly | Gln   | Ser | Leu | Lys | Ile | Pro   | Ala | Lys | Ser | His | Thr   | Pro | Ser | Thr |
|     | 11045 |     |     |     |     | 11050 |     |     |     |     | 11055 |     |     |     |
| Arg | Pro   | Glu | Thr | Gly | Asp | Thr   | Leu | Lys | Lys | Ile | Arg   | Ala | Leu | Pro |
|     | 11060 |     |     |     |     | 11065 |     |     |     |     | 11070 |     |     |     |
| Gln | Thr   | Pro | Lys | Leu | Pro | Ser   | Phe | Pro | Gly | Ser | His   | Ala | Thr | Ser |
|     | 11075 |     |     |     |     | 11080 |     |     |     |     | 11085 |     |     |     |
| Ser | Glu   | Phe | Asp | Phe | Gln | Ile   | Pro | Ser | Thr | Val | Lys   | Asn | Val | Thr |
|     | 11090 |     |     |     |     | 11095 |     |     |     |     | 11100 |     |     |     |
| Arg | Pro   | Ala | Pro | Asn | Gly | Arg   | Pro | Ser | Leu | Gly | Gln   | Ser | Pro | Ser |
|     | 11105 |     |     |     |     | 11110 |     |     |     |     | 11115 |     |     |     |
| Ser | Leu   | Pro | Lys | Phe | Lys | Gln   | Leu | Ile | Cys | Ile | Leu   | Thr | Arg | Thr |
|     | 11120 |     |     |     |     | 11125 |     |     |     |     | 11130 |     |     |     |
| Lys | Ser   | Leu | Arg | Tyr | Ile | Ile   | Asp | Asp |     |     |       |     |     |     |
|     | 11135 |     |     |     |     | 11140 |     |     |     |     |       |     |     |     |

&lt;210&gt; 16

&lt;211&gt; 11128

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificially Synthesized

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1997)..(1997)

&lt;223&gt; Xaa can be any naturally occurring amino acid

&lt;400&gt; 16

His His Gln Tyr Thr Ser Asn Phe Trp Cys Ala Leu Ile Cys Lys Ala  
 1 5 10 15

Val Ile Trp Gly Gly Arg Lys Val Ile Gly Arg Glu Thr Gly Asp Arg  
 20 25 30

Gly Arg Gly Gly Arg Phe Asp Asp Val Ala Val Arg Arg Ser Arg Phe  
 35 40 45

Ala Ser Ser Arg Gly Lys Ser Asp Val Lys Arg Gly Val Val Thr Arg  
 50 55 60

Lys Tyr Ser Ile Phe Pro Arg Ser Leu Thr Gly Asn Glu Val Phe Leu  
 65 70 75 80

Gly Gly Cys Lys Lys Arg Ala Ile Phe Ala Arg Lys Leu Asn Glu Glu  
 85 90 95

Val Lys Ile Val Ile Ser Arg Leu Trp Gln Gly Gly Val Phe Ala Glu  
 100 105 110

Gly Arg Val Asp Phe Asp Arg Leu Arg Gly Gly Phe Asp Tyr Arg Ile  
 115 120 125

Phe His Leu Asn Phe Arg Val Arg Cys Gln Ser Pro Val Phe Leu Arg  
 130 135 140

Thr Ile Ser Phe Pro Arg Lys Cys His Leu Thr Val Thr Ile Thr Val  
 145 150 155 160

Leu Arg Arg Lys Leu Arg Ser Pro Asp Pro Leu Trp Cys Thr Leu Ser  
 165 170 175

Thr Ile Cys Ser Asp Ala Ala Leu Ser Gln Tyr Leu Leu Pro Ala Cys  
 180 185 190



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Val Leu Glu Val Ala Glu Cys Ala Ser Lys Ile Ala Thr Thr Arg Gln  
 195 200 205  
 Gly Leu Thr Asp Asn Cys Met Lys Asn Leu Leu Arg Val Arg Arg Phe  
 210 215 220  
 Ala Leu Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg His Leu Leu Thr  
 225 230 235 240  
 Ser Met Pro Ser Thr Pro Pro Ile Asp Val Asn Asp Gly Lys Trp Pro  
 245 250 255  
 Ala Trp His Tyr Ala Gln Tyr Met Thr Leu Trp Asp Phe Pro Thr Trp  
 260 265 270  
 Gln Tyr Ile Tyr Val Leu Val Ile Ala Ile Thr Met Val Met Arg Phe  
 275 280 285  
 Trp Gln Tyr Ile Asn Gly Arg Gly Arg Phe Asp Ser Arg Gly Phe Pro  
 290 295 300  
 Ser Leu His Pro Ile Asp Val Asn Gly Ser Leu Phe Trp His Gln Asn  
 305 310 315 320  
 Gln Arg Asp Phe Pro Lys Cys Arg Asn Asn Ser Ala Pro Leu Thr Gln  
 325 330 335  
 Met Gly Gly Arg Arg Val Arg Trp Glu Val Tyr Ile Ser Arg Ala Arg  
 340 345 350  
 Leu Val Asn Arg Gln Ile Thr Arg Ser Phe Ile Ala Val Val Tyr His  
 355 360 365  
 Ser Ile Ala Asn Ala Val Ser Ala Ser Asp Thr Thr Val Ser Asn Leu  
 370 375 380  
 Arg Leu Glu Phe Asp Ala Thr Met Arg Val Arg Gly Ile Pro Arg Asn  
 385 390 395 400  
 Trp Pro Gln Trp Trp Ile Trp Gly Ile Leu Gly Phe Trp Met Ile Ile  
 405 410 415  
 Ile Cys Arg Val Val Gly Asn Leu Asp Leu Trp Val Thr Val Tyr Tyr  
 420 425 430  
 Gly Val Pro Val Trp Lys Glu Ala Lys Thr Thr Leu Phe Cys Ala Ser  
 435 440 445

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Asp Ala Lys Ala Tyr Asp Lys Glu Val His Asn Val Trp Ala Thr His  
 450 455 460  
 Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu Glu Asn  
 465 470 475 480  
 Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met Val Asp Gln Met  
 485 490 495  
 His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val  
 500 505 510  
 Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Lys Asn Val Asn Ile  
 515 520 525  
 Ser Ala Asn Ala Asn Ala Thr Ala Thr Leu Asn Ser Ser Met Asn Gly  
 530 535 540  
 Glu Ile Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Leu Arg Asp Lys  
 545 550 555 560  
 Lys Gln Lys Val Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu  
 565 570 575  
 Asn Gly Gly Glu His Asn Glu Thr Gly Glu Tyr Ile Leu Ile Asn Cys  
 580 585 590  
 Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro  
 595 600 605  
 Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys  
 610 615 620  
 Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr  
 625 630 635 640  
 Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu  
 645 650 655  
 Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Val Arg Ser Glu Asn  
 660 665 670  
 Leu Thr Asn Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser Val  
 675 680 685  
 Glu Ile Lys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg  
 690 695 700

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Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp  
705 710 715 720

Ile Arg Glu Ala His Cys Asn Ile Ser Arg Glu Thr Trp Asn Ser Thr  
725 730 735

Leu Ile Gln Val Lys Glu Lys Leu Arg Glu His Tyr Asn Lys Thr Ile  
740 745 750

Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Val Thr Thr His Ser  
755 760 765

Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Thr Lys Leu Phe  
770 775 780

Asn Glu Thr Lys Leu Phe Asn Glu Ser Glu Tyr Val Asp Asn Lys Thr  
785 790 795 800

Ile Ile Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu  
805 810 815

Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys  
820 825 830

Lys Ser Asn Ile Thr Gly Leu Leu Leu Thr Trp Asp Gly Gly Glu Asn  
835 840 845

Ser Thr Glu Gly Val Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn  
850 855 860

Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu  
865 870 875 880

Gly Val Ala Pro Thr Lys Ser Lys Arg Lys Val Val Gly Arg Glu Lys  
885 890 895

Arg Ala Val Gly Leu Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala  
900 905 910

Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg  
915 920 925

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala  
930 935 940

Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys

945                      950                      955                      960  
 Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln  
                          965                      970                      975  
 Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys Ala Thr  
                          980                      985                      990  
 Ala Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Leu Gly Asp Ile  
                          995                      1000                      1005  
 Trp Asp Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Ser Asn  
                          1010                      1015                      1020  
 Tyr Thr Asn Thr Ile Phe Arg Leu Leu Glu Asp Ser Gln Asn Gln  
                          1025                      1030                      1035  
 Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys  
                          1040                      1045                      1050  
 Asn Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr Ile  
                          1055                      1060                      1065  
 Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile  
                          1070                      1075                      1080  
 Ile Phe Gly Val Leu Ala Ile Val Lys Arg Val Arg Gln Gly Tyr  
                          1085                      1090                      1095  
 Ser Pro Leu Ser Phe Gln Thr Leu Ile Pro Asn Pro Arg Gly Pro  
                          1100                      1105                      1110  
 Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Glu Gln Asp Lys  
                          1115                      1120                      1125  
 Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp  
                          1130                      1135                      1140  
 Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Gln Leu Arg  
                          1145                      1150                      1155  
 Asp Phe Ile Leu Thr Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg  
                          1160                      1165                      1170  
 Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Val Leu Lys Tyr  
                          1175                      1180                      1185

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|     |      |     |     |     |     |      |     |     |     |     |      |      |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|------|-----|-----|
| Leu | Gly  | Asn | Leu | Val | Gln | Tyr  | Trp | Gly | Leu | Glu | Leu  | Lys  | Arg | Ser |
|     | 1190 |     |     |     |     | 1195 |     |     |     |     |      | 1200 |     |     |
| Ala | Ile  | Asn | Leu | Phe | Asp | Thr  | Ile | Ala | Ile | Ala | Val  | Ala  | Glu | Gly |
|     | 1205 |     |     |     |     | 1210 |     |     |     |     | 1215 |      |     |     |
| Thr | Asp  | Arg | Ile | Ile | Glu | Val  | Ile | Gln | Arg | Ile | Cys  | Arg  | Ala | Ile |
|     | 1220 |     |     |     |     | 1225 |     |     |     |     | 1230 |      |     |     |
| Arg | Tyr  | Ile | Pro | Thr | Arg | Ile  | Arg | Gln | Gly | Phe | Glu  | Ala  | Ala | Leu |
|     | 1235 |     |     |     |     | 1240 |     |     |     |     | 1245 |      |     |     |
| Leu | Gly  | Thr | Ser | Arg | Val | Asp  | Pro | Gly | Gly | Gln | Thr  | Ala  | Asp | Gln |
|     | 1250 |     |     |     |     | 1255 |     |     |     |     | 1260 |      |     |     |
| Pro | Arg  | Leu | Cys | Leu | Leu | Val  | Ala | Ser | His | Leu | Leu  | Phe  | Ala | Pro |
|     | 1265 |     |     |     |     | 1270 |     |     |     |     | 1275 |      |     |     |
| Pro | Pro  | Cys | Leu | Pro | Pro | Trp  | Lys | Val | Pro | Leu | Pro  | Leu  | Ser | Phe |
|     | 1280 |     |     |     |     | 1285 |     |     |     |     | 1290 |      |     |     |
| Pro | Asn  | Lys | Met | Arg | Lys | Leu  | His | Arg | Ile | Val | Val  | Gly  | Val | Ile |
|     | 1295 |     |     |     |     | 1300 |     |     |     |     | 1305 |      |     |     |
| Leu | Phe  | Trp | Gly | Val | Gly | Trp  | Gly | Arg | Thr | Ala | Arg  | Gly  | Arg | Ile |
|     | 1310 |     |     |     |     | 1315 |     |     |     |     | 1320 |      |     |     |
| Gly | Lys  | Thr | Ile | Ala | Gly | Met  | Leu | Gly | Met | Arg | Trp  | Ala  | Leu | Trp |
|     | 1325 |     |     |     |     | 1330 |     |     |     |     | 1335 |      |     |     |
| Leu | Leu  | Arg | Arg | Lys | Glu | Pro  | Ala | Asp | Leu | Gln | Ile  | Ile  | His | Leu |
|     | 1340 |     |     |     |     | 1345 |     |     |     |     | 1350 |      |     |     |
| Cys | Arg  | Val | Arg | Arg | Lys | Arg  | Asn | Gly | Ile | Met | Gly  | Ile  | Met | Gly |
|     | 1355 |     |     |     |     | 1360 |     |     |     |     | 1365 |      |     |     |
| Leu | His  | Ile | Gly | Gln | Ile | Ser  | Ile | Cys | Trp | Pro | Pro  | Cys  | Met | Pro |
|     | 1370 |     |     |     |     | 1375 |     |     |     |     | 1380 |      |     |     |
| Arg | Thr  | Pro | Ala | Arg | His | Gly  | Pro | Ser | Ser | Ser | Thr  | Thr  | Ser | Pro |
|     | 1385 |     |     |     |     | 1390 |     |     |     |     | 1395 |      |     |     |
| Asp | Ala  | Met | Cys | Thr | Trp | Gly  | Pro | Ala | Glu | Ala | Cys  | Ser  | Cys | Pro |
|     | 1400 |     |     |     |     | 1405 |     |     |     |     | 1410 |      |     |     |
| Thr | Ser  | Ala | Thr | Cys | Asn | Leu  | Arg | Cys | Cys | Trp | Ser  | Pro  | Met | Pro |
|     | 1415 |     |     |     |     | 1420 |     |     |     |     | 1425 |      |     |     |

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Cys | Pro  | Glu | Ala | Arg | Gly | Cys  | Leu | Thr | Met | Trp | Ser  | Cys | Gly | Lys |
|     | 1430 |     |     |     |     | 1435 |     |     |     |     | 1440 |     |     |     |
| Phe | Asp  | Met | Met | Asn | Pro | Arg  | Pro | Gly | Ala | Gly | Pro  | Ala | Asn | Ala |
|     | 1445 |     |     |     |     | 1450 |     |     |     |     | 1455 |     |     |     |
| Glu | Ala  | Ser | Thr | Pro | Gly | Phe  | Ser | Pro | Cys | Val | Trp  | Arg | Arg | Arg |
|     | 1460 |     |     |     |     | 1465 |     |     |     |     | 1470 |     |     |     |
| Thr | Cys  | Asp | Pro | Ile | Ile | Trp  | Cys | Cys | Pro | Ala | Thr  | Gly | Arg | Ser |
|     | 1475 |     |     |     |     | 1480 |     |     |     |     | 1485 |     |     |     |
| Ser | Ala  | Pro | Ala | Gly | Lys | Asn  | Leu | Thr | Arg | Val | Ser  | Ser | Val | Trp |
|     | 1490 |     |     |     |     | 1495 |     |     |     |     | 1500 |     |     |     |
| Gly | Arg  | Trp | Arg | Ala | Cys | Met  | Arg | Gly | Arg | Met | Thr  | Lys | Ile | Cys |
|     | 1505 |     |     |     |     | 1510 |     |     |     |     | 1515 |     |     |     |
| Val | Phe  | Leu | Cys | Val | Ala | Ala  | Ala | Ala | Glu | Ala | Pro  | Pro | Leu | Arg |
|     | 1520 |     |     |     |     | 1525 |     |     |     |     | 1530 |     |     |     |
| Glu | Gly  | Tyr | Ser | Ala | Leu | Ile  | Arg | Gly | Val | Ser | Pro  | Pro | Gly | Arg |
|     | 1535 |     |     |     |     | 1540 |     |     |     |     | 1545 |     |     |     |
| Glu | Cys  | Val | Arg | Met | Trp | Asp  | Pro | Arg | Trp | Thr | Ala  | Gly | Pro | Cys |
|     | 1550 |     |     |     |     | 1555 |     |     |     |     | 1560 |     |     |     |
| Ser | Pro  | Arg | Thr | Leu | Gln | Pro  | Pro | Thr | Arg | Pro | Ala  | Pro | Arg | Pro |
|     | 1565 |     |     |     |     | 1570 |     |     |     |     | 1575 |     |     |     |
| Trp | Thr  | Gln | Leu | Pro | Pro | Gln  | Leu | Leu | Leu | Pro | Pro  | Pro | Ala | Pro |
|     | 1580 |     |     |     |     | 1585 |     |     |     |     | 1590 |     |     |     |
| Cys | Ala  | Glu | Trp | Pro | Trp | Ala  | Pro | Ala | Thr | Thr | Ala  | Leu | Trp | Trp |
|     | 1595 |     |     |     |     | 1600 |     |     |     |     | 1605 |     |     |     |
| Pro | Thr  | Arg | Leu | Pro | Pro | Ile  | Ile | Pro | Pro | Ala | Thr  | Arg | Arg | Ser |
|     | 1610 |     |     |     |     | 1615 |     |     |     |     | 1620 |     |     |     |
| Cys | Cys  | Cys | Trp | Pro | Ser | Ser  | Arg | Pro | Pro | Ser | Ala  | Trp | Ala | Ser |
|     | 1625 |     |     |     |     | 1630 |     |     |     |     | 1635 |     |     |     |
| Pro | Ser  | Arg | Trp | Leu | Ser | Cys  | Arg | Arg | Arg | Arg | Gly  | Pro | Arg | Leu |
|     | 1640 |     |     |     |     | 1645 |     |     |     |     | 1650 |     |     |     |
| Pro | Arg  | Lys | Pro | Asn | Lys | Lys  | Ile | Asn | Lys | Thr | Glu  | Thr | Val | Val |
|     | 1655 |     |     |     |     | 1660 |     |     |     |     | 1665 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp  | Phe | Asn | Thr | Glu | Ser | Ile  | Phe | Ile | Phe | Phe | Ala  | Arg | Gly | Arg |
| 1670 |     |     |     |     |     | 1675 |     |     |     |     | 1680 |     |     |     |
| Pro  | Trp | Thr | Thr | Gly | Leu | Asp  | His | Ala | Pro | Gly | Gly  | Phe | Phe | Pro |
| 1685 |     |     |     |     |     | 1690 |     |     |     |     | 1695 |     |     |     |
| Gly  | Pro | Gly | Arg | Gly | Gly | Leu  | Gly | Cys | Gly | Thr | Trp  | Ala | Ala | Arg |
| 1700 |     |     |     |     |     | 1705 |     |     |     |     | 1710 |     |     |     |
| Pro  | Gly | Gly | Gly | Gly | Ser | Ser  | Ile | Ala | Gly | Pro | Arg  | Ala | Arg | Gly |
| 1715 |     |     |     |     |     | 1720 |     |     |     |     | 1725 |     |     |     |
| Trp  | Cys | Cys | Lys | Ser | Pro | Ser  | His | Ser | Arg | Gly | Ala  | Gly | Arg | Gly |
| 1730 |     |     |     |     |     | 1735 |     |     |     |     | 1740 |     |     |     |
| Ala  | Ala | Arg | Cys | Pro | Gly | Gly  | Asp | Trp | Pro | Arg | Ala  | Ala | Pro | Trp |
| 1745 |     |     |     |     |     | 1750 |     |     |     |     | 1755 |     |     |     |
| Cys  | Arg | Cys | Arg | Thr | Cys | Ala  | Gly | Arg | Asp | Ala | Cys  | Gly | Gly | Arg |
| 1760 |     |     |     |     |     | 1765 |     |     |     |     | 1770 |     |     |     |
| Asp  | Ala | Ser | Trp | Pro | Gly | Ser  | Asp | Trp | Arg | Cys | Ser  | Arg | Pro | Asp |
| 1775 |     |     |     |     |     | 1780 |     |     |     |     | 1785 |     |     |     |
| Pro  | Ala | Gly | Gly | Ser | Cys | Cys  | Ala | Gly | Pro | Pro | Ala  | Arg | Cys | Ile |
| 1790 |     |     |     |     |     | 1795 |     |     |     |     | 1800 |     |     |     |
| Arg  | Arg | Thr | Trp | Gly | Ile | Cys  | His | Ala | Thr | Trp | Lys  | Gly | Arg | Arg |
| 1805 |     |     |     |     |     | 1810 |     |     |     |     | 1815 |     |     |     |
| Glu  | Arg | Ile | Trp | Arg | Arg | Pro  | Cys | Asp | Arg | Pro | Gly  | Phe | Pro | Cys |
| 1820 |     |     |     |     |     | 1825 |     |     |     |     | 1830 |     |     |     |
| Thr  | His | Pro | Trp | Arg | Trp | Ala  | Arg | Gly | Arg | Arg | Pro  | Gly | Gln | Arg |
| 1835 |     |     |     |     |     | 1840 |     |     |     |     | 1845 |     |     |     |
| Arg  | Phe | Gly | Gly | Arg | Thr | His  | Arg | Ser | Cys | Gly | Pro  | Gly | Ala | Arg |
| 1850 |     |     |     |     |     | 1855 |     |     |     |     | 1860 |     |     |     |
| His  | Arg | Pro | Phe | Ile | Trp | Gly  | Gly | Gly | Cys | Pro | Thr  | Gly | Gly | Arg |
| 1865 |     |     |     |     |     | 1870 |     |     |     |     | 1875 |     |     |     |
| Arg  | Cys | Pro | Arg | Ser | Arg | Gly  | Arg | Ser | Cys | Pro | Arg  | Arg | Ser | Ala |
| 1880 |     |     |     |     |     | 1885 |     |     |     |     | 1890 |     |     |     |
| Ser  | Pro | Arg | Pro | Ala | Arg | Arg  | Gly | Gly | Ser | Cys | Pro  | Pro | Ala | Gly |

1895

1900

1905

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Lys  | Lys | Arg | Phe | Pro | Gly  | Arg | Gly | Arg | Ala | Gly  | Pro | Lys | Ala |
|     | 1910 |     |     |     |     | 1915 |     |     |     |     | 1920 |     |     |     |
| Gly | Ser  | Gly | Ala | Ala | Gly | Thr  | Cys | Arg | Ser | Arg | Trp  | Gly | Arg | Arg |
|     | 1925 |     |     |     |     | 1930 |     |     |     |     | 1935 |     |     |     |
| Pro | Arg  | Pro | Ala | Ala | Gly | Gly  | Ser | Gly | Arg | Asp | Ser  | Cys | Arg | Pro |
|     | 1940 |     |     |     |     | 1945 |     |     |     |     | 1950 |     |     |     |
| Arg | Gly  | Gly | Gly | Gly | Pro | Pro  | Arg | Ser | Ser | Ser | Arg  | Ala | His | Ala |
|     | 1955 |     |     |     |     | 1960 |     |     |     |     | 1965 |     |     |     |
| Cys | Ser  | Arg | Ala | Arg | Val | Pro  | Pro | Gly | Gly | Ala | Arg  | Pro | Pro | Ala |
|     | 1970 |     |     |     |     | 1975 |     |     |     |     | 1980 |     |     |     |
| Arg | Gly  | Ala | Leu | Ala | Ala | Arg  | Arg | Ser | Phe | Ser | Ala  | Ala | Xaa | Arg |
|     | 1985 |     |     |     |     | 1990 |     |     |     |     | 1995 |     |     |     |
| Arg | Pro  | Trp | Ala | Phe | Trp | Arg  | Gly | Ser | Val | Ala | Arg  | Val | Pro | Asp |
|     | 2000 |     |     |     |     | 2005 |     |     |     |     | 2010 |     |     |     |
| Gly | Pro  | Arg | Ala | Arg | Cys | Ala  | Leu | Gly | His | Leu | Asp  | Pro | Ala | Asp |
|     | 2015 |     |     |     |     | 2020 |     |     |     |     | 2025 |     |     |     |
| Leu | Leu  | Val | Ser | Arg | Val | Gly  | Ala | Thr | Ala | Gly | Val  | Gly | His | Gln |
|     | 2030 |     |     |     |     | 2035 |     |     |     |     | 2040 |     |     |     |
| Ala | Met  | Gly | Val | Gln | Arg | Gly  | Gln | Gly | Pro | Val | Leu  | Pro | Gly | Ser |
|     | 2045 |     |     |     |     | 2050 |     |     |     |     | 2055 |     |     |     |
| Gln | Gly  | Pro | Arg | Gln | Arg | Gly  | Leu | Arg | His | Gly | Glu  | Gly | Val | Arg |
|     | 2060 |     |     |     |     | 2065 |     |     |     |     | 2070 |     |     |     |
| Ala | Gly  | Leu | Gly | Ala | Cys | Glu  | Gly | Ala | Leu | Gln | Ala  | His | Pro | Ala |
|     | 2075 |     |     |     |     | 2080 |     |     |     |     | 2085 |     |     |     |
| Gly | Arg  | Glu | Pro | Leu | Pro | Val  | Gly | Ala | Leu | Arg | Val  | Gly | Gln | Val |
|     | 2090 |     |     |     |     | 2095 |     |     |     |     | 2100 |     |     |     |
| Ala | Ile  | Glu | His | Glu | Phe | Val  | Val | Glu | Arg | Leu | Gly  | Arg | Val | Ala |
|     | 2105 |     |     |     |     | 2110 |     |     |     |     | 2115 |     |     |     |
| Leu | Gly  | Ala | Glu | Leu | Thr | Phe  | Gly | Ser | Val | Ser | Ala  | Asp | Gly | Thr |
|     | 2120 |     |     |     |     | 2125 |     |     |     |     | 2130 |     |     |     |



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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Glu | Glu  | Gly | Leu | Glu | Gly | Val  | Glu | Leu | Gly | Gly | Glu  | Glu | Asp | Gly |
|     | 2135 |     |     |     |     | 2140 |     |     |     |     | 2145 |     |     |     |
| Leu | Gly  | Gly | Val | Gly | Val | Arg  | Ala | Ala | Ala | Gly | Ala  | Asp | Gly | Leu |
|     | 2150 |     |     |     |     | 2155 |     |     |     |     | 2160 |     |     |     |
| Ala | Leu  | His | Glu | Pro | Gly | Glu  | Val | Gly | Pro | Val | Gly  | Val | Lys | Asn |
|     | 2165 |     |     |     |     | 2170 |     |     |     |     | 2175 |     |     |     |
| Glu | Val  | Ser | Ser | Val | Leu | Phe  | Asp | Ala | Phe | Leu | Thr  | Ser | Gly | Leu |
|     | 2180 |     |     |     |     | 2185 |     |     |     |     | 2190 |     |     |     |
| His | Glu  | Leu | Val | Ser | Pro | Leu  | Gly | Asp | Lys | Glu | Ala  | Val | Arg | Val |
|     | 2195 |     |     |     |     | 2200 |     |     |     |     | 2205 |     |     |     |
| Pro | Val  | Asp | Arg | Leu | Tyr | Gly  | Pro | Val | Leu | Glu | Arg  | Gly | Ala | Ala |
|     | 2210 |     |     |     |     | 2215 |     |     |     |     | 2220 |     |     |     |
| Val | Leu  | Val | Val | Glu | Glu | Pro  | Arg | Pro | Leu | Arg | Asp  | Glu | Gly | Pro |
|     | 2225 |     |     |     |     | 2230 |     |     |     |     | 2235 |     |     |     |
| Gly | Pro  | Gly | Gln | His | Glu | Gly  | Gly | His | Val | Gly | Gly  | Val | Ala | Val |
|     | 2240 |     |     |     |     | 2245 |     |     |     |     | 2250 |     |     |     |
| Val | Val  | His | Gln | Arg | Val | His  | Leu | Leu | Gln | Gly | Met  | Gln | Ala | His |
|     | 2255 |     |     |     |     | 2260 |     |     |     |     | 2265 |     |     |     |
| Val | Pro  | Leu | Val | His | Ile | Gln  | Glu | Gly | Asp | Trp | Leu  | Val | Ser | Val |
|     | 2270 |     |     |     |     | 2275 |     |     |     |     | 2280 |     |     |     |
| Gly | His  | Val | Thr | Gly | Gly | Pro  | Gly | Arg | Gly | Gly | Ile  | Lys | Gly | Gly |
|     | 2285 |     |     |     |     | 2290 |     |     |     |     | 2295 |     |     |     |
| Gly | Pro  | Leu | Leu | Val | Leu | Thr  | Val | Phe | Arg | Ile | Ala  | Val | Gln | Glu |
|     | 2300 |     |     |     |     | 2305 |     |     |     |     | 2310 |     |     |     |
| Arg | Gln  | Leu | Leu | Gly | Val | Phe  | Pro | Leu | Glu | Gly | Trp  | His | Asn | Leu |
|     | 2315 |     |     |     |     | 2320 |     |     |     |     | 2325 |     |     |     |
| Gly | Thr  | Gln | Val | Val | Ser | Phe  | Lys | Arg | Gly | Gly | Phe  | Asp | Ile | Asp |
|     | 2330 |     |     |     |     | 2335 |     |     |     |     | 2340 |     |     |     |
| Gly | Ala  | Val | Gly | Asp | Ala | Phe  | His | Glu | Pro | Leu | Val  | His | Leu | Val |
|     | 2345 |     |     |     |     | 2350 |     |     |     |     | 2355 |     |     |     |
| Arg | Lys  | Asp | Asp | Leu | Phe | Val  | Val | Glu | Leu | Gly | Gly  | Glu | Gly | Ala |
|     | 2360 |     |     |     |     | 2365 |     |     |     |     | 2370 |     |     |     |

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Val Glu Gly Val Gly Glu Glu Leu Gly Asp Gly Ala His Gly Leu  
 2375 2380 2385  
 Val Leu Phe Leu Val Gly Ala Leu Leu Gly Gly Asp Val Glu Leu  
 2390 2395 2400  
 His Val Leu Ala Arg His Ala Leu Pro Phe Gly Glu Asp Gly Gly  
 2405 2410 2415  
 Glu Leu Val Gly His Asp Ser Asp Pro Pro Ala Ala Val Val Gln  
 2420 2425 2430  
 Gly Asp Glu Val His Ala Gly Gly His Leu Ala Ala Gln Gly Leu  
 2435 2440 2445  
 Val Gly Pro Ala Glu Ala Pro Ala Leu Ala Arg Ala Glu Gly Gly  
 2450 2455 2460  
 Gln Arg Val Gln His Glu Leu Val Gly Gly Val Gly Val His Gly  
 2465 2470 2475  
 Glu Asp Ala Gly Gln Lys Leu Gly Val Glu Val Ala Asp Ala Gly  
 2480 2485 2490  
 Val Gln Ile Val Gln Arg Arg Leu Pro Val Ala His Gly Gln Arg  
 2495 2500 2505  
 Ala Leu Val Gly Ala Glu Gly Arg Ala Pro Gly His Gly Val Arg  
 2510 2515 2520  
 Glu Arg Gly Gly Val His Ala Ala Asp Val Val Asp Val Glu Gly  
 2525 2530 2535  
 Leu Leu Glu Asp Ala Asp Val Gly Gly Val Ala Ala Pro Pro Ala  
 2540 2545 2550  
 Asp Ala Gly Ala His Val Val Val Gln Leu Val Arg Gly Arg Glu  
 2555 2560 2565  
 Glu Pro Arg Ala Glu Val Gly Ala Leu Arg Leu Phe Gly Ala Val  
 2570 2575 2580  
 Asp Asp Leu Ala Glu Asp Gly Val Gly Val Gly Gly Asp Gly Gly  
 2585 2590 2595  
 Pro Leu Glu Asp Val Glu Val Gly Val Gly Gln Ala Asp Arg Val  
 2600 2605 2610

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Pro Asp Glu Val Gly Val Gly Val Leu Gln Leu Gly Asp Glu Leu  
2615 2620 2625

Gly Gly Asp Glu Asp Val Gln Gly Ala Val Val Glu Gly Leu Leu  
2630 2635 2640

Asp Asp Val Val Leu Glu Leu Ala Leu Leu Leu Pro Gln Leu Ala  
2645 2650 2655

Val Glu Lys Glu Leu Phe Ala Val Leu Pro Val Leu Phe Glu Gly  
2660 2665 2670

Glu Pro Val Leu Ile Gly Thr Val Arg Ala His His Val Glu Leu  
2675 2680 2685

Val Asp Gly Leu Val Gly Ala Ala Ala Leu Leu His Gly Glu Gly  
2690 2695 2700

Val Ser Leu Cys Gly Leu Ala Gln Gly Gly Val Gly Glu Gly Glu  
2705 2710 2715

Gly Val Ala His His Asp Leu Glu Glu Leu Val Leu Glu Val Glu  
2720 2725 2730

Val Val Ala Ala Ala Leu Leu Pro Glu Leu Glu Val Arg Ala Leu  
2735 2740 2745

Leu Val Gly Gly Val Gly Gln Ser Glu Ser Asn Ile Val Glu Glu  
2750 2755 2760

Asp Leu Ala Arg Ala Gly His Glu Val Ala Ser Asp Ala Glu Arg  
2765 2770 2775

Leu Gly His Leu Gly Pro Val Val Asp Asp Leu Gly Gly Glu Asp  
2780 2785 2790

Asp Leu Val Glu Ala Val Asp Val Val Pro Asp Asp Val Glu Phe  
2795 2800 2805

His Glu Ser Arg Ala Ala Leu Asn Val Gly Gln Leu Leu Glu Leu  
2810 2815 2820

Val Val Gly Glu Leu Gly Gly Val Ala Glu Pro Val Leu Leu Glu  
2825 2830 2835

Gly Pro Val Gly Asp Val Gly Val Gly Ala Glu Glu Gly Ser Pro

2840

2845

2850

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Glu | Ile  | His | Gly | Gln | Gly | Gly  | Leu | Gln | Ala | Val | Pro  | Val | Leu | Thr |
|     | 2855 |     |     |     |     | 2860 |     |     |     |     | 2865 |     |     |     |
| Glu | Leu  | Leu | Ala | His | Gly | His  | Phe | Phe | Gly | Gly | Asp  | Ala | Val | Glu |
|     | 2870 |     |     |     |     | 2875 |     |     |     |     | 2880 |     |     |     |
| Gly | Ala  | Gly | Val | Ala | Val | Pro  | Ala | Val | Pro | Leu | Glu  | Leu | Glu | Gly |
|     | 2885 |     |     |     |     | 2890 |     |     |     |     | 2895 |     |     |     |
| Glu | Val  | Val | Gly | Glu | Leu | Asp  | Glu | Arg | Arg | Val | Pro  | Gly | Glu | Phe |
|     | 2900 |     |     |     |     | 2905 |     |     |     |     | 2910 |     |     |     |
| His | Asp  | Gln | His | Glu | Gly | Asp  | Glu | Leu | Leu | Ala | Glu  | Gly | Pro | His |
|     | 2915 |     |     |     |     | 2920 |     |     |     |     | 2925 |     |     |     |
| Pro | Gly  | Val | Gly | Phe | His | Ile  | Val | Gly | Glu | Glu | Glu  | Pro | Phe | Gly |
|     | 2930 |     |     |     |     | 2935 |     |     |     |     | 2940 |     |     |     |
| Ala | Arg  | Met | Arg | Ala | Asp | Gly  | Glu | Glu | Leu | Asp | Leu  | Leu | Pro | Pro |
|     | 2945 |     |     |     |     | 2950 |     |     |     |     | 2955 |     |     |     |
| Val | Gly  | Gly | Met | Ala | Val | Asp  | Val | Met | Glu | Val | Glu  | Met | Pro | Thr |
|     | 2960 |     |     |     |     | 2965 |     |     |     |     | 2970 |     |     |     |
| Ala | Arg  | Arg | Ala | Leu | Val | Leu  | Val | Phe | Ile | Gln | Ala  | Ser | Ala | Val |
|     | 2975 |     |     |     |     | 2980 |     |     |     |     | 2985 |     |     |     |
| Leu | Ala  | Thr | Leu | His | Gly | Met  | His | Val | Leu | His | Glu  | Leu | Tyr | Leu |
|     | 2990 |     |     |     |     | 2995 |     |     |     |     | 3000 |     |     |     |
| Gly | Ser  | Phe | Asp | Glu | Glu | Phe  | Gln | Trp | Ala | Val | Glu  | Arg | Trp | Arg |
|     | 3005 |     |     |     |     | 3010 |     |     |     |     | 3015 |     |     |     |
| Leu | His  | Leu | Val | Leu | Tyr | Tyr  | Val | Leu | Ala | Ile | Gly  | Val | Ala | Ile |
|     | 3020 |     |     |     |     | 3025 |     |     |     |     | 3030 |     |     |     |
| Val | Cys  | Leu | Asp | Gly | Gly | His  | Ala | Asp | Glu | Pro | Ala  | Arg | Glu | Ala |
|     | 3035 |     |     |     |     | 3040 |     |     |     |     | 3045 |     |     |     |
| Gly | Pro  | Asp | Phe | Gly | Ser | Asp  | Gly | Ser | Glu | Ser | Glu  | Asp | Glu | Gly |
|     | 3050 |     |     |     |     | 3055 |     |     |     |     | 3060 |     |     |     |
| Ala | Gln  | Ala | Gly | Ala | Val | Gln  | Gly | Pro | Glu | Thr | Leu  | Arg | Ser | Gln |
|     | 3065 |     |     |     |     | 3070 |     |     |     |     | 3075 |     |     |     |

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Val Ser Gly Gln Arg Arg Arg Ala Val Asp Leu Gln Glu Leu Phe  
 3080 3085 3090  
  
 Gln Gly Ala Arg Glu Val Gln Met Val Leu Asp Leu His Gly Ala  
 3095 3100 3105  
  
 Val Gly Gly Asp Val His Gly Leu Gln Gly Pro Val Pro Leu Gly  
 3110 3115 3120  
  
 Arg His His Arg Ala Pro Phe Leu Leu Gly Arg Cys Phe His Ala  
 3125 3130 3135  
  
 Gly Gln Lys Arg Arg Arg Gly Arg Ala Pro Gly Gly Arg Gly Gly  
 3140 3145 3150  
  
 Ser Gly Pro Gly Gly Arg Gly Gly Arg Gly Thr Ser Ala Pro Arg  
 3155 3160 3165  
  
 Ala Gly Arg Phe Trp Tyr Cys Ala Arg Arg Arg Leu Ala Ala Thr  
 3170 3175 3180  
  
 Thr Arg Arg Leu Thr Ser Trp Ile Arg Leu Trp Val Lys Ala Thr  
 3185 3190 3195  
  
 Gly Pro Val Ser Leu Asn Leu Lys Glu Ser Ser Thr Glu Ser Ile  
 3200 3205 3210  
  
 Ser Val Ser Leu Thr Ala Ala Cys Arg Arg Ile Ser Cys Thr Ser  
 3215 3220 3225  
  
 Pro Glu Leu Ser Trp Ala Ile Ser Val Met Asn Cys Ser Ile Ser  
 3230 3235 3240  
  
 Ser Ser Arg Ser Pro Arg Pro Ala Arg Ser Thr Val Ala Ala Arg  
 3245 3250 3255  
  
 Ser Leu Glu Met Arg Pro Met Ser Cys Glu Lys Ala Phe Met Pro  
 3260 3265 3270  
  
 Ala Ser Phe Gln Thr Arg Leu Thr Thr Ala Pro Ser Gly Ser Arg  
 3275 3280 3285  
  
 Ala Arg Met Thr Thr Trp Ala Arg Leu Ser Ser Thr Trp Arg Val  
 3290 3295 3300  
  
 Lys Thr Ala Leu Gln Arg Arg Trp Arg Leu Ser Val Val Ala Met  
 3305 3310 3315

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Cys Ser Val Thr Lys Lys Tyr Met Ile Gln Arg Arg Ser Gly Ile  
 3320 3325 3330  
 Ser Leu Thr Ser Pro Arg Ala Ser Lys Arg Ser Met Ala Ser Lys  
 3335 3340 3345  
 Ser Thr Ala Lys Leu Lys Asn Trp Glu Leu Arg Ala Glu Thr Val  
 3350 3355 3360  
 Asn Ser Ser Ser Arg Arg Arg Met Ser Ser Ala Met Val Ala Arg  
 3365 3370 3375  
 Thr Ser Arg Ser Lys Ala Pro Gly Gly Ser Ser Ser Ser Ile Ser  
 3380 3385 3390  
 Ser Ser Ser Thr Asn Ile Ser Ser Thr Ser Ser Ser Gly Gly Gly  
 3395 3400 3405  
 Gly Gly Gly Gly Ala Leu Arg Arg Arg Arg Arg Thr Gly Arg Arg  
 3410 3415 3420  
 Ser Met Lys Arg Ser Met Val Ser Pro Arg Arg Arg Arg Met Val  
 3425 3430 3435  
 Ser Val Thr Ala Arg Pro Ser Ser Arg Gly Arg Ser Val Lys Thr  
 3440 3445 3450  
 Pro Pro Arg Ile Ser Arg Trp Pro Pro Gly Gly Ser Pro Leu Gly  
 3455 3460 3465  
 Arg Glu Arg Ala Leu Thr Met His Leu Ile Asn Trp Pro Val Gly  
 3470 3475 3480  
 Thr Pro Arg Lys Asp Leu Ser Val Ser Arg Ser Thr Gly Ser Glu  
 3485 3490 3495  
 Asn Arg Thr Lys Ala Ser Ser Gln Ser Gln Ser Gln Gly Arg Leu  
 3500 3505 3510  
 Ser Pro Val Ser Cys Ser Ser Gly Ile Ser Gly Gly Gly Arg Ala  
 3515 3520 3525  
 Met Leu Leu Val Met Lys Leu Lys Ala Val Leu Arg Arg Arg Met  
 3530 3535 3540  
 Val Ala Arg Ser Thr Arg Ser Leu Gly Pro Ala Cys Trp Met Arg  
 3545 3550 3555

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Arg  | Ser | Ala | Met | Pro | Gln  | Ala | Trp | Ser | His | Leu  | Ala | Arg | Ser |
|     | 3560 |     |     |     |     | 3565 |     |     |     |     | 3570 |     |     |     |
| Leu | Ser  | Cys | Met | Ser | Arg | Ser  | Thr | Gly | Thr | Ser | Ser  | Ser | Pro | Ala |
|     | 3575 |     |     |     |     | 3580 |     |     |     |     | 3585 |     |     |     |
| Arg | Pro  | Cys | Met | Arg | Val | Ser  | Pro | Asn | Pro | Arg | Trp  | Gly | Trp | Thr |
|     | 3590 |     |     |     |     | 3595 |     |     |     |     | 3600 |     |     |     |
| Ser | Ala  | Arg | Ser | Ala | Thr | Thr  | Arg | Ser | Ala | Arg | Met  | Ala | Cys | Cys |
|     | 3605 |     |     |     |     | 3610 |     |     |     |     | 3615 |     |     |     |
| Ile | Trp  | Val | Arg | Val | Val | Trp  | Lys | Ser | Ser | Lys | Ser  | Thr | Lys | Arg |
|     | 3620 |     |     |     |     | 3625 |     |     |     |     | 3630 |     |     |     |
| Trp | Ala  | Pro | Val | Leu | Met | Val  | Glu | Gln | Leu | Ala | Met  | Thr | Asp | Gln |
|     | 3635 |     |     |     |     | 3640 |     |     |     |     | 3645 |     |     |     |
| Leu | Thr  | Val | Trp | Trp | Pro | Gly  | Arg | Thr | Ser | Ser | Trp  | Tyr | Leu | Arg |
|     | 3650 |     |     |     |     | 3655 |     |     |     |     | 3660 |     |     |     |
| Arg | Glu  | Ala | Arg | Val | Ser | Lys  | Met | Ser | Leu | Gln | Val  | Arg | Thr | Arg |
|     | 3665 |     |     |     |     | 3670 |     |     |     |     | 3675 |     |     |     |
| Tyr | Trp  | Tyr | Pro | Thr | Arg | Lys  | Cys | Gly | Gly | Gly | Trp  | Arg | Ser | Gly |
|     | 3680 |     |     |     |     | 3685 |     |     |     |     | 3690 |     |     |     |
| His | Arg  | Ser | Val | Ala | Gly | Ala  | Pro | Gly | Ala | Arg | Ser  | Ser | Ser | Met |
|     | 3695 |     |     |     |     | 3700 |     |     |     |     | 3705 |     |     |     |
| Arg | Arg  | Trp | Pro | Met | Tyr | Leu  | Asp | Ile | Gln | Val | Met  | Pro | Ala | Ala |
|     | 3710 |     |     |     |     | 3715 |     |     |     |     | 3720 |     |     |     |
| Val | Val  | Glu | Ala | Arg | Gly | Asn  | Ser | Arg | Thr | Arg | Phe  | Gln | Met | Leu |
|     | 3725 |     |     |     |     | 3730 |     |     |     |     | 3735 |     |     |     |
| Arg | Ser  | Gly | Arg | Lys | Phe | Met  | Val | Ala | Ala | Val | Trp  | Pro | Val | Arg |
|     | 3740 |     |     |     |     | 3745 |     |     |     |     | 3750 |     |     |     |
| Arg | Ala  | Gln | Ser | Trp | Met | Leu  | Thr | Tyr | Gly | Gln | Lys  | Arg | Lys | Arg |
|     | 3755 |     |     |     |     | 3760 |     |     |     |     | 3765 |     |     |     |
| Ser | Ala  | Ala | Arg | Leu | Arg | Gly  | Leu | Glu | Ala | Lys | Arg  | Thr | Gly | Trp |
|     | 3770 |     |     |     |     | 3775 |     |     |     |     | 3780 |     |     |     |
| Ala | Ala  | Arg | Val | Pro | Arg | Phe  | Glu | Ser | Arg | Ile | Arg  | Leu | Glu | Pro |

3785

3790

3795

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gln | Leu  | Thr | Trp | Tyr | Trp | His  | Ser | Arg | Leu | Asp | Pro  | Ser | Leu | Leu |
|     | 3800 |     |     |     |     | 3805 |     |     |     |     | 3810 |     |     |     |
| Thr | Lys  | Pro | Pro | Gly | Tyr | Gly  | Gly | Gly | Ser | Phe | Phe  | Gly | Leu | Gly |
|     | 3815 |     |     |     |     | 3820 |     |     |     |     | 3825 |     |     |     |
| Arg | Trp  | Ser | Lys | Thr | Ser | Lys  | Arg | Gly | Lys | Arg | Pro  | Pro | Ala | Met |
|     | 3830 |     |     |     |     | 3835 |     |     |     |     | 3840 |     |     |     |
| Ala | Arg  | Cys | Arg | Ser | Leu | Glu  | Lys | Glu | Ser | Pro | Gly  | Leu | Arg | Cys |
|     | 3845 |     |     |     |     | 3850 |     |     |     |     | 3855 |     |     |     |
| Gly | Val  | Pro | Arg | Phe | Glu | Pro  | Gln | Arg | Ser | Ala | Pro  | Ala | Gly | Phe |
|     | 3860 |     |     |     |     | 3865 |     |     |     |     | 3870 |     |     |     |
| Arg | Gly  | Arg | Gly | Arg | Gly | Cys  | Pro | Val | Val | Ser | Lys  | Thr | Pro | Pro |
|     | 3875 |     |     |     |     | 3880 |     |     |     |     | 3885 |     |     |     |
| Ala | Asp  | Phe | Ser | Ser | Tyr | Gly  | Ala | Ser | Pro | Ser | Phe  | Ser | Cys | Val |
|     | 3890 |     |     |     |     | 3895 |     |     |     |     | 3900 |     |     |     |
| Phe | Ala  | Arg | Cys | Ile | Pro | Tyr  | Cys | Gly | Arg | Cys | Ala  | Pro | Thr | Leu |
|     | 3905 |     |     |     |     | 3910 |     |     |     |     | 3915 |     |     |     |
| His | Leu  | Asn | Arg | Pro | Tyr | Arg  | Arg | Ser | Ser | Ser | Asn  | Ser | Arg | Arg |
|     | 3920 |     |     |     |     | 3925 |     |     |     |     | 3930 |     |     |     |
| Phe | Cys  | Pro | Arg | Pro | Ser | Ser  | Ser | Gln | Pro | Leu | Pro  | Arg | Arg | Pro |
|     | 3935 |     |     |     |     | 3940 |     |     |     |     | 3945 |     |     |     |
| Pro | Ala  | Glu | Pro | Ala | Phe | Ser  | Met | Thr | Trp | Pro | Trp  | Lys | Arg | Ala |
|     | 3950 |     |     |     |     | 3955 |     |     |     |     | 3960 |     |     |     |
| Arg | Gly  | Trp | Arg | Gly | Trp | Gly  | Arg | Arg | Arg | Arg | Ser  | Gly | Thr | Arg |
|     | 3965 |     |     |     |     | 3970 |     |     |     |     | 3975 |     |     |     |
| Ala | Cys  | Arg | Lys | Gly | Thr | Leu  | Ala | Arg | Pro | Thr | Cys  | Pro | Ser | Arg |
|     | 3980 |     |     |     |     | 3985 |     |     |     |     | 3990 |     |     |     |
| Thr | Cys  | Ser | Glu | Thr | Gly | Ala  | Ala | Arg | Ser | Pro | Arg  | Arg | Cys | Ala |
|     | 3995 |     |     |     |     | 4000 |     |     |     |     | 4005 |     |     |     |
| Pro | Pro  | Ala | Ser | Thr | Arg | Gly  | Gly | Ser | Cys | Gly | Ala  | Ala | Trp | Thr |
|     | 4010 |     |     |     |     | 4015 |     |     |     |     | 4020 |     |     |     |



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Glu Ser Gly Cys Gly Thr Arg Ile Ser Arg Arg Thr Ser Arg Gly  
 4025 4030 4035  
  
 Ser Ala Pro Arg Ala Arg Thr Trp Pro Arg Pro Thr Trp Ser Arg  
 4040 4045 4050  
  
 Arg Thr Ser Arg Pro Arg Arg Arg Ala Thr Ser Lys Asn Pro Ser  
 4055 4060  
  
 Thr Thr Thr Cys Ala Arg Ser Arg Ala Arg Arg Pro Trp Ala Cys  
 4070 4075 4080  
  
 Thr Cys Gly Thr Cys Trp Arg Pro Ser Cys Arg Thr Pro Arg Ala  
 4085 4090 4095  
  
 Ser Arg Arg Arg Ser Cys Phe Trp Trp Cys Ser Thr Val Gly Thr  
 4100 4105 4110  
  
 Thr Arg Arg Ser Gly Arg Arg Cys Ile Ser Pro Ser Pro Arg Ala  
 4115 4120 4125  
  
 Ala Gly Ser Trp Thr Trp Thr Phe Cys Arg Ala Ser Trp Cys Arg  
 4130 4135 4140  
  
 Ser Ala Gly Cys Arg Cys Pro Arg Ser Trp Arg Leu Ser Thr Ser  
 4145 4150 4155  
  
 Arg Cys Ala Trp Ala Ser Thr Thr Leu Gly Arg Ser Thr Arg Pro  
 4160 4165 4170  
  
 Arg Thr Cys Pro Thr Arg Arg Arg Ser Thr Gly Phe Thr Cys Ala  
 4175 4180 4185  
  
 Pro Lys Cys Pro Ala Thr Ile Trp Gly Cys Thr Ala Thr Thr Gly  
 4190 4195 4200  
  
 Cys Thr Ala Arg Ala Pro Ala Ala Gly Ala Ser Ala Thr Arg Ser  
 4205 4210 4215  
  
 Cys Thr Ala Cys Ser Gly Pro Pro Gly Pro Gly Pro Arg Gly Arg  
 4220 4225 4230  
  
 Ala Thr Leu Thr Trp Ala Arg Thr Cys Ala Gly Ser Pro Ala Ala  
 4235 4240 4245  
  
 Gly Pro Trp Lys Leu Pro Ala Val Pro Pro Thr Trp Arg Arg Trp  
 4250 4255 4260

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Thr | Met  | Arg | Arg | Arg | Arg | Ala  | Ser | Thr | Trp | Lys | Thr  | Asp | Gly | Ala |
|     | 4265 |     |     |     |     | 4270 |     |     |     |     | 4275 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Thr | Val  | Phe | Leu | Leu | Asp | Ala  | Ala | Thr | Ala | Thr | Ala  | Ser | Ser | Arg |
|     | 4280 |     |     |     |     | 4285 |     |     |     |     | 4290 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Asp | Ala  | Gly | Gly | Ala | Ala | Glu  | Pro | Ala | Val | Arg | His  | Leu | Leu | Gly |
|     | 4295 |     |     |     |     | 4300 |     |     |     |     | 4305 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg | Leu  | Asp | Pro | Gly | His | Ala  | Thr | His | His | Gly | Ala  | Asp | Asp | Pro |
|     | 4310 |     |     |     |     | 4315 |     |     |     |     | 4320 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gln | Ser  | Arg | Ser | Leu | Thr | Ala  | Ala | Ser | Gly | Gln | Pro  | Ala | Leu | Gly |
|     | 4325 |     |     |     |     | 4330 |     |     |     |     | 4335 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| His | Pro  | Gly | Gly | Arg | Gly | Ala  | Leu | Ala | Leu | Glu | Pro  | His | Ala | Arg |
|     | 4340 |     |     |     |     | 4345 |     |     |     |     | 4350 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Glu | Gly  | Ala | Gly | His | Arg | Glu  | Arg | Ala | Gly | Gly | Glu  | Gln | Gly | His |
|     | 4355 |     |     |     |     | 4360 |     |     |     |     | 4365 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro | Arg  | Arg | Arg | Gly | Arg | Ala  | Gly | Val | Gln | Arg | Ala  | Ala | Gly | Ala |
|     | 4370 |     |     |     |     | 4375 |     |     |     |     | 4380 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg | Gly  | Pro | Leu | Gln | Gln | His  | Gln | Arg | Ala | Asp | Glu  | Pro | Gly | Pro |
|     | 4385 |     |     |     |     | 4390 |     |     |     |     | 4395 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| His | Gly  | Asp | Arg | Arg | Ala | Arg  | Gly | Gly | Val | Ala | Ala  | Arg | Ala | Val |
|     | 4400 |     |     |     |     | 4405 |     |     |     |     | 4410 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro | Pro  | Arg | Val | Glu | Pro | Gly  | Leu | His | Gly | Gly | Ala  | Glu | Arg | Leu |
|     | 4415 |     |     |     |     | 4420 |     |     |     |     | 4425 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro | Glu  | His | Ala | Ala | Arg | Gln  | Arg | Ala | Pro | Gly | Pro  | Gly | Gly | Leu |
|     | 4430 |     |     |     |     | 4435 |     |     |     |     | 4440 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| His | Gln  | Leu | His | Gln | Arg | Ala  | Ala | Ala | Asp | Gly | Gly  | Arg | Gly | Ala |
|     | 4445 |     |     |     |     | 4450 |     |     |     |     | 4455 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro | Glu  | Arg | Gly | Val | Pro | Val  | Gly | Ala | Gly | Leu | Leu  | Leu | Pro | Asp |
|     | 4460 |     |     |     |     | 4465 |     |     |     |     | 4470 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gln | Ser  | Pro | Gly | Leu | Ala | Asp  | Arg | Glu | Pro | Glu | Pro  | Gly | Phe | Gln |
|     | 4475 |     |     |     |     | 4480 |     |     |     |     | 4485 |     |     |     |
|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Glu | Leu  | Ala | Gly | Thr | Val | Gly  | Arg | Ala | Gly | Pro | Gly  | Arg | Gly | Pro |
|     | 4490 |     |     |     |     | 4495 |     |     |     |     | 4500 |     |     |     |

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Arg Asp Gly Val Glu Pro Ala Asp Ala Glu Leu Ala Pro Ala Ala  
4505 4510 4515

Ala Ala Gly Gly Ala Leu His Gly Gln Arg Gln Arg Glu Pro Arg  
4520 4525 4530

Leu Val Pro Gly Leu Pro Ala Pro Val Pro Arg Gly His Arg Ala  
4535 4540 4545

Gly Ala Arg Gly Arg Ala Asp Leu Pro Gly Asp His Pro Arg Glu  
4550 4555 4560

Pro Arg Ala Gly Pro Gly Gly Pro Gly Gln Pro Gly Gly His Pro  
4565 4570 4575

Glu Leu Pro Ala Asp Gln Pro Val Ala Glu Asp Pro Ala Pro Val  
4580 4585 4590

Arg Ala Glu His Arg Gly Gly Ala His Pro Ala Leu Arg Ala Ala  
4595 4600 4605

Glu Arg Gly Ala Val Pro Asp Ala Gly Gly Gly His Ala Gln Arg  
4610 4615 4620

Arg Ala Arg His Asp Arg Ala Gln His Gly Ala Gln His Val Arg  
4625 4630 4635

Ser Gln Pro Pro Val His Gln Ala Asp Gly Leu Leu Ala Ser Gly  
4640 4645 4650

Gly Arg His Glu Leu Gly Leu Leu Tyr Gln Arg His Leu Glu Pro  
4655 4660 4665

Ala Leu Ala Pro Ala Ala Arg Val Leu His Gly Arg Val Arg His  
4670 4675 4680

Ala Arg Pro Gln Arg Arg Val Pro Val Gly Arg Arg Gly Gln Gln  
4685 4690 4695

Arg Val Leu Ala Ala Pro Arg His His Arg Val Glu Glu Arg Gly  
4700 4705 4710

Arg Gly Pro Ala Ala Val Leu Gly Ala Val Arg Ser Arg Gly Cys  
4715 4720 4725

Cys Arg Gly Gly Ala Gly Arg Gln Pro Leu Pro Glu Pro Ala Leu

4730

4735

4740

Phe Ala Glu Gln Arg Ala Gln Gln Arg Ala Gly Ser Ala Asp Ala  
 4745 4750 4755

Ala Ala Pro Ala Gly Arg Gly Gly Val Pro Glu Arg Leu Leu Val  
 4760 4765 4770

Glu Ala Arg Ala Arg Glu Glu Leu Pro Gln Arg Asp Arg Glu Pro  
 4775 4780 4785

Gly Gly Gln Asp Glu Pro Leu Glu Asp Val Arg Ala Arg Ala Gln  
 4790 4795 4800

Gly Arg Ala Pro Ser Gln Gln Arg Arg His Pro Thr Pro Ala Thr  
 4805 4810 4815

Arg Gln Ala Ala Gly Ser Gly Val Gly Arg Gly Phe Arg Arg Arg  
 4820 4825 4830

Gln Gln Arg Val Gly Leu Gly Trp Glu Trp Trp Trp Pro Val Arg  
 4835 4840 4845

Ser Leu Ala Pro Pro Tyr Arg Ala Pro Asp Val Arg Ile Lys Asn  
 4850 4855 4860

Lys Lys Arg Tyr Ser Pro Arg Pro Trp Arg Pro Ala Cys Val Leu  
 4865 4870 4875

Leu Cys Cys Leu Tyr Asp Glu Ala Arg Val Pro Gly Gly Ser Ser  
 4880 4885 4890

Ser Leu Val Arg Glu Arg Asp Ala Ala Gly Gly Gly Gly Gly Asp  
 4895 4900 4905

Ala Ala Pro Ala Gly Gly Ala Leu Arg Ala Pro Ala Val Pro Gly  
 4910 4915 4920

Ala Tyr Gly Gly Ala Glu Gln His Ser Leu Leu Gly Ala Gly Thr  
 4925 4930 4935

Leu Val Arg Tyr His Pro Val Val Pro Gly Gly Gln Gln Val Gly  
 4940 4945 4950

Gly His Arg Leu Ala Glu Leu Pro Glu Arg Pro Gln Gln Leu Pro  
 4955 4960 4965

## 368530-7006W01\_SequenceListing\_ST25.txt

Asp His Arg Gly Ala Glu Gln Arg Phe His Pro His Gly Gly Gln  
 4970 4975 4980  
  
 His Pro Asp His Gln Leu Arg Ala Leu Ala Val Gly Arg Pro Ala  
 4985 4990 4995  
  
 Glu Asn His His Ala His Gln His Ala Gln Arg Glu Arg Val His  
 5000 5005 5010  
  
 Val Gln Gln Gln Val Gln Gly Ala Gly Asp Gly Leu Ala Gln Asp  
 5015 5020 5025  
  
 Pro Gln Trp Gly Arg Gly Gly Glu Leu Trp Ser Gly Arg Ala Asp  
 5030 5035 5040  
  
 Leu Arg Val Gly Gly Val Ala Ala Arg Gly Gln Leu Leu Gly Asp  
 5045 5050 5055  
  
 His Asp His Arg Ser Asp Glu Gln Arg His His Arg Gln Leu Leu  
 5060 5065 5070  
  
 Gly Gly Gly Ala Ser Glu Arg Gly Ala Gly Glu Arg His Arg Arg  
 5075 5080 5085  
  
 Glu Val Arg His Ala Gln Leu Pro Ala Gly Leu Gly Pro Arg Asp  
 5090 5095 5100  
  
 Arg Ala Gly Asp Ala Gly Arg Val His Gln Arg Gly Leu Pro Pro  
 5105 5110 5115  
  
 Arg His Arg Pro Ala Ala Arg Leu Arg Arg Gly Leu His Arg Glu  
 5120 5125 5130  
  
 Pro Pro Gln Gln Pro Ala Gly His Pro Gln Ala Ala Ala Leu Pro  
 5135 5140 5145  
  
 Gly Gly Leu Pro Asp Pro Val Arg Gly Pro Gly Gly Gly Gln His  
 5150 5155 5160  
  
 Pro Arg Ala Leu Gly Cys Arg Ser Leu Glu Lys Gln Gly Gly Gly  
 5165 5170 5175  
  
 Arg Arg Ser Gly Asp Arg Ser Arg Gly His Arg Leu Tyr Arg Gly  
 5180 5185 5190  
  
 Ala Gly Arg Phe Cys Arg Arg Gly Ser Gly Arg Gly Gly Asn Arg  
 5195 5200 5205

## 368530-7006W01\_SequenceListing\_ST25.txt

Lys Asp Ser His Pro Ala Gly Gly Glu Gly Gln Gln Gly Gln Glu  
 5210 5215 5220  
 Leu Gln Arg Ala Arg Gly Gln Glu Lys His Arg Leu Pro Gln Leu  
 5225 5230 5235  
 Val Pro Gly Leu Gln Leu Arg Arg Pro Arg Glu Gly Arg Ala Leu  
 5240 5245 5250  
 Leu Asp Ala Ala His His Leu Gly Arg His Leu Arg Arg Gly Ala  
 5255 5260 5265  
 Ser Leu Leu Val Ala Ala Arg His Asp Ala Arg Pro Gly His Leu  
 5270 5275 5280  
 Pro Leu His Ala Ser Ser Gln Leu Pro Gly Gly Gly Arg Arg Ala  
 5285 5290 5295  
 Pro Ala Arg Leu Leu Gln Glu Leu Leu Gln Arg Ala Gly Arg Leu  
 5300 5305 5310  
 Leu Ala Ala Ala Ala Arg Leu His Leu Ala His Ala Arg Leu Gln  
 5315 5320 5325  
 Pro Leu Pro Arg Glu Pro Asp Pro Arg Pro Pro Ala Arg Ala His  
 5330 5335 5340  
 His Tyr His Arg Gln Lys Arg Ser Cys Ser His Arg Ser Arg Asp  
 5345 5350 5355  
 Pro Ala Ala Ala Gln Gln Tyr Pro Gly Ser Pro Ala Arg Asp Arg  
 5360 5365 5370  
 His Arg Gln Thr Pro His Leu Pro Leu Arg Leu Gln Gly Pro Gly  
 5375 5380 5385  
 Arg Ser Arg Ala Ala Arg Pro Leu Glu Pro His Leu Leu Lys Asn  
 5390 5395 5400  
 Val His Ser His Leu Ala Gln His Arg Leu Gly Pro Ala Arg Ala  
 5405 5410 5415  
 Gln Gln Asp Val Arg Arg Arg Ser Pro Thr Leu His Ala Thr Pro  
 5420 5425 5430  
 Arg Ala Arg Ala Arg Ala Leu Pro Arg Ser Leu Gly Arg Pro Gln  
 5435 5440 5445

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Gly | Pro  | Arg | Ala | Leu | Ala | His  | His | Arg | Arg | Arg | Arg  | Asp | Arg | Pro |
|     | 5450 |     |     |     |     | 5455 |     |     |     |     | 5460 |     |     |     |
| Gly | Gly  | Gly | Arg | Arg | Ala | Gln  | Leu | His | Ala | Arg | Arg  | Arg | Ala | Arg |
|     | 5465 |     |     |     |     | 5470 |     |     |     |     | 5475 |     |     |     |
| Leu | His  | Arg | Gly | Arg | Arg | His  | Arg | Gln | Arg | Gly | Gly  | Arg | Cys | Ala |
|     | 5480 |     |     |     |     | 5485 |     |     |     |     | 5490 |     |     |     |
| Pro | Val  | Arg | Pro | Arg | Gln | Glu  | Pro | Ala | Ala | Ala | His  | Arg | Pro | Ala |
|     | 5495 |     |     |     |     | 5500 |     |     |     |     | 5505 |     |     |     |
| Ala | Pro  | Glu | His | Pro | Arg | His  | Ala | Arg | Gly | Ala | Ser  | Leu | Ala | Ala |
|     | 5510 |     |     |     |     | 5515 |     |     |     |     | 5520 |     |     |     |
| Gln | Gly  | Gln | Ala | His | Gly | Thr  | Gln | Gly | His | Ala | Gln  | Gly | Gly | Gln |
|     | 5525 |     |     |     |     | 5530 |     |     |     |     | 5535 |     |     |     |
| Thr | Arg  | Gly | Leu | Arg | Gln | Gln  | Gln | Arg | Arg | Gln | Asp  | Pro | Gln | Thr |
|     | 5540 |     |     |     |     | 5545 |     |     |     |     | 5550 |     |     |     |
| Arg | Gly  | His | Gly | Gly | Gly | Gly  | Gly | His | Arg | Gln | His  | Val | Pro | Pro |
|     | 5555 |     |     |     |     | 5560 |     |     |     |     | 5565 |     |     |     |
| Ala | Ala  | Arg | Gln | Arg | Val | Leu  | Gly | Ala | Arg | Arg | Arg  | His | Arg | Cys |
|     | 5570 |     |     |     |     | 5575 |     |     |     |     | 5580 |     |     |     |
| Ala | Arg  | Ala | Arg | Ala | His | Pro  | Pro | Pro | Ser | His | Leu  | Lys | Met | Leu |
|     | 5585 |     |     |     |     | 5590 |     |     |     |     | 5595 |     |     |     |
| Thr | Ser  | Arg | Cys | Cys | Val | Pro  | Ala | Ala | Arg | Arg | Met  | Ser | Lys | Arg |
|     | 5600 |     |     |     |     | 5605 |     |     |     |     | 5610 |     |     |     |
| Lys | Tyr  | Lys | Glu | Glu | Met | Leu  | Gln | Val | Ile | Ala | Pro  | Glu | Ile | Tyr |
|     | 5615 |     |     |     |     | 5620 |     |     |     |     | 5625 |     |     |     |
| Gly | Pro  | Ala | Val | Lys | Glu | Glu  | Arg | Lys | Pro | Arg | Lys  | Leu | Lys | Arg |
|     | 5630 |     |     |     |     | 5635 |     |     |     |     | 5640 |     |     |     |
| Val | Lys  | Lys | Asp | Lys | Lys | Glu  | Glu | Glu | Asp | Val | Asp  | Gly | Leu | Val |
|     | 5645 |     |     |     |     | 5650 |     |     |     |     | 5655 |     |     |     |
| Glu | Phe  | Val | Arg | Glu | Phe | Ala  | Pro | Arg | Arg | Arg | Val  | Gln | Trp | Arg |
|     | 5660 |     |     |     |     | 5665 |     |     |     |     | 5670 |     |     |     |
| Gly | Arg  | Lys | Val | Lys | Pro | Val  | Leu | Arg | Pro | Gly | Thr  | Thr | Val | Val |

5675

5680

5685

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Phe | Thr  | Pro | Gly | Glu | Arg | Ser  | Gly | Ser | Ala | Ser | Lys  | Arg | Ser | Tyr |
|     | 5690 |     |     |     |     | 5695 |     |     |     |     | 5700 |     |     |     |
| Asp | Glu  | Val | Tyr | Gly | Asp | Glu  | Asp | Ile | Leu | Glu | Gln  | Ala | Val | Glu |
|     | 5705 |     |     |     |     | 5710 |     |     |     |     | 5715 |     |     |     |
| Arg | Leu  | Gly | Glu | Phe | Ala | Tyr  | Gly | Lys | Arg | Ser | Arg  | Pro | Ala | Pro |
|     | 5720 |     |     |     |     | 5725 |     |     |     |     | 5730 |     |     |     |
| Leu | Lys  | Glu | Glu | Ala | Val | Ser  | Ile | Pro | Leu | Asp | His  | Gly | Asn | Pro |
|     | 5735 |     |     |     |     | 5740 |     |     |     |     | 5745 |     |     |     |
| Thr | Pro  | Ser | Leu | Lys | Pro | Val  | Thr | Leu | Gln | Gln | Val  | Leu | Pro | Ser |
|     | 5750 |     |     |     |     | 5755 |     |     |     |     | 5760 |     |     |     |
| Ala | Ala  | Pro | Arg | Arg | Gly | Phe  | Lys | Arg | Glu | Gly | Gly  | Glu | Asp | Leu |
|     | 5765 |     |     |     |     | 5770 |     |     |     |     | 5775 |     |     |     |
| Tyr | Pro  | Thr | Met | Gln | Leu | Met  | Val | Pro | Lys | Arg | Gln  | Lys | Leu | Glu |
|     | 5780 |     |     |     |     | 5785 |     |     |     |     | 5790 |     |     |     |
| Asp | Val  | Leu | Glu | His | Met | Lys  | Val | Asp | Pro | Glu | Val  | Gln | Pro | Glu |
|     | 5795 |     |     |     |     | 5800 |     |     |     |     | 5805 |     |     |     |
| Val | Lys  | Val | Arg | Pro | Ile | Lys  | Gln | Val | Ala | Pro | Gly  | Leu | Gly | Val |
|     | 5810 |     |     |     |     | 5815 |     |     |     |     | 5820 |     |     |     |
| Gln | Thr  | Val | Asp | Ile | Lys | Ile  | Pro | Thr | Glu | Pro | Met  | Glu | Thr | Gln |
|     | 5825 |     |     |     |     | 5830 |     |     |     |     | 5835 |     |     |     |
| Thr | Glu  | Pro | Val | Lys | Pro | Ser  | Thr | Ser | Thr | Met | Glu  | Val | Gln | Thr |
|     | 5840 |     |     |     |     | 5845 |     |     |     |     | 5850 |     |     |     |
| Asp | Pro  | Trp | Met | Pro | Ala | Pro  | Ala | Ser | Thr | Thr | Arg  | Arg | Arg | Arg |
|     | 5855 |     |     |     |     | 5860 |     |     |     |     | 5865 |     |     |     |
| Lys | Tyr  | Gly | Ala | Ala | Ser | Leu  | Leu | Met | Pro | Asn | Tyr  | Ala | Leu | His |
|     | 5870 |     |     |     |     | 5875 |     |     |     |     | 5880 |     |     |     |
| Pro | Ser  | Ile | Ile | Pro | Thr | Pro  | Gly | Tyr | Arg | Gly | Thr  | Arg | Phe | Tyr |
|     | 5885 |     |     |     |     | 5890 |     |     |     |     | 5895 |     |     |     |
| Arg | Gly  | Tyr | Thr | Ser | Ser | Arg  | Arg | Lys | Thr | Thr | Thr  | Arg | Arg | Arg |
|     | 5900 |     |     |     |     | 5905 |     |     |     |     | 5910 |     |     |     |



|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg | Arg  | Arg | Thr | Arg | Arg | Ser  | Ser | Thr | Ala | Thr | Ser  | Ala | Ala | Ala |
|     | 5915 |     |     |     |     | 5920 |     |     |     |     | 5925 |     |     |     |
| Leu | Val  | Arg | Arg | Val | Tyr | Arg  | Ser | Gly | Arg | Glu | Pro  | Leu | Thr | Leu |
|     | 5930 |     |     |     |     | 5935 |     |     |     |     | 5940 |     |     |     |
| Pro | Arg  | Ala | Arg | Tyr | His | Pro  | Ser | Ile | Ala | Ile | Leu  | Cys | Arg | Arg |
|     | 5945 |     |     |     |     | 5950 |     |     |     |     | 5955 |     |     |     |
| Leu | Leu  | Leu | Ala | Asp | Met | Ala  | Leu | Thr | Cys | Arg | Leu  | Arg | Val | Pro |
|     | 5960 |     |     |     |     | 5965 |     |     |     |     | 5970 |     |     |     |
| Ile | Thr  | Gly | Tyr | Arg | Gly | Arg  | Lys | Pro | Arg | Arg | Arg  | Arg | Leu | Thr |
|     | 5975 |     |     |     |     | 5980 |     |     |     |     | 5985 |     |     |     |
| Gly | Asn  | Gly | Leu | Arg | Arg | His  | His | His | Arg | Arg | Arg  | Arg | Ala | Ile |
|     | 5990 |     |     |     |     | 5995 |     |     |     |     | 6000 |     |     |     |
| Ser | Lys  | Arg | Leu | Gly | Gly | Gly  | Phe | Leu | Pro | Ala | Leu  | Ile | Pro | Ile |
|     | 6005 |     |     |     |     | 6010 |     |     |     |     | 6015 |     |     |     |
| Ile | Ala  | Ala | Ala | Ile | Gly | Ala  | Ile | Pro | Gly | Ile | Ala  | Ser | Val | Ala |
|     | 6020 |     |     |     |     | 6025 |     |     |     |     | 6030 |     |     |     |
| Val | Gln  | Ala | Ser | Gln | Arg | His  | Asp | Thr | Ala | Trp | Lys  | Ile | Cys | Asn |
|     | 6035 |     |     |     |     | 6040 |     |     |     |     | 6045 |     |     |     |
| Lys | Lys  | Met | Asp | Arg | Ser | Trp  | Ser | Cys | Asp | Val | Cys  | Phe | Met | Glu |
|     | 6050 |     |     |     |     | 6055 |     |     |     |     | 6060 |     |     |     |
| Asp | Ile  | Asn | Phe | Ser | Ser | Leu  | Ala | Pro | Arg | His | Gly  | Thr | Arg | Pro |
|     | 6065 |     |     |     |     | 6070 |     |     |     |     | 6075 |     |     |     |
| Phe | Met  | Gly | Thr | Trp | Ser | Asp  | Ile | Gly | Asn | Ser | Gln  | Leu | Asn | Gly |
|     | 6080 |     |     |     |     | 6085 |     |     |     |     | 6090 |     |     |     |
| Gly | Ala  | Phe | Asn | Trp | Ser | Ser  | Leu | Trp | Ser | Gly | Leu  | Lys | Asn | Phe |
|     | 6095 |     |     |     |     | 6100 |     |     |     |     | 6105 |     |     |     |
| Gly | Ser  | Thr | Leu | Lys | Thr | Tyr  | Gly | Asn | Lys | Ala | Trp  | Asn | Ser | Ser |
|     | 6110 |     |     |     |     | 6115 |     |     |     |     | 6120 |     |     |     |
| Thr | Gly  | Gln | Ala | Leu | Arg | Glu  | Lys | Leu | Lys | Glu | Gln  | Asn | Phe | Gln |
|     | 6125 |     |     |     |     | 6130 |     |     |     |     | 6135 |     |     |     |
| Gln | Lys  | Val | Val | Asp | Gly | Leu  | Ala | Ser | Gly | Ile | Asn  | Gly | Val | Val |
|     | 6140 |     |     |     |     | 6145 |     |     |     |     | 6150 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asp  | Leu | Ala | Asn | Gln | Ala | Val  | Gln | Lys | Gln | Ile | Asn  | Ser | Arg | Leu |
| 6155 |     |     |     |     |     | 6160 |     |     |     |     | 6165 |     |     |     |
| Asp  | Ala | Val | Pro | Pro | Ala | Gly  | Ser | Val | Glu | Met | Pro  | Gln | Val | Glu |
| 6170 |     |     |     |     |     | 6175 |     |     |     |     | 6180 |     |     |     |
| Glu  | Glu | Leu | Pro | Pro | Leu | Asp  | Lys | Arg | Gly | Asp | Lys  | Arg | Pro | Arg |
| 6185 |     |     |     |     |     | 6190 |     |     |     |     | 6195 |     |     |     |
| Pro  | Asp | Ala | Glu | Glu | Thr | Leu  | Leu | Thr | His | Thr | Asp  | Glu | Pro | Pro |
| 6200 |     |     |     |     |     | 6205 |     |     |     |     | 6210 |     |     |     |
| Pro  | Tyr | Glu | Glu | Ala | Val | Lys  | Leu | Gly | Leu | Pro | Thr  | Thr | Arg | Pro |
| 6215 |     |     |     |     |     | 6220 |     |     |     |     | 6225 |     |     |     |
| Val  | Ala | Pro | Leu | Ala | Thr | Gly  | Val | Leu | Lys | Pro | Ser  | Ser | Ser | Ser |
| 6230 |     |     |     |     |     | 6235 |     |     |     |     | 6240 |     |     |     |
| Gln  | Pro | Ala | Thr | Leu | Asp | Leu  | Pro | Pro | Pro | Ala | Ser  | Arg | Pro | Ser |
| 6245 |     |     |     |     |     | 6250 |     |     |     |     | 6255 |     |     |     |
| Thr  | Val | Ala | Lys | Pro | Leu | Pro  | Pro | Val | Ala | Val | Ala  | Ser | Arg | Ala |
| 6260 |     |     |     |     |     | 6265 |     |     |     |     | 6270 |     |     |     |
| Pro  | Arg | Gly | Arg | Pro | Gln | Ala  | Asn | Trp | Gln | Ser | Thr  | Leu | Asn | Ser |
| 6275 |     |     |     |     |     | 6280 |     |     |     |     | 6285 |     |     |     |
| Ile  | Val | Gly | Leu | Gly | Val | Gln  | Ser | Val | Lys | Arg | Arg  | Arg | Cys | Tyr |
| 6290 |     |     |     |     |     | 6295 |     |     |     |     | 6300 |     |     |     |
| Lys  | Thr | Leu | Arg | Leu | Thr | Cys  | Leu | Ser | Val | Cys | Ile  | Cys | Met | Ser |
| 6305 |     |     |     |     |     | 6310 |     |     |     |     | 6315 |     |     |     |
| Ala  | Asp | Gln | Lys | Glu | Glu | Glu  | Ala | Arg | Arg | Arg | Val  | Ala | Arg | Trp |
| 6320 |     |     |     |     |     | 6325 |     |     |     |     | 6330 |     |     |     |
| Pro  | Pro | His | Arg | Cys | Cys | Pro  | Ser | Gly | Arg | Thr | Cys  | Thr | Ser | Pro |
| 6335 |     |     |     |     |     | 6340 |     |     |     |     | 6345 |     |     |     |
| Asp  | Arg | Thr | Leu | Arg | Ser | Thr  | Val | Arg | Val | Trp | Cys  | Ser | Ser | Pro |
| 6350 |     |     |     |     |     | 6355 |     |     |     |     | 6360 |     |     |     |
| Ala  | Pro | Gln | Thr | Pro | Thr | Ser  | Val | Trp | Gly | Thr | Ser  | Leu | Gly | Thr |
| 6365 |     |     |     |     |     | 6370 |     |     |     |     | 6375 |     |     |     |
| Pro  | Arg | Trp | Arg | Pro | Arg | Thr  | Met | Pro | Pro | Thr | Ala  | Ala | Ser | Gly |
| 6380 |     |     |     |     |     | 6385 |     |     |     |     | 6390 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | Cys | Ala | Ser | Cys | Pro | Trp  | Thr | Ala | Arg | Thr | Thr  | Pro | Thr | Arg |
| 6395 |     |     |     |     |     | 6400 |     |     |     |     | 6405 |     |     |     |
| Thr  | Lys | Cys | Ala | Thr | Arg | Trp  | Pro | Trp | Ala | Thr | Thr  | Ala | Cys | Trp |
| 6410 |     |     |     |     |     | 6415 |     |     |     |     | 6420 |     |     |     |
| Thr  | Trp | Pro | Ala | Pro | Thr | Leu  | Thr | Ser | Ala | Ala | Cys  | Trp | Ile | Gly |
| 6425 |     |     |     |     |     | 6430 |     |     |     |     | 6435 |     |     |     |
| Gly  | Pro | Ala | Ser | Asn | Pro | Thr  | Pro | Ala | Pro | Pro | Thr  | Thr | Ala | Trp |
| 6440 |     |     |     |     |     | 6445 |     |     |     |     | 6450 |     |     |     |
| Leu  | Pro | Arg | Glu | Arg | Pro | Thr  | Leu | Ala | Ser | Gly | His  | Ile | Lys | Leu |
| 6455 |     |     |     |     |     | 6460 |     |     |     |     | 6465 |     |     |     |
| Val  | Ile | Leu | Ile | Gln | Lys | Lys  | Pro | Ile | His | Met | Glu  | Met | His | Leu |
| 6470 |     |     |     |     |     | 6475 |     |     |     |     | 6480 |     |     |     |
| Cys  | Lys | Ala | Leu | Ala | Leu | Gln  | Arg | Met | Val | Phe | Asn  | Leu | Glu | Leu |
| 6485 |     |     |     |     |     | 6490 |     |     |     |     | 6495 |     |     |     |
| Thr  | Ala | Met | Val | Arg | Gln | Ser  | Met | Gln | Thr | Lys | Leu  | Ile | Asn | Gln |
| 6500 |     |     |     |     |     | 6505 |     |     |     |     | 6510 |     |     |     |
| Ser  | Leu | Lys | Trp | Val | Met | Leu  | Asn | Gly | Met | Thr | Ser  | Leu | Val | Leu |
| 6515 |     |     |     |     |     | 6520 |     |     |     |     | 6525 |     |     |     |
| Met  | Lys | Asn | Met | Glu | Ala | Glu  | Leu | Leu | Ser | Leu | Thr  | Pro | Lys | Ser |
| 6530 |     |     |     |     |     | 6535 |     |     |     |     | 6540 |     |     |     |
| Leu  | Ala | Met | Val | Leu | Leu | Pro  | Ser | Leu | Pro | Ile | Lys  | Lys | Glu | Ala |
| 6545 |     |     |     |     |     | 6550 |     |     |     |     | 6555 |     |     |     |
| Arg  | Gln | Met | Lys | Pro | Lys | Gln  | Ala | Val | Pro | Lys | Asn  | Met | Thr | Leu |
| 6560 |     |     |     |     |     | 6565 |     |     |     |     | 6570 |     |     |     |
| Thr  | Trp | His | Ser | Ser | Ile | Ile  | Glu | Val | Gln | Leu | Pro  | Pro | Ala | Pro |
| 6575 |     |     |     |     |     | 6580 |     |     |     |     | 6585 |     |     |     |
| Gln  | Lys | Leu | Phe | Cys | Ile | Leu  | Arg | Met | Trp | Ile | Trp  | Lys | Leu | Gln |
| 6590 |     |     |     |     |     | 6595 |     |     |     |     | 6600 |     |     |     |
| Ile  | Pro | Ile | Leu | Tyr | Thr | Arg  | Gln | Val | Gln | Met | Thr  | Val | Ala | Leu |
| 6605 |     |     |     |     |     | 6610 |     |     |     |     | 6615 |     |     |     |
| Leu  | Ser | Ile | Trp | Val | Ser | Ser  | Pro | Cys | Pro | Thr | Asp  | Pro | Thr | Thr |

6620

6625

6630

Leu Ala Ser Glu Thr Thr Leu Ser Val Cys Thr Thr Thr Ala Leu  
6635 6640 6645

Ala Ile Trp Val Tyr Trp Leu Asp Arg Pro Pro Ser Met Leu Trp  
6650 6655 6660

Trp Thr Cys Arg Thr Glu Thr Pro Asn Cys Pro Thr Ser Ser Cys  
6665 6670 6675

Leu Thr Leu Trp Val Thr Glu Pro Gly Ile Ser Val Cys Gly Ile  
6680 6685 6690

Arg Arg Trp Thr Val Met Thr Pro Met Cys Ala Leu Leu Lys Ile  
6695 6700 6705

Thr Val Trp Arg Met Asn Phe Leu Thr Ile Ala Ser Pro Trp Met  
6710 6715 6720

Leu Trp Val Glu Leu Ile Leu Thr Arg Glu Leu Arg Pro Met Val  
6725 6730 6735

Ile Ile Lys Pro Pro Gly Pro Lys Met Ile Leu Leu Met Met Leu  
6740 6745 6750

Met Asn Trp Ala Arg Ala Ile Leu Ser Pro Trp Arg Ser Thr Ser  
6755 6760 6765

Arg Pro Thr Cys Gly Gly Thr Ser Ser Thr Arg Thr Trp Arg Cys  
6770 6775 6780

Thr Cys Pro Thr Pro Thr Ser Thr Arg Arg Pro Thr Ser Arg Cys  
6785 6790 6795

Pro Pro Thr Pro Thr Pro Thr Ile Thr Thr Ala Ala Trp Trp Arg  
6800 6805 6810

Pro Arg Trp Trp Thr Pro Thr Ser Thr Ser Gly Arg Ala Gly Arg  
6815 6820 6825

Trp Thr Pro Trp Thr Thr Ser Thr Pro Ser Thr Thr Thr Ala Thr  
6830 6835 6840

Arg Ala Cys Asp Thr Ala Pro Cys Ser Trp Ala Thr Gly Ala Thr  
6845 6850 6855

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Cys  | Pro | Ser | Thr | Ser | Arg | Cys  | Pro | Lys | Ser | Phe | Ser  | Pro | Ser | Arg |
| 6860 |     |     |     |     |     | 6865 |     |     |     |     | 6870 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Ser | Cys | Ser | Cys | Pro | Gly  | Pro | Thr | Pro | Thr | Ser  | Gly | Thr | Ser |
| 6875 |     |     |     |     |     | 6880 |     |     |     |     | 6885 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Arg | Thr | Ser | Thr | Ser | Cys  | Arg | Ala | Pro | Ser | Ala  | Thr | Thr | Cys |
| 6890 |     |     |     |     |     | 6895 |     |     |     |     | 6900 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Arg | Thr | Gly | Pro | Pro | Ser  | Pro | Ser | Pro | Ala | Ser  | Thr | Ser | Thr |
| 6905 |     |     |     |     |     | 6910 |     |     |     |     | 6915 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Pro | Ser | Ser | Pro | Trp | Arg  | Thr | Thr | Pro | Pro | Pro  | Arg | Ser | Arg |
| 6920 |     |     |     |     |     | 6925 |     |     |     |     | 6930 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Cys | Cys | Ala | Thr | Thr | Pro  | Thr | Thr | Ser | Pro | Ser  | Thr | Thr | Thr |
| 6935 |     |     |     |     |     | 6940 |     |     |     |     | 6945 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser  | Arg | Arg | Pro | Thr | Cys | Ser  | Thr | Pro | Ser | Arg | Pro  | Thr | Pro | Pro |
| 6950 |     |     |     |     |     | 6955 |     |     |     |     | 6960 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Thr  | Cys | Pro | Ser | Pro | Ser | Pro  | Arg | Ala | Thr | Gly | Pro  | Pro | Ser | Ala |
| 6965 |     |     |     |     |     | 6970 |     |     |     |     | 6975 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Gly | Pro | Ser | Arg | Ala | Ser  | Arg | Pro | Ala | Arg | Arg  | Pro | Arg | Ser |
| 6980 |     |     |     |     |     | 6985 |     |     |     |     | 6990 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ala  | Pro | Gly | Ser | Thr | Pro | Thr  | Ser | Ser | Thr | Arg | Ala  | Pro | Ser | Pro |
| 6995 |     |     |     |     |     | 7000 |     |     |     |     | 7005 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Thr  | Ser | Thr | Ala | Pro | Ser | Thr  | Ser | Thr | Thr | Pro | Ser  | Arg | Arg | Ser |
| 7010 |     |     |     |     |     | 7015 |     |     |     |     | 7020 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Ser | Pro | Ser | Thr | Pro | Pro  | Ser | Ala | Gly | Pro | Ala  | Thr | Thr | Ala |
| 7025 |     |     |     |     |     | 7030 |     |     |     |     | 7035 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Ser  | Arg | Pro | Thr | Ser | Ser | Lys  | Ser | Ser | Ala | Pro | Ser  | Thr | Glu | Arg |
| 7040 |     |     |     |     |     | 7045 |     |     |     |     | 7050 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Gly  | Thr | Thr | Trp | Pro | Ser | Ala  | Thr | Pro | Arg | Thr | Gly  | Ser | Trp | Ser |
| 7055 |     |     |     |     |     | 7060 |     |     |     |     | 7065 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Arg  | Cys | Trp | Pro | Thr | Thr | Thr  | Ser | Ala | Thr | Arg | Ala  | Ser | Thr | Cys |
| 7070 |     |     |     |     |     | 7075 |     |     |     |     | 7080 |     |     |     |
|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
| Pro  | Arg | Ala | Thr | Arg | Thr | Ala  | Cys | Thr | Pro | Ser | Ser  | Ala | Thr | Ser |
| 7085 |     |     |     |     |     | 7090 |     |     |     |     | 7095 |     |     |     |

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Ser Pro Ala Ala Arg Ser Trp Thr Arg Ser Thr Thr Arg Thr Thr  
 7100 7105 7110  
 Arg Pro Ser Pro Trp Pro Thr Ser Thr Thr Thr Arg Ala Ser Ser  
 7115 7120 7125  
 Ala Thr Ser Arg Pro Pro Cys Ala Arg Ala Ser Pro Thr Pro Pro  
 7130 7135 7140  
 Thr Thr Pro Thr Arg Ser Ser Ala Arg Ala Pro Ser Pro Ala Ser  
 7145 7150 7155  
 Pro Arg Lys Ser Ser Ser Ala Thr Gly Ser Cys Gly Ala Ser Pro  
 7160 7165 7170  
 Ser Pro Ala Thr Ser Cys Pro Trp Ala Arg Ser Pro Thr Ser Ala  
 7175 7180 7185  
 Arg Thr Cys Ser Thr Pro Thr Pro Pro Thr Arg Thr Ile Ser Lys  
 7190 7195 7200  
 Ser Thr Pro Trp Met Ser Pro Pro Phe Ser Met Leu Ser Ser Lys  
 7205 7210 7215  
 Ser Ser Thr Ser Ser Glu Cys Thr Ser Pro Thr Ala Ala Ser Ser  
 7220 7225 7230  
 Arg Pro Ser Thr Cys Ala Arg Pro Ser Arg Pro Ala Thr Pro Pro  
 7235 7240 7245  
 Pro Lys Pro Leu Ala Ser Cys Lys Met Thr Ala Cys Ala Gly Ser  
 7250 7255 7260  
 Gly Glu Gln Glu Leu Arg Ala Ile Leu Arg Asp Leu Gly Cys Gly  
 7265 7270 7275  
 Pro Cys Phe Leu Gly Thr Phe Asp Lys Arg Phe Pro Gly Phe Met  
 7280 7285 7290  
 Ala Pro His Lys Leu Ala Cys Ala Ile Val Asn Thr Ala Gly Arg  
 7295 7300 7305  
 Glu Thr Gly Gly Glu His Trp Leu Ala Phe Ala Trp Asn Pro Arg  
 7310 7315 7320  
 Ser His Thr Cys Tyr Leu Phe Asp Pro Phe Gly Phe Ser Asp Glu  
 7325 7330 7335

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Arg Leu Lys Gln Ile Tyr Gln Phe Glu Tyr Glu Gly Leu Leu Arg  
7340 7345 7350

Arg Ser Ala Leu Ala Thr Glu Asp Arg Cys Val Thr Leu Glu Lys  
7355 7360 7365

Ser Thr Gln Thr Val Gln Gly Pro Arg Ser Ala Ala Cys Gly Leu  
7370 7375 7380

Phe Cys Cys Met Phe Leu His Ala Phe Val His Trp Pro Asp Arg  
7385 7390 7395

Pro Met Asp Lys Asn Pro Thr Met Asn Leu Leu Thr Gly Val Pro  
7400 7405 7410

Asn Gly Met Leu Gln Ser Pro Gln Val Glu Pro Thr Leu Arg Arg  
7415 7420 7425

Asn Gln Glu Ala Leu Tyr Arg Phe Leu Asn Ala His Ser Ala Tyr  
7430 7435 7440

Phe Arg Ser His Arg Ala Arg Ile Glu Lys Ala Thr Ala Phe Asp  
7445 7450 7455

Arg Met Asn Gln Asp Met Ser Gly Val Cys Met Met Leu Tyr Ser  
7460 7465 7470

Ser Thr Ala His Val Tyr Ala Thr Phe Ser Glu Ala Leu Thr Leu  
7475 7480 7485

Phe Arg Asn Arg Arg Gly Ser Ala Gly Ser Arg His Gly Pro Arg  
7490 7495 7500

Ala Gly Ile Arg Cys Gly Thr Gly Thr Trp Ala Ala Thr Thr Arg  
7505 7510 7515

Gly Ser Ala Ala Ser Ala Arg Gly Gly Arg Gly Thr Ser Arg Ser  
7520 7525 7530

Thr Ala Cys Ala Val Ala Gly Arg Pro Ala Gly Arg Ala Arg Arg  
7535 7540 7545

Ser Asn Arg Ser Trp Asp Pro Arg Ser Ala Arg Glu Ser Tyr Gly  
7550 7555 7560

Thr Arg Gly Cys Ser Thr Gly Thr Pro Ser Gly Pro Gly Ala Ser

7565

7570

7575

Arg Ser Pro Ala Pro Ser Arg Arg Cys Pro Pro Arg Pro Asp Pro  
 7580 7585 7590

Arg Arg Trp Pro Ser Arg Arg Gly Ser Ser Cys Arg Ser Ala Ala  
 7595 7600 7605

Pro Cys Trp Ala Arg Ser Arg Ala Cys Gly Cys Asn Arg Ser Ala  
 7610 7615 7620

Gly Gly Ser Ala Ser Ser Gly Pro Ala Arg Ser Ser Cys Pro Gly  
 7625 7630 7635

Thr Trp Pro Ser Lys Pro Pro Ala Gly Gly Arg Pro Ala Ala Pro  
 7640 7645 7650

Cys Arg Pro Arg Arg Arg Pro Arg Arg Thr Cys Arg Thr Gly Trp  
 7655 7660 7665

Trp Arg Ser Gln Arg Arg Ala Arg Ser Ser Ala Arg Arg Cys Trp  
 7670 7675 7680

Pro Ala Ala Pro Arg Cys Ala Pro Ser Gly Ser Gly Ser Trp Pro  
 7685 7690 7695

Gly Arg Gly Ser Pro Ser Ala Arg Ala Ala Arg Ser Arg Ser Pro  
 7700 7705 7710

His Pro Ser Arg Ser Cys Ala Pro Ser Gly Ser Ser Arg Ser Arg  
 7715 7720 7725

Ala Gly Thr Ala Ala Cys Pro Arg Pro Arg Cys Thr Arg Ala Ala  
 7730 7735 7740

Thr Ala Arg Ser Arg Cys Ser Pro Ser Ser Cys Gly Arg Ser Gly  
 7745 7750 7755

Ser Ala Ser Ala Arg Ser Pro Ala Gly Ser Gly Pro Ser Ser Trp  
 7760 7765 7770

Ser Gly Ser Cys Cys Trp Arg Ser Ala Glu Cys Arg Gly Ala Pro  
 7775 7780 7785

Arg Ser His Thr Gly Gly Arg Tyr Gly Gly Thr Pro Arg Pro Ala  
 7790 7795 7800



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Arg Ala Ser Ala Gly Arg Arg Thr Ser Gly Arg Ser Pro Arg Gly  
 7805 7810 7815  
 Thr Gly Pro Ser Ala Ala Ser Ser Leu Pro Cys Pro Ser Pro Arg  
 7820 7825 7830  
 Pro Lys Arg Ser Ala Gly Ser Gly Gly Ser Ser Pro Leu Ser Ser  
 7835 7840 7845  
 Ser Pro Pro Pro Lys Ser Gly Gly Arg Ser Arg Pro Gly Ser Gln  
 7850 7855 7860  
 Thr Leu Ala Cys Arg Pro Ser Arg Cys Ala Arg Gly Glu Ser Ser  
 7865 7870 7875  
 Pro Arg Pro Pro Ala Pro Pro Arg Pro Ala Phe Arg Pro Arg Cys  
 7880 7885 7890  
 Pro Gly Cys Leu Ala Lys Ala His Ala Trp Ser Cys Gly Val Ser  
 7895 7900 7905  
 Phe Trp Ala Ala Glu Ala Ala Ala Glu Thr Cys Trp Ala Ser Ala  
 7910 7915 7920  
 Ser Ser Arg Ser Pro Arg Leu Phe Leu Leu Leu Gly Arg Arg Pro  
 7925 7930 7935  
 Arg Pro Arg Gly Gly Arg His Ala Ser Ser Gly Ala Glu Ala Glu  
 7940 7945 7950  
 Ala Thr Gly Ser Arg Gly Ser Ala Gly Gly Trp Gln Ser Pro Phe  
 7955 7960 7965  
 Arg Val Arg Gly Cys Ala Pro Gly Gly Ala Ala Leu Thr Asp Phe  
 7970 7975 7980  
 Leu Arg Gly Arg Pro Leu Cys Ser Pro Arg Glu Gln Ala Trp Arg  
 7985 7990 7995  
 Leu Ser His Arg Arg Gln His Arg His Leu Pro Pro Pro Pro Pro  
 8000 8005 8010  
 Thr Arg Thr Ser Ser Ser Arg Met Lys Ala Pro Pro Arg Arg Pro  
 8015 8020 8025  
 Ala Pro Pro Pro Thr Pro Gln Pro Gln Thr Cys Lys Arg Trp Arg  
 8030 8035 8040

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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Asn | Pro  | Ser | Arg | Leu | Thr | Trp  | Ala | Thr | Arg | Pro | Arg  | Ser | Thr | Arg |
|     | 8045 |     |     |     |     | 8050 |     |     |     |     | 8055 |     |     |     |
| Arg | Ser  | Trp | Gln | Arg | Ala | Phe  | Gln | Pro | Arg | Lys | Arg  | Thr | Thr | Lys |
|     | 8060 |     |     |     |     | 8065 |     |     |     |     | 8070 |     |     |     |
| Ser | Ser  | Gln | Ser | Arg | Lys | Gln  | Arg | Ala | Ser | Arg | Thr  | Arg | Leu | Gly |
|     | 8075 |     |     |     |     | 8080 |     |     |     |     | 8085 |     |     |     |
| Ser | Ser  | Met | Ala | Thr | Thr | Ala  | Gly | Gln | Arg | Thr | Cys  | Ser | Ser | Ser |
|     | 8090 |     |     |     |     | 8095 |     |     |     |     | 8100 |     |     |     |
| Ile | Trp  | Pro | Ala | Asn | Ala | Ser  | Ser | Ser | Arg | Thr | Arg  | Cys | Ser | Thr |
|     | 8105 |     |     |     |     | 8110 |     |     |     |     | 8115 |     |     |     |
| Ala | Pro  | Arg | Cys | Pro | Ser | Ala  | Trp | Arg | Ser | Ser | Ala  | Ala | Pro | Thr |
|     | 8120 |     |     |     |     | 8125 |     |     |     |     | 8130 |     |     |     |
| Ser | Ala  | Thr | Ser | Ser | Arg | Arg  | Ala | Cys | Pro | Pro | Ser  | Ala | Ser | Pro |
|     | 8135 |     |     |     |     | 8140 |     |     |     |     | 8145 |     |     |     |
| Thr | Ala  | Pro | Ala | Ser | Pro | Thr  | Arg | Ala | Ser | Thr | Ser  | Thr | Arg | Ser |
|     | 8150 |     |     |     |     | 8155 |     |     |     |     | 8160 |     |     |     |
| Ser | Arg  | Cys | Pro | Arg | Pro | Trp  | Pro | Pro | Thr | Thr | Ser  | Phe | Ser | Arg |
|     | 8165 |     |     |     |     | 8170 |     |     |     |     | 8175 |     |     |     |
| Thr | Lys  | Gly | Ser | Pro | Ser | Pro  | Ala | Ala | Pro | Thr | Ala  | Pro | Ala | Pro |
|     | 8180 |     |     |     |     | 8185 |     |     |     |     | 8190 |     |     |     |
| Thr | Pro  | Cys | Ser | Thr | Trp | Ala  | Pro | Ala | Pro | Ala | Tyr  | Leu | Ile | Ser |
|     | 8195 |     |     |     |     | 8200 |     |     |     |     | 8205 |     |     |     |
| Pro | Pro  | Trp | Lys | Arg | Phe | Pro  | Arg | Ser | Ser | Arg | Val  | Trp | Ala | Ala |
|     | 8210 |     |     |     |     | 8215 |     |     |     |     | 8220 |     |     |     |
| Thr | Arg  | Leu | Gly | Pro | Arg | Thr  | Leu | Cys | Lys | Glu | Ala  | Glu | Arg | Ser |
|     | 8225 |     |     |     |     | 8230 |     |     |     |     | 8235 |     |     |     |
| Met | Ser  | Thr | Thr | Ala | Pro | Trp  | Trp | Ser | Trp | Lys | Ala  | Thr | Thr | Arg |
|     | 8240 |     |     |     |     | 8245 |     |     |     |     | 8250 |     |     |     |
| Ala | Trp  | Arg | Ser | Ser | Ser | Ala  | Arg | Ser | Ser | Pro | Thr  | Ser | Pro | Thr |
|     | 8255 |     |     |     |     | 8260 |     |     |     |     | 8265 |     |     |     |
| Arg | Arg  | Ser | Thr | Cys | Pro | Pro  | Arg | Ser | Ala | Pro | Ser  | Trp | Thr | Arg |
|     | 8270 |     |     |     |     | 8275 |     |     |     |     | 8280 |     |     |     |

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Cys Ser Ser Ser Ala Pro Arg Pro Ser Arg Arg Arg Arg Cys Arg  
 8285 8290 8295  
 Thr Pro Arg Ala Arg Thr Arg Ala Ser Pro Trp Ser Ala Thr Ser  
 8300 8305 8310  
 Ser Trp Arg Ala Gly Trp Glu Arg Val Ala Pro Pro Arg Ala Trp  
 8315 8320 8325  
 Lys Ser Gly Ala Ser Ser Trp Pro Trp Ser Trp Pro Trp Ser Trp  
 8330 8335 8340  
 Ser Val Cys Ala Ala Ser Ser Pro Thr Arg Arg Pro Cys Ala Arg  
 8345 8350 8355  
 Ser Arg Arg Thr Cys Thr Thr Ser Ser Asp Thr Gly Ser Cys Ala  
 8360 8365 8370  
 Arg Pro Ala Arg Ser Pro Thr Trp Ser Pro Thr Trp Ser Pro Thr  
 8375 8380 8385  
 Trp Ala Ser Cys Thr Arg Thr Ala Trp Gly Arg Thr Cys Cys Thr  
 8390 8395 8400  
 Pro Pro Cys Ala Gly Arg Pro Ala Ala Thr Thr Ser Ala Thr Ala  
 8405 8410 8415  
 Ser Thr Cys Thr Ser Ala Thr Pro Gly Arg Arg Ala Trp Ala Cys  
 8420 8425 8430  
 Gly Ser Ser Ala Trp Arg Ser Arg Thr Lys Ser Ser Ala Ser Ser  
 8435 8440 8445  
 Cys Arg Arg Thr Ser Arg Pro Cys Gly Pro Gly Ser Thr Ser Ala  
 8450 8455 8460  
 Pro Pro Pro Arg Thr Trp Pro Thr Ser Ser Ser Pro Ser Ala Cys  
 8465 8470 8475  
 Gly Arg Cys Ala Thr Gly Cys Pro Thr Leu Ala Lys Ala Cys Cys  
 8480 8485 8490  
 Lys Thr Phe Ala Leu Ser Ser Ser Asn Ala Pro Gly Ser Cys Pro  
 8495 8500 8505  
 Pro Pro Ala Pro Arg Cys Pro Arg Thr Ser Cys Arg Pro Ser Ala

8510

8515

8520

|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ser  | Ala | Pro | Arg | Arg | Ser | Gly  | Ala | Thr | Ala | Thr | Cys  | Cys | Ala | Trp |
| 8525 |     |     |     |     |     | 8530 |     |     |     |     | 8535 |     |     |     |
| Pro  | Thr | Thr | Trp | Pro | Thr | Thr  | Arg | Thr | Ser | Arg | Thr  | Ser | Ala | Ala |
| 8540 |     |     |     |     |     | 8545 |     |     |     |     | 8550 |     |     |     |
| Arg  | Ala | Cys | Ser | Ser | Ala | Thr  | Ala | Ala | Ala | Thr | Ser  | Ala | Arg | Arg |
| 8555 |     |     |     |     |     | 8560 |     |     |     |     | 8565 |     |     |     |
| Thr  | Ala | Pro | Trp | Pro | Ala | Thr  | Pro | Ser | Cys | Ala | Arg  | Pro | Arg | Ser |
| 8570 |     |     |     |     |     | 8575 |     |     |     |     | 8580 |     |     |     |
| Ser  | Ala | Pro | Ser | Ser | Cys | Lys  | Ala | Pro | Ala | Arg | Ala  | Arg | Gly | Val |
| 8585 |     |     |     |     |     | 8590 |     |     |     |     | 8595 |     |     |     |
| Asn  | Ser | Pro | Arg | Gly | Cys | Gly  | Pro | Arg | Pro | Thr | Cys  | Ala | Ser | Ser |
| 8600 |     |     |     |     |     | 8605 |     |     |     |     | 8610 |     |     |     |
| Cys  | Pro | Arg | Thr | Thr | Ile | Pro  | Ser | Arg | Ser | Gly | Ser  | Thr | Arg | Thr |
| 8615 |     |     |     |     |     | 8620 |     |     |     |     | 8625 |     |     |     |
| Asn  | Pro | Ser | Arg | Pro | Arg | Pro  | Ser | Cys | Arg | Pro | Ala  | Ser | Ser | Pro |
| 8630 |     |     |     |     |     | 8635 |     |     |     |     | 8640 |     |     |     |
| Arg  | Gly | Pro | Ser | Trp | Pro | Asn  | Cys | Lys | Pro | Ser | Arg  | Asn | Pro | Ala |
| 8645 |     |     |     |     |     | 8650 |     |     |     |     | 8655 |     |     |     |
| Lys  | Asn | Phe | Cys | Lys | Arg | Ala  | Thr | Gly | Ser | Thr | Trp  | Thr | Pro | Arg |
| 8660 |     |     |     |     |     | 8665 |     |     |     |     | 8670 |     |     |     |
| Pro  | Glu | Arg | Ser | Ser | Thr | Pro  | Ala | Ser | Pro | Arg | Met  | Pro | Arg | Gly |
| 8675 |     |     |     |     |     | 8680 |     |     |     |     | 8685 |     |     |     |
| Ser  | Ser | Lys | Lys | Leu | Lys | Val  | Glu | Leu | Pro | Pro | Pro  | Pro | Glu | Asp |
| 8690 |     |     |     |     |     | 8695 |     |     |     |     | 8700 |     |     |     |
| Leu  | Glu | Glu | Asp | Trp | Glu | Ser  | Ser | Gln | Ala | Glu | Glu  | Glu | Glu | Met |
| 8705 |     |     |     |     |     | 8710 |     |     |     |     | 8715 |     |     |     |
| Glu  | Asp | Trp | Asp | Ser | Thr | Gln  | Ala | Glu | Glu | Asp | Ser  | Leu | Gln | Asp |
| 8720 |     |     |     |     |     | 8725 |     |     |     |     | 8730 |     |     |     |
| Ser  | Leu | Glu | Glu | Glu | Asp | Glu  | Val | Glu | Glu | Ala | Glu  | Glu | Glu | Ala |
| 8735 |     |     |     |     |     | 8740 |     |     |     |     | 8745 |     |     |     |

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Ala Ala Ala Arg Pro Ser Ser Ser Ala Glu Glu Glu Lys Ala Ser  
 8750 8755 8760  
  
 Ser Thr Asp Thr Ile Ser Ala Pro Gly Arg Gly Arg Gly Gly Arg  
 8765 8770 8775  
  
 Ala His Ser Arg Trp Asp Glu Thr Gly Arg Phe Pro Asn Pro Thr  
 8780 8785 8790  
  
 Thr Gln Thr Gly Lys Lys Glu Arg Gln Gly Tyr Lys Ser Trp Arg  
 8795 8800 8805  
  
 Gly His Lys Asn Ala Ile Val Ser Cys Leu Gln Ala Cys Gly Gly  
 8810 8815 8820  
  
 Asn Ile Ser Phe Thr Arg Arg Tyr Leu Leu Phe His Arg Gly Val  
 8825 8830 8835  
  
 Asn Phe Pro Arg Asn Ile Leu His Tyr Tyr Arg His Leu His Ser  
 8840 8845 8850  
  
 Pro Tyr Tyr Cys Phe Gln Glu Glu Ala Glu Thr Gln Gln Gln Gln  
 8855 8860 8865  
  
 Gln Gln Gln Lys Thr Ser Gly Ser Ser Lys Ile His Ser Gly Gly  
 8870 8875 8880  
  
 Arg Trp Thr Glu Asp Arg Gly Glu Arg Ala Gly Ala Asp Pro Gly  
 8885 8890 8895  
  
 Ala Glu Glu Pro Asp Leu Ser His Pro Leu Cys His Leu Pro Ala  
 8900 8905 8910  
  
 Glu Ser Gly Ala Arg Ala Gly Thr Glu Ser Gln Glu Pro Phe Ser  
 8915 8920 8925  
  
 Ala Leu Ala His Pro Gln Leu Ser Val Ser Gln Glu Arg Arg Pro  
 8930 8935 8940  
  
 Thr Ser Ala His Ser Arg Gly Arg Arg Gly Ser Leu Gln Gln Val  
 8945 8950 8955  
  
 Leu Arg Ala His Ser Arg Val Ala Arg Ala Arg Pro His Thr Glu  
 8960 8965 8970  
  
 Lys Gly Gly Asn Tyr Val Thr Thr Cys Ala Leu Arg Pro Thr Ile  
 8975 8980 8985

## 368530-7006W01\_SequenceListing\_ST25.txt

|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Ile | Met  | Ser | Lys | Glu | Ile | Pro  | Thr | Pro | Tyr | Met | Trp  | Ser | Tyr | Gln |
|     | 8990 |     |     |     |     | 8995 |     |     |     |     | 9000 |     |     |     |
| Pro | Gln  | Met | Gly | Leu | Ala | Ala  | Gly | Ala | Ala | Gln | Asp  | Tyr | Ser | Thr |
|     | 9005 |     |     |     |     | 9010 |     |     |     |     | 9015 |     |     |     |
| Arg | Met  | Asn | Trp | Leu | Ser | Ala  | Gly | Pro | Ala | Met | Ile  | Ser | Arg | Val |
|     | 9020 |     |     |     |     | 9025 |     |     |     |     | 9030 |     |     |     |
| Asn | Asp  | Ile | Arg | Ala | His | Arg  | Asn | Gln | Ile | Leu | Leu  | Glu | Gln | Ser |
|     | 9035 |     |     |     |     | 9040 |     |     |     |     | 9045 |     |     |     |
| Ala | Ile  | Thr | Ala | Thr | Pro | Arg  | His | His | Leu | Asn | Pro  | Arg | Asn | Trp |
|     | 9050 |     |     |     |     | 9055 |     |     |     |     | 9060 |     |     |     |
| Pro | Ala  | Ala | Leu | Val | Tyr | Gln  | Glu | Ile | Pro | Gln | Pro  | Thr | Thr | Val |
|     | 9065 |     |     |     |     | 9070 |     |     |     |     | 9075 |     |     |     |
| Leu | Leu  | Pro | Arg | Asp | Ala | Gln  | Ala | Glu | Val | Gln | Leu  | Thr | Asn | Ser |
|     | 9080 |     |     |     |     | 9085 |     |     |     |     | 9090 |     |     |     |
| Gly | Val  | Gln | Leu | Ala | Gly | Gly  | Ala | Ala | Leu | Cys | Arg  | His | Arg | Pro |
|     | 9095 |     |     |     |     | 9100 |     |     |     |     | 9105 |     |     |     |
| Ala | Gln  | Gly | Ile | Lys | Arg | Leu  | Val | Ile | Arg | Gly | Arg  | Gly | Thr | Gln |
|     | 9110 |     |     |     |     | 9115 |     |     |     |     | 9120 |     |     |     |
| Leu | Asn  | Asp | Glu | Val | Val | Ser  | Ser | Ser | Leu | Gly | Leu  | Arg | Pro | Asp |
|     | 9125 |     |     |     |     | 9130 |     |     |     |     | 9135 |     |     |     |
| Gly | Val  | Phe | Gln | Leu | Ala | Gly  | Ser | Gly | Arg | Ser | Ser  | Phe | Thr | Pro |
|     | 9140 |     |     |     |     | 9145 |     |     |     |     | 9150 |     |     |     |
| Arg | Gln  | Ala | Val | Leu | Thr | Leu  | Glu | Ser | Ser | Ser | Ser  | Gln | Pro | Arg |
|     | 9155 |     |     |     |     | 9160 |     |     |     |     | 9165 |     |     |     |
| Ser | Gly  | Gly | Ile | Gly | Thr | Leu  | Gln | Phe | Val | Glu | Glu  | Phe | Thr | Pro |
|     | 9170 |     |     |     |     | 9175 |     |     |     |     | 9180 |     |     |     |
| Ser | Val  | Tyr | Phe | Asn | Pro | Phe  | Ser | Gly | Ser | Pro | Gly  | His | Tyr | Pro |
|     | 9185 |     |     |     |     | 9190 |     |     |     |     | 9195 |     |     |     |
| Asp | Glu  | Phe | Ile | Pro | Asn | Phe  | Asp | Ala | Ile | Ser | Glu  | Ser | Val | Asp |
|     | 9200 |     |     |     |     | 9205 |     |     |     |     | 9210 |     |     |     |
| Gly | Tyr  | Asp | Met | Ser | His | Gly  | Gly | Ala | Ala | Asp | Leu  | Ala | Arg | Leu |
|     | 9215 |     |     |     |     | 9220 |     |     |     |     | 9225 |     |     |     |

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|      |     |     |     |     |     |      |     |     |     |     |      |     |     |     |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Arg  | His | Leu | Asp | His | Cys | Arg  | Arg | Phe | Arg | Cys | Phe  | Ala | Arg | Asp |
| 9230 |     |     |     |     |     | 9235 |     |     |     |     | 9240 |     |     |     |
| Leu  | Ala | Glu | Phe | Ala | Tyr | Phe  | Glu | Leu | Pro | Glu | Glu  | His | Pro | Gln |
| 9245 |     |     |     |     |     | 9250 |     |     |     |     | 9255 |     |     |     |
| Gly  | Pro | Ala | His | Gly | Val | Arg  | Ile | Val | Val | Glu | Gly  | Gly | Leu | Asp |
| 9260 |     |     |     |     |     | 9265 |     |     |     |     | 9270 |     |     |     |
| Ser  | His | Leu | Leu | Arg | Ile | Phe  | Ser | Gln | Arg | Pro | Ile  | Leu | Ala | Glu |
| 9275 |     |     |     |     |     | 9280 |     |     |     |     | 9285 |     |     |     |
| Arg  | Glu | Gln | Gly | Gln | Thr | Leu  | Leu | Thr | Leu | Tyr | Cys  | Ile | Cys | Asn |
| 9290 |     |     |     |     |     | 9295 |     |     |     |     | 9300 |     |     |     |
| His  | Pro | Gly | Leu | His | Glu | Ser  | Leu | Cys | Cys | Leu | Leu  | Cys | Thr | Glu |
| 9305 |     |     |     |     |     | 9310 |     |     |     |     | 9315 |     |     |     |
| Tyr  | Asn | Lys | Ser | Asp | Gln | Arg  | Leu | Leu | Arg | Thr | Ser  | Val | Cys | Ser |
| 9320 |     |     |     |     |     | 9325 |     |     |     |     | 9330 |     |     |     |
| Cys  | Tyr | Gln | Pro | Val | Pro | Val  | Leu | His | Arg | Glu | Arg  | Asp | Arg | Ala |
| 9335 |     |     |     |     |     | 9340 |     |     |     |     | 9345 |     |     |     |
| Pro  | Ala | Pro | Val | Ala | Pro | Gln  | Glu | Val | Pro | His | Leu  | Ala | Val | Pro |
| 9350 |     |     |     |     |     | 9355 |     |     |     |     | 9360 |     |     |     |
| Gly  | Leu | Ser | Asp | Arg | Arg | Cys  | Gln | Pro | Leu | Arg | Gln  | Arg | Arg | Ser |
| 9365 |     |     |     |     |     | 9370 |     |     |     |     | 9375 |     |     |     |
| Pro  | Ala | Glu | Arg | Pro | Cys | Gln  | Pro | Tyr | Phe | Phe | His  | Pro | Gln | Lys |
| 9380 |     |     |     |     |     | 9385 |     |     |     |     | 9390 |     |     |     |
| Gln  | Ala | Pro | Ala | Leu | Pro | Thr  | Leu | Pro | Pro | Arg | Asp  | Leu | Ser | Val |
| 9395 |     |     |     |     |     | 9400 |     |     |     |     | 9405 |     |     |     |
| Arg  | Leu | Gly | Thr | Leu | Pro | Ser  | His | Leu | Pro | Pro | Asp  | Pro | Glu | Tyr |
| 9410 |     |     |     |     |     | 9415 |     |     |     |     | 9420 |     |     |     |
| His  | Ser | Val | Ala | Pro | Arg | Tyr  | Gln | Pro | Asn | Tyr | Pro  | Pro | Thr | Pro |
| 9425 |     |     |     |     |     | 9430 |     |     |     |     | 9435 |     |     |     |
| Pro  | Ser | Arg | Pro | Arg | Thr | Cys  | Thr | Glu | Leu | Glu | Lys  | Tyr | Ala | Thr |
| 9440 |     |     |     |     |     | 9445 |     |     |     |     | 9450 |     |     |     |
| Ile  | His | Ala | His | Ile | Arg | Leu  | Gly | Arg | Ala | Thr | Ala  | Thr | His | Ala |

9455

9460

9465

Pro Arg Tyr Leu Leu Gln Ser Asn Arg Arg Arg Leu Thr His Trp  
 9470 9475 9480

Pro Thr Thr Thr Ser Thr Thr Phe Ser Trp Thr Trp Thr Ala Ala  
 9485 9490 9495

Pro Arg Ser Ser Asp Ser Pro Asn Phe Ala Phe Ala Ser Ser Arg  
 9500 9505 9510

Arg Glu Pro Ser Arg Ser Cys Arg Thr Ala Pro Ser Thr Ser Ala  
 9515 9520 9525

Arg Lys Ala Ser Ser Ala Trp Asn Arg Pro Arg Ser Pro Thr Arg  
 9530 9535 9540

Ser Pro Arg Pro Thr Ile Ala Ser Pro Thr Ser Ser Cys Ser Ser  
 9545 9550 9555

Ala Arg Ser Ser Pro Ala Trp Ser Glu Ser Thr Pro Ser Ser Ser  
 9560 9565 9570

Pro Ser Ser Arg Ala Ile Pro Arg Gly Ala Ser Thr Ala Pro Ala  
 9575 9580 9585

Thr Pro Pro Thr Ala Ser Thr Leu Ser Arg Pro Ser Ala Ala Ser  
 9590 9595 9600

Ala Thr Ser Ser Pro Thr Asn His Pro Leu Ile Gln Asn Lys Tyr  
 9605 9610 9615

His Ile Asp Asp Asp Leu Asn Lys Lys Ser Phe Asp Leu Lys Arg  
 9620 9625 9630

Tyr Asn His Ile Asp Asp Leu Ser Phe Lys Lys Arg Ile Thr Tyr  
 9635 9640 9645

Leu Lys Ser Asp Thr Arg Ser Leu Ser Met Phe Ser Ala Asn Thr  
 9650 9655 9660

Thr Ser Leu Pro Ser Ser Gln Leu Trp Tyr Cys Arg Pro Arg Arg  
 9665 9670 9675

Ala Ala Asn Phe Leu His Thr Leu Lys Gly Met Ser Asn Ser Ser  
 9680 9685 9690



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|     |      |     |     |     |     |      |     |     |     |     |      |     |     |     |
|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Cys | Pro  | Ser | Ile | Phe | Ile | Leu  | Ser | Ser | Ile | Arg | Cys  | Pro | Lys | Ser |
|     | 9695 |     |     |     |     | 9700 |     |     |     |     | 9705 |     |     |     |
| Ala | Ser  | Gly | Trp | Met | Met | Thr  | Ser | Thr | Pro | Ser | Thr  | Pro | Thr | Met |
|     | 9710 |     |     |     |     | 9715 |     |     |     |     | 9720 |     |     |     |
| Gln | Thr  | Thr | His | Arg | Pro | Cys  | Pro | Ser | Ser | Thr | Pro  | Pro | Ser | Ser |
|     | 9725 |     |     |     |     | 9730 |     |     |     |     | 9735 |     |     |     |
| Leu | Gln  | Met | Asp | Ser | Lys | Arg  | Ser | Pro | Trp | Gly | Cys  | Cys | Pro | Cys |
|     | 9740 |     |     |     |     | 9745 |     |     |     |     | 9750 |     |     |     |
| Asp | Trp  | Leu | Thr | Pro | Ser | Pro  | Pro | Arg | Thr | Gly | Lys  | Ser | Pro | Ser |
|     | 9755 |     |     |     |     | 9760 |     |     |     |     | 9765 |     |     |     |
| Ser | Trp  | Glu | Arg | Gly | Trp | Thr  | Ser | Thr | Pro | Arg | Glu  | Asn | Ser | Ser |
|     | 9770 |     |     |     |     | 9775 |     |     |     |     | 9780 |     |     |     |
| Pro | Thr  | Arg | Pro | Pro | Arg | Pro  | Pro | Pro | Leu | Ser | Val  | Phe | Pro | Thr |
|     | 9785 |     |     |     |     | 9790 |     |     |     |     | 9795 |     |     |     |
| Thr | Pro  | Phe | Pro | Leu | Thr | Trp  | Ile | Pro | Leu | Phe | Ile  | Pro | Lys | Met |
|     | 9800 |     |     |     |     | 9805 |     |     |     |     | 9810 |     |     |     |
| Glu | Asn  | Tyr | Pro | Tyr | Lys | Phe  | Leu | His | Arg | Thr | Tyr  | Asn | Gln | Pro |
|     | 9815 |     |     |     |     | 9820 |     |     |     |     | 9825 |     |     |     |
| Phe | Thr  | His | Leu | Leu | Met | Asp  | Gln | Val | Asp | Val | Val  | Ala | Leu | Leu |
|     | 9830 |     |     |     |     | 9835 |     |     |     |     | 9840 |     |     |     |
| Leu | Gln  | Tyr | Ser | Trp | Pro | Leu  | His | Ser | Leu | Leu | Met  | Lys | Lys | Glu |
|     | 9845 |     |     |     |     | 9850 |     |     |     |     | 9855 |     |     |     |
| Ile | Leu  | Lys | Leu | Thr | Pro | Val  | Val | His | Gln | Leu | Met  | Gln | Val | Asp |
|     | 9860 |     |     |     |     | 9865 |     |     |     |     | 9870 |     |     |     |
| Leu | Val  | Ser | Thr | Ala | Lys | Glu  | Gly | Ser | Leu | Ser | Leu  | Pro | Gln | Glu |
|     | 9875 |     |     |     |     | 9880 |     |     |     |     | 9885 |     |     |     |
| Met | Gln  | Leu | Lys | Ala | Thr | Ala  | Gly | Leu | Lys | Val | Asp  | Leu | Lys | Val |
|     | 9890 |     |     |     |     | 9895 |     |     |     |     | 9900 |     |     |     |
| Met | Ala  | Leu | Gln | Thr | Leu | Ala  | Glu | Asp | Trp | Asn | Leu  | Glu | Pro | Leu |
|     | 9905 |     |     |     |     | 9910 |     |     |     |     | 9915 |     |     |     |
| Val | Gln  | Arg | Leu | Met | Ser | Gln  | Met | His | Thr | Gln | Phe  | Lys | Leu | Asn |
|     | 9920 |     |     |     |     | 9925 |     |     |     |     | 9930 |     |     |     |

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Trp Val Leu Ala Leu Pro Leu Thr Val Gln Ala Pro Leu Leu Leu  
 9935 9940 9945  
  
 Gly Thr Lys Arg Met Ile Asn Leu His Tyr Gly Pro Gln Pro Thr  
 9950 9955 9960  
  
 Pro Arg Gln Ile Ala Lys Tyr Thr Leu Lys Lys Met Pro Asn Ser  
 9965 9970 9975  
  
 His Phe Ala Gln Ser Val Glu Val Lys Phe Trp Val Leu Leu Tyr  
 9980 9985 9990  
  
 Trp Gln Ile Met Glu Val Ser Thr Gln Ser Gln Thr Gln Ala Leu  
 9995 10000 10005  
  
 His Ser Ser Pro Ser Ser Leu Met Gln Val Glu Phe Cys Ala Ala  
 10010 10015 10020  
  
 Pro His Thr Lys Asn Ile Gly Thr Ser Glu Arg Glu Met Leu His  
 10025 10030 10035  
  
 Leu Leu Ser Pro Ile Leu Met Leu Val Leu Cys Leu Thr Arg Pro  
 10040 10045 10050  
  
 Ile Leu Lys Thr His Leu Gln Leu Gln Lys Ala Ile Leu Ser Val  
 10055 10060 10065  
  
 Lys Phe Ile Ser Met Gly Met Arg Pro Asn His Cys Leu Leu Leu  
 10070 10075 10080  
  
 Leu Met Lys Leu Arg Met Gln Leu Ala Pro Thr Val Ser Leu Phe  
 10085 10090 10095  
  
 Asn Gly Asn Gly Ile Val Leu Ser Thr Gln Val Lys His Leu Leu  
 10100 10105 10110  
  
 Pro Ala Pro Ser Pro Ser Pro Thr Ser Pro Lys Asn Glu His Cys  
 10115 10120 10125  
  
 Ile Pro Pro Cys Met Pro Thr Leu Pro Thr Pro Leu Cys Leu Trp  
 10130 10135 10140  
  
 Lys Lys Leu Ser Thr Lys Asn Lys Val Gln Val Phe Tyr Phe Asn  
 10145 10150 10155  
  
 Ser Phe Thr Gly Phe Glu Gln Leu Phe Phe Leu His Pro Pro Arg  
 10160 10165 10170

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|     |       |     |     |     |     |       |     |     |     |     |       |     |     |     |
|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|-----|-------|-----|-----|-----|
| Thr | Trp   | Asn | Thr | Pro | Pro | Ser   | Pro | Pro | Ala | Gln | Pro   | Thr | Ser | Glu |
|     | 10175 |     |     |     |     | 10180 |     |     |     |     | 10185 |     |     |     |
| Cys | His   | Trp | Trp | Thr | Cys | Phe   | Trp | Ser | Pro | Arg | Ser   | Thr | Gln | Phe |
|     | 10190 |     |     |     |     | 10195 |     |     |     |     | 10200 |     |     |     |
| Gln | Ser   | Glu | Pro | Val | Ser | Gly   | Arg | Ser | Gly | Arg | Asn   | Pro | Pro | Gly |
|     | 10205 |     |     |     |     | 10210 |     |     |     |     | 10215 |     |     |     |
| Thr | Pro   | Ala | Ser | Ala | Pro | His   | Ser | Ser | Thr | Ala | Glu   | Asp | Cys | Pro |
|     | 10220 |     |     |     |     | 10225 |     |     |     |     | 10230 |     |     |     |
| Arg | Trp   | Ser | Gly | Ser | Arg | Leu   | Ser | Gly | Arg | Ser | Arg   | Arg | Ala | Ala |
|     | 10235 |     |     |     |     | 10240 |     |     |     |     | 10245 |     |     |     |
| Val | Gly   | Ile | Ile | Val | Arg | Glu   | Arg | Asp | Arg | Pro | Val   | Val | Ser | His |
|     | 10250 |     |     |     |     | 10255 |     |     |     |     | 10260 |     |     |     |
| Gln | Ala   | Pro | Gln | Gln | Ser | Leu   | Pro | Pro | Pro | Leu | Arg   | Gln | Ala | Ala |
|     | 10265 |     |     |     |     | 10270 |     |     |     |     | 10275 |     |     |     |
| Ala | Gln   | Gly | Val | Arg | Val | Gln   | Gly | Leu | Pro | Gln | His   | Asp | Ala | His |
|     | 10280 |     |     |     |     | 10285 |     |     |     |     | 10290 |     |     |     |
| Gly | Pro   | Gln | His | Gln | Ser | Ser   | Gly | Ala | Ala | Gly | Ala   | Ala | Ala | His |
|     | 10295 |     |     |     |     | 10300 |     |     |     |     | 10305 |     |     |     |
| Ala | Asp   | Leu | Ala | Gln | Val | Ala   | Ala | Val | Arg | Ala | Thr   | Gln | Asp | His |
|     | 10310 |     |     |     |     | 10315 |     |     |     |     | 10320 |     |     |     |
| Gln | Val   | Val | Gln | Gln | Ser | Ile   | Val | Gln | His | Ala | Pro   | Ala | Glu | Thr |
|     | 10325 |     |     |     |     | 10330 |     |     |     |     | 10335 |     |     |     |
| His | Arg   | Gly | Lys | Asp | Ala | Thr   | His | Val | Ala | Val | Val   | Pro | Asp | Pro |
|     | 10340 |     |     |     |     | 10345 |     |     |     |     | 10350 |     |     |     |
| Gln | Val   | Asn | Gln | Val | Ala | Leu   | Pro | Pro | Glu | His | Ala   | Ala | His | Val |
|     | 10355 |     |     |     |     | 10360 |     |     |     |     | 10365 |     |     |     |
| His | Asp   | Leu | Leu | Gly | His | Val   | Ala | Val | His | His | Leu   | Pro | Val | Pro |
|     | 10370 |     |     |     |     | 10375 |     |     |     |     | 10380 |     |     |     |
| His | His   | Pro | Leu | Val | Glu | His   | Ala | Ala | Pro | Asp | Asp   | Pro | Ala | Glu |
|     | 10385 |     |     |     |     | 10390 |     |     |     |     | 10395 |     |     |     |
| Pro | Gln   | Gly | Gln | His | Arg | Pro   | Ala | Arg | His | Ala | Ala   | Lys | Arg | Pro |

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10400

10405

10410

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| Arg | Val   | Pro | Ala | Met | Ala | Met   | Glu | Asp | Pro | Pro | Leu   | Val | Pro | Val |
|     | 10415 |     |     |     |     | 10420 |     |     |     |     | 10425 |     |     |     |
| Asp | His   | Leu | Gly | Ala | Glu | Gln   | Val | Tyr | Val | Gly | Thr   | Ala | Gln | Ala |
|     | 10430 |     |     |     |     | 10435 |     |     |     |     | 10440 |     |     |     |
| Tyr | Ala   | His | Ala | Ser | Leu | Gln   | His | Ser | Gln | Leu | Leu   | Gly | Gly | Gln |
|     | 10445 |     |     |     |     | 10450 |     |     |     |     | 10455 |     |     |     |
| Asn | His   | Ile | Pro | Gly | His | Gly   | Glu | Leu | Leu | Gln | Asp   | Ser | Glu | Pro |
|     | 10460 |     |     |     |     | 10465 |     |     |     |     | 10470 |     |     |     |
| Arg | Arg   | Thr | Gly | Gln | Ser | Ser   | His | Ile | Thr | Tyr | Ile   | Val | His | Gly |
|     | 10475 |     |     |     |     | 10480 |     |     |     |     | 10485 |     |     |     |
| Gln | Gly   | Ile | Ala | Ile | Arg | Gln   | His | Arg | Val | Ile | Leu   | His | Gln | Arg |
|     | 10490 |     |     |     |     | 10495 |     |     |     |     | 10500 |     |     |     |
| Ser | Ala   | Gly | Leu | Gly | Leu | Leu   | Thr | Ala | Trp | Gly | Gly   | Arg | Pro | Ile |
|     | 10505 |     |     |     |     | 10510 |     |     |     |     | 10515 |     |     |     |
| Arg | Val   | Met | Ala | Gly | Arg | Gly   | Ser | Cys | Ser | Arg | Pro   | Cys | His | Asp |
|     | 10520 |     |     |     |     | 10525 |     |     |     |     | 10530 |     |     |     |
| Ala | Val   | Ala | Phe | Gly | His | Phe   | Arg | Thr | Cys | Cys | Ser   | Arg | Thr | Trp |
|     | 10535 |     |     |     |     | 10540 |     |     |     |     | 10545 |     |     |     |
| Ser | Gly   | Arg | Cys | Thr | Pro | Ile   | Ala | Gly | Gly | Gly | Pro   | Gly | Ala | Trp |
|     | 10550 |     |     |     |     | 10555 |     |     |     |     | 10560 |     |     |     |
| Asn | Ala   | Arg | Cys | Asn | Cys | Lys   | Thr | Ala | Thr | Leu | Ser   | Asp | Arg | Ala |
|     | 10565 |     |     |     |     | 10570 |     |     |     |     | 10575 |     |     |     |
| Ala | Asp   | Leu | Gly | Pro | Gln | Glu   | Arg | Ser | His | His | Ala   | Leu | Ser | His |
|     | 10580 |     |     |     |     | 10585 |     |     |     |     | 10590 |     |     |     |
| Arg | Pro   | Pro | Trp | Asn | Gly | Pro   | Asp | Pro | Ala | Arg | Cys   | Asn | Phe | Val |
|     | 10595 |     |     |     |     | 10600 |     |     |     |     | 10605 |     |     |     |
| Gly | Phe   | Arg | Arg | Arg | Gly | Arg   | Glu | Glu | Gln | Glu | Glu   | Pro | Leu | Thr |
|     | 10610 |     |     |     |     | 10615 |     |     |     |     | 10620 |     |     |     |
| Phe | Asn   | Pro | Asn | Gly | Leu | Gly   | Ala | Leu | Gln | Asn | Glu   | Gly | Arg | Gly |
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|       |     |     |     |     |     |       |     |     |     |     |       |     |     |     |
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| Asp   | Gly | Thr | Ser | Arg | Pro | Arg   | Cys | Val | Gly | Gly | Lys   | Gln | Pro | Gly |
| 10640 |     |     |     |     |     | 10645 |     |     |     |     | 10650 |     |     |     |
| Gln   | Arg | Tyr | Gly | Ser | Arg | Asp   | Val | Pro | Arg | Trp | Leu   | Pro | Ala | Lys |
| 10655 |     |     |     |     |     | 10660 |     |     |     |     | 10665 |     |     |     |
| Pro   | Pro | Arg | Ala | His | Pro | Glu   | Thr | Arg | Gln | Arg | Lys   | Arg | Glu | Gly |
| 10670 |     |     |     |     |     | 10675 |     |     |     |     | 10680 |     |     |     |
| Ser   | Leu | Ile | Pro | Gln | Ser | Ser   | Cys | Tyr | Thr | Pro | Ala   | Pro | Ser | Pro |
| 10685 |     |     |     |     |     | 10690 |     |     |     |     | 10695 |     |     |     |
| Asp   | Asn | Phe | His | Phe | Ser | Ser   | Leu | Glu | Phe | Glu | Leu   | Val | Pro | Glu |
| 10700 |     |     |     |     |     | 10705 |     |     |     |     | 10710 |     |     |     |
| Val   | Asn | Pro | Ser | Gln | Pro | Arg   | Ala | Arg | Ala | Glu | Arg   | Pro | Pro | Pro |
| 10715 |     |     |     |     |     | 10720 |     |     |     |     | 10725 |     |     |     |
| Ala   | Phe | Leu | Ser | Thr | Pro | Ser   | Phe | Gln | Asp | Ile | Leu   | Leu | Leu | Val |
| 10730 |     |     |     |     |     | 10735 |     |     |     |     | 10740 |     |     |     |
| His   | Leu | Gln | Gln | Ile | Asp | Lys   | Arg | Asn | Ile | Lys | Ile   | Ser | Ala | Ala |
| 10745 |     |     |     |     |     | 10750 |     |     |     |     | 10755 |     |     |     |
| Ile   | Pro | Lys | Leu | Leu | Pro | Gln   | Gln | Leu | Val | Leu | Phe   | His | Ile | Leu |
| 10760 |     |     |     |     |     | 10765 |     |     |     |     | 10770 |     |     |     |
| Ser   | Glu | Ile | Phe | Ser | His | Arg   | Thr | Thr | Arg | Asn | Lys   | Ile | Arg | Ala |
| 10775 |     |     |     |     |     | 10780 |     |     |     |     | 10785 |     |     |     |
| Ser   | His | Ser | Thr | Asp | Lys | Pro   | Lys | Ser | Ser | Pro | Val   | Ser | Ile | Ala |
| 10790 |     |     |     |     |     | 10795 |     |     |     |     | 10800 |     |     |     |
| Lys   | Cys | Lys | Thr | Ala | Ile | Ser   | Met | Leu | Ala | Arg | Pro   | Gly | Asp | Ile |
| 10805 |     |     |     |     |     | 10810 |     |     |     |     | 10815 |     |     |     |
| Phe   | Gln | Ile | Thr | Gly | Gln | Lys   | Ile | Thr | Gln | Ala | Ile   | Phe | Lys | Lys |
| 10820 |     |     |     |     |     | 10825 |     |     |     |     | 10830 |     |     |     |
| Ile   | Asn | Lys | Arg | Lys | Ile | Leu   | Gln | Val | His | Val | Ser   | Leu | Gly | Asn |
| 10835 |     |     |     |     |     | 10840 |     |     |     |     | 10845 |     |     |     |
| Asn   | Asp | Glu | Val | Asn | Ala | Ser   | Gly | Ala | Phe | Gln | His   | Gly | Leu | Ala |
| 10850 |     |     |     |     |     | 10855 |     |     |     |     | 10860 |     |     |     |
| Asp   | Leu | Lys | Thr | Lys | Asn | Lys   | Thr | Leu | Asn | His | Ala   | Ser | Leu | Ala |
| 10865 |     |     |     |     |     | 10870 |     |     |     |     | 10875 |     |     |     |

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|              |     |     |     |     |     |              |     |     |     |     |              |     |     |     |
|--------------|-----|-----|-----|-----|-----|--------------|-----|-----|-----|-----|--------------|-----|-----|-----|
| Asn<br>10880 | Arg | Trp | Val | Asn | Arg | Ser<br>10885 | Leu | Gln | His | Gln | Ala<br>10890 | Gly | His | Gly |
| Val<br>10895 | Ser | Gly | Ala | Thr | Leu | Val<br>10900 | Lys | Ile | Val | Ala | Met<br>10905 | Ile | Glu | Asn |
| His<br>10910 | His | Arg | Glu | Thr | Phe | Pro<br>10915 | Val | Ala | Gly | Val | Asn<br>10920 | Asp | Ser | Thr |
| Arg<br>10925 | Ile | His | Pro | Arg | Asn | Ile<br>10930 | Gly | Val | Arg | Glu | Lys<br>10935 | Lys | Ala | Pro |
| Glu<br>10940 | Glu | Ala | Ile | Arg | His | Tyr<br>10945 | Asn | Ala | Gln | Ser | Gln<br>10950 | Val | Gln | Gln |
| Ser<br>10955 | Asp | Ala | Met | Arg | Met | Lys<br>10960 | His | Lys | Ile | Leu | Arg<br>10965 | Cys | Val | Gln |
| Asn<br>10970 | Val | Ile | Thr | Pro | Leu | Leu<br>10975 | His | Arg | Gln | Arg | Ser<br>10980 | Pro | Arg | Ser |
| Leu<br>10985 | Gln | Ile | His | Ile | Gln | Ser<br>10990 | Leu | Ser | Val | His | Ser<br>10995 | Leu | Pro | Ser |
| Ser<br>11000 | Ser | Thr | Gln | Gln | Ala | Gln<br>11005 | Glu | Ser | Glu | Lys | Gly<br>11010 | Ala | Leu | Thr |
| Cys<br>11015 | Pro | Pro | Ala | Leu | Cys | Ser<br>11020 | Ile | Tyr | Ser | Pro | Asp<br>11025 | Leu | His | Arg |
| Lys<br>11030 | Gly | Gln | Ser | Leu | Lys | Ile<br>11035 | Pro | Ala | Lys | Ser | His<br>11040 | Thr | Pro | Ser |
| Thr<br>11045 | Arg | Pro | Glu | Thr | Gly | Asp<br>11050 | Thr | Leu | Lys | Lys | Ile<br>11055 | Arg | Ala | Leu |
| Pro<br>11060 | Gln | Thr | Pro | Lys | Leu | Pro<br>11065 | Ser | Phe | Pro | Gly | Ser<br>11070 | His | Ala | Thr |
| Ser<br>11075 | Ser | Glu | Phe | Asp | Phe | Gln<br>11080 | Ile | Pro | Ser | Thr | Val<br>11085 | Lys | Asn | Val |
| Thr<br>11090 | Arg | Pro | Ala | Pro | Asn | Gly<br>11095 | Arg | Pro | Ser | Leu | Gly<br>11100 | Gln | Ser | Pro |
| Ser<br>11105 | Ser | Leu | Pro | Lys | Phe | Lys<br>11110 | Gln | Leu | Ile | Cys | Ile<br>11115 | Leu | Thr | Arg |

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368530-7006W01\_SequenceListing\_ST25.txt  
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